InterDrought-V

Hyderabad, India

21-25 February, 2017

Collaborative Partners

USAID FROM THE AMERICAN PEOPLE

ICAR

Platinum Sponsors

illumina

premas life sciences

MARS

THE PEANUT FOUNDATION

DUPONT PIONEER

syngenta thoughtseeders

METALHANDS INSTRUMENTS PVT. LTD. LAB AUTOMATION DESIGN & CONSULTING FIRM

MB MANYARA BIOTECH

Diamond Sponsor

华大基因 BGI

Gold Sponsors

MACROGEN Advancing through Genomics

agrigenome

ILS YOUR PARTNER IN LIFE

affymetrix Biology for a better world

NRGene

Silver Sponsors

THERAGEN ETEX

LGC

Bronze Sponsors

DSS TaKaRa

PHENOSPEX

LemnaTec

Novogene 诺禾致源

Worldwide No.1 WINTERSTEIGER in field research equipment.

Media Partners

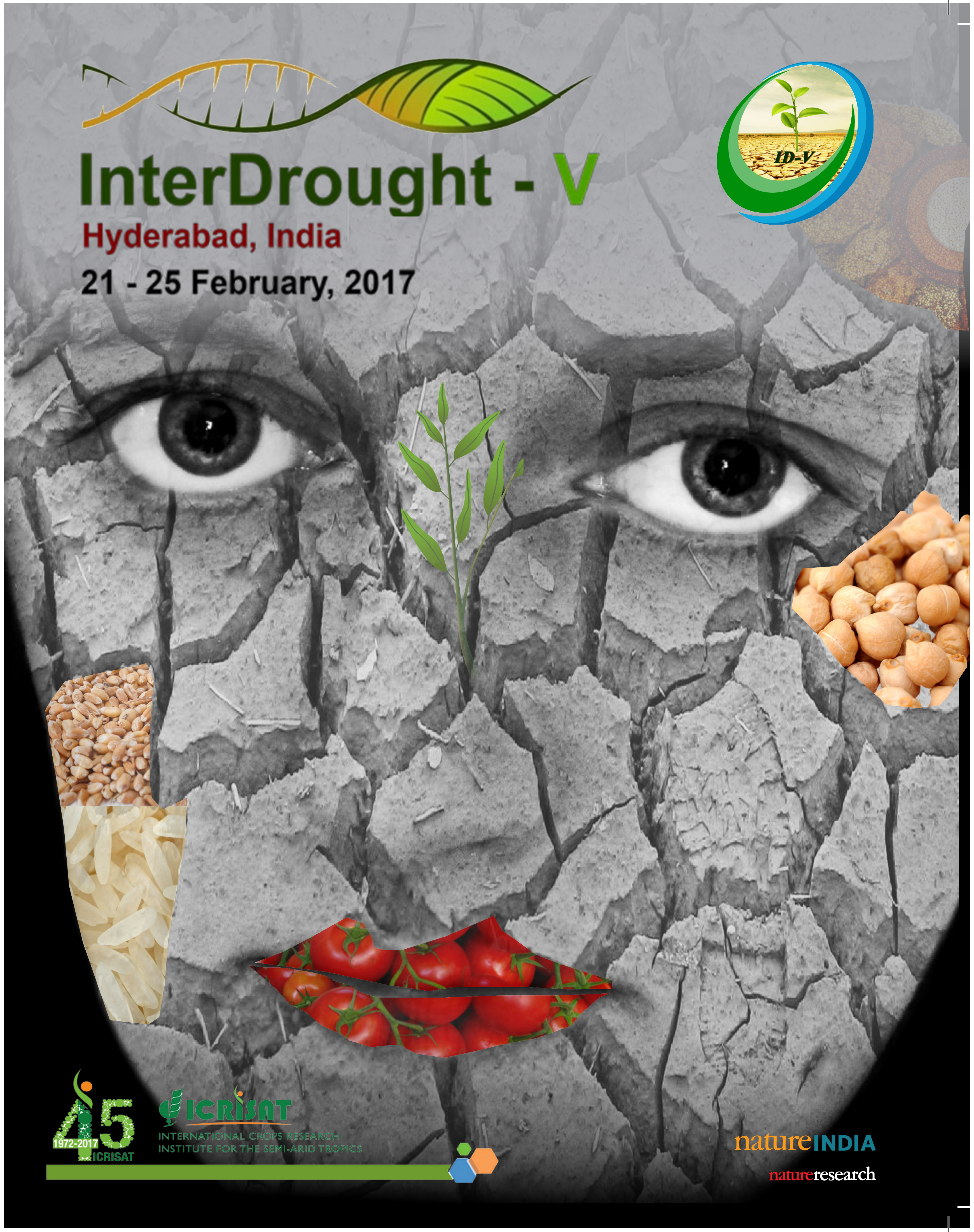
natureINDIA

Journal of Experimental Botany

FUNCTIONAL PLANT BIOLOGY

InterDrought - V

natureINDIA



InterDrought - V

Hyderabad, India

21 - 25 February, 2017

45 1972-2017 ICRISAT

ICRISAT INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

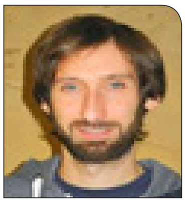
natureINDIA

natureresearch

International Organizing Committee

Dorothea Bartels

University of Bonn
Germany

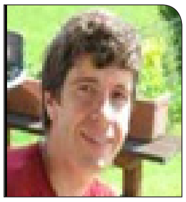


Andrea Carminati

University of Goettingen
Germany

Mark Cooper

Dupont Pioneer
USA



Xavier Draye

University of Catholique
de Louvain
Belgium

Delphine Fleury

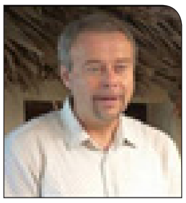
Australian Centre
for Plant Functional
Genomics
Australia

Graeme Hammer

The University of
Queensland
Australia

Jonathan Lynch

University of Penn State
USA

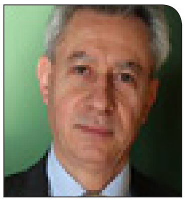


Jean-Marcel Ribaut

Integrated Breeding
Platform (IBP)
Mexico

Robert Sharp

University of Missouri
USA



Pasquale Steduto

Food and Agriculture
Organization (FAO)
Egypt

Francois Tardieu

National Institute of
Agronomic Research
(INRA)
USA

Roberto Tuberosa

University of Bologna
Italy

Neil Turner

The University of
Western Australia
Australia

Vincent Vadez

International Crops
Research Institute for
the Semi-Arid Tropics
(ICRISAT)
India

Rajeev Varshney

International Crops
Research Institute for
the Semi-Arid Tropics
(ICRISAT)
India

Lizhong Xiong

Huazhong Agricultural
University
China

Jianhua Zhang

Chinese University of
Hong Kong
Hong Kong

National Organizing Committee

Peter Carberry

Deputy Director
General-Research
International Crops
Research Institute for
the Semi-Arid Tropics
(ICRISAT)
Patancheru, Telangana

Swapan Datta

Pro - Vice Chancellor
Visva - Bharati
University
Santiniketan,
West Bengal

Anil Grover

Professor
University of Delhi -
South campus
New Delhi

HS Gupta

Former Director General
Borlaug Institute for
South Asia (BISA)
New Delhi

PK Gupta

Emeritus Professor
Ch Charan Singh
University (CCS)
Meerut, Uttar Pradesh

Renu Khanna-Chopra

National Fellow
Indian Agricultural
Research Institute
(IARI)
New Delhi

T Radhakrishnan

Director
ICAR - Directorate of
Groundnut Research
(DGR)
Junagadh, Gujarat

KRS Sambasiva Rao

Professor
Acharya Nagarjuna
University
Nagarjuna Nagar,
Andhra Pradesh

Narendra Singh

Director
ICAR - Indian Institute
of Pulses Research
(IIPR)
Kanpur, Uttar Pradesh

Shoba Sivasankar

Director - CRP Grain
Legumes & CRP Dryland
Cereals International Crops
Research Institute for the
Semi-Arid Tropics (ICRISAT)
Patancheru, Telangana

Ch Srinivasa Rao

Director
ICAR - Central
Research Institute for
Dryland Agriculture
(CRIDA)
Hyderabad, Telangana

Vilas Tonapi

Director
ICAR - Indian Institute
of Millets Research
(IIMR)
Hyderabad, Telangana

O P Yadav

Director
ICAR - Central Arid
Zone Research Institute
(CAZRI)
Jodhpur, Rajasthan

InterDrought-V
Hyderabad International Convention Center (HICC), Hyderabad, India
21-25 February, 2017

Chief Patrons
David Bergvinson
Director General, ICRISAT
MS Swaminathan
Founder & Mentor, MSSRF

Co-Patrons
T Mohapatra
Director General, ICAR &
Secretary, DARE
K VijayRaghavan
Secretary, DBT

InterDrought Chair
Francois Tardieu
Res. Director, INRA

InterDrought Vice- Chair
JS Sandhu
Deputy DG-CS, ICAR

InterDrought Past Chair
Roberto Tuberosa
Professor, *Univ.of Bologna*

Conference Org. Chair
Rajeev Varshney
Res. Prog. Director, ICRISAT

International Org. Committee
Dorothea Bartels, *Germany*
Andrea Carminati, *Germany*
Mark Cooper, *USA*
Xavier Draye, *Belgium*
Delphine Fleury, *Australia*
Graeme Hammer, *Australia*
Jonathan Lynch, *USA*
Jean-Marcel Ribaut, *Mexico*
Robert Sharp, *USA*
Pasquale Steduto, *Egypt*
Francois Tardieu, *France*
Roberto Tuberosa, *Italy*
Neil Turner, *Australia*
Vincent Vadez, *India*
Rajeev Varshney, *India*
Lizhong Xiong, *China*
Jianhua Zhang, *Hong Kong*

National Org. Committee
Peter Carberry, ICRISAT
Swapan Datta, Visva-Bharati
Anil Grover, UDSC
HS Gupta, BISA
PK Gupta, CCS University
Renu Khanna-Chopra, IARI
T Radhakrishnan, ICAR-DGR
KRS Sambasiva Rao, ANU
Ch Srinivasa Rao, ICAR-CRIDA
NP Singh, ICAR-IIPR
Shoba Sivasankar, ICRISAT
Vilas Tonapi, ICAR-IIMR
OP Yadav, ICAR-CAZRI

Contacts
InterDrought-V
c/o CEG, Bldg # 300
ICRISAT, Patancheru 502324, Hyd, India
Tel: +91-40-30713345, 30713387
Fax: +91-40-30713074, 30713075
Email: id5.icrisat@gmail.com;
r.k.varshney@cgiar.org
Web: *http://ceg.icrisat.org/idV/*
Follow us at
https://facebook.com/InterDroughtV
https://twitter.com/InterDroughtV

Welcome Message

It gives us immense pleasure to welcome you all to the InterDrought-V conference in Hyderabad, India. This conference is being organized in continuation of earlier InterDrought Conferences held in France (ID-I, 1995), Italy (ID-II, 2005), China (ID-III, 2009) and Australia (ID-IV, 2013). InterDrought conferences serve as a platform for presenting and debating key issues and strategies relevant for improving drought tolerance in crops. The main mission of the conference is to cross-fertilization of disciplines, and explore scientific and technological applications.

We are also pleased to share that InterDrought-V is the largest conference in the series of InterDrought conferences with more than 850 participants from 56 countries. The conference includes 23 invited, 26 contributory presentations across 8 sessions. In addition to the main conference, 55 presentations in 8 workshops and one panel discussion have also been organized. In addition, two poster sessions have also been included for enabling young researchers to present their work and interact with eminent scientists. We are thankful to all the participants especially speakers, co-chairs, special invitees for accepting our request and agreeing to participate in the conference that has made the programme scientifically rich.

We would like to thank the members of International Organizing Committee (Roberto Tubrerosa in particular), National Organizing Committee and Local Organizing Committee for their support. We would like to put on record the contribution of ICRISAT and INRA for allowing us to organize the conference. It has been pleasure to have USAID and ICAR as collaborative partners. Thanks are also due to all of our sponsors, exhibitors, and media partners (please see last pages of the book). Special thanks to the InterDrought-V core team members especially to Ms. Anu Chitikineni for spending quality time in organizing the conference.

We are doing our best to ensure your participation in the conference and stay in Hyderabad fruitful and enjoyable. Please do not hesitate to contact us or members from the team in case we can be of any help during your stay. We hope that the conference would be scientifically rewarding as well as enjoyable for all of you.

In summary, we strongly believe that the InterDrought-V conference will provide a suitable platform for researchers to share their ideas/experience and have intense discussions about the issues and strategies relevant for improving drought tolerance in crops.

Have a happy and fruitful stay in Hyderabad, India!

Francois Tardieu

Rajeev Varshney

ICRISAT INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

With the announcement of Sustainable Development Goals in 2015, there is renewed optimism that poverty, hunger, malnutrition and environmental degradation can be addressed by the global community working in concert for equity and sustainability. To achieve these goals, agriculture must manage the risks of climate variability that especially threaten the poorest and most vulnerable who farm the drylands. Agriculture research has a key role in combating the major constraint of recurrent drought to dryland agriculture, especially as it is exacerbated by climate change.

The InterDrought-V conference brings together the disciplines of plant and crop physiology, genomics, genetics and breeding. It aims at presenting recent advances in these fields related to plant responses to water deficit and climate change, phenotyping and genetic variability. Technology revolution will dramatically increase our capacity to utilize genetic diversity and develop robust and drought tolerant varieties in a faster and cheaper manner.

The InterDrought-V Conference series is a sustained effort to bring together scientists who research drought in agriculture. This conference is in continuation of earlier InterDrought Conferences held in France (ID-I, 1995), Italy (ID-II, 2005), China (ID-III, 2009) and Australia (ID-IV, 2013).

It gives me great pleasure to welcome you to InterDrought-V organized by ICRISAT. We are grateful for the opportunity to host this important international gathering to exchange ideas, identify best practices and build strong, international partnerships to harness the power of modern tools to better serve the needs of smallholder farmers in the developing world. InterDrought-V 2017 brings together over 850 participants from 55 countries who are leaders in their respective fields and provides a platform to discuss new ideas and cutting-edge science related to key issues and strategies relevant for improving drought and other stress tolerance in crops.

I wish you a productive meeting as you learn and map out the next steps to advance our research to address drought and factors associated with climate change.

A warm welcome to Hyderabad!

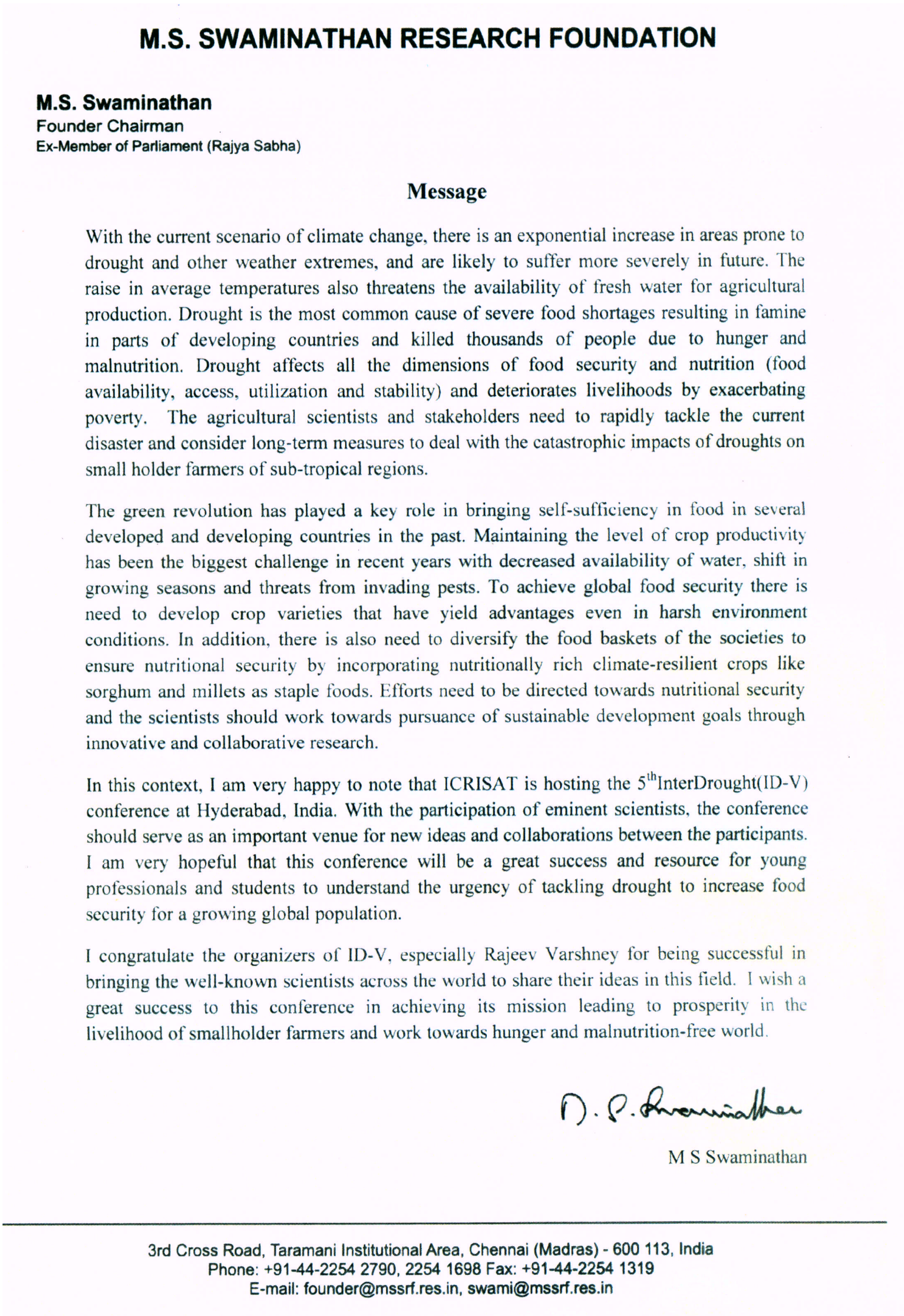
Kind regards,

David Bergvinson

David Bergvinson
Director General

Headquarters:
Patancheru 502 324, Telangana, India
Tel +91 40 30713071, **Fax** (O) +91 40 3071 3074, +91 40 3071 3075
E-mail icrisat@cgiar.org

www.icrisat.org
ICRISAT's scientific information: **http://EXPLORE*it*.icrisat.org**
ICRISAT is a member of the CGIAR System Organization



M.S. SWAMINATHAN RESEARCH FOUNDATION

M.S. Swaminathan
Founder Chairman
Ex-Member of Parliament (Rajya Sabha)

Message

With the current scenario of climate change, there is an exponential increase in areas prone to drought and other weather extremes, and are likely to suffer more severely in future. The raise in average temperatures also threatens the availability of fresh water for agricultural production. Drought is the most common cause of severe food shortages resulting in famine in parts of developing countries and killed thousands of people due to hunger and malnutrition. Drought affects all the dimensions of food security and nutrition (food availability, access, utilization and stability) and deteriorates livelihoods by exacerbating poverty. The agricultural scientists and stakeholders need to rapidly tackle the current disaster and consider long-term measures to deal with the catastrophic impacts of droughts on small holder farmers of sub-tropical regions.

The green revolution has played a key role in bringing self-sufficiency in food in several developed and developing countries in the past. Maintaining the level of crop productivity has been the biggest challenge in recent years with decreased availability of water, shift in growing seasons and threats from invading pests. To achieve global food security there is need to develop crop varieties that have yield advantages even in harsh environment conditions. In addition, there is also need to diversify the food baskets of the societies to ensure nutritional security by incorporating nutritionally rich climate-resilient crops like sorghum and millets as staple foods. Efforts need to be directed towards nutritional security and the scientists should work towards pursuance of sustainable development goals through innovative and collaborative research.

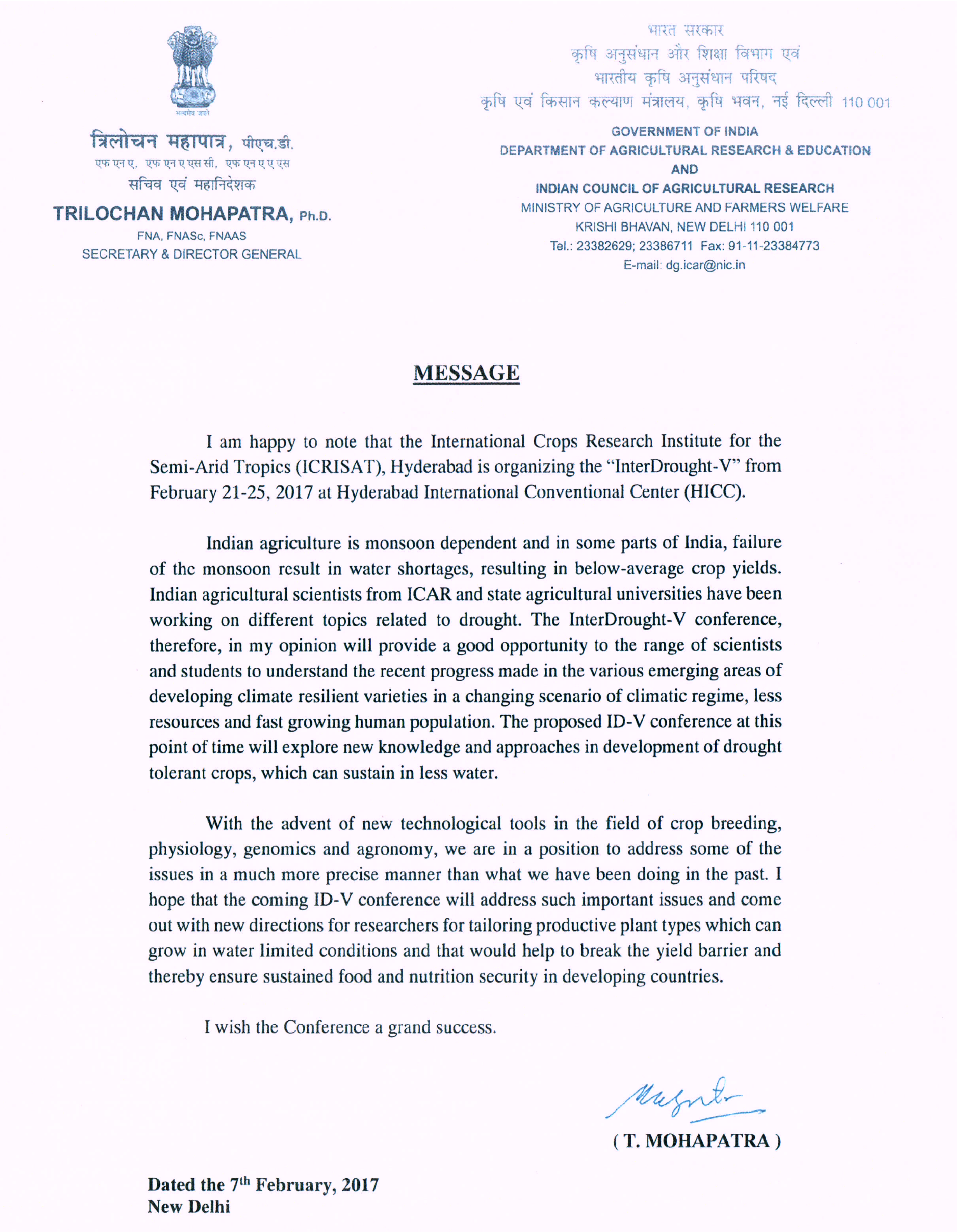
In this context, I am very happy to note that ICRISAT is hosting the 5th InterDrought(ID-V) conference at Hyderabad, India. With the participation of eminent scientists, the conference should serve as an important venue for new ideas and collaborations between the participants. I am very hopeful that this conference will be a great success and resource for young professionals and students to understand the urgency of tackling drought to increase food security for a growing global population.

I congratulate the organizers of ID-V, especially Rajeev Varshney for being successful in bringing the well-known scientists across the world to share their ideas in this field. I wish a great success to this conference in achieving its mission leading to prosperity in the livelihood of smallholder farmers and work towards hunger and malnutrition-free world.

M. S. Swaminathan

M S Swaminathan

3rd Cross Road, Taramani Institutional Area, Chennai (Madras) - 600 113, India
Phone: +91-44-2254 2790, 2254 1698 Fax: +91-44-2254 1319
E-mail: founder@mssrf.res.in, swami@mssrf.res.in



त्रिलोचन महापात्र, पीएच.डी.
एफ एन ए, एफ एन ए एस सी, एफ एन ए ए एस
सचिव एवं महानिदेशक
TRILOCHAN MOHAPATRA, Ph.D.
FNA, FNASc, FNAAS
SECRETARY & DIRECTOR GENERAL

भारत सरकार
कृषि अनुसंधान और शिक्षा विभाग एवं
भारतीय कृषि अनुसंधान परिषद
कृषि एवं किसान कल्याण मंत्रालय, कृषि भवन, नई दिल्ली 110 001
GOVERNMENT OF INDIA
DEPARTMENT OF AGRICULTURAL RESEARCH & EDUCATION
AND
INDIAN COUNCIL OF AGRICULTURAL RESEARCH
MINISTRY OF AGRICULTURE AND FARMERS WELFARE
KRISHI BHAVAN, NEW DELHI 110 001
Tel.: 23382629; 23386711 Fax: 91-11-23384773
E-mail: dg.icar@nic.in

MESSAGE

I am happy to note that the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad is organizing the "InterDrought-V" from February 21-25, 2017 at Hyderabad International Conventional Center (HICC).

Indian agriculture is monsoon dependent and in some parts of India, failure of the monsoon result in water shortages, resulting in below-average crop yields. Indian agricultural scientists from ICAR and state agricultural universities have been working on different topics related to drought. The InterDrought-V conference, therefore, in my opinion will provide a good opportunity to the range of scientists and students to understand the recent progress made in the various emerging areas of developing climate resilient varieties in a changing scenario of climatic regime, less resources and fast growing human population. The proposed ID-V conference at this point of time will explore new knowledge and approaches in development of drought tolerant crops, which can sustain in less water.

With the advent of new technological tools in the field of crop breeding, physiology, genomics and agronomy, we are in a position to address some of the issues in a much more precise manner than what we have been doing in the past. I hope that the coming ID-V conference will address such important issues and come out with new directions for researchers for tailoring productive plant types which can grow in water limited conditions and that would help to break the yield barrier and thereby ensure sustained food and nutrition security in developing countries.

I wish the Conference a grand success.

(T. MOHAPATRA)

Dated the 7th February, 2017
New Delhi

natureINDIA

Media Partner of InterDrought-V

natureINDIA
www.natureasia.com/en/nindia

Springer Nature
7th Floor, Vijaya Building
17 Barakhamba Road
New Delhi 110001
Ph: +91 11 48755814

EDITORIAL
Editor: Subhra Priyadarshini
Copy Editor: T. V. Padma
Art and design: Ajay Kumar Bhatt

ADVERTISING & SPONSORSHIP
Product Manager, Nature jobs and Advertising:
Sonia Sharma, +91 11 48755814; M: +91 9650969959
sonia.sharma@nature.com

SUBSCRIPTIONS & REPRINTS
Sonia Sharma: +91 11 48755814, M: +91 9650969959,
naturejobs.india@nature.com

NATURE JOURNAL QUERIES
Manager, Sales Support, NPG: Jacob Thomas
M: +91 9818171996
jacob.thomas@nature.com

Cover image illustration by Ajay Kumar Bhatt

Connect with us on

facebook.com/npgindia
@NatureInd

natureresearch

Looking for a Plan C in water-scarce times

An issue that stirs emotions among scientists, policy makers and the general public alike is 'water'. Or, in the present times, the lack thereof.

In these water-scarce times, in India, as in many other parts of the world, the issue of groundwater depletion is a subject of concern and serious study. And so, apart from the parched patches that the world inherited from the 20th century, we are looking at times of new aridity triggered by plummeting groundwater tables. It's actually a vicious circle – news studies are now suggesting that excessive pumping of water for agriculture may not be the reason behind the plunging groundwater levels after all. Long-term changes in monsoon rainfall could instead be influencing this, and that in turn is forcing farmers to dig deeper for water.

Why this preamble on water? Especially when water-scarcity is an issue almost embedded in the DNA of scientists attending InterDrought conferences.

Essentially because it's nice to take a step back once a while and look at the larger canvas. For scientists and technologists working on a Plan B to counter drought – that is, to still be able to grow nutritionally-rich, drought-resistant crops – these conferences are a wonderful reminder of the big picture. Interestingly, InterDrought-V is hoping to be the largest such congregation in recent times with over 850 scientists from around 55 countries. This provides a canvas bigger than ever before to create new milestones, fortify strategies that have worked so far, and solemnly bury the ones that don't work so well in the changing climate scenarios.

The Nature Research Group devotes significant energies to the coverage of the "Grand Challenges", which include our coverage of climate, water and food – issues that resonate well with InterDrought-V. Nature India, a showcase of India's science, is proud to be associated with the conference as its media partner. We hope that the conference, bringing together the who's who of the discipline from across the world, will identify issues and concerns to evolve a futuristic Plan C for drought-friendly agriculture.

Priyadarshini

Subhra Priyadarshini
Editor

natureINDIA

Contents

- Program xiii
- Inaugural Session xxiii
- Inaugural Lecture 7
- **Session I |** Setting the Biophysical Context: Climatic/Soil Constraints 11
- **Session II** | Maximising Dryland Crop Production: Crop Design 17
- **Session III** | Plant Productivity under Drought I: Effective Capture of Water 23
- **Session IV** | Plant Productivity under Drought II: Transpiration Efficiency 29
- **Session V** | Plant Productivity under Drought III: Vegetative Growth 37
- **Session VI** | Reproductive Development, Yield, Yield Quality 43
- **Session VII** | Breeding for Water-Limited Environments.. 51
- **Session VIII** | Agronomic Management/Cropping Systems for Water-Limited Environments, Broad Approaches... 59
- **Workshops Program** 68
- **Workshop I** | Abiotic Stress Tolerance in Cereals... 73
- **Workshop II** | Abiotic Stress Tolerance in Legumes 79
- **Workshop III** | Tolerance to Heat Stress for Crop Improvement.. 85
- **Workshop IV** | Genetic Engineering for Abiotic Stress 91
- **Workshop V** | GWAS and GS for Crop Improvement 97
- **Workshop VI** | Drought Stress and Aflatoxin Contamination in Crops 105
- **Workshop VII** | IPPN Workshop on Precision Phenotyping for Improved Stress Tolerance 111
- **Workshop VIII** | Next Generation Genomics & Molecular Breeding Platforms 117
- Panel Discussions on Climate Smart Agriculture 121
- List of Posters.. 127
- List of Participants 161
- Notes.. 204
- Sponsors 211

Program

InterDrought-V

Hyderabad International Convention Center (HICC)
Hyderabad, India
21-25 February, 2017

Technical Program

Tuesday, February 21, 2017		
09:00 hrs onwards	**Registration**	
10:00 – 16:00 hrs **(Hall MRG 1, 2, 3, 4, 5, 6, 1.05, 1.06)** *(Please see the workshop program sheet for workshop details)*	**Parallel Workshops**	
17:00 – 20:00 hrs **(Hall 4)**	**Opening Ceremony**	
	Welcome	**Rajeev Varshney** *Conference Org. Chair*
	Welcome message	**J S Sandhu** *InterDrought Vice Chair* & Deputy Director General (Crop Science), *Indian Council of Agricultural Research*
	Introduction to the Conference Topic	**Francois Tardieu** *InterDrought Chair*
	Opening address	**David Bergvinson** Director General, *ICRISAT*
	Inspirational address	**Shobhana K Pattanayak** Secretary, *Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Govt of India*
	Inaugural Address ***Science to Reduce Risk in the Quest to End Hunger***	**Rob Bertram** Chief Scientist, Bureau of Food Security *USAID*, USA
20:00 hrs onwards	***Welcome Cocktail and Dinner*** ***(Poolside Lawns, Hotel Novotel)***	

Wednesday, February 22, 2017

08:30 – 10:15 hrs **(Hall 4)**	**Session I: Setting the biophysical context: climatic/soil constraints** **Co-Chairs: Gurbachan Singh, *ASRB, India*** **Moses Siambi, *ICRISAT RP- ESA, Kenya***	
08:30 – 09:00 hrs	Climate change impact on crops – linking research to the scales of problem perception	**Frank A. Ewert** *University of Bonn* Germany
09:00 – 09:30 hrs	Plant water use and carbon gain and the isotopologues of carbon dioxide (in the context of climate change)	**Graham Farquhar** *Australian National University* Australia
09:30 – 10:00 hrs	Water flow to roots: dynamic effects of soil drying, transpiration rates and the properties of the root-soil interface	**Andrea Carminati** *University of Goettingen* Germany
10:00 – 10:15 hrs	Facilitated discussion	
10:15 – 10:45 hrs	*Tea / Coffee Break*	
10:45 – 12:30 hrs **(Hall 4)**	**Session II: Maximising dryland crop production – crop design** **Co-Chairs: Jairo Palta, *The University of Western Australia, Australia*** **Himanshu Pathak, *ICAR-NRRI, India***	
10:45 – 11:15 hrs	New tools for characterizing plant and soil water status	**Baret Frederic** *French National Institute for Agricultural Research* France
11:15 – 11:45 hrs	The possibilities of breeding: What can/has been changed, what can/has not?	**Mark Cooper** *Dupont Pioneer* USA
11:45 – 12:15 hrs	Is E well enough considered in GxExM analyses?	**Peter Carberry** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* India
12:15 – 12:30 hrs	Facilitated discussion	
12:30 – 14:15 hrs	*Lunch*	
14:15 – 16:15 hrs **(Hall 4)**	**Session III: Plant productivity under drought I Effective capture of water** **Co-Chairs: Neil Turner, The University of Western Australia, *Australia*** **OP Yadav, *ICAR- CAZRI, India***	
14:15 – 14:45 hrs	Root system architecture beyond geometry: new opportunities or undue complexity?	**Xavier Draye** *Universite catholique de Louvain* Belgium
14:45 – 15:15 hrs	Roles of root aquaporins under drought and salinity	**Stephen Tyerman** *University of Adelaide* Australia
15:15 – 15:25 hrs	Characterising root trait variability in chickpea (*Cicer arietinum* L.) germplasm for adaptation to dryland environments	**Kadambot Siddique** *The University of Western Australia* Australia

15:25 – 15:35 hrs	Root type matters: measurement of water uptake by seminal, crown and lateral roots in maize	**Mutez Ahmed** *University of Goettingen* Germany
15:35 – 15:45 hrs	Enhancing drought tolerance in chickpea using genomics approaches	**Mahendar Thudi** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* India
15:45 – 15:55 hrs	Trait introgression to evolve Rice cultivars suitable for the water saving aerobic cultivation: Evidence for physiological breeding	**Sheshshayee Sreeman** *University of Agricultural Sciences (UAS)-Bangalore* India
15:55 – 16:15 hrs	Facilitated discussion	
16:15 – 16:45 hrs	*Tea / Coffee Break*	
16:45 – 18:30 hrs (Hall 1, 2 & 3)	**Poster Session I- Themes IDT1, IDT2, IDT3, IDT4, IDT5, IDT 6 & IDT8**	

Thursday, February 23, 2017

08:30 – 10:40 hrs (Hall 4)	**Session IV: Plant productivity under drought II Transpiration efficiency** **Co-Chairs: Graeme Hammer, *University of Queensland, Australia*** **Shoba Sivasankar, Director, *CRPs GLs and Cereals, India***	
08:30 – 09:00 hrs	Adapting crops for semi-arid-tropical (SAT) agricultural systems; progress in TE research	**Jana Kholova** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* India
09:00 – 09:20 hrs	Towards genetic improvement of root system architecture to enhance rice productivity under drought stress	**Yusaku Uga** *National Agricultural and Food Research Organization (NARO)* Japan
09:20 – 09:30 hrs	Characterization of the maize ABA receptor and PP2C gene families reveal a subset of maize ABA receptors contribute to water use efficiency in early development	**Michael Bartsch** *Syngenta Crop Protection,* Switzerland
09:30 – 09:40 hrs	Mining soybean genetic diversity to identify genetic markers and physiological mechanisms underlying carbon isotope discrimination	**Arun Dhanapal** *University of Missouri* USA
09:40 – 09:50 Hrs	Introgression of drought tolerance traits into adapted Kenyan chickpea varieties using marker assisted backcrossing (MABC)	**Alice Kosgei** *Machakos University College* Kenya
09:50 – 10:00 Hrs	Breeding grapevine for an efficient use of water by lowering night-time transpiration	**Aude Coupel-Ledru** *INRA-LEPSE* France

10:00 – 10:10 Hrs	Stay-green QTL Stg3B is the key QTL associated with improved grain and stover yield under post-rainy sorghum growing conditions	**Harvinder Talwar** *ICAR-Indian Institute of Millets Research (IIMR)* India
10:10 – 10:40 hrs	Facilitated discussion	
10:40 – 11:10 hrs	*Tea / Coffee Break*	
11:10 – 15:10 hrs **(Hall 4)**	**Session V: Plant productivity under drought III Vegetative Growth** **Co-Chairs: Lizhong Xiong, *Huazhong Agri University, China*** **Kailash Bansal, *ICAR- NAHEP, India***	
11:10 – 11:40 hrs	Physiological controls of maize nodal root growth under drought: a (re)heightened priority	**Robert Sharp** *University of Missouri* *USA*
11:40 – 12:10 hrs	Genetic variability of plant responses to evaporative demand and water deficit, a forward integration from phenotyping to simulation of plant performances in the field	**Boris Parent** *INRA LEPSE* France
12:10 – 14:00 hrs	*Lunch*	
14:00 – 14:10 hrs	Analysing desiccation tolerance using transcriptome and genome sequence information	**Dorothea Bartels** *University of Bonn* Germany
14:10 – 14:20 hrs	Dissection of physiological, genetic, and metabolic traits in two tall fescue genotypes with contrasting drought tolerance	**Yun Kang** *The Samuel Roberts Noble Foundation* USA
14:20 – 14:30 hrs	Negative regulation of drought tolerance in rice by jasmonic acid : evidences from physiological traits, root proteome and metabolites	**Rohit Dhakarey** *Karlsruhe Institute of Technology* Germany
14:30 – 14:40 hrs	Bridging the generation gap: On the hunt to solve stress tolerance during vegetative and reproductive development	**Amal Johnston** *University of Heidelberg* Germany
14:40 – 15:10 hrs	Facilitated discussion	
15:10 – 15:30 hrs	*Tea / Coffee Break*	
15:30 – 18:00 hrs **(Hall 5 & 6)**	***Workshop - Next Generation Genomics & Molecular Breeding Platforms*** **Co-Chairs: Dave Edwards, *The University of Western Australia, Australia*** **Rajeev K Varshney, *ICRISAT RP- Genetic Gains, India*** *(Please see the workshop program sheet for workshop details)*	
19:00 hrs onwards	***Cultural Program (Hall 4) and Gala Dinner (Hall 1, 2 & 3)***	
Friday, February 24, 2017		
08:30 – 10:40 hrs **(Hall 4)**	**Session VI: Reproductive development, yield, yield quality** **Co-Chairs: Tony Fischer, *CSIRO, Australia*** **Victor Nwosu, *MARS Inc., USA***	
08:30 – 09:00 hrs	Maize reproductive development and kernel set under limited plant growth environments	**Lucas Borras** *Universidad Nacional de Rosario* Argentina

09:00 – 09:30 hrs	Genetic basis of wheat yield under dry and hot climates	**Delphine Fleury** *University of Adelaide* Australia
09:30 – 09:40 hrs	Efforts and strategies for alleviation of drought tolerance in chickpea in India	**Sushil Chaturvedi** *ICAR-Indian Institute of Pulses Research (IIPR)* India
09:40 – 09:50 hrs	Transgenic and CRISPR Cas approaches to improving the grain yield of maize under drought stress conditions	**Amitabh Mohanty** *Dupont Pioneer* India
09:50 – 10:00 hrs	Elaborating a unique regulon for rice yield under drought: component genes underpin or are affected by transcriptional, post-translational, biochemical and epigenetic mechanisms	**Ajay Kohli** *International Rice Research Institute (IRRI)* Philippines
10: 00 – 10:10 hrs	Exploring QTLxE in a network of fields: identification of QTLs associated with scenarios of heat and drought for predicting yields in future climates	**Emilie Millet** *INRA-LEPSE* France
10: 10 – 10:20 hrs	Molecular genetic analysis of root system architecture and drought tolerance in soybean	**Babu Valliyodan** *University of Missouri* USA
10:20 – 10:40 hrs	Facilitated discussion	
10:40 – 11:10 hrs	*Tea / Coffee Break*	
11:10 – 15:40 hrs (Hall 4)	**Session VII: Breeding for water-limited environments** **Co-Chairs: KHM Siddique, *UWA Institute of Agriculture, Australia*** **Shiv Kimothi, *ADG-ICAR, India***	
11:10 – 11:40 hrs	The definition and development of water-saving and drought-resistance Rice (WDR)	**Lijun Luo** *Shanghai Agrobiological Gene Center* China
11:40 – 12:10 hrs	Climate-resilient sorghum breeding in West Africa Sudano-Sahelian environments	**Niaba Teme** *Institut d'Economie Rurale (IER)* Mali
12:10– 14:00 hrs	*Lunch*	
14:00 – 14:30 hrs	Success stories in rice breeding for drought tolerance in India	**HE Shashidhar** *University of Agricultural Sciences – Bangalore* India
14:30 – 14:40 hrs	Genetic control of nodal root angle is associated with drought tolerance in sorghum	**Vijaya Singh** *University of Queensland* Australia
14:40 – 14:50 hrs	Drought tolerant cowpea lines derived through Marker Assisted Recurrent Selection	**Ousmane Boukar** *International Institute of Tropical Agriculture (IITA)* Nigeria

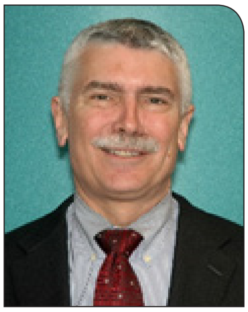
14:50 – 15:00 hrs	Chickpea breeding for water-limited environments	**Pooran Gaur** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* India
15:00 – 15:10 hrs	Wheat (*Triticum aestivum* L.) genotypes present high variability of stem carbohydrates and differences in the expression of genes regulating fructan metabolism under contrasting water regimes	**Alejandro del Pozo** *Universidad de Talca* Chile
15:10 – 15:20 hrs	Legume breeding and seed systems for improved livelihoods and impact	**Emmanuel Monyo** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* Kenya
15:20 – 15:40 hrs	Facilitated discussion	
15:40 – 16:00 hrs	*Tea / Coffee Break*	
16:00 – 18:00 hrs (Hall 1, 2 & 3)	**Poster session: IDT7 & IDT9**	

Saturday, February 25, 2017

08:30 – 11:45 hrs (Hall 4)	**Session VIII: *Agronomic management / cropping systems* for water-limited environments, broad approaches** **Co-Chairs: Steven Brown, *The Peanut Foundation, USA*** **Anthony Whitbread, *ICRISAT RP-Innovation Systems, India***	
08:30 – 09:00 hrs	Understanding and quantifying the drivers of yield under drought and yield potential	**Victor Sadras** *South Australian Research and Development Institute* Australia
09:00 – 09:30 hrs	Pushing rain-fed agriculture towards aridity: Success and surprise in the plains of Argentina	**Esteban Jobbagy** *Grupo de Estudios Amblentales* Argentina
09:30 – 10:00 hrs	Irrigation strategies coupled with genotypes	**Elias Fereres** *University of Cordoba* Spain
10:00 – 10:30 hrs	*Tea / Coffee Break*	
10:30 – 10:40 hrs	Rainfall, soil sand content, and depth of soil compaction predominantly affect rice yield reduction by reproductive-stage drought at varietal screening sites in Bangladesh, India, and Nepal	**Amelia Henry** *International Rice Research Institute (IRRI)* Philippines
10:40 – 10:50 hrs	Comparison between groundwater withdrawals for irrigation and estimated crop water requirements in the Kairouan plain	**Fajr Fradi** *National Agricultural Research Institute of Tunisia* Tunisia

10:50 –11:00 hrs	N-fertilising rainfed wheat and barley to intensify cereal production in the Mediterranean basin	**Roxana Savin** *University of Lleida* Spain
11:00 – 11:10 hrs	Adoption of soil and water conservation practices under different farming systems in the Sahel region of northern Mali	**Birhanu Zemadim** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* Mali
11:10 – 11:20 hrs	Effect of plastic film mulching and nitrogen on N2O emission in dryland maize	**Shanchao Yue** *Northwest A&F University* China
11:20 – 11:30 hrs	Intercropped woody species in the Sahel to resist drought: beneficial microorganisms and common mycorrhizal hyphal networks to reduce water stress.	**Richard Dick** *Ohio state University* USA
11:30 – 11:45 hrs	Facilitated discussion	
11:45 – 12:30 hrs	ID-V General Assembly	
12:30 – 14:00 hrs	*Lunch*	
14:00 – 16:30 hrs (Hall 4)	**Closing Session** **Chief Guest: Shri Krishna Byre Gowda, Hon. Minister of Agriculture, *Government of Karnataka, India***	
14:00 – 15:00 hrs	Forum by young scientists nominated by the steering committee : Questions raised by the congress, future, what they have learnt	
15:00 – 15:30 hrs	Poster prize distribution	
15:30 - 15:45 hrs	Inspirational Address	**Shri Krishna Byre Gowda** *Hon. Minister of Agriculture Government of Karnataka, India*
15:45-16:00 hrs	Conclusion : Main points raised during the congress	**Francois Tardieu** *Institut National De La Recherche Agronomique (INRA)* France
16:00-16:10 hrs	Concluding remarks	**Peter Carberry** *DDG-Research, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),* India
16:10-16:20 hrs	Acknowledgements	**Rajeev Varshney** *International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)* India
16:20 – 16:30 hrs	Next Congress	
16:30 hrs	Close	

Inaugural Session



Robert Bertram

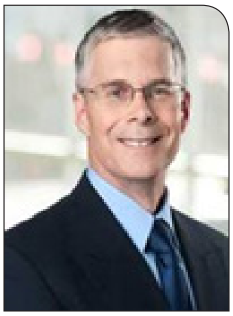
Cheif Scientist
USAID's Bureau for Food Security
USA

Shobhana K Pattanayak

Secretary, DAC & FW
Ministry of Agriculture
Government of India

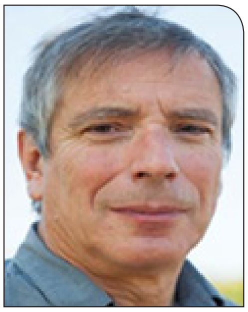
J S Sandhu

Deputy Director General, Crop Sciences
Indian Council of Agricultural Research
(ICAR)
India



David Bergvinson

Director General
International Crops Research Institute for the
Semi-Arid Tropics (ICRISAT)
India



Francois Tardieu

Research Director
National Institute of Agronomic Research
(INRA)
France

Rajeev K Varshney

Research Program Director - Genetic Gains
International Crops Research Institute for
the Semi-Arid Tropics (ICRISAT)
India

Session II

Maximising Dryland Crop Production: Crop Design

Co-chairs

Dr Jairo Palta

Adj. Professor
The University of Western Australia
Australia

Dr. Himanshu Pathak

Director
ICAR-National Rice Research Institute (NRRI)
India

Dr. Frederic Baret
INRA-EMMAH/ UMT-CAPTE,
84914 Avignon
France
E-mail: baret@avignon.inra.fr

Dr. Frederic Baret received a PhD in the use of remote sensing for crop monitoring in 1986. He is currently Research Director at INRA, leading the remote sensing team. Dr. Baret has coordinated several national and European projects; and is involved in the development of radiative transfer models at several scales (soil, leaf, canopy) and their use for the retrieval of vegetation biophysical variables. He has developed retrieval algorithms (CYCLOPES, GEOV1, GEOV2, GEOV3) from satellite and airborne sensors as well as close range remote sensing. Dr. Baret is also deeply involved in the validation of remote sensing products and has chaired the CEOS/LPV working group. He recently expanded his activity on high throughput phenotyping with the development of measurement systems as well as interpretation methods. Dr. Baret is in charge of the development of phenotyping methods in field conditions within the French Plant Phenotyping Network (PHENOME) project. This includes the application of drone observations as well as the development of phenomobiles (fully automatic robot rover). He has authored more than 200 research papers (h=47 from WoK).

New tools for characterizing plant and soil water status

Baret F.[1]*, Doussan C.[1], de Solan B.[2], Madec S.[1],Comar A.[3], Jezequel S.[4], Simon Carrière[1], F. Postik[1]

[1]INRA-EMMAH/ UMT-CAPTE, 84914 Avignon, France
[2]Arvalis Institut du végétal / UMT CAPTE, 84914 Avignon, France
[3]HIPHEN, 84914 Avignon, France
[4]Arvalis Institut du végétal / UMT CAPTE, 04800 Gréoux, France
*E-mail: baret@avignon.inra.fr

Characterizing water stress under field conditions is mandatory for an integrated evaluation of genotype performances under realistic environments. It is first required to accurately describe the soil variability over the experimental platform to prevent confounding local environmental effects with genotypic ones. Several traits can then be investigated, based either on below or above ground observations, using the new available tools. Electric resistivity tomography (ERT) was exploited to monitor the distribution of soil moisture over a set of microplots and compute the water balance. Above the ground, the impact of water stress can be observed over integrated structure variables such as crop height or the green area index that are accessible from LiDAR, high resolution RGB or multispectral imagery acquired aboard unmanned aerial (UAV) or ground (UGV) vehicles. The dynamics of these variables reveals important genotypic differences. Conversely, the observation of the diurnal variation of leaf rolling and canopy temperature provides access to the short term reaction of the plant to water stress. The use of these new tools is illustrated over wheat and maize field experiments with concurrent ground measurements used to quantify the associated accuracy and precision. However, these several type of measurements repeated along the growth cycle need to be combined together to get a more comprehensive insight of the mechanisms that govern plant resistance or resilience under drought conditions as well as their genotypic control. The assimilation of such observations into crop functioning models is foreseen as the approach that should be privileged in the coming years.

Dr. Mark Cooper
DuPont Pioneer,
8305 NW 62nd Avenue,
Johnston IA 50131,
USA
E-mail: mark.cooper@pioneer.com

Dr. Mark Cooper has been involved in research and breeding for drought tolerance of cereals. He is a Research Fellow for DuPont Pioneer, working as a member of a global team with responsibilities for developing molecular, phenotyping and modeling technologies to improve yield stability of maize. As a maize breeder he has developed a number of drought-tolerant maize hybrids that are currently grown by farmers across the US Corn Belt and in Europe. Drought tolerant maize germplasm from Dr. Cooper's breeding program has been deployed globally.

The possibilities of breeding: what can be/has been changed, what can/has not?

Mark Cooper[1]*, Charlie Messina[1], Matt Smalley[1], Neil Hausmann[1], John Arbuckle[1]

[1]DuPont Pioneer, 8305 NW 62nd Avenue, Johnston IA 50131, USA
*E-mail: mark.cooper@pioneer.com

Water availability frequently limits the productivity of cropping systems. Future productivity targets have been defined. However, our ability to achieve such targets is still the subject of much debate. In all projection scenarios, there is an expectation that gains in productivity will come in part from further genetic improvements through breeding. Therefore, it is worth grounding ourselves in the reality of what is possible through breeding. The possibilities to change crop productivity through breeding will be reviewed using three broad phases: (1) the historical perspective, which provides an assessment of the changes that have been made and successfully delivered to farmers, (2) the current perspective, which examines the genetic diversity accessible within the current breeding cycle and the current research and breeding strategies that are being used to manipulate the accessible genetic diversity to deliver new products in the short to medium term, and (3) the future perspective, which uses our understanding of all available methods for creating and accessing novel and usable genetic diversity and applying breeding strategies to harness this diversity to create improved products from the future cycles of the breeding programs. Foundational to realizing the opportunities of all future scenarios is ensuring that the improved products can be delivered to and successfully used by farmers. These three phases are applicable for any crop or cropping system. Breeding maize for the corn-belt of North America will be discussed as an example and used as a reference for other scenarios and targets.

Dr. Peter Carberry
ICRISAT,
Patancheru, 502324, Telangana, State
India
E-mail: P.Carberry@cgiar.org

Dr. Peter Carberry, an Australian national, is the Deputy Director General- Research at ICRISAT. Dr. Carberry received his PhD in Agriculture from the University of Sydney. Before joining ICRISAT, Peter was Chief Research Scientist and Partnership Leader (CSIRO-DFAT Africa Food Security Initiative), Commonwealth Scientific and Industrial Research Organization (CSIRO), Australia. His expertise is in crop physiology and in the development and application of systems models. He is a key developer of the Agricultural Production Systems Simulator (APSIM) cropping systems model. Peter has held several important scientific positions, including Board Director of the Australian Institute of Agricultural Science and Technology; President, Australian Society of Agronomy; Grains Research & Development Corporation, Senior Fellowship 2007; Board Member, International Crop Science Congress (2004).

He is Associate Editor, Food Security journal and member of the Editorial Board of the Journal of Integrative Agriculture. He has 87 journal papers, 29 book chapters, four guest editorships, and has contributed to over a hundred conference papers, newsletters and other publications.

Is E well enough considered in GxExM analyses?

Carberry P*[1],Vadez V[1]

[1]ICRISAT, Patancheru, 502324, Telangana, India
E-mail: P.Carberry@cgiar.org

Genotype x Environment x Management (GxExM) is an appropriate framing, both to understand agricultural systems performance and to identify priority interventions for systems improvement. While genetic gain (G) and agronomic management (M) are well enough considered in agricultural research, the influence of the environment (E) is often underestimated and, in significant ways, overlooked for much of rainfed agriculture.

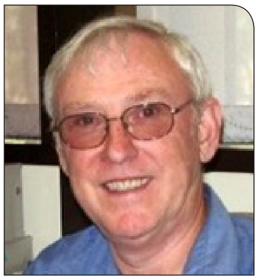
First, extremes in climate, forever relevant but now more so with climate change, must be included when considering E. High temperature effects on flowering and seed set at last are critical considerations in developing new varieties for the SAT. Second, most researchers ignore the influence of soils, despite crop performance often being governed by resource supply and not by demand. Soil characterisation is treated cursorily in most GxExM analyses – rarely are measurements taken to the full depth of rooting. The soil environment further governs the attainment of plant stands, notoriously low and variable in the SAT due to inadequate moisture for germination, high soil strength and crusting, and extreme soil surface temperatures. Third, the environment encompasses pressures from biotic pests – weeds, diseases and insects. While breeding does emphasise screening for resistance to major diseases and insects, the environment is rarely defined by the inherent weed pressure experienced in target ecologies, with the possible exception of Striga.

The environment is dynamic with time and agricultural practice. In this paper, we suggest a lack of attention to E in agricultural research in the SAT can lead to distorted priorities and less than effective interventions.

Session III

Plant Productivity under Drought I: Effective Capture of Water

Co-chairs



Prof. Neil Turner

Senior Principal Research Fellow
The University of Western Australia
Australia

Dr. OP Yadav

Director
ICAR-Central Arid Zone Research Institute
India

Dr. Xavier Draye
Crop Physiology and Plant Breeding,
Universitécatholique de Louvain
Earth and Life Institute,
Louvain-la-Neuve,
Belgium
E-mail: xavier.draye@uclouvain.be

Dr. Xavier Draye is Professor of Crop Physiology and Plant Breeding at the Universitécatholique de Louvain. He uses a combination of experimental and modelling (FSPM) strategies, from the organ to the plant scales, to understand the dynamics of root system architecture and hydraulics. Dr. Draye interacts closely with soil hydrologists and molecular biologists to develop novel views of crop water use that integrate notions of growth, development, root hydraulic properties and soil water dynamics. He is also active in the development of root image analysis tools and standards (RSML) and in the development of phenotyping systems. He has contributed to the DROPs project and is involved in the modelling section of the EMPHASIS infrastructure.

Root system architecture beyond geometry : new opportunities or undue complexity?

René Civava[4], Aleksander Ligeza[1], Valentin Couvreur[1], Beata Orman[2], Mathieu Devos[1], Adrien Dockx[1], Sixtine Passot[1], François Chaumont[1], Guillaume Lobet[1],[3], Mathieu Javaux[1],[3], Xavier Draye[1]

[1]Université catholique de Louvain, Earth and Life Institute, Louvain-la-Neuve, Belgium
[2]University of Liège, PhytoSystems, Liège, Belgium
[3]FZ Juelich, Juelich, Germany
[4]Evangelic University of Africa, Bukavu, Congo
*E-mail: xavier.draye@uclouvain.be

Root system architecture is classically seen as the geometrical side of plant strategies to capture soil water. In our quest to optimise water extraction under drought, target architectural phenotypes have been proposed and several paths (phenes) to achieve them have been identified. Nevertheless, recent progress in phenotyping, biology and modelling indicate that the contribution of root system architecture in the capture of water is more complex than what we have considered. A first avenue ahead of us relates to the temporal dynamics of root system architecture. Progress in phenotyping and modelling helps us capture rules constraining the variability of root growth, which, in combination with field shovelomics data, provides the access to critical variables such as deep soil exploration. A second avenue relates to the plasticity of root development. Current research in model and crop species has identified novel mechanisms of root response to soil water heterogeneity, including hydrotropism, hydropatterning and lateral root repression. This knowledge will help us to build more realistic and less empirical models of field root architecture. A third avenue relates to the multi-scale complexity of the soil-root hydraulic continuum. The most recent models of soil-root hydraulic architecture now include rhizosphere properties, aquaporin expression and cell-wall decorations at the cell level, root anatomy and root development, which are within the reach of phenomics. The presentation reviews our progress in these avenues and discusses whether these represent new opportunities to achieve efficient capture.

Prof. Stephen Tyerman
Department of Plant Science,
University of Adelaide,
Australia
E-mail: steve.tyerman@adelaide.edu.au

Prof. Stephen Tyerman's research interests lie in the area of plant physiology and, in particular, how plants acquire their mineral nutrients and water for optimum growth. He has a biophysical background and brings this it to bear by using novel sensor technology for probing plant performance and responses to stress. Prof. Tyerman has researched membrane transport systems, nutrition, salinity and water relations in plants. He is currently the Head of the Department of Plant Science at the University of Adelaide and is one of 10 chief investigators responsible for the overall management of the Australian Research Council Centre of Excellence in Plant Energy Biology that has nodes in Perth, Canberra and Melbourne, employing over 130 staff and research higher degree students and with total funding over $40 million. Prof. Tyerman's research interests include sustainable use of water resources and this has lead him into positions on committees addressing the consequences of global warming. Steve's research and community engagement was recognised by the award of Fellowship of the Australian Academy of Science in 2004.

Roles of root aquaporins under drought and salinity

Tyerman S.D.[1]*

[1]Australian Research Council Centre of Excellence in Plant Energy Biology, University of Adelaide, School of Agriculture, Food and Wine, Department of Plant Science
*E-mail: steve.tyerman@adelaide.edu.au

An update on the roles of root aquaporins will be given highlighting some outstanding questions on their roles under drought and salinity. Root hydraulic conductance appears to track shoot demand (transpiration) and this is achieved by variation in the activity and expression of certain root aquaporins. We have found this for a variety of species, including grapevine and soybean, where we have also demonstrated rapid signaling from the shoot that alters root expression of aquaporins and hydraulic conductivity in response to shoot wounding. In grapevine abscisic acid and salinity can alter the response between hydraulic conductance and transpiration to enable easier extraction of water from the soil and to restrict salt uptake. We identify at least two likely candidate aquaporins involved, and suggest that the signal may be changes in xylem tension. One of these aquaporins from soybean when over expressed increases salinity tolerance. Recent work from the group has shown that a highly expressed aquaporin in Arabidopsis (AtPIP2;1) can function as non-selective cation channel when expressed in heterologous systems with biophysical properties similar to that of the non-selective cation channels found in root plasma membranes of a variety of species and thought to be responsible for sodium influx. The implications of this discovery for salinity tolerance and coupled water and ion transport will be discussed.

Characterising root trait variability in chickpea (*Cicer arietinum* L.) germplasm for adaptation to dryland environments

Siddique K H M[1]*, Chen Y[1], Ghanem M E[2]

[1]The UWA Institute of Agriculture, The University of Western Australia, LB 5005, Perth WA 6001, Australia
[2]International Centre for Agricultural Research in the Dry Areas, North-Africa Platform, Rabat, Morocco
*E-mail: kadambot.siddique@uwa.edu.au

Chickpea (*Cicer arietinum* L.) is an important grain legume crop, but its sustainable production is challenged by predicted by climate changes which are likely to increase production limitations and uncertainty. Characterising the variability in root architecture traits in a core collection of chickpea germplasm will provide the basis for breeding new germplasm with suitable root traits for the efficient acquisition of soil resources and adaptation to drought and other abiotic stresses. This study used a semi-hydroponic phenotyping system for assessing root trait variability across 270 chickpea genotypes. The genotypes exhibited large variation in rooting patterns and branching manner. Thirty root-related traits were characterised, 17 of which had larger variation among genotypes with coefficients of variation ≥0.30. The Pearson correlation matrix showed a strong correlation among most of the selected traits ($P \leq 0.05$). Principal component analysis revealed three principal components with eigen values >1 capturing 81.5% of the total variation.An agglomerative hierarchical clustering analysis, based on root trait variation, identified three genotype homogeneous groups (rescaled distance of 15) and 16 sub-groups (rescaled distance of 5). The chickpea genotypes characterised in this study with vastly different root properties could be used for further studies in glasshouse and field trials; and for molecular markers, gene mapping and modelling simulations, ultimately aimed at breeding gremplasm with root traits for improved adaptation to drought and other specific environments.

Root type matters: measurement of water uptake by seminal, crown and lateral roots in maize

Ahmed MA[1]*, Zarebanadkouki M[1], Kaestner A[2], Carminati A[1]

[1]Georg-August University of Goettingen, Goettingen, Germany
[2]Paul Scherrer Institute, Villigen, Switzerland
*E-mail: mahmed@gwdg.de

The ability of crops to capture water from the soil depends on the root architecture and anatomical root traits that determine their radial and axial hydraulic conductance. These properties are not constant but vary along roots and among different root types and their measurement as well as their effect on the location of water uptake remain an open scientific challenge. The objectives of this study were to measure water uptake by maize roots in soils and estimate differences between seminal, nodal and lateral roots.

We traced the transport of deuterated water (D_2O) in the roots of five weeks-old maize in sandy soil using neutron radiography. The transport of D_2O was simulated using a diffusion-convection numerical model, which gave the radial permeability and the water uptake of the different root segments. The root architecture of five weeks-old maize consisted of seminal roots with long laterals and crown (nodal) roots with shorter and fewer laterals. Water was mainly taken up by crown roots and their laterals, while laterals of seminal roots, which were the main location of water uptake in younger plants, stopped to take up water. In contrast to seminal roots, crown roots were able to take up water also from their most distal segments.

Although seminal roots have been heavily investigated, they do not present the main location of water uptake of a mature maize root system. The ability of crown roots to take up water from their most distal segments can provide an advantage to extract water from deep soil layers and tolerate drought.

Enhancing drought tolerance in chickpea using genomics approaches

Mahendar Thudi[1],*, Pooran M Gaur[1], L Krishnamurthy[1], Srinivasan Samineni[1], Rajeev Varshney[1],[2],*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana State, India.
[2]School of Plant Biology and Institute of Agriculture, The University of Western Australia, Crawley, WA, 6009 Australia
*E-mail: t.mahendar@cgiar.org; r.k.varshney@cgiar.org

Terminal drought is one of the major constraints in chickpea (*Cicer arietinum* L.) leading to more than 50% production losses. To overcome these production losses due to drought, a range of translational genomics approaches are being used in chickpea breeding to develop improved chickpea varieties for enhancing food and nutritional security in developing countries in the context of climate change. For understanding the complex nature of drought tolerance, precise phenotypic data (20 drought component traits evaluated in one to seven seasons at one to five locations in India on two intra-specific mapping populations - ICC 4958 × ICC 1882 and ICC 283 × ICC 8261) together with extensive genotyping data was analyzed. As a result, nine QTL clusters containing QTLs for several drought tolerance traits have been identified, which can be targeted for molecular breeding. Among these clusters, one cluster harbouring 48% robust M-QTLs for 12 traits and explaining about 58.20% phenotypic variation present on CaLG04 has been referred as "*QTL-hotspot*". This genomic region contains seven SSR markers (ICCM0249, NCPGR127, TAA170, NCPGR21, TR11, GA24 and STMS11). This QTL region has been introgressed in several leading varieties (e.g. JG 11, Chefe, KAK2) by using marker-assisted backcrossing (MABC) approach. Multi-location evaluation of these MABC lines provided several lines that have up to 24% higher yield than the recurrent parents. Introgression of this region into other elite cultivars will enhance production and productivity in chickpea.

Trait introgression to evolve rice cultivars suitable for the water saving aerobic cultivation: evidence for physiological breeding.

Prathibha MD[1].,Puspa D[1].,Preethi NV[1]., Raju BR[2].,Mohankumar MV[3]., Sowmya HR[1]., Pooja B[1]., Smitharani JA[1]., Rajanna MP[4] , Sheshshayee MS[1]

[1]Department of Crop Physiology, University of Agricultural Sciences, GKVK, Bengaluru 560065
[2]Department of Agronomy, Kansas State University Manhattan, USA, KS-66505
[3]Bayer Crop Science, Bengaluru
[4]Rice breeding division, Zonal Agricultural Research Station, VC Farm, Mandya, India
*E-mail: msshesh1@uasbangalore.edu.in

Evolving suitable rice cultivars is crucial for harnessing the water-saving advantage of semi-irrigated aerobic cultivation practice. Though several drought adaptive traits have been identified and validated, introgressing several of these onto the same genetic background alone can enhance crop performance under semi-irrigated aerobic conditions. We developed novel phenotyping approaches based on stable isotopes of carbon and oxygen to capture the genetic variability, water use efficiency and water use; and also developed strategies to assess root traits using specially designed root structures. A temperature induction response technique was developed to screen for variability in acquired tolerance traits. Using these phenotyping approaches, we screened a set of diverse *indica* rice germplasm for trait diversity. Around 300 genome wide SSR markers revealed significant molecular diversity and a population structure segregating the population into six subgroups. Association mapping revealed several robust QTL governing the variability in these drought adaptive traits which were validated using bi-parental mapping populations.

The best root, WUE and acquired tolerance trait donor genotypes, AC39020 and IET16348, were identified and crossed separately with a mega rice variety, IR64. The F1 plants were inter-mated and the resultant double-cross F1 was backcrossed with IR64 till BC3F1. At each generation, QTL-markers were used for foreground selection and a set of 120 genome wide SSRs for background selection, and phenotyped for yield and Δ13C. This marker assisted-phenotypic selection led to the identification of superior lines with trait improvement with more than 97% of IR64 genome recovered demonstrating the power of physiological breeding.

Session IV

Plant Productivity under Drought II: Transpiration Efficiency

Co-chairs

Prof. Graeme Hammer

Centre Director
The University of Queensland
Australia

Dr. Shoba Sivasankar

Director
CRP Grain Legumes & CRP Dryland Cereals
India

Dr. Jana Kholová
Crop Physiology Laboratory
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT),
Patancheru
Telangana,
India
E-mail: J.Kholova@cgiar.org

Dr. Jana Kholová obtained her MSc degree, with specialization in plant genetics & physiology at the Dept. of Genetics and Microbiology, Charles University in Prague, Faculty of Science. From 2006- 2010, she did her Ph.D, specializing in plant genetics & physiology. Since 2009, Dr. Kholová is serving as Scientist at the Dept. of Crops Physiology, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India. Her work areas include plant stress physiology & modeling; genetics; plant biochemistry; molecular biology; plant nutrition; and interdisciplinary research along the SAT-crops value-chain.

Adapting crops for semi-arid-tropical (SAT) agricultural systems: progress in TE research

Jana Kholová[1], Graeme L. Hammer[2], Tharanya Murugesan[1], Sivasakthi Kaliamoorthi[1], Greg McLean[3], Surjit Vikraman[1], Erik van Oosterom[2], Keerthi Chandavalada[1], Vincent Vadez[1] *

[1]International Crops Research Institute for the Semi–Arid Tropics (ICRISAT), Crop Physiology Laboratory, Patancheru 502324, Telangana, India
[2]The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane,QLD 4072, Australia
[3]Agri-Science Queensland, Department of Agriculture and Fisheries, Toowoomba, QLD 4350, Australia
*E-mail v.vadez@cgiar.org

Increasing the efficiency of water conversion into biomass (TE) is in focus for improvement of crop productivity under water-limited environments. The last ID conference highlighted that stomatal regulation under high vapor pressure can increase TE, which represented a new opportunity for crop improvement. While increasing TE leads to enhanced crop production under drought stress, managing water to assure its availability for the grain filling period is necessary. Particularly, we will focus on traits that alter the crop water-use profile during the season (e.g. canopy size and development), increase TE (e.g. canopy conductivity and structure), or achieve both. For these water-use related traits, the range of genetic variability has been explored and this allowed designing crops suitable for either agro-systems intensification or resilience. Yet, the interactions of physiological processes responsible for plant water use with environments are not fully understood and this talk will provide an update on these aspects. We will also show how the crop and socio-economic models are used to quantify the benefits and evaluate the trade-offs associated with different crop water-use strategies in semi-arid tropics agro-ecologies. Results indicate that variation in water-use related traits is frequently associated with grain versusstover production trade-offs. Therefore, the economic value of a particular technology intervention depends on the nature and type of commodity demand within the specific agro-system. We will discuss the possibilities of enhancing the crop value in the systems with high demand for staple food grains ormore complex dual purpose (food and fodder)crop production systems.

Dr. Yusaku Uga
National Agriculture and Food Research Organization (NARO), Japan
3 Chome-1-1 Kannondai, Tsukuba, Ibaraki Prefecture 305-8517,
Japan
E-mail: yuga@affrc.go.jp

Yusaku's research aims are to identify and apply QTLs associated with root system architecture for genomic-based breeding to improve crop production under abiotic stress like drought and nitrogen deficiency. Recently, his group reported cloning and characterization of DRO1, a rice QTL for deep rooting (Uga et al., 2013, Nature Genetics). For the first time, he showed the feasibility of using a gene controlling deep rooting to develop new crop cultivars with high adaptability to drought. In addition to DRO1, he is going on with cloning of other QTLs for root system architectures such as root growth angle and root length. He is currently the principal researcher of Breeding Material Development Unit, Institute of Crop Science, National Agriculture and Food Research Organization. Yusaku's basic and applied study was recognaized by the many awards: Niigata International Food Award in 2016, Japan Prize in Achievement Award for Young Scientists in 2014, Young Scientist Award of Japanese Society of Breeding in 2013.

Towards genetic improvement of root system architecture to enhance rice productivity under drought stress

Yusaku Uga

National Agriculture and Food Research Organization (NARO), Tsukuba, Japan
E-mail: yuga@affrc.go.jp

Drought is one of the most serious abiotic stresses affecting crop production in the world. Under drought conditions, water exists disproportionately in the deep soil layers. The survival of most terrestrial plants is needed to the ability of their roots to obtain water from soil. Deep root system appears to be an efficient adaptation strategy for avoiding drought stress because it enables a plant to absorb more water from deep soil layers. Therefore, deeper rooting may be a key trait in the enhancement of drought avoidance in crops. Root growth angle (RGA), which determines the direction of root elongation in the soil, affects the area in which roots capture water. Our group have isolated quantitative trait locus controlling RGA, DRO1, in rice. We also have developed a near-isogenic line (NIL) that carries a functional allele of DRO1 derived from the deep-rooting cultivar 'Kinandang Patong' in the genetic background of the shallow-rooting variety 'IR64', which has a non-functional allele of DRO1. Using this NIL, we demonstrated that introducing of RGA gene improved yield performance in rice under drought. To develop varieties that can be adapted to a wide range of drought stresses, it would be necessary to identify and characterize additionally QTLs for root system architecture (RSA) other than DRO1. Recently, our group isolated another RGA QTL, qSOR1, in rice. We developed four NILs having functional or non-functional allele of DRO1 and/or qSOR1. These lines showed several types of RGA ranging from shallow to steep, suggesting that we could make genetic variation of RGA by using only two QTLs. We also identified several QTLs for root length because root length may be another important trait which determines the area in which roots absorb water. These QTLs for RSA will be useful genetic resources for breeding of RSA to enhance drought avoidance in rice.

Characterization of the maize ABA receptor and PP2C gene families reveal a subset of maize ABA receptors contribute to water use efficiency in early development

Michael L Nuccio, Sang Youl Park, Sean Cutler, Julie Green, Jian Lv, Xi Chen, Andrew DeBrecht, Esteban Bortiri, Michael Bartsch*

Syngenta Crop Protection, LLC, USA
E-mail: michael.bartsch@syngenta.com

Abscisic Acid (ABA) is a potent plant hormone involved in plant water use, seed maturation, germination and response to the environment. The PYR/PYL/RCAR family of ABA receptors has been shown to be the major mechanism by which ABA signaling initiates in plant cells. This gene family consists of at least 12 members in many plant species. Here we characterize the 12-member maize ABA receptor (ZmPYL) gene family. We show that most gene family members are related to *Arabidopsis* PYR/PYL/RCARs and can be arranged into three clades based on sequence homology and ligand sensitivity. We find that most maize ABA receptors are widely expressed throughout development, suggesting that many may have overlapping functions. Each ZmPYL interacts with *Arabidopsis* HAB1 and ABI1 as well as some maize PP2Cs in an ABA-dependent manner. Over-expression of each ZmPYL in transgenic maize suggests that six are directly involved in maize water use during vegetative development. These data show which ZmPYLs represent critical control points for water use and might be the basis for traits to improve crop water use and response to water deficit.

Mining soybean genetic diversity to identify genetic markers and physiological mechanisms underlying carbon isotope discrimination

Fritschi FB[1], Dhanapal AP[1]*, Sanz-Saez A[1], Naylor B[1], Ray JD[2], Smith JR[2], Purcell L[3], King CA[3]

[1]University of Missouri, Columbia, Missouri, 65211, USA.
[2]USDA-ARS, Stoneville, Mississippi, 38776, USA.
[3]University of Arkansas, Fayetteville, Arkansas 72704, USA.
*E-mail: dhanapala@missouri.edu

Limited water resources can severely reduce soybean (Glycine max) yields on a regional scale and may have devastating effects at the farm level. Soybean genotypes with superior water use efficiency (WUE) may be leveraged to develop cultivars with increased yield under drought. In this research, 373 diverse soybean genotypes were characterized for WUE under field conditions using carbon isotope discrimination (CID)as a surrogate measure. Genome-wide association analyses over four environments revealed 39 SNP markers tagging 21 putative loci. Phenotypic extremes were selected to develop bi-parental mapping populations and for in-depth physiological characterization under manipulated field and controlled environment conditions. Measurements of WUE of phenotypic extremes revealed >1.5-fold difference between low and high CID genotypes. Photosynthesis measurements suggested that stomatal rather than non-stomatal limitations were the primary driver underlying the differences in CID between the extreme phenotypes examined in these experiments. Nonetheless, differences in non-stomatal limitations among genotypes warrant further investigations into both stomatal and non-stomatal limitations of soybean photosynthesis. Thermal image based assessments of canopy temperature depression (CTD) revealed a positive correlation of CTD and CID, indicating that thermal imaging may be useful to identify genotypes differing in WUE. Further research is needed to confirm the genetic markers and evaluate their usefulness for selecting genotypes with increased WUE in soybean. The contrasting genotypes identified in this study offer avenues to develop a more complete understanding of mechanisms contributing to CID in soybean, and to clarify the relationship of CID, WUE, and yield under different environmental conditions.

Introgression of drought tolerance traits into adapted Kenyan chickpea varieties using marker assisted backcrossing (MABC)

Kosgei AJ[1], *,Kimurto PK[2], Gaur PM[3], YeboahMA[4], Offei SK[5], Danquah EY[5], Muriuki RW[2], Thudi M[3] , Varshney RK[3]

[1]Machakos University, Machakos, Kenya
[2]EgertonUniversity, Njoro, Kenya
[3]International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, India
[4]The World Vegetable Center (AVDRC), Messa Yaoundé, Cameroon
[5]West Africa Centre for Crop Improvement (WACCI), University of Ghana, Legon, Ghana
* E-mail: songj.aliz@gmail.com

Drought is the major constraint causing considerable yield reduction in chickpea. Roots play a critical role in enhancing drought tolerance. The main objective of the study was to introgress drought tolerant root traits into Kenyan chickpea varieties through marker assisted breeding (MABC). Eight simple sequence repeat (SSR) markers, linked to quantitative trait loci (QTL) for root and yield traits, were used to screen the parents at ICRISAT, India. In addition, 1144 single nucleotide polymorphic markers (SNPs) were also used in genotyping these parents at Legume Genomics Center, United Kingdom. Crosses were made between two selected varieties, ICCV 92944 (*Chania Desi II*) and ICCV 00108 (*LDT 068*) and *'QTL-hotspot'* donor parent ICC 4958 that has extensive rooting system. Polymorphic SSR and SNP markers were used to select progenies with root QTL at F1, BC1F1 and BC2F1 that were later advanced to BC2F3. The BC2F3 populations were evaluated for root traits at Egerton University in randomized complete block design with two replications in pot experiment. The BC2F3 families were significantly different for root dry weight (RDW), shoot dry weight (SDW), total plant dry weight (PDW) and root to shoot dry weight (R/S) ratio (R/S) for *Chania Desi II* x ICC 4958 and R/S for *LDT 068* x ICC 4958. These lineshad significantly improved root traits compared the recurrent parents. MABC is aneffective and efficient method of introgressing complex drought tolerant traits which leads to improvement in yield especially under drought conditions.

Breeding grapevine for an efficient use of water by lowering night-time transpiration

Coupel-Ledru A[1], Lebon E[1], Christophe A[1], Gallo A[1], Gago P[2], Pantin F[3], Doligez A[1], Simonneau T[1] *

[1]INRA, Montpellier, F-34060, France
[2]MBG-CSIC, 36143 Pontevedra, Spain
[3]Montpellier SupAgro, Montpellier, F-34060, France
*E-mail: audecoupel.ledru@yahoo.fr

In the face of increasing water scarcity, breeding for higher transpiration efficiency (TE), that is, the biomass produced per unit of water transpired, has become crucial. This could be achieved by reducing plant transpiration through a better closure of the stomatal pores at the leaf surface. However, this strategy generally also lowers growth, as stomatal opening is necessary for the capture of atmospheric CO2 that feeds daytime photosynthesis. Here, we considered the reduction in transpiration rate at night (En), when photosynthesis is inactive, as a possible strategy to limit water use without altering growth. We carried out a genetic analysis for En and TE in grapevine, a major crop in drought-prone areas. A 3 year experiment was conducted on the F1 progeny from a cross between Syrah and Grenache cultivars using a phenotyping platform coupled to a controlled-environment chamber, under well-watered and moderate soil water deficit scenarios. High genetic variability was found for En and 5 QTLs were detected. An experiment was also performed outdoors which confirmed the significance of this genetic variability. We further highlighted a major role of residual stomatal opening at night and a minor, yet significant contribution of the cuticle in determining this genetic variability. Strikingly, 4 of the QTLs detected for En co-localized with QTLs for TE. Moreover, genotypes with favourable alleles on these common QTLs exhibited reduced En without altered growth. These original results (Coupel-Ledru et al., PNAS, 2016) open new horizons for breeding crops with lower water loss at night for higher TE.

Stay-green QTL Stg3B is the key QTL associated with improved grain and stover yield under post-rainy sorghum growing conditions

H.S. Talwar[1]*, S.P. Deshpande[2], R. Madhusudhana[1], Shiwesh Kumar[1], V. Vadez[2] and VA Tonapi[1]

[1]ICAR-Indian Institute of Millets Research (ICAR-IIMR), Rajendranagar, Hyderabad, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: talwar@millets.res.in

Stay-green is the best characterized trait contributing to the adaptation of sorghum to postflowering drought conditions. Using B35 as stay-green donor, QTL introgression lines (ILs) were generated in two genetic backgrounds (S35 and R16). These lines along with local checks, recurrent parent and stay-green donor were evaluated in two years during the post-rainy season under both well-watered (WW) and water-stressed (WS) conditions at four locations. Stay-green ILs had improvement in green leaf area retention at maturity (GLAM) in both genetic backgrounds under both WW and WS, and more so under WS condition. R16 was more responsive to the QTL introgression than S35 in terms of GLAM, suggesting that effect of individual stay-green QTL introgression interacted with genetic backgrounds. Stg3B was the key stay-green QTL in enhancing the GLAM, particularly under WS conditions. Under WS conditions, the introgressions with Stg3B improved grain yield (GY) and total dry matter (TDM) by 16% and 9%, respectively over recurrent parent. No improvement in GY and TDM was recorded in ILs compared to recurrent parent under WW conditions in S35 background, while 8% increase in both GY and TDM was recorded under WS conditions with Stg3B introgressions in S35 background. The recipient genetic background and soil moisture conditions during postflowering growth stages played an important role in the expression of stay-green QTLs. Our results, also clearly established the superiority of Stg3B in enhancing the GY and TDM accumulation over other individual QTLs or in combination under both the genetic backgrounds, particularly under WS conditions.

Session V

Plant Productivity under Drought III: Vegetative Growth

Co-chairs

Prof. Lizhong Xiong

Professor
Huazhong Agricultural University
China

Dr. Kailash Chander Bansal

Director
ICAR-NAHEP
India

Dr. Robert E Sharp
University of Missouri,
Columbia, Missouri 65211,
USA
E-mail: sharpr@missouri.edu

Dr. Robert Sharp is a Professor of Plant Sciences and Director of the Interdisciplinary Plant Group at the University of Missouri (MU), USA. He received his Ph.D. from Lancaster University, UK, where he began his studies of plant water stress physiology. After postdoctoral work at the University of Illinois-Urbana, and the University of California-Davis, Dr. Sharp joined the faculty at MU in 1986. His research emphasizes the physiology of plant adaptation to drought, with a primary focus on root growth regulation. Studies have taken advantage of kinematic analyses of spatial patterns of cell expansion, in combination with transcriptome and proteome (cell wall and plasma membrane) analyses, to investigate the complexity and coordination of processes involved in root growth responses to water stress. Current projects include "scaling up" from model seedling systems to address maize nodal root development under drought via an integrated “lab-to-the-field” approach. Dr. Sharp was appointed as Director of the Interdisciplinary Plant Group (IPG, http://ipg.missouri.edu/) in 2011. The IPG is a community of 60 faculty-led teams from across the MU campus, and fosters interdisciplinary and collaborative research and education through community activities including an annual symposium, training programs, and national and international partnerships. Dr. Sharp is a Fellow of the American Association for the Advancement of Science (AAAS) and of the American Society of Plant Biologists.

Physiological controls of maize nodal root growth under drought: a (re)heightened priority

Sharp RE[1]*, Riggs KJ[1], Yamaguchi M[1], Thompson HJ[1], Fritschi FB[1]

[1]University of Missouri, Columbia, Missouri 65211, USA
*E-mail: sharpr@missouri.edu

The nodal roots are essential for development of the mature root system in maize (Zea mays L.) and other grasses. Under drought conditions, nodal roots, which are produced sequentially from multiple stem nodes, may need to grow through dry upper soil to reach available water. Despite early findings that maize nodal roots have a superior ability to continue elongation under water deficits relative to other organs, the physiological controls that determine this ability remain poorly understood. Recent progress in understanding nodal root growth responses to water deficit will be reviewed, using model system approaches and extending to drought conditions in the field. In controlled environment studies, a divided-chamber system was developed to characterize nodal root growth responses to precise variations in soil water potential. Results from these studies show substantial differences in growth sensitivity, both between genotypes and between roots from different nodes, and highlight the importance of hydraulic properties that determine the relation between root growth zone and soil water status. To investigate how nodal roots respond metabolically to water deficits under field conditions, a rainout shelter was used to control the duration and intensity of drought, and the root growth zone was harvested for metabolic profiling. The results reveal both region-specific (within the growth zone) and node-specific (between nodes) patterns of response that provide novel insights into root growth adaptation to water deficits. This knowledge will build a foundation for the long-term goal of developing innovative approaches to improve water capture and crop productivity under water-limiting conditions.

Dr. Boris Parent
INRA-LEPSE,
Montpellier,
France
E-mail: boris.parent@inra.fr

Dr. Boris Parent graduated from INSA Toulouse in 2005 (French engineer school), and obtained a PhD in plant ecophysiology at the LEPSE-INRA laboratory (Montpellier, France) in 2008, with a thesis on leaf development in rice and maize in response to temperature and water deficit. After four years of Post Doctoral Fellowship at ACPFG, (Adelaide, Australia), where he worked on the development of systematic analyses of plant responses to drought and high temperature in wheat and barley, Dr. Parent rejoined the LEPSE-INRA laboratory with a permanent position in 2013. He now focuses on the analysis of the intra- and inter-specific diversity of plant responses to drought and high temperatures, and the modelling of its effect on plant performances in various environmental scenarios. The main idea of Dr. Parent's research project is that genotype by environment interactions (GEI) are emergent properties of simple biological processes which all respond differently to the plant micro-environment. He uses phenotyping platforms, allowing the analysis of responses traits, independent from the environment, on hundreds of genotypes and species. Dr. Parent develops ecophysiological models for several plant processes which are parametrized with platform results. The integration of such ecophysiological models and sets of parameter values in crop models allows testing the comparative advantages of any combination of trait / allele values in hundreds of environments over Europe.

Genetic variability of plant responses to evaporative demand and water deficit, a forward integration from phenotyping to simulation of plant performances in the field

Boris Parent[1]*, Emilie J. Millet[1], Santiago Alvarez Prado[1], Aude Coupel-Ledru[1], Llorenç Cabrera-Bosquet[1], Sēbastien Lacube[1], Claude Welcker[1], Adel Meziane[1], François Tardieu[1]

[1]INRA LEPSE, Montpellier, France
*E-mail: boris.parent@inra.fr

Crop improvement for drought is based on the selection of alleles that increase yield in dry or hot conditions. The Genotype by Environment Interactions (GxE) is typically high in these environments, with alleles conferring either positive or negative effects, depending on drought scenarios (Tardieu, 2012). Rather than trying to over-simplify GxE, for instance, in managed drought experiments, we propose an integrative approach using genome wide association studies (GWAS), phenotyping and modelling. It aims at predicting in which drought scenarios a combination of trait/allele could confer advantages (Parent and Tardieu, 2015). Indeed, (i) we phenotype the intra- and inter-specific variability of development and growth responses to temperature, evaporative demand and water deficit with phenotyping platforms. (ii) We develop ecophysiological models with parameters which can be directly extracted from measurements in platforms and in the field. (iii) We carry out GWAS at different scales, from -omic to plant scale in platform, and to yield components in network of field experiments to identify QTLs linked to conditional allelic effects depending on environmental conditions, and to values of model parameters. (iv) We use either direct measurements or the allelic compositions at target QTLs to determine the phenotypic profiles (set of parameter values) of real or virtual genotypes. (v) We simulate genotypic performance and the contribution of genomic regions under current and future stress situations over Europe via modelling. Results are compared to the observed genetic variability in networks of field experiments and are used as feedbacks for improving our phenotyping routines and ecophysiological models.

Analysing desiccation tolerance using transcriptome and genome sequence information

Dorothea Bartels

University of Bonn, IMBIO, Kirschallee 1, D-53115 Bonn, Germany
E-mail: dbartels@uni-bonn.de

Limited water availability in some areas of the earth has resulted in evolution of mechanisms to live with restricted water supply. The majority of higher plants are unable to survive desiccation to an air-dried state; only seeds or pollen can withstand this condition. However, a small group of vascular angiosperm plants, termed resurrection plants, have evolved unique mechanisms of desiccation tolerance. Resurrection plants can tolerate severe water loss, and mostly adjust their water content with the relative humidity in the environment. The plants grow in ecological niches where rainfall occurs seasonal. Resurrection plants can remain in the desiccated state, comparable to dry seeds. When rainfall occurs, the plants take advantage of the conditions; they resurrect, grow and produce seeds before other species growing from seeds can do so. Our studies are focused on the desiccation tolerant resurrection plant *Craterostigma plantagineum* and the desiccation tolerant grass *Oropetium thomaeum*. Recently the genome sequence of *Oropetium thomaeum* was determined. *Oropetium thomaeum* has the smallest known genome among grasses and shows colinearity to genomes of agricultural relevant grasses such as sorghum or maize. The analyses of comparative transcriptome analyses in resurrection plants and non-tolerant plants will be discussed. We expect that the understanding of desiccation tolerance will provide novel biotechnological targets for improving growth of agricultural plants in environments with water limitations and seasonal rainfall.

Dissection of physiological, genetic, and metabolic traits in two tall fescue genotypes with contrasting drought tolerance

Kang Y[1], Talukder S[1], An Z[2], Torres-Jerez I[1], Saha M[1], Udvardi MK[1]*

[1]The Samuel Roberts Noble Foundation, Ardmore, Oklahoma, USA
[2]Rubber Research Institute(CATAS), Danzhou, Hainan, China
*E-mail:mudvardi@noble.org

Drought is the most prevailing abiotic stress that causes significant crop yield loss world-wide. Tall fescue is an important cool-season perennial forage grass throughout Europe and USA. Under natural conditions, tall fescue usually forms mutualistic symbiotic relationship with endophytes for enhanced biotic and abiotic stress tolerance. In the current study, we aim at revealing the mechanisms underlying different drought sensitivities among tall fescue genotypes, as well as the role of endophytes under drought. Over 1000 tall fescue genotypes were screened, both in the field and the greenhouse, through multiple years; and two genotypes, T400 and S279, with extreme performances under drought were selected. Further greenhouse physiological characterization showed that compared to S279, tolerant genotype T400 has narrower and thicker leaves, longer roots, lower stomata density, and lower shoot water loss rate under both well-watered and drought stress conditions. In addition, leaf cell osmotic pressure increased more in T400 than S279 under drought. Endophyte did not affect shoot growth under drought in either genotype, however, it greatly enhanced root growth in S279, which presumably is beneficial under field drought conditions. In further experiments, root and shoot tissues were collected from well-watered, mildly (soil volumetric water content, VWC, ~10%), moderately (VWC, 5%), and severely (VWC, 1%), drought-stressed plants of both genotypes (with or without endophytes). RNAseq and GC-MS analyses were conducted to reveal genetic and metabolic mechanisms underlying the different responses of these two tall fescue genotypes to drought as well as the role of endophytes under drought stress.

Negative regulation of drought tolerance in rice by jasmonic acid : evidences from physiological traits, root proteome and metabolites

Dhakarey R[1,3], Raorane ML[1,3], Treumann A[2], Preshobha KP[1], Sahi V[1], Schendel R[1], Hause B[4], Henry A[3] , Kohli A[3], Riemann M[1] *

[1]Karlsruhe Institute of Technology, Karlsruhe, Germany
[2]Newcastle University, Newcastle Upon Tyne, United Kingdom
[3]International Rice Research Institute, Los Baños, Philippines
4Leibniz Institute of Plant Biochemistry (IPB), Halle, Germany
*E-mail: michael.riemann@kit.edu

Various adaptive responses of drought stressed plants are strongly influenced by chemical messengers called phytohormones, which regulate the plants growth and development during such adverse conditions. One such important phytohormone is jasmonic acid (JA). Previously, the rice mutant cpm2 was shown to be less sensitive to salt stress. This cpm2 mutant is impaired in the function of allene oxide cyclase (AOC), a key enzyme in JA biosynthesis. In the present study, a targeted approach - at levels of morpho-physiology, proteomics and metabolites - was undertaken to analyze the drought response of cpm2. The mutant had lower stomatal conductance, higher water use efficiency and increased shoot ABA levels under drought as compared to the WT. Importantly, roots of cpm2 were better developed under both control and moderate drought stress. To assess if the roots of cpm2 and WT respond differentially to drought at the molecular level, high-throughput comparative root proteome analysis was performed. AOC was unique to WT and highly abundant under drought, which confirmed the lack of AOC in cpm2. Identification of differentially expressed proteins revealed increased ROS detoxification, more secondary metabolism and cell wall modifications in cpm2 under drought. Metabolite and cytological analysis also revealed differential accumulation of cell wall components in WT and cpm2 roots. These results suggested that JA signaling might negatively influence drought tolerance by orchestrating a block on critical morpho-physiological and molecular changes necessary for stress adaptation. Mutant analysis suggested benefits of blocking JA synthesis might be useful for drought tolerance in rice.

Bridging the generation gap: on the hunt to solve stress tolerance during vegetative and reproductive development

Amal J. Johnston

Laboratory of Germline Genetics & Evo-Devo, Centre for Organismal Studies, University of Heidelberg, Heidelberg, Germany
E-mail: amal.johnston@greentechlab.net; amal.johnston@cos.uni-heidelberg.de

Due to their sessile nature, plants frequently encounter unfavorable growth conditions such as drought, salinity, and extreme light and temperatures. Needless to say, the overall global agricultural productivity is severely constrained by daunting stress conditions, with abiotic stress alone being the primary cause of reduced yield in major crop plants by over 50%. Abiotically stressed plants may suffer cellular oxidative damage due to excess of reactive-oxygen-species (ROS), inhibition of photosynthesis, and dysfunction of metabolism, leading to defective growth and development, reduced fertility, and precocious senescence. Although abiotic stress amelioration starts right from the vegetative phase (sporophytic generation), the importance of germline-specific (gametophytic generation) sink strength and seed/grain-filling under drought has recently received increasing attention. Challenging approaches to understand reproductive development, starting from early female and male germline until late seed development, under stress are certainly complementary to the ongoing approaches of the stress studies on vegetative tissues. By understanding how plants buffer stress across the two major generations, we would gain a holistic view of source-sink relationships, fitness trade-offs underlying stress tolerance, and selective pressures on the stress-regulatory pathways. By studying an essential regulator that controls the entire plant life cycle, we were able to uncover an intriguing mechanism underlying osmotic and drought stress during vegetative and reproductive development in the model plant *Arabidopsis*. I would like to present recent results and insights into an underlying epigenetic memory that faithfully propagates constitutive stress response and stress amelioration, and discuss about the opportunities to transfer this knowledge to agricultural crops.

Session VI

Reproductive Development, Yield, Yield Quality

Co-chairs

Dr. Tony Fischer

Honorary Research Fellow
CSIRO
Australia

Dr. Victor Nwosu

Program Manager
Mars Inc.,
USA

Dr. Lucas Borrás
Universidad Nacional de Rosario,
Campo Experimental Villarino S/N, Zavalla,
S2125ZAA, Prov. de Santa Fe,
Argentina
E-mail: lborras@unr.edu.ar

Dr. Lucas Borrás obtained his PhD at the Universidad de Buenos Aires, Argentina, in 2004. Dr. Borrás is currently Professor at the Universidad Nacional de Rosario, Argentina, and is a scientist at CONICET, the Argentine National Research Council. His research is dedicated to the understanding of yield determination of field crops under different management and environmental conditions, with emphasis on maize, soybean and sorghum. He is part of the editorial board of Crop Science and Field Crops Research.

Maize reproductive development and kernel set under limited plant growth environments

Borrás, L.[1*]

[1]Universidad Nacional de Rosario, Campo Experimental Villarino S/N, Zavalla, S2125ZAA, Prov. de Santa Fe, Argentina.
*E-mail: lborras@unr.edu.ar

Maize grain yield is highly related to the number of kernels that are established during the flowering period. Kernel number depends on ear biomass accumulation and kernel set efficiency (i.e., kernels set per unit ear biomass). Ear growth can be decomposed into the rate of plant biomass accumulation and the proportion of this biomass that is allocated to the ear. In contrast to other major crops, the proportion of plant biomass that maize allocates to the ear is not constant across plant growth rates, being almost zero in stressful situations. Fortunately, there is genetic variability for this trait, with large practical implications for crop management and plant breeding. Because female flower development and silk extrusion are biomass dependent processes, conditions that inhibit plant growth commonly generate delays in silk appearance relative to that of the male flowers. This reproductive synchrony can be used as a marker

Dr. Delphine Fleury
University of Adelaide, Glen Osmond, 5064,
South Australia,
Australia
E-mail: delphine.fleury@acpfg.com.au

Dr. Delphine Fleury completed her PhD in 2001 at the ENSAT (Toulouse, France) and her postdoctoral training in 2005 at the Department of Plant Systems Biology (VIB, Ghent, Belgium). Dr. Fleury joined the Australian Centre for Plant Functional Genomics in Adelaide (Australia) in 2006. She runs the genetics program aiming to improve the tolerance of wheat and barley to drought using quantitative genetics, physiology and omics. Her group particularly focused on the positional cloning of quantitative trait loci increasing yield under low rain-fed environment. She is also co-investigator with the ARC Industrial Transformation Hub linked to Australian breeding companies on genetics diversity and molecular breeding for wheat in a hot and dry climate.

Genetic basis of wheat yield under dry and hot climates

Pauline Thomelin[1], Fabio Arsego[1], Habtamu Tura[1], Melissa Garcia[1], Penny Tricker[1], Paul Eckermann[1], Boris Parent[2], Delphine Fleury[1]

[1]University of Adelaide, Glen Osmond, 5064, South Australia, Australia
[2] INRA LEPSE, Montpellier, 34060, France
*E-mail: delphine.fleury@acpfg.com.au

In Australian dryland agriculture, grain crop yields are approximately 50% of their potential and are highly unpredictable. During the 1990's, the rate of productivity increase in Australian broad acre cropping improved by 3.4% annually but has since slowed and declined by -1.4% in drought years. A way to improve the drought tolerance of crops varieties is to discover new genes and alleles that allow plants to continue to grow and yield grain under water limited conditions. Although many quantitative trait loci (QTL) have been identified in wheat, few have been deployed in breeding programmes.

We cumulated QTL over 10 years on three wheat populations for yield, agronomical, physiological and morphological traits in various locations in Australia, India and Mexico. Genomic resources now enable us make progress in fine mapping and positional cloning of QTL in wheat. Target QTL that increases yield and yield components in hot and dry climates were fine mapped to genes level using the cv Chinese Spring reference sequence and whole genome shotgun sequences of Australian parental lines. We also investigated QTL function under controlled conditions to measure growth rate, transpiration, stomatal traits, and semi-controlled evironments using deep soil bins, rainout shelter and irrigation. By measuring accurately the environmental variables and using ecophysiological models, we can dissect the response to the environment into elementary and simpler traits and identify the conditions where a QTL is specifically expressed. Such detailed information on QTL x environment interaction, physiological mechanism and fine mapping is crucial for breeding application.

Efforts and strategies for alleviation of drought tolerance in chickpea in India

Chaturvedi, SK[1]*, Singh, NP[1], Gaur, PM[2], Mishra, N[1], Das, Alok[1], Sonkar, Sumit[3] and Varshney, RK[2]

[1]ICAR-Indian Institute of Pulses Research, Kanpur 208 024, India
[2]International Crops Research Institute for the semi Arid Tropics, Patancheru 502 324 India
[3] Malviya National Institute of Technology, Jaipur, India
*E-mail: sushilk.chaturvedi@gmail.com

Among the various cool season pulses grown in India, chickpea (*Cicer arietinum* L.) occupies an important position in rainfed agriculture. Chickpea is largely grown (>67% area) on conserved/residual moisture, contributing about 45% to the total pulses production in India. Being a rainfed crop, it often faces terminal drought stress. When chickpea sowing is delayed in fields vacated by paddy in the presence of terminal heat, soil moisture stress further limits its productivity. This necessitates the adoption of suitable strategies to alleviate *per se* drought tolerance in chickpea. Two main strategies, integrated breeding and transgenic technology, have been adopted for developing drought-tolerant varieties. The third potential strategy is utilization of nanotechnology, which has not been tried under Indian NARES. Systematic breeding efforts resulted in development of varieties having *per se* drought tolerance (RSG 44, Vijay, RSG 888, JG 74, Pusa 2024), and escape (JG 11, JG 16, JSC 56, IPC 2006-77 etc.) exploiting earliness. QTLs responsible for drought tolerance have been identified in chickpea genotype ICC 4958, which have been transferred, and drought-tolerant elite breeding lines have been developed. MAGIC and NAM populations combining drought and heat tolerance are now becoming available for identification of elite breeding lines having combined tolerance to both stresses for their possible release. Exploitation of transgenic technology using DREB gene has also shown promise. The use of nano-particles in enhancing root development and growth vigour in chickpea has opened the doors for exploitation of nanotechnology for alleviation of *per se* drought tolerance.

Transgenic and CRISPR Cas approaches to improving the grain yield of maize under drought stress conditions

Habben JE[1]*, Shi J[1], Gao H[1], Lafitte R[1], Hakimi S[1], Weers B[1], Amitabh Mohanty

[1]DuPont Pioneer, Johnston, IA, U.S.A.
*E-mail: jeffrey.habben@pioneer.com

There is a significant challenge to meeting the crop productivity demands for feeding an increasing global population. Lack of sufficient water is a major limiting factor to crop production, and the development of drought-tolerant germplasm is desired. We have used multiple approaches to show that modifying ethylene biosynthesis or signaling can enhance drought tolerance of maize. Initially, we demonstrated that reducing the expression of *ACS6* (a gene that encodes an ethylene biosynthetic protein) by approximately 50% can increase grain yield under field drought stress conditions. Subsequently, we discovered a family of novel negative regulators of ethylene signal transduction in *Arabidopsis* and maize. These regulators are encoded by the *ARGOS* gene family, and in transgenic plants over-expression of ARGOS genes reduces ethylene sensitivity. Field testing showed that ARGOS8 maize transgenic events had a greater grain yield relative to controls under both drought-stress and well-watered conditions.We then employed a CRISPR-Cas-enabled advanced breeding technology to generate novel variants of ARGOS8. The native maize GOS2 promoter, which confers a moderate level of constitutive expression, was inserted into the 5′-untranslated region of the native ARGOS8 gene or was used to replace the native promoter of ARGOS8. A field study showed that relative to the comparator, the ARGOS8 variants increased grain yield by five bushels per acre under flowering-stress conditions and had no yield loss under well-watered conditions. We believe that continued advancement in our understanding of the key biological processes in maize will enable significant improvements in crop productivity.

Elaborating a unique regulon for rice yield under drought: component genes underpin or are affected by transcriptional, post-translational, biochemical and epigenetic mechanisms

Kohli A[1]*, Longkumer T[1], Raorane M[1],[2], Oane RH[1], Pabuayon IM[1],[3], Pandey A[1],[4], Trinidad J[1], Gotrakar D[1], Serafin-Lozada L[1],[5], Varthini V[1], Yamamoto N[1], Miro B[1], Mahdi S[1], Sabariappan R[6], Kapoor S[7], Hsing YIC[8], Henry A[1], Kumar A[1]

[1]International Rice Research Institute, Manila, 1226, Philippines
[2]Karlsruhe Institute of Technology, Karlsruhe, 76133, Germany
[3]Texas Tech University, Lubbock, Texas, 79409-2122, USA
[4]Pohang University of Science and Technology, Pohang, South Korea
[5]University of Philippines Los Banos, Laguna, 4031, Philippines
[6]Tamil Nadu Agricultural University, Coimbatore, 641003, India
[7]University of Delhi South Campus, New Delhi, 110021, India
[8]IPMB, Academia Sinica, Nankang, Taipei 11529, Taiwan
E-mail: a.kohli@irri.org

A limited number of regulons have been characterized in the eukaryotes. Similarly, limited information exists on characterization of large-effect QTLs (LEQ). We recently suggested that an LEQ for rice yield under drought was composed of multiple genes that were necessary for its full impact, and which functioned in a manner similar to that of a regulon. Here we report characterization of four of the nine essential genes at this locus. Each of the four genes highlights a separate component of the complex panoply of regulatory mechanisms at play in response to drought stress. One of the genes is a transcription factor. It regulates two downstream target genes in *cis*. One, an amidohydrolase, modulates the epigenome, and other, a phosphodiesterase. affects critical biochemical components in the reproductive organs. The fourth gene, a kinase, potentially affects transcriptional splice variants. In parallel, the transcription factor is differentially SUMOylated under drought and this post-translational modification potentially alters the genes regulated by the transcription factor. Transcriptomics, proteomics and metabolomics-mediated analyses of a near isogenic line (NIL) containing the LEQ reveal novel features and present a holistic overview, captured by its unique regulon like gene content, on the plants' response to drought stress. The LEQ is already part of rice varieties released for drought tolerance. Dissection of the molecular mechanisms in breeding lines generated through molecular genetics is useful because markers/genes can be easily tracked. The molecular genetics and molecular biology interface generates field-relevant, and gene and/or mechanism-based data that is robust and dependable for other varieties/crops.

Exploring QTLxE in a network of fields: identification of QTLs associated with scenarios of heat and drought for predicting yields in future climates

Millet E[1], Kruijer W[2], Nicolas S[3], Coupel-Ledru A[1], Charcosset A[3], Van Eeuwijk F[2], Tardieu F[1], Welcker C[1]*

[1]INRA Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux, IBIP,34060, Montpellier,France
[2]WUR, Biometrics-Applied Statistics, Department of Plant Science, Wageningen, Netherlands
[3]INRA Génétique Quantitative etEvolution, 91190 Gif-sur-Yvette, France
E-mail :claude.welcker@inra.fr

Genetic analysis of tolerance to climate change is hampered by climatic variability that generates GxE interactions depending on the timing and intensity of water or heat stresses. We have performed a genome-wide analysis of yield in 29 fields over Europe, with irrigated and rainfed treatments in each location. Six scenarios of heat and drought were first identified by clustering observations over 60 European sites x 35 years. A detailed environmental characterisation was carried out in all experiments, which were ascribed to environmental scenarios. A panel of 244 maize hybrids genotyped with 832K polymorphic SNPs was analysed in these experiments, together with a characterization of phenology in a phenotyping platform. We have first identified by GWAS genomic regions (QTLs) associated with grain yield. Nearly all QTLs had scenario-dependent allelic effects, with positive, negative or null effects depending on heat/drought scenarios. Second, by combining information coming from the field and the platform, we have estimated the responses of yield components to environmental conditions via regression analysis over the whole dataset. We have identified in this way massive effects of temperature and water deficit at flowering time, and of intercepted light during the vegetative stage. The slopes of these responses largely differed between hybrids and were dissected into QTLs. A model combining environmental conditions with QTL of responses accounted for 72% of the variance of yield, including in eight new experiments. This work, therefore, allows prediction of genotypes to cope with climate changes. (*Millet et al 2016, Plant Physiology 72:1).*

Molecular genetic analysis of root system architecture and drought tolerance in soybean

Valliyodan B[1]*, Prince S[1], Murphy M[1], Ye H[1], Song L[1], Nguyen HT[1]

[1]University of Missouri, Columbia, 65211, Missouri, United States of America
*E-mail: valliyodanb@missouri.edu

Continuous climate changes cause irregular precipitation patterns worldwide, which is leading to more frequent drought events and consequent reduction in crop production. Root system architectures (RSA) are quantitative traits determined by polygenes and affected by growing environments. Developing a better root system is a promising strategy to improve crop productivity under optimum and stress environments. In soybean, promising germplasm accessions have been identified for extensive fibrous rooting, increased root length, or varied root angle under drought stress. Examination of the root anatomy of 41 soybean lines showed a number of metaxylem elements in roots to be correlated with drought tolerance in soybean. Promising lines with larger numbers of metaxylem elements under drought were identified as a potential donor source for drought tolerance breeding. Currently, eight QTL/QTL-clusters have been mapped to regulate root length, fibrous rooting/lateral-root number, or root thickness. One gene, *Glycine-Lateral-Root-1* (*GLR1*) was identified from a GWAS using a core set of 397 diverse lines and the rare alleles (0.5%) of this locus was found to increase lateral root number by regulating cortex cell shape and size. The *GLR1* encodes a protein with unknown function and its role in regulating lateral root growth was confirmed by transgenic soybean hairy root system. Soybean accessions with the rare allele were found to produce better root system and plant performance under water limited and optimal field conditions. These findings are expected to provide genetic and genomic resources for soybean productivity under drought, through the modification of RSA.

Session VII

Breeding for Water-Limited Environments

Co-chairs

Prof. Kadambot Siddique

Hackett Professor of Agriculture Chair and Director
UWA Institute of Agriculture
The University of Western Australia
Australia

Dr. Shiv Kimothi

Assistant Director General
Indian Council of agricultural Research
India

Dr. Lijun Luo
Shanghai Agrobiological Gene Center,
Shanghai 201106,
China
E-mail: lijun@sagc.org.cn

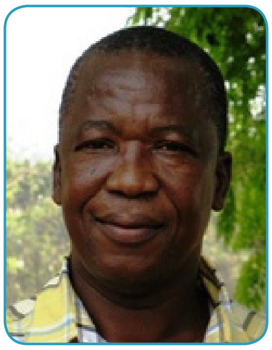
Dr. Lijun Luo is director and principal scientist at Shanghai Agrobiological Gene Center, China. He is involved in the development of drought resistance evaluation standards, germplasm identification, phenotyping in field conditions, QTL mapping and candidate gene discovery, functional genomics, and breeding for drought resistance of rice. Dr. Lijun has proposed a new strategies on developing water-saving and drought- resistance rice(WDR) and released a number of WDR (both inbred and hybrid) that are currently grown by farmers in China and several Asian and African countries.

The definition and development of water-saving and drought-resistance rice (WDR)

Luo LJ[1]

[1]Shanghai Agrobiological Gene Center, Shanghai 201106, China
*E-mail: lijun@sagc.org.cn

Upland and lowland rice (*Oryza sativa L*) are two of the most important rice ecotypes adapted to ago-ecosystems with contrasting soil-water conditions. Upland rice, domesticated in the water –limited environment, contains valuable drought-resistant characters, but has been less applied in rice breeding programs. Water-saving and drought-resistance rice (WDR) is defined as new type of rice variety which has both high yield potential and good quality as the current irrigated rice, as well as the capacity of water-saving and drought resistance as the upland rice. There is abundant genetic diversity on DR performance in rice germplasm resources. Based on the scientific evaluation in the field, several elite DR germplasm were identified and used in genetic and molecular studies as well as in breeding programs. More than 100 drought resistant candidate genes were cloned and studied on its functional genomes. Drought resistant CMS lines and several WDR varieties were developed and released to the farmers, and they demonstrated significant water saving and drought resistant ability in farmer's field in recent years. The whole-genome sequencing and transcriptome analyses indicated that there are obvious genomic variations between WDR and its upland (or lowland) parents. Conventional breeding actually can effectively integrate different drought resistant genes and its interacting networks.



Dr. Niaba Teme
Institut d'Economie Rurale du Mali,
BP 258, Rue Mohamed V,
Bamako,
Mali
E-mail: niabateme@gmail.com

Dr. Niaba Teme is a specialist in sorghum lines and hybrid development at the Institute of Rural Economy (IER), Bamako, Mali. He was a senior technician from 1980 to 1995. He earned his PhD in 2006 at the University of Texas Tech, Texas, specializing in plant breeding. Since 2010, Dr. Teme has been running the IER Biotechnology Laboratory and has been an active member of the Consultative Group on Biotechnology (CGB) with the aim to inform civil society, government employees and other activists on biotechnology issues. To date, Niaba Teme has implemented several projects on sorghum, the first being a pilot study on dual-purpose sorghum to improve cattle milk production during dry season in central Mali.

He further implemented two projects funded by the Generation Challenge Program (GCP), MARS and BCNAM, to boost sorghum grain yield and quality in Western African countries.

The fourth one was a "Production Marketing" project that aimed at improving farmer yield and income through sustainable intensive production and marketing. The fifth project (BIOSORG) concerned the assessment of the industrial, feed and food quality of sorghum. And the latest project focused on identifying sorghum lines for enhanced heterosis under sustainable intensification for food and feed.

Beside his main professional tasks, Dr. Teme is currently supervising and examining theses from the University of Bamako and the West Africa Center for Crop Improvement (WACCI), from the University of Ghana. His next undertaking will be on the assessment of allelic diversity of economically valuable millet, sorghum, rice in order for breeders to handle diversified and limited numbers of varieties per species.

Dr. Teme's entire professional career has been devoted to sorghum breeding. He therefore strongly believes that he can make a difference in getting this job done.

Climate-resilient sorghum breeding in West Africa Sudano-Sahelian environments

Niaba Teme[1]*, Mohamed Lamine Tēkētē[1], Salifou Sissoko[1], Mamoutou Kouressy[1], Michel Vaksmann[2], Karim Dagno[1], Jean François Rami[2], Baptiste Guiton[2], Korotimi Thera[1], Abdoulaye G. Diallo[1], Sidi B. Coulibaly[1], Mamourou Diourtē[1]

1Institut d'Economie Rurale du Mali, BP 258, Rue Mohamed V, Bamako, Mali.
2La Recherche Agronomique pour le Développement. Avenue Agropolis, 34398 Montpellier Cedex 5 France
*E-mail: niabateme@gmail.com

Rainfed sorghum production in West Africa semi-arid environments depends largely on rainfall patterns, which vary strongly both geographically and between years. The most important adaptation trait of sorghum to climate variability is photoperiod sensitivity which instigates flowering towards rainy season end regardless of sowing date. This trait adjusts vegetative duration phase according to biotic and abiotic stresses. Varieties maturing before rainy season end are extremely susceptible to insect attacks, grain molds and bird damages. Variety flowering beyond end of rainy season faces terminal drought risks. Consequently, producers still crop mostly photoperiod sensitive varieties with early planting yield increase.

Photoperiod sensitivity was eliminated by most sorghum breeders to develop early maturing varieties with a broader adaptation for temperate zone and drought escape in Africa. This approach was not fruitful as the problem is not short cropping season but its variability in both time and space. Evidence is now that simultaneous improvement of yield, production, stability and grain quality requires the development of photoperiod-sensitive varieties.

BCNAM and MARS sorghum populations, developed by IER, include 3600 backcross lines derived from 23 donors and 2 recurrent parents. These populations were genotyped and phenotyped. Genetic analysis focused on photoperiod sensitivity, yield components, grain quality, feeding value and resistance to foliar diseases.

Understanding sorghum flowering genetic regulation makes it possible to implement new breeding options based on adaptation to climate variability, and to climate change scenarios. Photoperiod-sensitive varieties with high and stable yields, tolerating delayed planting are being developed to mitigate late season drought and biotic stresses.

Dr. H.E. Shashidhar
Genetics and Plant Breeding,
University of Agricultural Sciences, Bangalore,
India
E-mail: heshashidhar@gmail.com; heshashidhar@rediffmail.com

Dr. H E Shashidhar is a Professor of Genetics and Plant Breeding at University of Agricultural Sciences, Bangalore. He has worked on saving water for rice cultivation while maintaining the yield potential and enhancing the nutritive value of grains. Studies on root morphological traits in germplasm accessions, mapping populations, isogenic and near-isogenic lines contributed to elucidating the molecular genetics of the traits, identification of molecular markers and quantitative trait loci linked to root traits and yield. Desirable roots traits, which influence whole-plant architecture, grain and water productivity, were used to maximize access to soil moisture at all stages of plant growth. Direct seeding and maintaining soil under aerobic condition was found to impact plant growth rate positively due to the altered soil biogeochemistry, and micro-flora, thus enhancing water productivity, and enhanced zinc and iron in polished rice. The holistic approach based on budgeting of water during the process of selecting for roots, biomass and productivity among segregants and simultaneous selections while forwarding generations in the target habitats led to Dr. Shashidhar's success.

The work resulted in ARB 6, an eco-friendly aerobic rice variety. Mechanized direct seeding of only six kilograms seeds per acre in well-spaced rows and no impound water at any stage of crop resulted in saving water, labor, fertilizer, enhancing productivity and profits. In collaboration with University of Bangor, UK and Birsa Agricultural University, Bihar, marker-assisted selection and QTL introgression from Kalinga III resulted in another rice variety performing exceedingly well in rainfed uplands of Bihar and Nepal.

Success stories in rice breeding for drought tolerance in India

H E Shashidhar

Genetics and Plant Breeding, University of Agricultural Sciences, Bangalore, India
E-mail: heshashidhar@gmail.com

Breeding for drought tolerance is a challenging but highly effective strategy to enable crops to not only survive stress, but also help in getting higher yield and better grain from progressively depleting resources. Historically, natural selection has succeeded in accumulating genes (in the form of unique germplasm accessions) with ability to survive multiple and severe stresses. These manifest as much valued local adaptability, a trait that has coevolved with the environment. This is true of other crops of Indian origin too. It is because of this that there are many success stories for drought tolerance breeding across crops in India. Some noteworthy examples of drought tolerance are N22, Kalinga-3, Devamallige, Budda in rice; M35-1 in sorghum. Discovery new traits, genes and alleles is common. Some of the traditional crops such as millets are known to be innately drought tolerant. In rice conventional breeding for drought tolerance has resulted in ARB 6 aerobic rice variety with high degree of tolerance to low-moisture stress. High yielding trait from the male parent was superimposed/introgressed onto deep rooting trait of a local female parent. Similar stories are seen in the use of Ashoka 200F, Ashoka 228 based on Kalinga 3 (Birsa Agricultural University, Ranchi), R-RF 75 based on Dagaddesi and other accessions (IGKVV, Raipur), IR74731 series from IRRI breeding programs across India, PKM 1, PKM2 (TNAU, Coimbatore) and MAS 26 & 94-1 (UAS,B). While success has been forthcoming, the potential and source of future improvements in drought tolerance will be discussed.

Genetic control of nodal root angle is associated with drought tolerance in sorghum

Singh V[1]*, van Oosterom EJ[1], Joshi DC[1], Jordan DR[2], Mace ES[3], Hammer GL[1]

[1]The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, QLD 4072, Australia
[2]The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Warwick QLD, Australia
[3]Department of Agriculture and Fisheries, Hermitage Research Facility, Warwick, QLD, Australia
*E-mail: v.singh@uq.edu.au

Genetic improvement of drought resistance in sorghum is essential to enhancing production under water-limiting environments. Recent research has demonstrated that the angle of the first flush of nodal roots is a key determinant of spatial patterns of water acquisition and can improve drought adaptation. Here we summarise studies on the genetic control of nodal root angle in sorghum seedlings and its effects on water extraction of mature plants. Phenotyping for nodal root angle in small soil-filled chambers indicated extensive genetic variation (15°-50°). Selected lines with contrasting root angle were grown in large soil-filled chambers to assess differences in root distribution patterns and water extraction patterns of mature plants. Lines with narrow root angle and a more vertical root distribution extracted more water from depth. Further phenotyping and genotyping of a mapping population identified four QTLs for nodal root angle, which explained 58.2% of phenotypic variance. These QTLs co-located with QTLs for stay green and were correlated with grain yield from breeding trials. Preliminary modelling of this effect on water extraction indicated significant yield advantage in many Australian sorghum production environments. This research suggests that nodal root angle can be used as a selection criterion in sorghum breeding to improve drought adaptation. A high-throughput phenotyping platform has been developed to phenotype sorghum mapping populations for nodal root angle to elucidate the underlying genetic architecture of the trait. It is anticipated that the results will support molecular breeding for drought adaptation by manipulation of root traits.

Drought tolerant cowpea lines derived through Marker Assisted Recurrent Selection

Boukar O[1]*, Belko N[1], Fatokun C[2], Close TJ[3], Roberts PA[3], Huynh B-L[3], Moukoumbi Y[1], Chamarthi S[1], Togola A[1]

[1]International Institute of Tropical Agriculture (IITA), Kano, Nigeria
[2]International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
[3]University of California, Riverside, California, United States of America
* E-mail: o.boukar@cgiar.org

Cowpea, Vigna unguiculata (L) Walp, contributes significantly to the livelihood of millions of people in Sub Saharan Africa (SSA). The relatively high protein and micronutrient (Fe, Zn) contents of its grain ensure a nutritionally balanced diet for consumers in both urban and rural communities. Cowpea haulms are also used as quality fodder for animals. Farmers in SSA get substantial income from the production of cowpea grain and fodder despite the low productivity of the crop due to several stress factors. Drought is one of the constraints that limit the production of cowpea considerably, despite its relatively better adaptation to drought-prone agro-ecologies compared to many crops. The main objective of cowpea breeding under the Tropical Legumes I project was to develop high-yielding, drought-tolerant lines using Marker-Assisted Recurrent Selection (MARS). To this end, two elite lines (IT84S-2246 and IT98K-1111-1), were selected and crossed to generate 298 F2:3 families. These families were phenotyped in two agro-ecologies and a total of 110 SNPs polymorphic between the two parents and distributed at an average of every 2 cM intervals on the genetic linkage map were used to genotype the 298 families. Two and five QTLs associated with grain yield and stay green characteristics under drought respectively were identified. A total of 177 genotypes fixed for all the favorable alleles at the seven QTLs have been derived. Field evaluations of these lines were conducted and those with good agro-physiological performance have been selected for potential release as new varieties.

Chickpea breeding for water-limited environments

Pooran M Gaur[1]*, Srinivasan Samineni[1], Mahendar Thudi[1], Sobhan B Sajja[1], Sushil K Chaturvedi[2], Veera Jayalakshmi[3], Anita Babbar[4], M Yasin[5], DM Mannur[6], AG Vijaykumar[7],Rajeev K Varshney[1], GP Dixit[2]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru, Hyderabad 502 324, India
[2]ICAR-Indian Institute of Pulses Research (IIPR), Kanpur 208 024, India
[3]ANGRAU Regional Agricultural Research Station, Nandyal518 502, AP, India
[4]Jawarharlal Nehru KrishiVishwaVidyalaya (JNKVV), Jabalpur 482 004, India
[5]RVSKVV-RAK College of Agriculture, Sehore 466 001, Madhya Pradesh, India
[6]UAS-Raichur Agricultural Research Station, Gulbarga 585 101, Karnataka, India
[7]UAS-Dharwad Regional Agricultural Research Station, Bijapur 586 101, Karnataka, India
*E-mail: p.gaur@cgiar.org

Chickpea (*Cicer arietinum* L.) is a dry season food legume and is largely grown on residual soil moisture after the rainy season. The crop often experiences moisture stress towards the end of the crop season (terminal drought). The crop may also face heat stress at the reproductive stage, if sowing is delayed. The increasing climate variability, reflected in wide fluctuations in temperatures and rainfall, is further aggravating risks of terminal drought and heat stresses to chickpea crop, particularly in the semi-arid tropics (SAT). The genetic approaches being used for managing terminal drought and heat stresses include development of varieties with early maturity and enhanced tolerance to these stresses. Excellent progress has been made in the development of early maturing varieties with high yield potential, which helped in bringing additional area under cultivation and enhancing productivity of chickpea in short-season SAT environments. Several varieties with improved drought tolerance have been developed by the classical approach of selecting for grain yield under moisture stress conditions. Similarly, selection for pod set in the crop, subjected to reproductive stage heat stress by delayed planting, has helped in development of heat-tolerant varieties. A genomic region called "QTL-hot spot", which controls a number of drought tolerance traits including root traits, has been introgressed into several popular cultivars using marker-assisted backcrossing (MABC); and introgression lines giving significantly higher yield than the popular cultivars under moisture stress conditions have been identified. Multi-parent advanced generation inter-cross (MAGIC) approach has been found promising in enhancing genetic recombination and developing lines with enhanced tolerance to terminal drought and heat stresses. Integrated breeding approaches involving, particularly, genomic tools, precision phenotyping, and rapid generation turnover techniques, have improved efficiency of chickpea breeding programs in developing varieties better adapted to water limited environments.

Wheat (*Triticum aestivum* L.) genotypes present high variability of stem carbohydrates and differences in the expression of genes regulating fructan metabolism under contrasting water regimes

del Pozo A[1]*, Yáñez A[2], Tapia G[3], Guerra F[4]

[1]Centro Mejoramiento y Fenómica, Facultad de Ciencias Agrarias, Universidad de Talca, Talca, Chile.
[2]Departamento de Ciencias Agrarias, Facultad de Ciencias Agrarias y Forestales, Universidad Católica del Maule, Curicó, Chile
[3]CRI-Quilamapu, Instituto de Investigaciones Agropecuarias, Chillán, Chile
[4]Instituto de Ciencias Biológicas, Universidad de Talca, Casilla 747, Talca, Chile
*E-mail: adelpozo@utalca.cl

The genetic and physiological mechanisms underlying the relationship between water-soluble carbohydrates (WSC) and water stress tolerance were investigated. The genotypic variability of stem weight, stem water-soluble carbohydrate content, grain yield (GY) and other agronomical traits was evaluated in a large collection of 384 wheat genotypes grown in field conditions under water stress, mild water stress and fully irrigated. Also, the dynamics of the main WSCs in stems, and the expression of genes involved in fructan metabolism were evaluated in water stress tolerant and susceptible genotypes, grown in a glasshouse under water stress (WS; 50% field capacity from heading) and fully irrigated (FI; 100% field capacity) conditions. The WSC content at anthesis presented a negative correlation with spikes per square meter, but a positive correlation with kernel per spike and grain weight. Consequently, the relationships between WSC content with GY were low or not significant in the three water regimes. In the glasshouse, the stress-tolerant genotype exhibited higher concentrations of WSCs, glucose, fructose and fructan in the stems, compared to FI. In addition, the stress-tolerant genotype exhibited higher up-regulation of the fructan 1-fructosyltransferase B (1-FFTB) and fructan 1-exohydrolase w2 (1-FEHw2) genes, whereas the susceptible cultivar presented an up-regulation of the fructan 6-fructosyltransferase (6-SFT) and fructan 1-exohydrolase w3 (1-FEHw3) genes. Our results indicated clear differences in the pattern of WSC accumulation and the expression of genes regulating fructan metabolism between the tolerant and susceptible genotypes.

Legume breeding and seed systems for improved livelihoods and impact

E S Monyo[1]*, H Desmae[2], O Boukar[3], C Mukankusi[4], P Gaur[5], P Okori[6], B Motagi[7], H Ajeigbe[7], C Fatokun[3], Y Moukumbi[3], A Kamara[3], L Omoigui[3], A Arega[8], K Mausch[1], R Bodo[7], S Beebe[9], C Ojiewo[10], J Rubyogo[11], E Akpo[1], R K Varshney[5]

[1]ICRISAT Nairobi
[2]ICRISAT Bamako
[3]IITA Kano,
[4]CIAT Kampala,
[5]ICRISAT India
[6]ICRISAT Malawi
[7]ICRISAT Kano
[8]IITA Malawi
[9]CIAT Colombia
[10]ICRISAT Addis Ababa
[11]CIAT Arusha
*E-mail: e.monyo@cgiar.org

The Tropical Legumes III project aims to reduce food insecurity in drought-prone areas of Sub Saharan Africa (SSA) and South Asia (SA), through improved productivity and production of four major grain legumes – chickpea, common bean, cowpea and groundnut. This is being sone by conducting research under three complementary research and delivery pillars: support for the development and release of farmer-preferred varieties; strengthening of the legume breeding capacity of partner CGIAR centers (ICRISAT, IITA and CIAT), and national partners Burkina Faso, Ghana, Mali, Nigeria, Ethiopia, Tanzania and Uganda; and establishment of sustainable seed delivery systems that service the needs of small-holderfarmers. Significant achievements have been recorded. Breeding program assessments have been completed in all countries and improvement plans developed for execution. New seed varieties (163) have been released and are fast replacing the old ruling seed varieties in all target countries. Thirty seven national partners were trained at MSc and PhD levels. As a result of the enhanced skills and knowledge of seed value chain actors, seed production significantly increased by 221% (from 139,048 to 446,359 tons) in seven years. Since 2007, improved varieties have been adopted on at least 2 million hectares and more than $448 million has been generated from the project funding and nearly $976 million from the project and investment partners. For each dollar invested, the project generated $9 with direct project investment or $20 with partnership's investment, and again $20 when using adoption rate based estimate. These achievements and implementation challenges will be discussed.

Session VIII

Agronomic Management/Cropping Systems for Water-Limited Environments, Broad Approaches

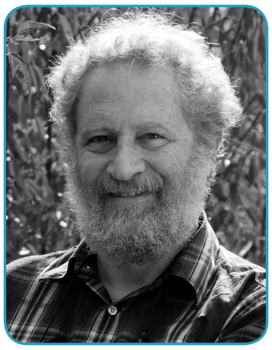
Co-chairs

Dr. Steve L. Brown

Executive Director
The Peanut Foundation
USA

Dr. Anthony Michael Whitbread

Research Program Director-ISD
ICRISAT
India



Dr. Victor Sadras
Principal Crop Ecophysiologist,
South Australian Research & Development Institute,
Adelaide,
Australia
E-mail: Victor.Sadras@sa.gov.au

Dr. Victor Sadras is the Principal Crop Ecophysiologist with the South Australian Research & Development Institute. His research interest is the adaptation of crops to environmental stresses, including water deficit, extreme temperatures, nutrient deficit, soil physical and chemical constraints (e.g. compaction, salinity), pathogens and insects. He has measured and modelled aspects of the water, carbon and nitrogen economies of annual and perennial crops in rain-fed and irrigated systems of Australia, Argentina, Spain and China. He is co-editor in chief of Field Crops Research, and associated editor of Crop and Pasture Science, and Irrigation Science.

Understanding and quantifying the drivers of yield under drought and yield potential

Victor Sadras

South Australian Research and Development Institute, Adelaide, Australia
E-mail: Victor.Sadras@sa.gov.au

Dryland farming in low rainfall environments is a risky business. A common strategy in Australian farms combines approaches to reduce financial losses in dry seasons, and the ability to capture the benefits of wetter seasons. Improved adaptation to drought must therefore consider and avoid trade-offs with yield potential.

Yield depends on the technology used to establish, protect, grow and harvest the crop, the environment where it is grown, and the interaction between environment and technology. In the short to medium term (5-10 years), the environment over-rides technology. In the long-term (decades), technology increases yield, whereas the environment contributes to often significant deviations around time trends. Despite its importance, the environment is often characterised superficially, e.g. nominally as location and season. In this paper, we quantify and compare the drought environments for wheat, field pea and chickpea in Australia, and their implications for crop improvement and management.

The GxE interaction is biologically interesting and agronomically important, as it is often a large component of the phenotypic variance of crop yield. Using an approach based on phenotypic plasticity, we untangle GxE interactions, including trade-offs between yield potential and yield under drought, and challenge the notion that “yield stability” is a desirable trait. Combining a plasticity perspective with Fst genome scan, we show genetic profiles associated with phenotypic plasticity of yield, nitrogen fixation and carbon isotope discrimination of chickpea crops in diverse water and thermal regimes.

We conclude with an update of level of organisation and scaling advanced in Intedrought-IV (JXB 65, 1981), reinforcing the notion that grain yield is primarily a population rather than a plant-level trait. Natural selection favours competitive plants whereas selection for seed yield in agriculture favours less competitive types, which conform to the phenotype of Donald’s “communal plant”.Experiments in chickpea showed high-yielding lines are less responsive to competition, in agreement with Donald’s theory and Fst genome scan highlights the lack overlap in the genetic architecture underlying yield of crop stands and yield under relaxed competition. The impact of plant-plant interactions is further illustrated in sunflower, where self-organisation of stands mediated by light quality is shown to increase oil production per unit land area.

Dr. Esteban Jobbágy
Grupo de Estudios Ambientales, CONICET
San Luis,
Argentina
E-mail: jobbagy@gmail.com

Dr. Esteban Jobbágy is a Principal Researcher in CONICET and Universidad Nacional de San Luis – Argentina. His research focuses on the reciprocal interactions between managed ecosystems (including crops, pastures, and tree plantations) and the hydrological system. Coupling between crops and shallow water tables; salinization processes; and farmer responses to drought and water availability fluctuations are some of the main themes of his current research. Dr. Jobbágy leads the GEA team of fifteen researchers settled in San Luis, on the semiarid edge of the Pampas.

Pushing rain-fed agriculture towards aridity: success and surprise in the plains of Argentina

Jobbagy EG[1]*, Baldi G[1], Gimenez R[1], Magliano P[1], Mercau JL[1], Murray F[1], Nosetto MD[1], Paez R[1]

[1]Grupo de Estudios Ambientales - IMASL, Universidad Nacional de San Luis & CONICET. San Luis (5700) Argentina
*E-mail: obbagy@gmail.com

How far into aridity is rain-fed agriculture feasible, profitable and sustainable? What technological breakthroughs support its dry migration? Answers are sought for the semiarid plains of Argentina, where extensive farming systems coined in humid environments are currently approaching an edge of 500 mm/yr. Compared to similar climatic zones, these farming systems are characterized by relative low inputs (very low fertilization, nil irrigation, N-fixing crop dominance), intermediate cultivation intensity (1.2 crops/year vs. 1.7 and 0.8 in India and Australia), and high individual crop yields (2.3 tons/crop vs. 2.0 and 1.7 in India and Australia). The above-ground NPP of farming systems declines linearly with aridity, matching the levels of pastures and woodlands for soybean and doubling them it for maize. No-till schemes combined with GMO weed/plague control were critical in improving the water economy of these systems. Bare soil evaporation rates dropped 6-fold under typical crop litter stocks vs. 2-fold drops under closed native forest canopies subject to grazing. Late sowing (up to 2-month after rainy season start), made feasible by herbicide/insect resistant crops, warranted moisture accumulation and water/heat stress risk reduction. As these systems expand and age, new problems emerge, such as the exponential rise of herbicide-resistant weeds and the onset of water logging and salinization driven by raising water tables. More adaptative crop cycles, deeper roots and salt/water logging tolerance combined with the use of opportunistic cover crops for deep drainage prevention, litter build-up, and weed control are needed.

Prof. Elias Fereres
Institute for Sustainable Agriculture-CSIC and
University of Cordoba, Cordoba, Spain
E-mail: ag1fecae@uco.es

Elias' professional area of expertise is centred on the sustainability of water-limited agriculture and on the role of water in agriculture and the environment. Research activities during his career included topics such as irrigation water management, deficit irrigation strategies, efficient use of limited water supplies in drought situations, optimization of agrcultural water use, modelling attainable yields, crop productivity as affected by water, water management at different scales, agriculture-environment interactions, and soil and water conservation, He is currently professor in the School of Agricultural and Forestry Engineering, University of Córdoba, Spain, and researcher at the Institute of Sustainable Agriculture, Scientific Research Council of Spain (IAS-CSIC). Co-author of the FAO publication I&D66 on crop yield response to water, and of the AquaCrop simulation model. Formerly a member of TAC of the CGIAR, he is a member of the Royal Academy of Engineering of Spain and of the Aademia Europaea. Currently, he is the Chief Editor of the journal Irrigation Science.

Irrigation strategies coupled with genotypes

Steduto P.[1]*, Fereres E.[2]

[1]FAO (Food and Agriculture Organization of the United Nations), Cairo, Egypt
[2]IAS-CSIC and University of Cordoba, Cordoba, Spain
*E-mail: pasquale.steduto@fao.org

Increased water scarcity suggests that, in the future, limited water for irrigation will be the norm rather than the exception. Limited irrigation will impose water deficits on crops resulting in yields which are lower than those obtained under unlimited water supply. Stress management via deficit irrigation may result in minimizing yield losses, but achievement of maximum crop productivity and farm profits under such conditions requires solving an optimization problem at different temporal and spatial scales. The problem is multidimensional but optimizing the use of different genotypes is one important component of the solution. Simulation models are essential tools to help solve this problem. Once the water supply constraint is known, genotype selection may be optimized by simulating the differential responses of all cultivars available to farmers. The same approach could assist breeders and agronomists to identify useful strategies for cultivar selection under limited irrigation. Important traits that could be optimized include the joint increase in carbon assimilation and water use efficiency by optimizing the response to VPD, the maintenance of harvest index by controlling the level of water deficit, and the manipulation of plant development to take advantage of high rainfall and/or low VPD periods, and to avoid severe water deficits. Future climate change scenarios will be explored to design optimal genotypes for use under the various irrigation strategies that are emerging in water-limited environments.

Rainfall, soil sand content, and depth of soil compaction predominantly affect rice yield reduction by reproductive-stage drought at varietal screening sites in Bangladesh, India, and Nepal

Suresh Prasad Singh[1], Abhinav Jain[2], M.S. Anantha[3], Santosh Tripathi[4], Subarna Sharma[4], Santosh Kumar[5], Archana Prasad[6], Bhawana Sharma[6], Biswajit Karmakar[7], Rudra Bhattarai[8], Sankar Prasad Das[9], Shravan K. Singh[10], Vinay Shenoy[2], R. Chandra Babu[11], S. Robin[11], Padmini Swain[12], J.L. Dwivedi[13], Ram Baran Yadaw[14], Nimai P. Mandal[3], T. Ram[15], Krishna Kumar Mishra[4], S.B. Verulkar[6], Tamal Aditya[7], Krishna Prasad[16], Puvvada Perraju[17], Ram Krishna Mahato[8], Sheetal Sharma[18], K. Anitha Raman[18], Arvind Kumar[18], Amelia Henry[18]*

[1]Bihar Agricultural University, Sabour, Bihar, India
[2]Barwale Foundation, Maharajpet, Andhra Pradesh, India
[3]Central Rainfed Upland Rice Research Station, Hazaribag, Jharkand, India
[4]Nepal Agricultural Research Council Regional Agriculture Research Station, Nepalgunj, Khajura, Banke Nepal
[5]Indian Council of Agricultural Research, Research Complex for Eastern Region, Patna, Bihar, India
[6]Indira Gandhi Agricultural University, Raipur, Chhattisgarh, India
[7]Bangladesh Rice Research Institute, Regional Station, Rajshahi, Bangladesh
[8]Regional Agricultural Research Station, Tarahara, Sunsari, Nepal
[9]ICAR Research Complex for North Eastern Hill Region, Lembucherra, Tripura, India
[10]Benaras Hindu University, Varanasi, Uttar Pradesh, India
[11]Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
[12]National Rice Research Institute, Cuttack, Odisha, India
[13]Crop Research Station, Narendra Dev University of Agriculture and Technology, Masodha, Kumar Ganj, Faizabad, Uttar Pradesh, India
[14]National Rice Research Program, Hardinath, Baniniya, Janakpurdham, Nepal
[15]Indian Institute of Rice Research, Patencheru, Telangana, India
[16]Birsa Agricultural University, Ranchi, Jharkhand, India
[17]Jawaharlal Nehru Krishi Viswa Vidyalaya, Rewa, Madhya Pradesh, India
[18]International Rice Research Institute, Los Baños, Laguna, Philippines
*E-mail: a.henry@irri.org

Drought is the major constraint to rainfed rice productivity in South Asia, but few reports provide detailed characterisation of the soil properties related to drought stress severity in the region. The aim of the study was to provide a compilation of drought breeding network sites and their respective levels of drought stress, and to relate soil parameters with yield reduction by drought. This study characterised levels of drought stress and soil nutrient and physical properties at 18 geographically distributed research station sites involved in rice varietal screening in Bangladesh, India, and Nepal, as well as at farmers' fields located near the research stations. Based on soil resistance to penetration profiles, a hardpan was surprisingly absent in about half of the sites characterised, which may be due to a greater degree of soil cracking at those sites. Significant relationships of sand content and depth of compaction and yield reduction by drought indicated the importance of field susceptibility to drainage, rather than water retention by clay, for plant water availability in this region. The main difference between research stations and nearby farmers' fields was in terms of soil compaction. These results present an initiative for understanding the range of severities of reproductive-stage drought stress in drought-prone rainfed lowland rice-growing areas in South Asia.

Comparison between groundwater withdrawals for irrigation andestimated crop water requirements in the Kairouan plain

Fradi F.[1]*, Massuel S.[2], Simonneaux V.[3], Calvez R.[2], Oueslati I.[1]

[1]Université de Carthage/ INAT, Institut National Agronomique de Tunisie, 43, Avenue Charles Nicolle 1082 –Tunis, Tunisie
[2]UMR G-EAU (IRSTEA, Ciheam-Iamm, Cirad, AgroParisTech, IRD, SupAgro), 361,rue Jean-François Breton, BP 5095, 34196 Montpellier Cedex 5
[3]CESBIO, UMR 5126 (CNES, CNRS, IRD, UPS), 18, Av Edouard Belin, 31401Toulouse, France
*E-mail: fradifajr@gmail.com

In the Kairouan plain, irrigated agriculture is largely supported by groundwater, and the continuous growing demand for groundwater threatens water balances. The problem for managers is that withdrawals are difficult to assess and, thus, to regulate because they are individual and scattered in the landscape. Methods need to be developed to provide such estimates. In this work, the main objective was to evaluate the farmers' irrigation practices. A comparison at farm scale between measured groundwater withdrawals and simulated volumes of water used for irrigation was done. The groundwater withdrawals were measured using a method based on temperature and discharge monitoring of the pumping equipment. The crop water requirements were determined using the SAMIR model (Satellite of Monitoring Irrigation), based on the FAO-56 dual crop coefficient approach fed with high resolution NDVI image time series. SAMIR updates the soil water content according to the precipitation rate, and then provides an irrigation schedule. Three irrigation scenarios were tested in order to analyse the situation: one with calibrated parameters, one with maximum irrigation and the last with economic irrigation.

The remotely sensed KCB values, significantly different from the FAO values, are specific to the growing conditions in this context. It shows the reliability of the remote sensing data in computing the crop coefficients.The comparison of the pumped volumes and estimated ones showed frequent over-irrigation. This means that either the farmers need to improve their crop water budget or that their constraints on irrigation practices need to be considered in groundwater draft assessment.

N-fertilising rainfed wheat and barley to intensify cereal production in the Mediterranean basin

Savin R[1]*, Cossani CM[1†], Dahan R[2], AyadJY[3], Albrizio R[4], TodorovicM[5], Karrou M[6], Slafer GA[1],[7]

[1]Department of Crop and Forest Sciences and AGROTECNIO (Center for Research in Agrotechnology), University of Lleida, Av. RoviraRoure 191,
[2]5198, Lleida, Spain
[2]Scientific Division/INRA-Morocco, Av. de la Victoire, BP 415 R.P., Rabat, Morocco
[3]Department of Horticulture and Crop Science, Faculty of Agriculture, University of Jordan, Amman11942, Jordan
[4] ConsiglioNazionaledelleRicerche - Istituto per i SistemiAgricoli e Forestali del Mediterraneo (CNR-ISAFOM), ViaPatacca 85, 80056, Ercolano, Napoli, Italy
[5]CIHEAM—Mediterranean Agronomic Institute of Bari (IAMB), Via Ceglie 9, 70010 Valenzano, BA, Italy
[6]Integrated Water and Land Management Program, ICARDA-Rabat, Morocco
[7]ICREA (Catalonian Institution for Research and Advanced Studies), Barcelona, Spain
†present address: South Australian Research and Development Institute – SARDI, PO Box 1783 Port Lincoln, SA, 5606, Australia
*E-mail: savin@pvcf.udl.cat

In the Mediterranean basin, water scarcity is the most critical yield-limiting factor. Nitrogen fertilisation has been proposed as a tool to increase yield by enhancing WUE. However, farmers are still reluctant to fertilise rainfed cereals because they expect no responses, or even yield penalties, in most years. This assumption is rooted on the Liebig's '*law of the minimum*'. However, the concept of this 'law' has been challenged from empirical and theoretical grounds. Therefore, we tested in a multi-location, multi-year study in four different areas of the Mediterranean Basin whether durum wheat and barley may respond positively to nitrogen fertilisation when grown in rainfed conditions and, therefore, whether fertilisation in water-stressed crops may become a tool for intensifying cereal production. The study involved 16 experiments, including different genotypes of durum wheat and barley sown at Morocco, Jordan, North-eastern Spain, and Southern Italy, with different nitrogen doses applied at sowing or early in crop development over four growing seasons. Averaging across all conditions (years-locations-species) yield increased 26% when fertilised. Most importantly, the average did not mask a cross-over response and, therefore, even under the lowest-yielding conditions (cases most limited by soil water) there was a generalised positive response to fertilisation (and naturally the response was greater under less water-limited conditions). Grain number per unit area, and not grain weight, was the main component related to grain yield. In addition, barley and durum wheat responded similarly to nitrogen fertilisation, against the widespread belief that barley responds less.

Adoption of soil and water conservation practices under different farming systems in the Sahel region of northern Mali

Diiro G[1], Birhanu ZB[2]*, Petri M[3], Tabo R[4]

[1]Lecturer Department of Agribusiness and Natural Resources Economics, Makerere University. Kampala.Uganda
[2]Scientist Land and Water Management, and Project Manager.International Crops Research Institute for theSemi-Arid Tropics (ICRISAT).West and Central Africa (WCA).Bamako. Mali
[3]Former Agronomist and Project Manager.ICRISAT.WCA. Bamako. Mali
[4]Principal Agronomist and Regional Director. ICRISAT.WCA. Bamako. Mali
*E-mail z.birhanu@cigar.org

Climate change remains a major development challenge in developing countries, particularly in the Sub Saharan African economies. A study was conducted to assess the adoption of SWC practices under three farming systems (rice, cereals and mixed based) in the northern region of Mali. Data was collected from 297 farmer households, 16 NGOs and 11 focus group discussions in 11 villages. Results indicated that SWC measures are the most critical entry points for improving land resource resilience and agricultural productivity. At least one SWC practice was implemented by more than half of the farmers in the studied villages. However, the rate of adoption of the individual measures is generally low. Zai was the most common practice (43%), and the likelihood of adoption of any of the other SWC measures is less than 25%. Significant variation was observed among the three farming systems in the adoption of most of the SWC measures. About 69% of farmers residing in the mixed farming system used Zai compared to 34% (cereal) and 32% (rice). About 35% of farmers in the mixed system used ponds relative to 16% of the users in the cereals system. The most common constraints to SWC noted by farmers were lack of finance (29.5%) and limited labor (28%). The low uptake of SWC measures may hamper farmer households from achieving sustainable resilience to climate change. Inclusive strategies that include the use of improved crop varieties, integrated soil fertility management practices, credit schemes, and agro-meteorological forecasts in the extension and advisory services are recommended.

Effect of plastic film mulching and nitrogen on N_2O emission in dryland maize

Yue SC[1],[2]*, Liu JC[2], Wang ZL[2], Shen YF[12], Li SQ[12]

[1]State Key Laboratory of Soil Erosion and Dryland Farming on the Loss Plateau, Northwest A&F University
[2]College of Natural Resources and Environment, Northwest A&F University
*E-mail: yueshanchao@nwafu.edu.cn

Understanding the response of N_2O emission to plastic film mulching is beneficial for improving management practices. We performed field experiments from 2014 to 2015 in northwestern China to measure the annual N_2Oemissions using the static chamber technique: plastic film mulching maize or no-mulching maize at different N levels (0 kg ha-1,100kg ha-1, 250 kg ha-1, and 400 kg ha-1). Compared to the no-mulching treatment, plastic film mulching markedly improved the soil temperature and moisture, which significantly increased the maize yields and N uptake, but did not increase the N_2O emissions. As a result, the yield-scaled N_2O emissions were markedly reduced in the plastic film mulching maize. However, the rate of N_2O emissions at different growth stages was affected by mulching. For the plastic film mulching treatment, N_2O emissions mainly concentrated in VE-V10 stage while it mainly concentrated in V10-R6 stage for no-mulching maize field.

Intercropped woody species in the sahel to resist drought: Agronomic performance and soil quality

R. Dick[1] *, M. Sene[2], M. Khouma (the late), A. Badiane[3], M. Bright[1], E. Dossa[4], L. Lardy[5] and K. Assigbetse[5],

[1]Ohio State University, USA
[2]Sciences du Sol, Institut Sénégalais de Recherches Agricoles (ISRA)/ CERAAS, Thiès, Sénégal
[3]UNOPS Dakar, Sénégal
[4]International Fertilizer Development Center, Accra, Ghana
[5]USAID/ Sénégal, Dakar, Sénégal
[5]Institut de Recherche pour le Développement - Intensification Ecologique des Sols Cultivés en Afrique de l'Ouest Dakar – SENEGAL
*E-mail: dick.78@osu.edu

The Sahel is an ecologically fragile environment where in-season drought periods are common, causing chronic low yields, crop failures, and long-term food insecurity. Green Revolution technology has not been successful in the region; hence, biologically based systems are needed that utilize local resources and can buffer against drought in the Sahel. Two native shrubs, *Piliostigma reticulatum* and *Guiera senegalensis*, coexist with row crops throughout the Sahel and until recently have largely been overlooked. Unfortunately, the current management of coppicing in the and residue burning prior to cropping, is not utilizing this organic matter effectively. Two long-term experiments (11 years) were conducted in Senegal that showed the intriguing ability of *G. senegalensis* and *P. reticulatum* under optimal conditions (optimized at ~1500 shrubs ha-1 with residue returns to soil) to dramatically increase yields of millet and groundnut, with or without fertilizer additions and maintain yields in drought years. Importantly, water use efficiency (WUE) (kg grain ha-1 mm-1 precipitation), showed that the presence of shrubs maintained this ratio in very dry years compared to non-shrub plots where this yield ratio tracked rainfall. Importantly, shrubs reduce time to harvest by about 15 days - a valuable asset for the semi-arid Sahel with its erratic rainfall patterns. These results are attributed to hydraulic lift and improved nutrient availability and soil quality. Shrub-intercropping is advantageous for subsistence farmers, because it is a local resource they are familiar with that does not require external inputs or new infrastructure.

Workshops

InterDrought-V

Hyderabad International Convention Center (HICC), Hyderabad, India

21-25 February, 2017

Workshops on February 21, 2017

Workshop / Time	W1: Abiotic stress tolerance in cereals	W2: Abiotic stress tolerance in legumes	W3: Tolerance to Heat Stress for Crop Improvement	W4: Genetic Engineering for Abiotic Stress	W5: GWAS and GS for Crop Improvement	W6: Drought Stress and Aflatoxin Contamination in crops	W7: IPPN workshop on precision phenotyping for improved stress tolerance
	(Venue: Hall MRG02) **Workshop Co-organizers:** Roberto Tuberosa, University of Bologna, Italy & Vilas Tonapi, IIMR, India	***(Venue: Hall MRG03)*** **Workshop Co-organizers:** Henry Nguyen, University of Missouri, USA & NP Singh, ICAR- IIPR, India	***(Venue: Hall MRG04)*** **Workshop Co-organizers:** PK Gupta, CCS University, India & HS Balyan, CCS University, India & Kulvinder Gill, WSU, USA	***(Venue: Hall MRG05)*** **Workshop Co-organizers:** Anil Grover, UDSC, India & Ashwani Pareek, JNU, India	***(Venue: Hall MRG06)*** **Workshop Co-organizer:** Jose Crossa, CIMMYT, Mexico & Hari D Upadhyaya, ICRISAT, India	***(Venue: Hall MRG1.05)*** **Workshop Co-organizers:** Baozhu Guo, USDA-ARS, USA & C Corley Holbrook, USDA-ARS, USA & Manish Pandey, ICRISAT, India	***(Venue: Hall MRG1.06)*** **Workshop Co-organizers:** Roland Pieruschka, IBG-2, Germany & Pervez Haider Zaidi, CIMMYT, India
1015 – 1030	*Setting the scene - Organizers*	*Setting the scene - Organizers*	*Setting the scene - Organizers*	*Setting the scene - Organizers*	*Setting the scene - Organizers*	*Setting the scene - Organizers*	*Setting the scene - Organizers*
1030 – 1100	Relating root phenotyping and genetic diversity to drought avoidance in rice ***Adam Price,*** University of Aberdeen, UK	Genetic regulation of root system architecture and plasticity in grain legumes ***Henry Nguyen,*** University of Missouri, USA	Heat Stress: Perception, response and resilience in crop plants ***PV Vara Prasad***, Kansas State University, USA	Application of genetic engineering to produce stress tolerant rice plants ***Anil Grover***, University of Delhi-South Campus, India	Genomic-enabled prediction using kernel models with genotype × environment interaction ***Jose Crossa,*** CIMMYT, Mexico	Deciphering drought-induced response patterns at the biochemical and molecular level in maize related to aflatoxin contamination resistance ***Baozhu Guo***, USDA-ARS, USA	Field-based phenotyping for drought tolerance in maize – focus on breeder's wish-list ***Pervez Haider Zaidi,*** CIMMYT, India
1100 – 1130	Pyramiding major QTLs for increased rice yield under drought: recent approaches and successes ***Arvind Kumar,*** IRRI, Philippines	Development of efficient drought escaping plant types of pulses through conserving micro-environmental moisture ***PS Basu***, ICAR-IIPR, India	Developing climate resilient wheat ***Kulvinder Gill***, Washington State University, USA	Two-component signaling (TCS) system in development and abiotic stress response in rice ***Ashwani Pareek***, JNU, India	Integrating statistical and crop growth modelling approaches to facilitate breeding for water-limited environments ***Fred Van Eeuwijk,*** WUR, Netherlands	Breeding peanut with drought tolerance and reduced aflatoxin contamination ***C Corley Holbrook***, USDA-ARS, USA	Yield maintenance under drought: expansive growth and hydraulics also matter in reproductive organs ***Francois Tardieu,*** INRA, France
1130 – 1200	Rapid genetic gains achieved by developing and deploying multiple abiotic and biotic stress tolerant rice varieties in Asia and Africa ***Jauhar Ali***, IRRI, Philippines	Breeding common bean (*Phaseolus vulgaris* L.) for multi-stressed environments ***Clare Mukankusi***, CIAT, Uganda	Breeding for heat tolerance in wheat, where we are? ***AK Joshi,*** BISA, India	Ensuring the food bowl for Masses: Raising crops for saline and dry areas ***Sneh Singla-Pareek***, ICGEB, India	A simpler method for GWAS and the use of significant markers in genome selection ***Juan Andres Burgueño***, CIMMYT, Mexico	Aflatoxin permissive transcriptional states in peanut seeds ***Peggy Ozias-Akins***, University of Georgia, USA	Transpiration Efficiency: Further insights from species, sink strength, and soil comparisons & LeasyScan: 3D scanning of crop canopy plus seamless monitoring of water use to harness the genetics of key traits for drought adaptation ***Vincent Vadez***, ICRISAT, India
1200 – 1230	Genetic dissection of root traits at jointing and grain filling stages in wheat ***Ruilian Jing***, CAAS, China	Hybrid Pigeonpea: Best Bet for maximizing productivity in dry lands ***CV Sameer Kumar,*** ICRISAT, India	How rising temperatures would be detrimental for cool and warm-season food legumes? ***Harsh Nayyar***, Panjab University, India	Identification and validation of genes for water use efficiency and grain yield under drought in rice ***Andy Pereira***, University of Arkansas, USA	Genomic selection in hybrid breeding ***Yusheng Zhao***, IPK-Gatersleben, Germany	Drought affects A. flavus and aflatoxin contamination and their association with drought tolerant traits in peanut genotypes ***Sanun Jogloy,*** Khon Kaen University, Thailand	Drought acclimation during multiple vegetative growth stages in wheat improves drought tolerance during generative growth: insights from proteomics and physiology ***Xiao Wang***, Nanjing Agricultural University, China
1230 – 1330	***Lunch***						
1330 – 1400	Development of drought tolerant wheat cultivars using wide hybridization, genomics and molecular breeding approaches ***HS Dhaliwal***, Eternal University, India	Retrospect and prospect of improving groundnut (*Arachis hypogaea* L.) for drought-prone areas of India ***T Radhakrishnan***, ICAR-Directorate of Groundnut Research, India	In-sillico characterization of Phosphoglucose isomerase (PGI) gene in *Triticum aestivum* ***Rakesh Singh***, ICAR- NBPGR, India	Engineering crops for enhanced tolerance to multiple abiotic stresses and improved N use efficiency via manipulating novel-stress associated proteins ***Om Parkash Dhanker***, UMass Amherst, USA	Genomic-enabled prediction model with genotype × environment interaction in elite chickpea lines ***Manish Roorkiwal***, ICRISAT, India	Management of aflatoxin contamination in groundnut by enhancing host-plant resistance ***Liao Bashou***, OCRI-CAAS, China	Precise monitoring of stress response and high throughput phenotyping for stress adaptive traits – Use of stable isotopes and Gravimetric approaches ***MS Sheshashayee,*** UAS-Bangalore, India

1400 – 1430	A genome-wide approach combining field and platform phenotyping to investigate plant responses to drought and high temperatures ***Claude Welcker***, INRA-LEPSE, France	The first high density genotyping 'Axiom_Arachis' 58K SNPs Array for genetic studies and molecular breeding in groundnut ***Manish Pandey***, ICRISAT, India	Mining for heat stress responsive genes by RNA-Seq based comprehensive gene expression analyses in chickpea (*Cicer arietinum* L.) ***Himabindu Kudapa***, ICRISAT, India	Functional diversity of plant stress hormone Abscisic Acid Receptors in rice ***Viswanathan Chinnusamy***, ICAR- IARI, India	Harnessing the genomic diversity of asian cultivated rice (*Oryza sativa* L.): SNPs, pan genomes and structural variation ***Zhikang Li***, CAAS, China	Drought stress and aflatoxin contamination: Transcriptional responses of *Aspergillus flavus* to oxidative stress are related to stress tolerance and aflatoxin production capability ***Jake Fountain***, University of Georgia, USA	
1430 – 1500	Genetic determinants of drought stress tolerance in Setaria ***Manoj Prasad***, NIPGR, India	Breeding chickpea for water limited environments: Selection indices and strategies ***Bharadwaj Chellapilla***, IARI, India	Towards developing rice genotypes adapted to warming climate ***M Raveendran***, TNAU, India	Drought tolerant Rice: Metabolic engineering and dissecting proteomics in understanding the system ***Karabi Datta***, University of Calcutta, India	Integrative genome-wide association studies (GWAS) to understand complex genetic architecture of quantitative traits in chickpea ***Swarup Parida,*** NIPGR, India	Combination of empirical and trait-based approaches for breeding drought tolerance in groundnut (*Arachis hypogaea* L) ***Janila Pasupuleti,*** ICRISAT, India	
1500 – 1530	**General Discussions**	**General Discussions**	**General Discussions**	Genetic engineering approaches for drought tolerance in grain legumes: Progress and prospects ***Pooja Bhatnagar,*** ICRISAT, India	Understanding the genetics of biomass formation in barley assessed by non-invasive phenotyping ***Kerstin Neumann***, IPK-Gatersleben, Germany	Molecular breeding tools improved drought tolerant groundnut variety for resistance to foliar fungal diseases ***Rathna Kumar Arulthambi Luke***, Directorate of Groundnut Research, India	

Panel Discussions on Climate Smart Agriculture

Co-Chairs: David Bergvinson & RS Paroda

(Venue: Hall MRG01, HICC, Hyderabad)

1330 - 1630 hrs

David Bergvinson Director General, ICRISAT, India	R S Paroda former Director General, ICAR, India	William D Dar former Director General, ICRISAT, India & President, Inanglupa, Philippines	Swapan Datta former Deputy Director General-Crop Science, ICAR & Vice Chancellor, Shantiniketan, India	Jeff Ehlers Senior Program Officer, Bill & Melinda Gates Foundation, USA	Usha Barwale Zehr Director-Research, MAHYCO, India	Shadrack Moephuli President and CEO, Agricultural Research Council, South Africa	KHM Siddique, Hackett Professor of Agriculture Chair and Director/Professor, Institute of Agriculture, University of Western Australia, Australia	A K Padhee Director, Country Relations and Business Affairs, ICRISAT, India

Workshop on February 23, 2017

W8: Next Generation Genomics & Molecular Breeding Platforms

(Venue: Hall 5 & 6, HICC, Hyderabad)

Time	1530 – 1600 hrs	1600 – 1630 hrs	1630 – 1700 hrs	1700 – 1730 hrs	1730 – 1800 hrs
Co-Organizers: Dave Edwards, University of Western Australia, Australia & Rajeev K Varshney, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India	The BGISEQ-500 sequencing platform for multiple research applications ***Xin Liu***, BGI Research, China	Using genomics to breed for the future: Sequencing and genotyping platforms ***Ryan Rapp,*** Illumina Inc., USA	Delivering higher rates of genetic gain to farmers in drought-prone environments ***Gary Atlin***, Bill & Melinda Gates Foundation, USA	The assembly, analysis and application of pangenomes ***Dave Edwards,*** University of Western Australia, Australia	Genotyping by Sequencing: Which application is right for me? ***Jacqueline Batley***, University of Western Australia, Australia

Workshop I

Abiotic Stress Tolerance in Cereals

Co-organizers

Prof. Roberto Tuberosa

Professor
University of Bologna
Italy

Dr. Vilas A Tonapi

Director
ICAR-IIMR
India

Relating root phenotyping and genetic diversity to drought avoidance in rice

Adam H Price

University of Aberdeen, Institute of Environmental and Biological Sciences, Aberdeen, AB24 3UU, UK
E-mail: a.price@abdn.ac.uk

Most of the research that I have conducted on rice genetics over nearly 25 years has focused on identifying ways in which understanding root form and function will help grow rice using less water, be it in drought-prone upland systems or lower water input irrigated systems. The research includes biotic interactions in the soil since it can be anticipated that the more rice is grown aerobically, the more interactions with nematodes, mycorrhizal and parasitic weeds will impact on performance. Highlights include the introduction of root growth QTLs from the cultivar *Azucena* into the Indian upland cultivar *Kalinga III* using marker assisted selection in collaboration with Bangor University (Steele et al 2013) and identifying genes underlying a QTL for rice-*Striga* interactions in a research collaboration with Wageningen (Cardoso et al. 2014). This talk will focus predominantly on two areas of current research. The first is the linking of a QTL for drought avoidance on rice chromosome 7 to allelic variation in aquaporins and the impact on root hydraulic conductance, unpublished research conducted by Farkhanda Khowaja and Zainab Abubakar. The second is on the development of a buried herbicide method for screening rooting depth which can be linked to field drought performance in the *Oryza* SNP set of 20 cultivars but whose value is best demonstrated in a study of 135 Sri Lankan landraces where genetic structure appears to be associated with root depth and drought avoidance, a study by Mayuri Munasinghe (Munasinghe and Price 2016).

Pyramiding major QTLs for increased rice yield under drought: Recent approaches and successes

Arvind Kumar[1]*, N.K. Singh[2], T. Ram[3], Satish Verulkar[4], N.P. Mandal[5], Amelia Henry[1], Ajay Kohli[1]

[1]International Rice Research Institute, Los Baños, Philippines
[2]National Research Center for Plant Biology, Indian Agricultural Research Institute, New Delhi, India
[3]Indian Institute of Rice Research, Rajendranagar, Hyderabad, India
[4]Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur, India
[5]Central Rainfed Upland Rice Research Station (CRURRS), Hazaribagh, India
*E-mail: a.kumar@irri.org

Drought is a regular problem on more than 20 million hectares rice in Asia. Breeding for traits rejected in post-Green Revolution era unknowingly has led to the continuous loss of drought-tolerant alleles in modern semi-dwarf varieties. Breeding based on direct selection for grain yield under drought helped breeders to combine drought tolerance with high yield potential. The approach led to the identification of seven stable QTLs for grain yield under drought. Better understanding of physiological mechanisms associated with each as well as QTLs combinations and gene/gene networks associated with some of the identified QTLs has helped breeders to introgress and pyramid QTLs in appropriate combinations to improve yield of several mega varieties by 0.5- 1.5 t per hectare under drought. IR 64 lines pyramided with *qDTY2.2* and *qDTY4.1* have been released as varieties in India, Nepal and Myanmar. Success with breakage of undesirable linkages of drought tolerance with low yield potential, tall plant height, early maturity as well as poor grain quality, and development of tightly-linked markers for identified QTLs has allowed several breeding programs across regions to freely use the *qDTYs* in backcross as well as forward breeding programs and combine drought tolerance with traits/genes needed for any ecosystem. The identification of QTL x QTL and QTLs x genetic background interactions shall help breeders increase the frequency of drought-tolerant alleles in modern varieties and, thereby, increase the level of drought tolerance. Over last five years, more than fifty rice breeding lines have been released as varieties in ten different countries,

Rapid genetic gains achieved by developing and deploying multiple abiotic and biotic stress tolerant rice varieties in Asia and Africa

Ali J[1]*, Xu JL[2], Franje N[1], Sevilla, MAL[1], Li ZK[2]

[1]International Rice Research Institute (IRRI), DAPO 7777, Metro Manila, Philippines;
[2]Chinese Academy of Agricultural Sciences (CAAS), Beijing, China.
*E-mail: J.Ali@irri.org

Breeding resilient rice varieties is vital for sustainable and stable yields. We bred 240 Green Super Rice (GSR) cultivars at IRRI for testing, released 20 GSR varieties and nominated 104 promising multiple abiotic and biotic stress tolerant materials into national yield trials across Asia and Africa within five years, adopting an innovative and skillful selection scheme and genomics assisted breeding strategy. Introgression breeding and designed QTL pyramiding (DQP) was employed for developing varieties with multiple abiotic and biotic stress tolerance without compromising on grain yield and quality. BC_1F_2 populations derived from HHZ, WTR1 and TME80518 (as recipient parents) and 16 donors at IRRI were screened simultaneously for three rounds for different abiotic (drought, salinity, submergence and low fertilizer input conditions) and biotic stresses (blast, BLB, BLS Tungro) and normal irrigated conditions, which resulted in identification of 1333 (HHZ-ILs) + 2232 (WTR 1-ILs) + 1408(TME80518-ILs) trait specific introgression lines (ILs) superior over tolerant checks. QTLs governing complex traits (drought, salinity, cold) were identified by genotyping 495 and 576 ILs in HHZ and WTR1 backgrounds respectively. We nominated 35 promising pyramiding lines (PLs) to AYT (MET0) in DS2015 from 45 DQP crosses and several lines were advanced to MET1 stage. Success in deriving rapid and high genetic gains may be attributed to a combination of effective selection skills, reduced breeding time and innovative genomics-assisted breeding approach. Currently, it is estimated that nearly 20 promising released IRRI bred GSR lines can cover an area of 1.2mha during WS2016 across Asia and Africa.

Genetic dissection of root traits at jointing and grain filling stages in wheat

Long Li, Zhi Peng, Xinguo Mao, Jingyi Wang, Xiaoping Chang, Ruilian Jing*

Institute of Crop Science, Chinese Academy of Agricultural Sciences/National Key Facility for Crop Gene Resources and Genetic Improvement, Beijing 100081, China
*E-mail: jingruilian@caas.cn

Root system is a vital organ of the plant for absorbing water and nutrients from the soil, but the genetic basis of root characters in wheat (*Triticum aestivum* L.) remains to be elucidated, especially in the late growth period, because it is hard to detect roots. The purpose of this study was to identify high quality alleles/QTLs controlling root depth (RD) and root dry weight (RDW) by combining linkage mapping and genome-wide association study (GWAS). A double haploid (DH) population with 150 lines and a natural population consisting of 323 accessions was grown in PVC tubes for phenotyping. The genotypes were identified with the wheat 660 KSNP (single nucleotide polymorphism) arrays. For linkage mapping, we constructed a set of high-density linkage map spanning 6186cM (1866 bins). Seventeen QTLs for RD and/or RDW were located on chromosomes 1A, 2D, 3A, 3B, 4A, 5A, 5B, 6B and 6D. For GWAS, we selected 283,369 high-quality SNPs, and 10 loci for two traits on chromosomes 2A, 2B, 2D, 4D, 5B, 5D and 6A were detected through LD-based association analysis. Among them, only one SNP was located on the same linkage group of 5B, which harbored a QTL. On comparing the GWAS results at the jointing stage and grain filling stage, one common locus on chromosome 2B showed a highly significant association with RDW. All significant candidate SNPs will be verified using two wheat groups with extreme root depth and root dry weight in the field, using a mini rhizotron system. The findings will enhance our knowledge of the genetic regulation of root growth and supply useful information for molecular breeding in wheat.

Development of drought tolerant wheat cultivars using wide hybridization, genomics and molecular breeding approaches

Dhaliwal, H. S.

Eternal University, Baru Sahib- 173101, India
*E-mail: hsdhaliwal07@gmail.com

More than 50% of the global wheat area is affected by periodic drought while 66% of the irrigated area receives only limited irrigation. The water stress during grain-filling period leads to reduced yield due to accelerated leaf senescence, oxidative damage to photo-assimilation and reduced grain-filling period, carbon assimilation, seed set and development. Some of the mechanisms for drought avoidance are early flowering and rapid grain filling and tolerance due to osmotic adjustment by compatible solutes, anti-oxidative defense, improved root architecture, translocation of reserves, and hormonal regulation. The landraces and related wild species constitute a reservoir of useful variability for breeding for drought tolerance. A spontaneous translocation of 1RS of *Secale cereale* in wheat possesses several QTLs, especially on its terminal region for root architecture, better canopy temperature, higher CID and increased stomatal conductance leading to 20% higher grain yield of wheat cultivars under limited water regimes. A region with three candidate genes for lateral root development and higher root and shoot biomass under water stress have also been identified on 7DL.7EL translocation in wheat. Genomic regions of a pre-Green Revolution drought-tolerant variety C306 have been identified using two different mapping populations. Combinations of suitable alleles of vernalization and photoperiod genes can be used to develop wheat cultivars for drought tolerance for different agro-climatic regions. All the above genes and other for drought tolerance on the syntenic genomic regions of other cereals can be explored in wheat germplasm and used for marker assisted breeding for drought tolerance.

A genome-wide approach combining field and platform phenotyping to investigate plant responses to drought and high temperatures

Welcker C[1]*, Millet E[1], Alvarez Prado S[1], Coupel Ledru A[1], Tsu Wei Chen[1], Cabrera Bosquet L, Tardieu F[1-]

[1]INRA Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux, IBIP, 34060, Montpellier, France
*E-mail: claude.welcker@inra.fr

Natural genetic resources need to be fully explored for designing novel genotypes able to cope with climate change, with special emphasis on identification of traits and allelic sources of adaptation to drought and high temperature. We base our approach on a combination of methods involving genetic analyses in phenotyping platforms and in the field. The rationale is that a given trait or allele confers advantages for yield in specific scenarios of water deficit or high temperature, but most often not in all of these scenarios. We have explored, in a network of field experiments, a series of environmental scenarios for identifying the scenarios where a given allele has positive, negative or no effect on yield. We have then dissected these effects into responses to specific environmental conditions and their genetic variability. The latter step involves phenotyping in an automated phenotyping platform, allowing one to infer traits that are impossible to measure in the field, such as radiation use efficiency, sensitivity of growth to water deficit or stomatal control. We have applied this strategy to a panel of 250 maize hybrids allowing a multi-scale multi environment whole-genome association study. Resulting pattern of QTL effects expressed as function of environmental variables and traits can be used for assessing the performance of genotypes and the contribution of genomic regions under current and future stress situations, and for accelerating the breeding for drought-prone environments.

Genetic determinants of drought stress tolerance in Setaria

Muthamilarasan M[1], Prasad M[1]*

[1]National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi
*E-mail: manoj_prasad@nipgr.ac.in

Cultivated foxtail millet (*Setaria italica*) and its wild progenitor (*S. viridis*) have collectively been considered as tractable model species for studying C4 photosynthesis, stress biology and biofuel traits. Being cultivated in arid and semi-arid tropics of the world, these species are well-adapted to harsh environments such as drought, heat and salinity. This adaptation or acclimation potential of *Setaria* spp. has drawn research interest, and attempts have been made to dissect the molecular mechanisms of stress tolerance. Compared to other stresses, drought response has been studied extensively in *S. italica* and many drought-responsive genes encoding for transcription factors, signaling molecules and enzymes have been identified and characterized. Several genome-wide studies have reported the identification of stress-responsive gene family members, and speculated on the potential for expansion and neo-functionalization of paralogs in these gene families. In this context, the present talk discusses the key genetic determinants identified for stress tolerance in *S. italica* and demonstrates their use in improving drought tolerance. In addition, strategies for identification of genes underlying stress tolerance are also described. Little effort has so far been made towards understanding the stress-tolerance characteristics of *Setaria* as compared to studies reported in other crops. Comprehensive functional studies along with the use of integrated -omics approaches are required to elucidate the genetics and genomics of stress tolerance in *Setaria,* as it is important to develop climate change resilient crops to meet the growing demand for food and feed.

Workshop II

Abiotic Stress Tolerance in Legumes

Co-organizers

Prof. Henry Nguyen

MSMC Endowed Professor & Director
University of Missouri
USA

Dr. NP Singh

Director
ICAR-IIPR
India

Genetic regulation of root system architecture and plasticity in grain legumes

Henry T. Nguyen[1]*

[1]Division of Plant Sciences, University of Missouri, Columbia, MO 65211, USA
*E-mail: nguyenhenry@missouri.edu

Climate change increases the occurrence of extreme weather patterns in the global agricultural areas, which can cause significant reduction in crop production and threaten food security. Meeting the food demand of the world's growing population requires a faster rate of yield increase for major crops, including grain legumes. Grain legumes are an essential commodity in optimal human diets and animal feed because of their unique seed composition. Root system architecture (RSA) is an important developmental and agronomic trait, which plays a vital role in plant adaptation and productivity under water-limited environments. A deeper and proliferate root system helps extract enough water and nutrients under these environmental conditions. Root biology and screening for natural genetic variations in the RSA in legumes lags far behind compared to above-ground traits. Our research program focuses on an integrated genetics and genomics approach to dissect molecular processes from genome to phenome, in order to achieve increased water capture and use efficiency. A combination of screening for natural genetic variation for RSA and large-scale genome sequencing in soybean enabled us to identify new genetic resources, and associated genes and markers. This approach helped us characterize the genetic diversity in root system developmental plasticity in response to water stress, and the genes and markers identified through the genotype-phenotype association are in the translational genomics pipeline. This presentation will highlight the importance of beneficial root traits and recent discoveries towards better root system architecture in legumes, with emphasis on soybean, for enhanced stress resistance and yield.

Development of efficient drought escaping plant types of pulses through conserving micro-environmental moisture

NP Singh[1], PS Basu[1]

[1]ICAR-Indian Institute of Pulses Research, Kanpur, India
*E-mail: psbsu59@gmail.com

Water retention capacity varies among pulses species. The sensitivity of different pulses to drought is, therefore, related to their water retention capacity which is primarily determined by cell elasticity and osmotic adjustment (OA). Despite large genetic differences in OA among pulse species, this trait has been little exploited in breeding programs due to its poor heritability and absence of a definite relationship with grain yield. On the other hand, OA plays an important role in sustainability, preventing crop species from dying even under severe stress, and promoting growth when favourable situations return. Among pulses, the pigeonpea has the highest OA values upto 1.6 MPa, followed by cowpea, horsegram, chickpea and lentils. On the contrary, *Vigna* species has very little or almost no osmotic adjustment. The irrigation demand of a pulse crop proportionately increases if the crop has low or no OA. A study conducted with a pigeonpea variety RVK 275 with high OA revealed very high tolerance to drought, and it did not show any drying symptoms as the level of stress increased beyond a threshold limit when other sensitive genotypes were completely knocked down. Thermal imaging of pigeonpea showed a graded canopy temperature with the highest values at the top and gradual decrease towards bottom, while the reverse trend was observed in relative water content (RWC). With prolonged drought under rainfed conditions, the terminal shoots of the tall pigeonpea plant type were subjected to severe decrease in the RWC, along with deprivation of soluble leaf sugars, due to complete drought-induced inhibition of photosynthesis, although there were no visible symptoms. Subsequently, when the tall plant types experienced chilling temperatures below 70 C, the starved apical meristem showed complete drying up due to freezing injury and loss of cell elasticity, as evidenced by increased electrolyte leakage which progressively intensified from top to bottom. This phenomenon was further supported by the complete disastrous effects of cold stress (<70C) in the rainfed pigeonpea variety *Maruthi* which was sown this year at Akola, Maharashtra, where an irrigated crop with the same variety was completely saved. The experimental trial conducted at IIPR, Kanpur, between tall vs dwarf variety revealed that the dwarf variety with a closed canopy and high OA conserves moisture within the plant canopy, modifies and maintains uniform RWC throughout the entire plant and, thus, protects the plant from drying up. The dwarf pigeonpea variety was found to have easy access to soil water as a result of decreased height, and under situations when the transpiration rate declines due to low temperatures. The situation remains comparable to pulse crops with shorter height, such as chickpea and lentil, which escape cold stress due to water saturation within the plant canopy. This evidence suggests that modification of plant microenvironment is desirable for developing new plant types for drought and cold tolerance; while looking for *Vigna* species with high OA is required to minimize water demand.

Breeding common bean (*Phaseolus vulgaris* L.) for multi-stressed environments

Mukankusi C.[1], *Beebe S.[2], Rao. I.[2], Raatz, B.[2] and Buruchara R.[3]

[1]International Center for Tropical Agriculture (CIAT), Kampala, Uganda
[2]International Center for Tropical Agriculture, Cali, Colombia
[3]International Center for Tropical Agriculture, Nairobi, Kenya
*E-mail: s.beebe@cgiar.org

The Bean Program of the International Center for Topical Agriculture (CIAT) aims to overcome production constraints of common bean (*Phaseolus vulgaris* L.) ranging from biotic to abiotic stress factors. A multidisciplinary team is developing a number of advanced lines of different market classes that combine stress tolerance with nutritional traits such as micronutrient (iron and zinc) and protein content in grain. Collaborative research efforts contribute to elucidating plant mechanisms governing pest (bruchids and bean stem maggot) and disease (common bacterial blight, angular leaf spot, root rot, bean common mosaic virus disease and anthracnose) resistance, abiotic stress (drought, heat, low P, low N and Al toxicity) tolerance and grain nutritional quality. Germplasm accessions from two sister species, *P. coccineus* and *P. accutifolius* have been utilized as sources of resistance to major production constraints and a number of interspecific lines developed to improve resilience to confront problem soils in the face of climate change. Molecular markers are routinely utilized for selecting resistance to key diseases and insect pests and major efforts made to utilize modern genomic tools to increase scale, efficiency, accuracy and speed of the program. A few key traits such as PHI, PPI, CT and root architecture have been shown to be correlated to yield performance under abiotic stress conditions. Elite breeding lines have been shared with partners in Africa and Latin America and improved bean varieties released in several African countries with 10-50% yield advantage over commercial checks. These new bean varieties will be key components of sustainable food systems in the tropics.

Hybrid pigeonpea: best bet for maximizing productivity in dry lands

Sameer Kumar CV[1]*, Hingane AJ[1] ,Shruthi HB[1], Sharma Mamta[1], Sudhakar C[2], Nagesh Kumar MV[2], Saxena RK[1], Varshney RK[1], Gaur PM[1], Wani SP[1]

[1]International Crops Research Institute for the Semi- Arid Tropics (ICRISAT), Hyderabad, India.
[2]Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India.
*E-mail: c.sameerkumar@cgiar.org

Pigeonpea is a hardy, widely adapted, drought tolerant crop and an integral component of cropping systems of small and marginal farmers of SAT regions of the globe. The global pigeonpea area, production and yield is approximately 6.23 mha, 4.74 MT and 762.4 kg ha -1 respectively (FAOSTAT 2015). Inflated market prices coupled with stagnant productivity have created a substantial demand supply gap. This alerted breeders to break the yield plateau by harnessing the inherent heterotic potential, as no further horizontal increase in area under pigeonpea was possible. Yield advantage in maize, rice, wheat and grain sorghum through hybrid technology triggered the adaptance of the latter in pigeonpea. As hand emasculation and pollination was not commercially feasible, male sterile lines became imperative for utilization of available natural out-crossing in pigeonpea. Thus, the first pigeonpea hybrid ICPH 8 was developed using GMS source in 1991, followed by PPH4, CoH1, AKPH4104 and AKPH2022.Though the bottlenecks of GMS system led to the development of the first CMS- based pigeonpea hybrid GTH-1 the first commercial CMS hybrid was ICPH 267. It has greater root mass, depth and ability to draw moisture from deeper soil profiles. Its fast root growth also helps in overcoming short spells of early season drought that is often encountered in July-sown rainfed crops. Hybrids have recorded 20% to 30% yield advantage over existing varieties and seed production technology has been standardized for large-scale production of commercial hybrids. SSR based hybrid purity assessment kits are also developed for testing GOT. The hydraulic characteristics of pigeonpea roots is an interesting asset for both nutrient and water uptake. In this context, hybrid pigeonpea is the best bet for maximizing dryland productivity.

Retrospect and prospect of improving groundnut (*Arachis hypogaea* L.) for drought-prone areas of India

Radhakrishnan T[1]*, Pal KK[1], Rathnakumar, L[1]., Ajay, BC[1]., Bosamia, T[1]

[1]ICAR-Directorate of Groundnut Research, Junagadh 362001, Gujarat, India
*E-mail: radhakrishnan@dgr.org.in

Groundnut in India is often cultivated with low inputs in marginal lands of arid and semi-arid tropics in around 5.5 million ha, with production of 7 million tonnes and productivity of about 1530 kg/ha. However, productivity is often affected by drought, the frequency and intensity of which is likely to increase in future owing to climate change. Though a few donor lines and released varieties have been claimed to be tolerant to early-, mid-, and end-off season drought, cultivars capable of assured production in limited water availability are still lacking. Success of transferring *mtlD*, *DREB,* genes for proline, glycine and betaine pathways to confer drought tolerance and improve the much-needed water-use efficiency has been limited. To cope with drought, identification of ideal plant ideotypes, use of identified QTLs related to drought stress tolerance, and water-use efficiency by genome assisted breeding to introgress the required traits in cultivated background are required. The screening methods currently used in conventional breeding need radical changes to produce drought-tolerant cultivars. To address the issues of reduction in photosynthesis, carbon gain and yield, and enhancement in photorespiration during drought stress, transfer of C4-photosynthetic machinery into C3-groundnut can be considered with enhanced water-use efficiency. Management of nutrient uptake and N-fixation in drought stress, along with use of endophytc microbes could also be part of the strategies to alleviate drought. The availability of genomic and transcriptomic data of wild and cultivated groundnut brightens the possibility of developing drought-tolerant groundnut cultivars in future.

The first high density genotyping 'Axiom_Arachis' 58K SNPs array for genetic studies and molecular breeding in groundnut

Pandey MK[1]*, Agarwal G[1,2], Kale SM[1], Clevenger J[2], Nayak SN[1], Sriswathi M[1], Chitikineni A[1], Chavarro C[3], Chen X[4], Upadhyaya HD[1], Vishwakarma MK[1], Leal-Bertioli S[3], Liang X[4], Bertioli DJ[3], Guo B[5], Jackson SA[3], Ozias-Akins P[2], Varshney RK[1,6]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]University of Georgia (UGA), Tifton, USA
[3]Center for Applied Genetic Technologies, University of Georgia (UGA), Athens, USA
[4]Crops Research Institute (CRI), Guangdong Academy of Agricultural Sciences (GAAS), Guangzhou, China
[5]Crop Protection and Management Research Unit, USDA-ARS, Tifton, USA
[6]The University of Western Australia, Crawley, Australia
*E-mail: m.pandey@cgiar.org; r.k.varshney@cgiar.org

Genome complexity and narrow genetic base are the major problems that hinder achieving accelerated genetic gains in groundnut or peanut, a major source of vegetable oil (48%) and protein (25%). High density genotyping is a must-have genomic resource in a crop for use in several genetic and breeding applications. Availability of genome sequence for both the diploid genome progenitors of cultivated groundnut has provided an opportunity for discovery of structural variations in large-scale including single nucleotide polymorphisms (SNPs), the most abundant DNA sequence variation in the genomes. In this context, we developed a high-density SNP array 'Axiom_*Arachis*' with 58K SNPs with uniform genome coverage. We identified initially a total of 163,782 SNPs that included 118,860 SNPs (58,438 SNPs for A-genome and 60,422 SNPs for B-genome) from 30 tetraploids and 44,922 SNPs (39,937 SNPs for A-genome and 4,985 SNPs for B-genome) from 11 diploids. Finally, a total of 58,233 highly informative SNPs with genome specificity were used for array development. In addition to cultivated groundnuts (*Arachis hypogaea)*, this array has fair representation of other diploids (*A. duranensis, A. stenosperma, A. cardenasii, A. magna* and *A. batizocoi*). Genotyping of the groundnut 'Reference Set' containing 300 genotypes identified 44,424 polymorphic SNPs and genetic diversity analysis provided in-depth insights into the genetic architecture of this material. In summary, this high-density SNP array will accelerate the process of trait dissection and molecular breeding including genomic selection for achieving higher genetic gains in groundnut.

Breeding chickpea for water limited environments: selection indices and strategies

Bharadwaj C[1]*, Patil BS[2], Madan Pal[1], Manu B[1], Tapan K[1], Neeraj K[1], Philanim S[1], Soren KR[3], Jain PK[4], Supriya S[1], Nazish N[1], Shruti R[1], Sarvjeet S[5], Tripathi S[1], Hegde VS[1], Varshney RK[6] and Chauhan SK[1]

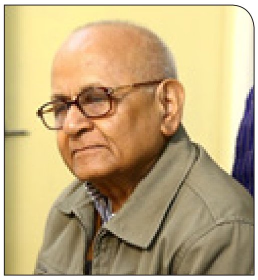
[1] ICAR-Indian Agricultural Research Institue, Pusa, New Delhi 110012
[2] ICAR-IARI Regional Centre, Dharwad, Karnataka
[3] ICAR-IIPR, Kanpur, Uttar Pradesh, India
[4] ICAR-NRCPB, Pusa, New Delhi 110012
[5] PAU, Ludhiana, India
[6]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: bharadwaj_gen@iari.res.in

Chickpea (*Cicer arietinum* L.) is the one of the most important pulse crops in the world and its production is limited by terminal drought. Unlike conventional breeding for yield, it is more challenging and requires to be measured in terms of its manifestation towards changing performance of a genotype under stress. An evaluation of a panel developed for drought and breeding studies has clearly identified the presence of large variability for drought tolerance. A large number of traits have been screened and it has been inferred that drought susceptibility index is the best way to identify genotypes that have resilience to terminal drought. However, different genotypes possessed various physiological mechanisms to cope with the effects of drought and, hence, provide ample opportunities to breeders to combine them to develop drought-tolerant genotypes. The chickpea genotypes L550, PG112 and ICC92944 have shown higher mean values for yield traits under stress and have desirable terminal drought-tolerant mechanisms for yield and other associated characters such as lower DSI, higher HI, higher BY and higher grain yield. They have, thus, emerged as stable genotypes for yield under stress situations. Though MABC for root traits has been identified, rapid screening techniques using CTD and identification of markers for MSI and RWC to be used for screening segregating generations appears to be promising in north Indian conditions. This is because unlike in south India, drought in the north India develops abruptly after a cold period, giving little time for the root system to respond. Thus, breeding for terminal drought tolerance would require concentrating on these traits too.

Workshop III

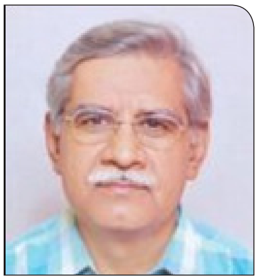
Tolerance to Heat Stress for Crop Improvement

Co-organizers



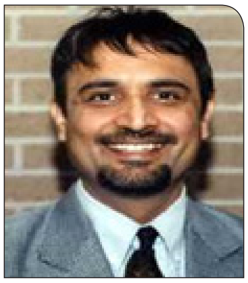
Prof. PK Gupta

Emeritus Professor
Ch Charan Singh University (CCS)
India



Prof. HS Balyan

Emeritus Professor
Ch Charan Singh University (CCS)
India



Prof. Kulvinder Gill

Professor
Washington State University
USA

Heat stress: perception, response and resilience in crop plants

P.V.V. Prasad[1]*, M. Djanaguiraman[1], S.V.K. Jagadish[1]

[1]Kansas State University, Manhattan, Kansas 66506, USA
*E-mail: vara@ksu.edu

High temperature (heat) stress is one of the most important abiotic factors that limit crop productivity and genetic gains in current and future climates. Perception and response of plants to stress determines the level of tolerance or susceptibility. Currently, significant progress has been achieved in understanding and underpinning mechanisms for improving resilience of crops plants to heat stress. The focus of the presentation will be on: (i) how plants perceive heat stress; (ii) impacts of heat stress on biochemical, anatomical, physiological processes and yield; (iii) mechanisms related to stress tolerance; and (iv) opportunities for improving resilience to heat stress. Yields of most field crops decrease when exposed to temperatures >35 degree Centigrade during sensitive stages of crop development. However, the threshold varies among crop species and genotypes. Reproductive stages of crop development, particularly gametogenesis, anthesis, embryo formation and rapid grain filling, are vulnerable to heat stress, leading to yield losses. Genetic variability exists for resilience to heat stress and all modes of stress mitigation strategies (escape, avoidance and tolerance) should be explored. Selected examples from field crops for traits associated with resilience will be presented. Emerging biochemical and molecular tools provide opportunities for rapid screening and identification of new sources of stress tolerance. Continued collaboration among biologists, breeders and agronomists is essential for developing genetic and agronomic strategies to minimize impacts of heat stress on yield.

Developing climate resilient wheat

Kulvinder S. Gill* and all partners of the Climate Resilient Wheat Innovation Lab

*Washington State University, Pullman, WA- 99164; and 17 other partner institutes
*E-mail: ksgill@wsu.edu

With the increasing temperature trends and unusual climatic changes, heat stress is a serious challenge to wheat production, as even 1°C rise in temperature above the optimal will result in yield losses of up to 4%-5%. Rainfed areas of the US are projected to decrease wheat production by 20%-40% due to climate change. Thus, developing climate-resilient wheat is crucial in today's context. As a public-private partnership, 'Feed the Future Innovation Lab-Climate Resilient Wheat' is developing heat-tolerant varieties. Evaluation of well-known heat-tolerant material from around the globe, both under controlled as well as field conditions, showed extensive natural variation for the trait, although only few lines maintained 'normal' productivity at 40oC. A short period of heat stress during germination had serious and long- term effect on plant development and yield. A ten-day heat stress at germination reduced germination percentage, coleoptile length, and yield. Sugars availability maybe a reason for the effect on germination as external application of sucrose showed significant recovery in germination percentage and coleoptile length. Heat stress during the vegetative phase significantly affected tiller number, flowering time, pollen fertility, plant height and yield. During the reproductive stage, heat stress adversely affected photosynthesis. The identified heat-tolerant lines are being used to transfer the trait into wheat cultivars by marker assisted background selection combined with simultaneous detection and utilization of QTLs. Various molecular and physiological studies for the trait are underway and an update will be presented.

Breeding for heat tolerance in wheat, where we are?

Arun Kumar Joshi[1,2]*, Ravi Prakash Singh[3], Uttam Kumar[2], Suchismita Mondal[3], Hans-Joachim Braun[3]

[1]International Maize and Wheat Improvement Center (CIMMYT), G-2, B-Block, NASC Complex, DPS Marg, New Delhi – 110012 India.
[2]Borlaug Institute for South Asia (BISA), G-2, B-Block, NASC Complex, DPS Marg, New Delhi – 110012 India.
[3]International Maize and Wheat Improvement Center (CIMMYT), Int. Apdo. Postal 6-641, 06600 Mexico, DF, Mexico
*E-mail: a.k.joshi@cgiar.org

Breeding for heat tolerance in wheat has been a subject of high significance for warmer areas from the day wheat became a staple crop in these regions. For a long time, terminal heat stress used to be the major issue. However, rising temperatures due to climate change has made heat stress tolerance at early growth stages equally important. In fact, heat stress is becoming more and more unpredictable, occurring at any stage of crop growth and, hence, climate-resilient wheat is the demand of the time. Over years, a successful breeding approach for heat tolerance depended on planting under late-sown conditions, followed by selection for lines that maintained better yields and kernel weight. It was also combined with selecting for early-maturing lines that can escape heat stress and yield well in heat stressed environments. Physiological traits, especially canopy temperature, also became a favorable trait for breeding for heat stress tolerance. A simultaneous enhancement of grain yield potential and heat stress tolerance of early-maturing wheat lines was found beneficial in South Asia to enhance productivity under temperature stress, while reducing the water use by cutting the last irrigation. In last decade, molecular markers were explored for heat tolerance. However, these markers so far lacked robustness and could not become a regular part of most breeding programs and remained restricted to identification of parental lines for breeding programs. Recently, the concept of genomic selection (GS) was introduced for breeding climate-resilient wheat. Our recent experience with GS on breeding climate resilient wheat for South Asia has demonstrated its ability to improve genetic gains during selection, however, phenotyping under heat stress remains critical to train GS models.

How rising temperatures would be detrimental for cool and warm-season food legumes

Harsh Nayyar[1]*, P.Gaur[2], Shiv Kumar[3], Sarvjeet Singh[4], H. Bindumadhava[5], R.M. Nair[6] P.V.Vara Prasad[7], Jitendra Kumar[8], K.H.M. Siddique[9]

[1]Department of Botany, Panjab University, Chandigarh, 160014 India,
[2]ICRISAT, Patancheru 502 324, Greater Hyderabad, Telangana, INDIA,
[3]ICARDA, Rabat 10112, Morocco,
[4]P.A.U., Ludhiana 141004, Punjab, India, Where is 5
[6]World Vegetable Center, South Asia, ICRISAT campus, Patancheru 502 324, Greater Hyderabad, Telangana, INDIA,
[7]Kansas State University, Kansas Manhattan, USA,
[8]Indian Institute of Pulses Research, Kanpur, India,
[9]The UWA institute of Agriculture, The University of Western Australia, Perth WA 6001, Australia
*E-mail: harshnayyar@hotmail.com

Rising temperatures are a major concern for the productivity of food legumes, grown in winter as well as summer-season, especially in tropical and sub-tropical regions. Our studies have indicated marked damage to the reproductive stage, resulting in reduction in pod set and seed yield of chickpea, lentil (cool-season legumes) and mungbean (warm-season legume) under high temperatures. Studies done in controlled and outdoor environments (late sowing) revealed that temperatures >35/20°C (as day and night) were highly detrimental for winter-season legumes; while >38/25°C markedly affected the summer-season legumes (mungbean). Urdbean, (a summer season legume), was found to be relatively more tolerant. The degree of damage varies depending upon the duration, timing and severity of stress. Among the reproductive components, pollen grains were more sensitive, became deformed and showed reduction in pollen viability, reduced germination and pollen tube growth. Stigma receptivity and ovule viability were also inhibited, which affected the pollen germination on stigma surface and restricted tube growth through style, and impaired fertilization to cause flower abortion. Assessment of the physiology of leaves, anthers and styles indicated decrease in sucrose production in all these organs due to inhibition of enzymes, which possibly affected the structural and functional aspects of the pollen grains and tube growth through style. Seed filling is another stage which becomes impaired as a result of inactivation of enzymes related to sucrose production, causing inhibition in sucrose translocation into seeds. Additionally, the composition of the seeds was adversely affected, resulting in small size and poor quality of seeds. The data related to these processes would be presented. Genetic variation for heat tolerance exists in our target legume crops, which needs further probing and use of heat tolerant germplasm in breeding programs. Screening for high temperature tolerance has led to identification of few heat-tolerant genotypes, which are able to maintain their gamete function at high temperature, unlike the sensitive genotypes. Future studies should focus on high throughput phenotyping techniques and/or physiological, biochemical or genetic markers that control the reproductive function. Information about the effects of heat stress on reproductive biology and seed filling events of chickpea, lentil and mungbean will be discussed.

In-sillico characterization of phosphoglucose isomerase (PGI) gene in *Triticum aestivum*

Rakesh Singh[1]

[1]Division of Genomic Resources, NBPGR, New Delhi-110012
*E-mail: *rakesh.singh2@icar.gov.in

Food security is a major concern in India; hence, it is necessary to devise strategies to enhance food grain production. Heat tolerance is a complex trait, with scant knowledge about its genetics, physiology and molecular biology. Activity assays for enzymes involved in grain starch synthesis can be one approach to address this trait. Phosphoglucose isomerase enzyme, also known as glucose-6-phosphate isomerase (GPI), has a major role in glucogenesis i.e. starch synthesis. It has also been reported that there is 50% reduction in starch synthesis with 50% reduction in PGI enzyme, which leads to reduction in grain size. Hence, characterization of the PGI gene is important to know in detail its role in starch synthesis. The protein sequence of PGI enzyme of wheat (*Triticum aestivum*) was downloaded from the protein database of NCBI, and analyzed to find the respective gene in *T. aestivum*. Three homologous gene copies of PGI were present on 1A, 1B and 1D chromosome of *Triticum aestivum*. The orthologous gene copies were also traced in grass family. Multiple Sequence Alignment tool was used for gene as well as protein sequences analysis in homologous as well as orthologous copies of PGI. To further study the gene sequence, gene structures (introns and exons) of homologous as well as orthologous PGI were constructed. Finally, to analyse the structure and function of the homologous and orthologous genes, 3D protein structure were predicted with the help of I-Tasser software which helped in understanding the mode of action of different PGI genes.

Mining for heat stress responsive genes by RNA-Seq based comprehensive gene expression analyses in chickpea (*Cicer arietinum* L.)

Kudapa H*, Agarwal G, Chitikineni A, Gaur PM, Krishnamurthy L, Varshney RK*

International Crops Research Institute for the Semi-Arid Tropics, Patancheru-502324, Hyderabad, India
*E-mail: k.himabindu@cgiar.org

Chickpea (*Cicer arietinum* L.), an important legume crop, is adversely affected by abiotic stresses such as heat, drought and salinity. Amongst these stresses, heat stress is the main abiotic stress that has an adverse impact on almost all aspects of plant development, growth, reproduction and yield. Development of genomic resources is a pre-requisite to develop heat-tolerant chickpea varieties. In this context, RNA-Seqbased transcriptome analysis was performed on vegetative (leaves and roots) and reproductive (leaves, roots and flowers) tissues of six contrasting heat responsive (tolerant - ICCV 92944, ICC 1356, ICC 15614 and sensitive - ICC 5912, ICC 4567, ICC 10685) genotypes. A total of ~514 million reads were generated and alignment of these reads against the available chickpea genome assembly resulted in mapping of 469 (92.9%) million reads. Furthermore, gene expression analysis resulted in identification of 7,670 significantly differentially expressed genes, including 874 novel genes between contrasting genotypes. A set of 56 stress responsive genes belonging to APETALA2/Ethylene Responsive Factor (AP2/ERF), Heat Shock Protein (HSP) and 90 families are selected for further validation using quantitative real time PCR. Moreover >22,456 single nucleotide polymorphisms (SNPs)/INDELs were identified between parental genotypes of two mapping populations (ICC15614 × ICC 4567 and ICC 1356 × ICC 4567). Novel differentially expressed genes along with the marker resources identified in this study should help breeders in developing heat tolerant chickpea varieties in efficient manner.

Towards developing rice genotypes adapted to warming climate

Raveendran M*, Sathishraj R, Mahendran R, Tsutomu Ishimaru, Jagadish Krishna

Tamil Nadu Agricultural University (TNAU), Coimbatore, India
*E-mail: raveendrantnau@gmail.com

Climate change is posing a serious threat to sustained increase in rice productivity and production. Current global climate models predict a mean increase in temperature by 1.0 to 3.7°C over most land areas by late 21st century (IPCC, 2013). Development of heat-resilient rice cultivars is needed for ensuring global food security. Development of reliable screening methods, identification of new donors for heat tolerance and understanding genetic and molecular basis of heat tolerance will accelerate development of heat-tolerant rice genotypes. Our field experiments using popular rice varieties under open and shaded field conditions during summer revealed that spikelet sterility was high under open conditions, and shading was found to offer significant protection of upto 40%. Evaluation of anthesis pattern in a popular rice variety CO 51 revealed that spikelet sterility increased with increase in temperature. Spikelets dehisced at noon time showed increased susceptibility to high temperature stress. Evaluation of an association mapping panel during *kharif* and summer seasons over two years revealed that key variables *viz.,* spikelet sterility, grain yield per plant and head rice recovery, can be used for large-scale evaluation of rice lines for their responses against high temperature. Our results indicated that tissue temperature, particularly leaf/panicle temperature, is a more predictive variable for assessing heat induced spikelet sterility in rice. Simulation studies predicted that 1 degree increase in day temperature during dry season may account for 11.5 % reduction in yield. New heat-tolerant genotypes *viz.,*IR 77298-14-1-2 and IR 1561-228-3-3 from Philippines, *Shonth* from India and *Loku Samba* from Sri Lanka, were also identified, which needs further investigation. Further experiments are in progress through GWAS to identify SNPs associated with heat tolerance traits. Our results have also revealed that early morning flowering trait can be utilized as an effective heat mitigating trait for breeding applications. Further efforts are in progress to develop heat-tolerant rice genotypes through marker assisted introgression of QTLs controlling heat escape (qEMF3) and heat tolerance (qHTSF1.1 and qHTSF4.1) related traits.

Workshop IV

Genetic Engineering for Abiotic Stress

Co-organizers

Prof. Anil Grover

Professor
University of Delhi - South Campus
India

Prof. Ashwani Pareek

Professor
Jawaharlal Nehru University (JNU)
India

Application of genetic engineering to produce stress tolerant rice plants

Anil Grover

Department of Plant Molecular Biology, University of Delhi South Campus, Benito Juarez Road, DhaulaKuan, New Delhi-110021, India
E-mail: anil.anilgrover@gmail.com

Drought and heat are the two most common stresses that affect crops and often these stresses co-occur. Plants respond to these stressful regimes in a coordinated manner through overlapping as well as stress-specific signalling pathways. Our work deals with the production of rice plants with enhanced heat stress tolerance. To search for the transgene(s) which may result in high level of heat stress tolerance, we carried out the transcriptional profile of heat stressed rice (*Oryza sativa* L.) plants using microarray-based method. It was noted that the rice transcript profile is significantly modulated within 10 min of heat stress (HS_10): analysis of differentially expressed genes (DEGs) revealed that 1,556 genes were rapidly up-regulated (≥twofold, $P<0.05$) at HS_10 as compared to 600 down-regulated genes. The enrichment of GO terms protein kinase activity/ protein serine kinase activity, and response to heat and reactive oxygen species in up-regulated genes after HS_10 signifies the role of signal transduction events and reactive oxygen species during early heat stress. The transcriptional profile shows that the response of rice to heat stress involves signal perception and transduction, activation/synthesis of heat shock factors, genomic and proteomic alterations, ROS metabolism and a host of other proteins associated with biochemical, cellular and physiological processes and 'unknown' functions. Rice ClpB/Hsp100 family proteins are constituted of three isoforms localized in three different cell compartments, namely, cytoplasm (ClpB-c), chloroplast (ClpB-p) and mitochondria (ClpB-m). Our focus is to analyse the role of ClpB-c/Hsp100 proteins in governing plant heat stress response.

Two-component signaling (TCS) system in development and abiotic stress response in rice

Priyanka Gupta[1], Soni P[1], Ashutosh Gupta[1], Nongipur R[1], Sneh L Singla Pareek[2], Ashwani Pareek[1],

[1]Stress Physiology and Molecular Biology Laboratory, School of Life Sciences, Jawaharlal Nehru University, New Delhi 110067
[2]Plant Molecular Biology, International Centre for Genetic Engineering and Biotechnology, ArunaAsaf Ali Road, New Delhi 110067
E-mail: ashwanip@mail.jnu.ac.in

Salinity stress accounts for a very significant yield reduction worldwide. The salinity stress response in crop plants is a complex multigenic network, involving crosstalk among multiple signaling pathways. Two-component signaling (TCS) system is highly conserved signaling machinery governing distinct physiological processes in plants, ranging from hormone signaling to abiotic stress signaling. We have identified 51 TCS genes in rice and categorized them into 11 histidine kinases (HKs), 5 histidine phosphotransfer proteins (HPTs) and 36 response regulators (RRs). qRT-PCR analyses revealed the expression of two sensory histidine kinases, OsHK3b and OsHK5, to be significantly induced under salinity and drought. Complementation assays in yeast osmosensing deficient d mutant, Δsln1Δsho1, revealed that both OsHK3b and OsHK5 could function as osmosensors in yeast, but the complementation by OsHK5 is cytokinin dependent. OsHK3b-overexpressing transgenic rice plants were tolerant to osmotic stresses and had higher yield in control as well as salinity and drought stress conditions, compared to the wildtype plants. OsHK3b under-expression in rice resulted in decreased tolerance to salinity and drought as well as decreased yield. Yeast two hybrid and bimolecular fluorescence complementation assays identified OsPHP3 as the interacting partner of OsHK3b. OsPHP3, in turn, interacts with OsRR26, a type-B response regulator localized in the nucleus and cytosol. OsRr26 expression is repressed under osmotic stresses. OsRR26 under-expression resulted in tolerance to salinity in seedlings as compared to the wildtype. The OsRr26 under-expression lines had lower number of tillers and abnormalities in seed development, leading to minimal grain filling and elongated awns. The role of these TCS members in development and stress response will be discussed.

Ensuring the food bowl for masses: raising crops for saline and dry areas

Sneh Lata Singla-Pareek[1] *

[1]Plant Stress Biology, International Centre for Genetic Engineering and Biotechnology, Aruna Asaf Ali Marg, New Delhi-110067, India
*E-mail: snehicgeb.res.in

To meet the rising food demand, there is an urgent need to boost crop production. Thus, we need to accelerate our understanding of reduction in crop yield occurring due to various climatic vagaries. Tremendous progress has been made over the past years in defining the molecular circuitry underlying cross talk between various plant hormones, defence-related machineries, development-associated proteins and environmental response networks. Here, we have attempted to bridge the yield gap in rice for sustainable food production by genetic manipulation of either stress-related genes or genes participating in hormone homeostasis. Taking clues from the stress tolerance capacity of plants over-expressing either the glyoxalase (Gly) pathway for enhanced cellular detoxification or sodium proton antiporters (NHX as well as SOS1), we developed transgenic rice plants expressing two different stack combinations of stress associated genes viz. GlyI, GlyII along with NHX1 or with SOS1. Evaluation of these multigenic transgenic plants via assessment of various morphological, physiological and agronomical parameters indicated improved tolerance to abiotic stress and enhanced yield. Simultaneously, we also raised transgenic rice plants with RNAi based knockdown of one of the key genes of cytokinin metabolism i.e., cytokinin oxidase-2. These transgenic plants showed better yield under both non-stress and stress conditions. Considering the complexity of stress response, our results suggest that a combinatorial approach targeting diverse pathways is better than the 'single gene approach' to tame the deleterious effects of environmental extremes of high salt and water deficit under field conditions.

Identification and validation of genes for water use efficiency and grain yield under drought in rice

Ambavaram M[1],[2], Krishnan A[1],[3],Gupta C[4], Basu S[4],Ramegowda V[4], Kumar A[4], Batlang U[1],[5], Ritu Mihani[4], Yingling S[4], Thomas J[4], Pereira A[1],[4]*

[1]Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA, USA
[2]MetabolixInc, Cambridge, MA, USA
[3]Lewis-Sigler Institute for Integrative Genomics, Princeton University, NJ, USA
[4]Crop Soil, and Environmental Sciences, University of Arkansas, Fayetteville, AR, USA
[5]Botswana College of Agriculture, Gaborone, Botswana
*E-mail: apereira@uark.edu

The response of plants to abiotic stresses is a complex system, from signal perception and transduction to protection. To dissect the complex traits of stress tolerance and grain yield in rice, we developed a Rice Environmental Coexpression Network (RECoN) and other regulatory gene networks to predict genes involved in stress regulatory pathways. A transcription factor termed HYR (Higher Yielding Rice) was found positively associated with photosynthetic carbon metabolism and other biological processes affected by environmental stresses. Over-expression of HYR in rice cultivars showed an increase in photosynthesis and vegetative growth; and higher grain yield and quality under control, drought and high night time temperature treatments at critical reproductive stages. Gene expression and ChIP analysis of HYR rice revealed the HYR-regulated pathway determining PCM and yield components, supporting the role of HYR as a key regulator of grain yield and stress tolerance. Morpho-physiological analysis of other predicted stress-responsive regulatory genes using knockout mutants revealed a class of mutants compromised in growth under drought (GUD), showing reduction in yield under stress conditions. To identify natural variation for stress response and productivity in rice, we conducted GWAS on the USDA mini-core collection and identified putative loci for multiple productivity traits, which are being characterized in a systems genetics approach using networks predicting biological functions. Integration of transcriptome data from mutants and over-expression lines of stress tolerance genes, as well as diverse stress tolerant genotypes, is being used to construct integrated regulatory networks to predict stress response and productivity in rice.

Engineering crops for enhanced tolerance to multiple abiotic stresses and improved N use efficiency via manipulating novel-stress associated proteins

Dhankher OP[1], Tomar P[1]*, Dixit A[1], Paulose B[2]

[1]Stockbridge School of Agriculture, University of Massachusetts Amherst, MA 01003
[2]Department of Plant Biology, Michigan State University, East Lansing, MI 48824-1312
*E-mail: parkash@umass.edu

Environmental stresses adversely affect the growth and productivity of crop plants and, thus, are serious threats to agriculture. Recently, members of Stress-Associated Proteins (SAP) gene family have been suggested to play significant roles in multiple abiotic stress responses in rice. However, their exact functions/ molecular mechanisms are not known. In *Arabidopsis* and rice genomes, 14 and 18 genes respectively, coding for SAP related proteins have been identified. Over-expression of AtSAP13 provided strong tolerance to multiple abiotic stresses such as salt, drought, and various toxic metals including zinc, cadmium, and arsenic, without causing a significant difference in metals accumulation. These plants attained significantly higher biomass and longer roots as compared to wild type plants under the stress condition. Whereas, the over-expression of AtSAP10 provided strong tolerance to heat, salt, zinc, nickel and manganese. We hypothesized that the expression of SAP genes might be regulated via the interaction of *cis*-elements present in the SAP promoters with abiotic stress related *trans* factors via protein-DNA interactions under different abiotic stresses. Through yeast one hybrid assay, we have proved this hypothesis and identified several transcription factors such as DREB, ERE, ZIP, and HSE that are interacting with the SAP promoters. Additionally, we have identified and over-expressed gamma-glutamyl cyclotransferase (GGCT), a gene from another stress related gene family, involved in GSH homeostasis. Over-expression of GGCT not only provided strong tolerance to oxidative stresses, but also improved N use efficiency in plants under stress conditions. Therefore, these novel stress associated genes are ideal for developing climate-resilient crops with enhanced tolerance to multiple abiotic stresses.

Functional diversity of plant stress hormone abscisic acid receptors in rice

Santosh Kumar VV[1], Shashank K Yadav[1], Rakesh K Verma[1], Sanya Shrivastava[1], Viswanathan Chinnusamy[1]*

[1]Division of Plant Physiology, ICAR-Indian Agricultural Research Institute, New Delhi-110012, India
*E-mail: viswanathan@iari.res.in

Rice, the major food crop of the world, is highly sensitive to drought stress. For environmental sustainability and food security, it is imperative to enhance WUE and drought tolerance of rice. Since the plant stress hormone ABA plays a key role in plant development and stress responses, ABA receptors (ABARs) are important targets for genetic improvement of WUE and drought tolerance of plants. Genome-wide analysis identified 12 ABAR homologs in rice genome. Real-time qRT-PCR expression analysis of *ABARs* in different tissues and stress conditions revealed differential expression patterns, suggesting non-redundant roles of *ABARs* in development and stress responses. The functional specificity/redundancy of ARARs in development and biotic and abiotic stress tolerance of rice needs to be established. Hence, we initiated work on functional characterization of ABAR gene family in rice by over-expression, RNAi silencing and CRISPR-Cas9 genome editing. Since, constitutive over-expression of ABAR6 severely impaired the plant development, transgenic rice lines with stress-inducible over-expression of ABARs were developed. These transgenics were confirmed by PCR, Southern blot and qRT-PCR analyses. Analysis of drought tolerance of *RD29A:ABAR6* transgenic rice lines in pot culture under greenhouse conditions revealed that *RD29A:ABAR6* transgenic rice lines use less water, and are more tolerant than non-transgenic lines. ABAR6 enhances drought tolerance of rice by enhancing dehydration avoidance through transpiration minimization, and cellular tolerance to dehydration. Functional diversity of ABARs was evident from differential developmental and stress phenotypes of ABARs. Precise regulation of ABARs can greatly save water and confer yield stability to rice.

Drought tolerant rice: metabolic engineering and dissecting proteomics in understanding the system

Karabi Datta[1]*, Swapan Datta[1]

[1]Translational Research laboratory for transgenic crops, Botany Department, University of Calcutta, Kolkata-700019
*E-mail: krbdatta@yahoo.com

Abiotic stress is a complex phenomenon which is less understood but causes severe yield losses in major crops globally. Since decades, work is in progress on developing climate-resilient crops using conventional breeding, molecular breeding, and genetic engineering to come up with designer crops suitably adapted across the ecosystems. With advancement of new tools including CRISPER-genome editing, new insights on better crop development might be gained in the near future. Earlier we developed *DREB1A*-based engineered rice driven by the drought/salinity responsive promoter rd29, and showed enhanced drought-tolerant rice (Datta et al 2012). It is well known that plant tolerance to drought is mediated by a number of physiological and biochemical processes, which means that it is a multi-gene trait. The activation of such genes must involve a distinctive set of transcription factors. By over-expressing transcription factor gene(s), it may be possible to change or to increase the level of expression of several downstream target genes responsible for drought (Varshney et al., 2011). Based on drought-tolerant rice plants by over-expressing *Arabidopsis DREB1A*, the metabolic network regulated in the drought-tolerant transgenic rice has been studied. We have demonstrated the comparative proteome analysis between the roots of wild type and transgenic DREB1A plants under drought stress condition. The study identified that stress- and defense-related proteins are especially up-accumulated under drought stress in both the plants (Paul et al 2016). A novel protein, R40C1, was reported to be significantly up-accumulated in roots of transgenic plants, which is likely to play a significant role in generation of drought-tolerant plants.

Genetic engineering approaches for drought tolerance in grain legumes: progress and prospects

Pooja Bhatnagar-Mathur[1]*, Vincent Vadez[1], Kiran K Sharma[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Telangana, India.
*E-mail: p.bhatnagar@cgiar.org

Inadequate water resources and the ensuing climate change over the recent years are posing major challenges for food production. Drought in various forms is responsible for major losses to global crop production, affecting millions of resource-poor farmers in the semi-arid tropics. While developing drought-tolerant cultivars could alleviate such economical strains, genetic improvement of grain legumes is difficult to achieve through conventional means due to their highly self-pollinating characteristics and conserved genomes with very little variability. To generate additional genetic diversity, we attempted to enhance drought tolerance in chickpea and peanut through genetic engineering approaches. Independent transgenic events with high transpiration efficiencies (TE) and desirable root and shoot traits were selected for further evaluation under a series of environments under glasshouse and confined field trials to comprehensively study the component traits of drought, and understand the stress adaptive mechanisms. Relationship between TE and its surrogate traits were explored, besides studying the role of biochemical changes in the anti-oxidative machinery under water-limiting conditions. Evaluations were based on water capture, effective use of captured water for producing biomass via photosynthesis, and converting assimilates into harvestable yield. Accordingly, critical assessment of drought tolerance and yield under contained field conditions proved the effectiveness of several events that showed substantial yield improvement under drought stress, without any accompanying yield penalty under irrigation. Details of various strategies to develop drought tolerant transgenc plants, and the results and scope of our own studies will be discussed.

Workshop V

GWAS and GS for Crop Improvement

Co-organizers

Dr. Jose Crossa

Ex-Head, Biometrics and Statistics Unit
International Maize and Wheat Improvement
Center (CIMMYT)
Mexico

Dr. Hari D Upadhyaya

Head - Genebank
International Crops Research Institute for
the Semi-Arid Tropics (ICRISAT)
India

Genomic-enabled prediction using kernel models with genotype × environment interaction

Jose Crossa[1]*, Massaine Bandeirae Sousa[2], Jaime Cuevas[3], Diego Jarquín[4], Paulino Pérez-Rodríguez[5], Juan Burgueño[1], Gustavo de los Campos[6], and Roberto Fritsche-Neto[2]

[1]Biometrics and Statistics Unit, International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600, Mexico DF, Mexico
[2]Department of Genetics, Luiz de Queiroz College of Agriculture, University of São Paulo, Piracicaba, São Paulo, Brazil
[3]University of Quintana Roo, Chetumal, Quintana Roo, Mexico
[4]Agronomy and Horticulture Department, University of Nebraska, 321 Keim Hall, Lincoln, NE, USA 68583-0915
[5]Colegio de Postgraduados, Montecillos, Edo. de Mexico, Mexico;
[6]Department of Epidemiology & Biostatistics, Michigan State University, 909 Fee Road, Room B601, East Lansing, MI 48824, USA.
*E-mail: j.crossa@cgiar.org

Implementation of genomic selection (GS) strategies in plant breeding needs to model, and predict genotype × environment interaction G×E. In this study we compare the prediction accuracy of four genomic prediction models: (1) single environment model (SE), (2) reaction norm model (RN) across environments (RNA), (3) RN with G×E (RNG×E), and (4) a G×E model that estimates the genomic main effect and the specific environment main effect. Each of the four models was computed with two kernel methods, linear GBLUP and a non-linear Gaussian kernel (GK). The eight model-method combinations were applied to extensive maize data sets having different number of maize entries evaluated in different environments and for grain yield, and plant and ear height. Results show that for grain yield models incorporating G×E have higher prediction accuracy than single-environment models, and that model with the non-linear Gaussian kernel method had superior predictive ability than models with the GBLUP method. The G×E model with the Gaussian kernel (G×E-GK) had the highest prediction accuracy closely followed by the reaction norm with G×E fitted with the non-linear kernel (RNG×E-GK). Non-linear kernels are more flexible than linear kernels and allow capturing small cryptic marker × marker interaction as well as marker × environment interaction.

Integrating statistical and crop growth modelling approaches to facilitate breeding for water-limited environments

Daniela Bustos-Korts[1], Marcos Malosetti[1], Martin P. Boer[1], Willem Kruijer[1], Scott Chapman[2], Fred van Eeuwijk[1]*

[1]Wageningen University and Research, Wageningen, the Netherlands
[2]CSIRO Agriculture, Australia
*E-mail: fred.vaneeuwijk@wur.nl

The combination of statistical and crop growth modelling provides a powerful way of studying the genotype by environment interactions (GEI) that occur between water-limited and well-watered conditions. For the latter conditions, statistical models for GEI are typically mixed models with terms for QTLs and QTL by environment interactions (QEI), as well as terms for residual genetic and non-genetic effects. The QTL terms are often chosen fixed, while the polygenic terms are random with variance-covariance structures that are constrained by genomic and pedigree relationships for the genotypes, while for the environments constraints are defined from similarities based on soil and meteorological information. This type of mixed model can be used for QTL detection, but it also serves as a basis for genomic prediction. Information on drought stress tolerance as obtained in phenotyping platforms or from crop growth models can be inserted in the above mixed model as fixed genotypic covariates to explain GEI terms, but it can also be introduced in the random part of the model to define a genetic covariance term for the field performance. Equally, environmental characterizations, for example as calculated from crop growth models, can be introduced as fixed environmental covariates and as environmental covariances. We extended the above multi-environment mixed model for GEI by introducing a multi-trait perspective capturing the dynamics of yield and yield components where we hybridize statistical and crop growth approaches. We illustrate our approach on real and simulated Australian wheat data using APSIM.

A simpler method for GWAS and the use of significant markers in genome selection

Juan Burgueño

International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico
E-mail: J.Burgueno@cgiar.org

Genome wide association studies and genome selection have become the most commonly used genetic tools in plant breeding in the last 15 years. However, many questions continue to open up, due to many practical situations in which GWAS can be applied and for which no standard method exists. In this talk I will pay attention to two issues. Models for GWAS usually assume that the vector of BLUP or adjusted means following a normal distribution with common variance, however BLUP come from an experiment that introduces correlation between BLUPs. We will present a method which takes in account this situation and does not need to adjust a mixed model for each marker; therefore it avoids the use of approximations to produce results quickly. The method adjusts the data in one step considering any covariables and structure of the data in a mixed model framework. After the vector of BLUP and their matrix of variance covariance are used to build a test to measure the significance of the effect for each marker. Genome wide association studies results have been used to improve prediction accuracy in genome selection, with der the idea that significant markers should provide better predictions than a larger set of markers with unknown effect, and at a lower cost. However a good predictive model will not necessarily be the model with most significant effects. To use this approach, we need to know the significant markers, but they vary for different sets of genotypes and environments. Results obtained in CIMMYT showed that using markers with unknown effects continues to be a good option.

Genomic selection in hybrid breeding

Zhao YS., Mette M. F., Reif J. C.*

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, 06466, Germany;
*E-mail: reif@ipk-gatersleben.de

While hybrid breeding is widely applied in outbreeding species, for many self-pollinating crop plants, it has only recently been established. This may have been a reason for the limitations of methods available for hybrid performance prediction, in particular when established heterotic pools were absent. Genomic selection has been suggested as a promising approach to resolve these limitations. We briefly introduce the principles of genomic selection as an extension of marker-assisted selection using genome-wide high-density molecular marker data and discuss the advantages and limitations of currently used algorithms. Including the outcome from a recent extended approach to hybrid wheat as a timely example, we summarize current progress in empirical studies on the application of genomic selection for prediction of hybrid performance. Here, we put emphasis on the factors affecting the accuracy of prediction, pointing in particular to the relevance of relatedness, genotype x environment interaction and experimental design. Finally, we discuss future research needs and potential applications.

Genomic-enabled prediction model with genotype × environment interaction in elite chickpea lines

Manish Roorkiwal[1], Diego Jarquin[2], Ankit Jain[1], Vanika Garg[1], Sandip Kale[1], Muneendra K. Singh[1], Samineni Srinivasan[1], Pooran M. Gaur[1], Abhishek Rathore[1], Bharadwaj Chellapilla[3], Shailesh Tripathi[3], Jose Crossa[2], Rajeev K. Varshney[1],[4]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]International Maize and Wheat Improvement Center (CIMMYT), Mexico, Mexico
[3]Indian Agricultural Research Institute, Delhi, India
[4]School of Plant Biology and the Institute of Agriculture, The University of Western Australia (UWA), Crawley, Australia
*E-mail: r.k.varshney@cgiar.org

Genomic selection (GS) allows safe phenotyping and reduces cost and shortening selection cycles. Incorporating of genotype × environment (G×E) interactions in genomic prediction models improves the predictive ability of lines performance across environments and in target environments. Phenotyping data on a set of 320 elite chickpea breeding lines on different traits (e.g., plant height, days to maturity, and seed yield), from three consecutive years for two different treatments at two locations were recorded. These lines were genotyped on DArTseq(1.6K) and Genotyping-by-Sequencing (GBS; 89K SNPs) platforms. Five different models were fitted, four of which included genomic information as main effects (baseline model) and/or G×E interactions. Three different cross-validation schemes that mimic real scenarios that breeders might face on fields were considered to assess the predictive ability of the models (CV2: incomplete field trials; CV1: newly developed lines; and CV0: new previously untested environments). Different prediction models gave different results for the different traits; however, some interesting patterns were observed. For CV1, analyzing yield seed interaction models improved baseline counterparts on an average between 55 and 92% using DArT and DArT combined with GBS data, respectively [between 9 and 112% for all traits]. While for CV2 these improvements varied b tween 65 and 102% [between 8 and 130% remaining traits]. In CV0, no clear advantage was observed considering the interaction term. These results suggest that GS models hold potential for breeder's applications on chickpea cultivar improvements.

Harnessing the genomic diversity of Asian cultivated rice (*Oryza sativa* L.): SNPs, pan-genomes and structural variation

Wensheng Wang[1], Zhiqiang Hu[2], Zhichao Wu[1,3], Min Li[1,3,4,5], Shuaishuai Tai[6], Kenneth L. McNally[7], Jianlong Xu[1,3,4], J. Ali[7], Hongliang Zhang[8], Binying Fu[1,4], Yongming Gao[1,4], Chen Sun[2], Fan Zhang[1], Xinyuan Zhang[3], Fei Shen[8], Xiao Cui[2], Hong Yu[9], Dmytro Chebotarov[7], Tianqing Zheng[1], Zichao Li[8], Miaolin Chen[2], Yongli Zhou[1,4], Xiuqin Zhao[1], Yue Zhao[2], Rui Li[2], Ben Jia[2], Jingyuan Lu[2], Xianchang He[2], Zhaotong Dong[2], Jianxin Shi[2], Jing Li[2], Dabing Zhang[2], Zhen Yue[6], Jiayang Li[1,9], Xiaodong Fang[6], RamilMauleon[7], Millicent Sanciangco[7], JinjieLi[8], Ye Yin[6], ChaochunWe[2,*], JueRuan[3,*], Gengyun Zhang[4,6,*], Nickolai Alexandrov[7,*], Zhikang Li[3,4,*]

[1]Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing 100081, China
[2]School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai200240, China;
[3]Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences 518120, Shenzhen, China;
[4]Shenzhen Institute for Innovative Breeding, Chinese Academy of Agricultural Sciences, Shenzhen 518120, China;
[5]Anhui Agricultural University, Hefei 230036, China;
[6]BGI-Shenzhen, Shenzhen 518083, China;
[7]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines;
[8]China Agricultural University, Beijing 100193, China;
[9]Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing 100101, China
*E-mail: lizhikang@caas.cn

Asian cultivated rice (*Oryza sativa* L.) is the staple food for the half world population, with rich diversity within species. We present here results from comprehensive analyses of the genome resequencing data of a core collection of 3,000 rice accessions released by the 3,000 Rice Genomes Project. Three important aspects of the population genomic diversity within *O. sativa* were revealed. First, over 42 million SNPs and ≥3 million small indels were discovered against five reference genomes. Population structure analysis discovered previously-unreported sub-populations within *O. sativa*. Secondly, the pan genome (PG) analyses led us to discover more than 12,000 novel protein-coding genes that are absent in the reference Nipponbare genome. The rice PG consists of 56.7% core genes that are essential and present in all rice lines, and 43.3% distributed genes that are present in only some of rice accessions and show a high level of diversity. Thirdly, we discovered more 90,000 structural variations (SVs) > 100 bpin the 3,000rice genomes, most of which are small transpositions and deletions. The SNPs, PG and SV variation clearly differentiate the 3,000 accessions into four major varietal groups, and multiple sub-populations within them. Significantly reduced diversity was found in genomic regions where over 1,000 agronomically important and domestication-related genes locate. GWAS analysis for grain length, grain width and bacterial blight resistance revealed both novel and previously reported loci, demonstrating the utility and effects of population structure for gene/QTL discoveries. The tremendous genome diversity and population differentiation within *O. sativa* are inferred to be the consequences of the long process of diploidization and transition from its direct outcrossing ancestor to a predominant self-fertilization species during evolution. Our results provide additional evidence supporting the hypothesis that rice domestication and its subsequent cultivation took place repeatedly at different times and locations across South Asia, S. East Asia and China. Now, all the SNP, PG and SV data are publicly available for further analyses and confirmation. Tremendous efforts have also been taken to phenotype the 3,000 rice accessions to exploit genes and alleles for important traits of rice and to establish a comprehensive database for rice functional genomics and molecular breeding for future rice improvement.

Integrative genome-wide association studies (GWAS) to understand complex genetic architecture of quantitative traits in chickpea

Parida SK[1]*, Kujur A[1], Bajaj D[1], Das S[1], Srivastava R[1], Badoni S[1], Laxmi[1], Thakro V[1], Basu U[1], Daware A[1], Upadhyaya HD[2], Tripathi S[3], Bharadwaj C[3]

[1]National Institute of Plant Genome Research (NIPGR), New Delhi, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[3]Division of Genetics, Indian Agricultural Research Institute (IARI), New Delhi, India
*E-mail: swarup@nipgr.ac.in

Development of high-yielding stress-tolerant chickpea cultivars is essential to enhance its yield potential and productivity amidst climate change scenario. Unfortunately, superior lines/recombinants producing higher pod and seed yield under stress are not available in world chickpea collection. Therefore, genetic dissection of complex stress tolerance and yield-contributing quantitative traits is the prime objective in current chickpea genomics and breeding research. Our study employed diverse GWAS-assisted integrated genomic strategies involving classical genetic inheritance analysis, QTL mapping, differential transcript profiling, molecular haplotyping and haplotype-based gene domestication/evolution study for rapid quantitative dissection of complex yield and stress tolerance traits in chickpea. To accomplish this, multi-location/years replicated yield traits-related field phenotyping and high-throughput marker genotyping information generated from numerous natural germplasm accessions (association panel) and multiple intra- and inter-specific mapping populations of chickpea were deployed in the aforesaid combinatorial genomic approaches. These analyses delineated 12 novel alleles and six haplotypes from 10 transcription factor genes and 16 major QTLs/eQTLs governing yield and stress tolerance traits that were mapped on 10 ultra-high density chickpea genetic linkage maps. The superior natural alleles/haplotypes of two major genes (QTLs) regulating seed weight and pod/seed number identified from cultivated and wild *Cicer* gene pools are being introduced into multiple high-yielding Indian varieties of chickpea for its marker-assisted genetic improvement. The potential molecular signatures delineated using integrated genomics-assisted breeding strategies have functional significance to understand the molecular genetic mechanism and natural allelic diversity-led domestication pattern underlying these complex quantitative traits at a genome-wide scale, leading to fast-paced translational genomics for chickpea genetic enhancement. These essential outcomes will be useful for devising the most efficient strategies to produce high-yielding climate-resilient chickpea cultivars for sustaining global food security.

Understanding the genetics of biomass formation in barley assessed by non-invasive phenotyping

Neumann K[1], Dhanagond S[1], Zhao Y[1], Liu G[1], Kilian B[1],[2], Reif JC[1], Graner A[1]

[1]Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, 06466, Germany,
[2]Global Crop Diversity Trust (GCDT), Bonn, 53113, Germany
E-mail: neumannk@ipk-gatersleben.de

Barley is the fourth most important cereal crop worldwide and Germany is the third largest barley-producing country. Despite the outstanding environmental adaptability of barley, which outcompetes any other cereal crop, future yield improvement is hampered by biotic and abiotic stresses.In Germany, barley yields showed a strong fluctuation during the last 15 years, reflecting the impact of climate change. One factor is the increased frequency of drought events, especially in spring during the vegetative growth phase. Understanding the genetics of biomass formation under well-watered and seasonal drought conditions can provide a basis for stabilizing and increasing grain yield. In our studies, a pot based imaging system was used to evaluate daily biomass assessed in a diverse reference collection of barley developed from the IPK genebank. The experimental setup comprised a drought period of 18 days with watering regime corresponding to 20% field capacity (well-watered: 90%) and a 14- day long recovery period. Drought treatment started in the tillering phase and experiments ended around tipping time. We obtained high heritability for biomass under both conditions over the whole observation period, which made this trait amenable for genome-wide association scans (GWAS). GWAS were performed for each day independently within the well-watered and within the drought stress treatments. Different genetic loci were identified for early and later vegetative biomass. Similarly, specific loci were identified for biomass under well-watered and stress conditions. Results point at candidate genes involved in plant growth hormone regulation and phenology. Although plants were quickly recovering upon the end of drought, the results demonstrate a strong effect of drought on grain yield. In addition, we observed a positive correlation of vegetative biomass to grain yield, which might blaze a trail to further increase yield potential.

Workshop VI

Drought Stress and Aflatoxin Contamination in Crops

Co-organizers

Dr. Baozhu Guo

Research Plant Pathologist
United States Department of
Agriculture - Research Service
USA

Dr. C Corley Holbrook

Research Geneticist
United States Department of
Agriculture - Research Service
USA

Dr. Manish Pandey

Scientist - Groundnut Genomics
International Crops Research
Institute for the Semi-Arid Tropics
India

Deciphering drought-induced response patterns at the biochemical and molecular level in maize related to aflatoxin contamination resistance

Yang L[1],[2], Fountain JC[1],[2], Jiang T[3], Ji P[1], Ni X[4], Lee RD[5], Kemerait RC[2], Chen S[6], Guo B[1],*

[1]USDA-ARS, Crop Protection and Management Research Unit, Tifton, GA, USA
[2]Department of Plant Pathology, University of Georgia, Tifton, GA, USA
[3]Northeast Forestry University, Key Laboratory of Forest Tree Genetic Improvement and Biotechnology, Harbin, China
[4]USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton, GA, USA
[5]Department of Crop and Soil Sciences, University of Georgia,Tifton, GA, USA
[6]Interdisciplinary Center for Biotechnology Research, Proteomics Facility, University of Florida, Gainesville, FL, USA
*E-mail: baozhu.guo@ars.usda.gov

Drought stress influences crop growth, decreases yield, and exacerbates *Aspergillus flavus* infection and pre-harvest aflatoxin contamination. In order to dissect drought stress-induced responses in maize, genotypes with contrasting levels of drought tolerance were used to investigate the physiological, biochemical, and molecular changes in seedlings and kernels under drought stress. Seedlings of drought-sensitive genotypes (B73 and Lo1016) exhibited higher production of reactive oxygen species (ROS) and nitric oxide levels, and rapid increases in stress-responsive enzyme activities compared to the tolerant lines (Lo964, Va35 and Grace E-5). Kernel proteomic analyses revealed that B73 exhibited a vigorous, induced response to stress while Lo964 displayed stable, constitutive expression of defense proteins. Comprehensive metabolomics analyses of developing kernels also found that drought stress induced higher sugar accumulation, and energy and unsaturated fatty acid metabolism in B73. Contrarily, Lo964 had higher sphingolipid metabolite accumulation, a higher glycolysis rate, and a lower TCA cycle rate in response to drought stress. In addition, pre-incubation of kernels in high humidity prior to inoculation during *A. flavus*-kernel screening assays resulted in enhanced visible sporulation and reduced aflatoxin production. Biochemical investigation showed that pre-incubation resulted in increases in ROS content at 2-3 days after inoculation (DAI) while kernels lacking pre-incubation exhibited increases at 3-4 DAI. Given that aflatoxin production is most active 3-4 DAI, reduced ROS exposure during this key period following pre-incubation may contribute to reduced contamination. These results indicate that drought sensitivity is associated with diverse metabolic processes in maize, and that ROS production may contribute to the exacerbated aflatoxin contamination during drought stress.

Breeding peanut with drought tolerance and reduced aflatoxin contamination

Holbrook CC*[1], Ozias-Akins P[2], Guo BZ[1], Wilson DM[2]

[1]USDA-ARS, Tifton, GA, 31794. USA.
[2]Univ. of Georgia, Tifton, GA, 31794. USA.
*E-mail: Corley.Holbrook@ars.usda.gov

Aflatoxin contamination costs the U.S. peanut (*Arachis hypogaea* L.) industry over $20 million annually. Our objective is to develop peanut cultivars with resistance to pre-harvest aflatoxin contamination (PAC) to reduce these costs. We have developed screening techniques that can measure genetic differences in aflatoxin contamination and have been using these techniques to identify genotypes that exhibit relatively low PAC in multiple environments. Significant reductions in PAC have also been identified in peanut genotypes with drought tolerance. These sources of resistance to PAC have been crossed with cultivars and breeding lines that have high yield. Evaluation of numerous breeding populations has identified several families and individual breeding lines that have relatively low PAC and relatively high yield. To increase breeding efficiency, studies on mechanisms of resistance to PAC are being conducted. The most promising mechanisms identified thus far are resistance to drought and resistance to the peanut root-knot nematode. Late generation breeding lines have been developed with resistance to drought, several of which also exhibited reduced aflatoxin contamination in multiple environments.

Aflatoxin permissive transcriptional states in peanut seeds

Clevenger J[1], Korani W[1], Chu Y[1], Karikari A[1], Holbrook CC[2], Ozias-Akins P[1]*

[1]University of Georgia, Institute of Plant Breeding, Genetics & Genomics, Tifton, GA 31793 USA
[2]USDA-ARS, Tifton, GA 31794 USA
*E-mail: pozias@uga.edu

Pre-harvest aflatoxin contamination of peanut seeds is highly variable and greatly enhanced under conditions of late season abiotic stress. To increase the probability of aflatoxin contamination, pod-zone drought was simulated in the field using rain-out shelters. *Aspergillus flavus/parasiticus* infected seeds without or contaminated with aflatoxin, plus uninfected controls, were harvested in order to compare their transcriptional landscapes. Relatively few genes were differentially expressed due to *Aspergillus* invasion among three genotypes, although over 500 genes were differentially expressed between seeds without or contaminated with aflatoxin. A significant difference in expression was observed for genes involved in ABA biosynthesis/activation, up-regulated in uncontaminated infected or uninfected seeds, while genes involved in repression of ABA signaling were upregulated in contaminated seeds. ABA signaling also regulates fatty acid biosynthesis, reviving an examination of the role seed fatty acid composition may play in aflatoxin contamination of peanut. To extend transcriptional profiling to post-harvest infection/aflatoxin contamination, seeds of ten peanut genotypes were infected by a Green Fluorescent Protein (GFP)-expressing strain of *A. flavus* and two genotypes representing resistant and susceptible responses were selected for in-depth analysis.

Drought affects A. *flavus* and *aflatoxin* contamination and their association with drought tolerant traits in peanut genotypes

Jogloy S[1],[2]*,Vorasoot N.[1]Arunyanark A[3], Girdthai T[4], Koolachart R[5]

[1]Department of Plant Science and Agricultural Resources, Faculty of Agriculture, Khon Kaen University, Khon Kaen, Thailand
[2]Peanut and Jerusalem Artichoke Improvement for Functional Food Research Group, Khon Kaen University, Khon Kaen, Thailand
[3]Department of Agronomy, Faculty of Agriculture, Kamphaeng Saen Campus, Kasetsart University, Nakhon Pathom, Thailand
[4]Suranaree University of Technology, Nakhon Ratchasima, Thailand
[5]Nong Khai Rubber Regulatory Center, Department of Agriculture, Nong Khai, Thailand
*E-mail: sjogloy@gmail.com

Drought not only reduces economic yield of peanut, but also increases *A. flavus* colonization and aflatoxin contamination. The effect of drought on aflatoxin contamination depends on plant growth stage, and the duration and severity of drought. The objectives of these studies were to i) investigate the effect of terminal and long-period drought on physiological traits related to drought resistance and aflatoxin contamination in peanut genotypes and ii) examine the association between drought tolerance traits and aflatoxin contamination under drought conditions. Peanut genotypes were evaluated under well watered and drought stress conditions at Khon Kaen University, Thailand. Our results revealed that terminal drought and long-period drought enhanced *A. flavus* colonization and aflatoxin contamination. The studies showed that drought tolerance traits, SPAD chlorophyll meter reading (SCMR), specific leaf area (SLA), relative water content (RWC) and root length density (RLD), were associated with aflatoxin contamination. Peanut genotypes with high SCMR, RWC and % RLD and low SLA had lower *A. flavus* colonization and aflatoxin contamination. The results indicated that some physiological traits related to drought resistance can be use as indirect selection criteria for reduced *A. flavus* colonization and aflatoxin contamination under drought prone environments.

Management of aflatoxin contamination in groundnut by enhancing host-plant resistance

Liao B[1]*, Lei Y[1], Jiang H[1], Yan L[1], Wan L[1], Huang L[1], Zhou X[1], Luo H[1], Chen Y[1], Wang H[1], Pandey M[2], Sudini H[2], Upadhaya UD[2], Varshney RK[2]

[1]Oil Crops Research Institute of Chinese Academy of Agricultural Sciences (OCRI-CAAS), Wuhan, China
[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: lboshou@hotmail.com

Groundnut (*Arachis hypogaea*) currently ranks first among oilseed crops in China in terms of annual production, average crop and oil yield, and total crop value. Aflatoxin contamination has been a crucial concern for food safety and market competitiveness in groundnut products in most warm regions where heat and drought stresses are generally serious. Genetic enhancement for resistance to aflatoxin has been regarded as the most cost-effective approach to reduce contamination risk in this crop. Based on continuous evaluation of groundnut germplasms, including the core collections from China, ICRISAT and USA, several lines have been identified as resistant to *Aspergillus* infection or aflatoxin production. Recently, more research efforts have been made in identifying materials with shell resistance to *Aspergillus* infection, through cooperation with ICRISAT. Efforts have also been made in identifying and enhancing germplasm lines with diverse resistance components or mechanisms. Several ICRISAT breeding lines have been used in improving aflatoxin resistance of groundnut in Chinese institutions. An elite cultivar developed at OCRI-CAAS, Zhonghua 6, with desirable resistance to aflatoxin production, bacterial wilt and pot rot has been extensively used in central China. Through RNA-seq profiling, it was found that relative higher resveratrol content in Zhonghua 6 was a key mechanism for its reduced aflatoxin production under high infection pressure of *Aspergillus* sp.

Drought stress and aflatoxin contamination: transcriptional responses of *Aspergillus flavus* to oxidative stress are related to stress tolerance and aflatoxin production capability

Fountain JC[1],[2], Bajaj P[3], Yang L[1], Pandey MK[3], Nayak SN[3], Kumar V[3], Jayale AS[3], Chitikineni A[3], Lee RD[4], Scully BT[5], Kemerait RC[1], Varshney RK[3],*, Guo B[2],*

[1]Department of Plant Pathology, University of Georgia, Tifton, GA, USA
[2]USDA-ARS Crop Protection and Management Research Unit, Tifton, GA, USA
[3]International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana, India
[4]Department of Crop and Soil Sciences, University of Georgia, Tifton, GA, USA
[5]USDA-ARS, U.S. Horticultural Research Laboratory, Ft. Pierce, FL, USA
*E-mail: r.k.varshney@cgiar.org, baozhu.guo@ars.usda.gov

Oilseed crops such as maize and peanut are staple food crops which are vital for global food security. The contamination of these crops with carcinogenic aflatoxins during infection by *Aspergillus flavus* under drought stress conditions is a serious threat to the safety of these commodities. In order to better understand the role of aflatoxin production in the biology of this pathogen under environmental stress, a collaborative transcriptome project was undertaken to examine the transcriptional responses of toxigenic and atoxigenic isolates of *A. flavus* to oxidative stress. Selected isolates were cultured in aflatoxin production-conducive and non-conducive media amended with varying levels of H2O2. Isolates which possessed greater tolerance to H2O2 stress and aflatoxin production capability exhibited fewer differentially expressed genes (DEGs) than those which possessed less tolerance and lower aflatoxin production. Primary metabolic mechanisms were also stimulated in response to stress along with antioxidant enzyme-encoding genes. Genes related to fungal development such as aminobenzoate degradation genes and conidiation regulators were also differentially expressed in response to stress. Secondary metabolite biosynthetic processes also formed a large component of the isolate responses to stress including those for aflatoxin, aflatrem, and kojic acid. Co-expression analyses also showed that aflatoxin biosynthetic gene expression along with antioxidant genes were highly correlated with toxigenic isolate biomass under variable stresses. These results along with others in the literature suggest that the production of these secondary metabolites may provide supplemental oxidative stress alleviation. Additional data validation using proteomics, metabolomics and whole genome resequencing (WGRS) approaches will also be discussed.

Combination of empirical and trait-based approaches for breeding drought tolerance in groundnut (*Arachis hypogaea* L.)

Janila P[1]*, VariathMT[1], Manohar SS[1]

[1]International Crops Research Institute for the Semi-Arid Tropics, Patancheru 502324, Hyderabad, India
*E-mail: p.janila@cgiar.org

Breeding groundnut varieties that combine improved pod yield under water-deficit stress, and enhanced water use efficiency (WUE) is an important strategy to overcome the challenges in water-limited conditions. SPAD chlorophyll meter reading (SCMR) and specific leaf area (SLA) are the two important traits associated with WUE. SCMR is simple, non-destructive and robust method. Maintaining high chlorophyll density under water stress conditions is associated with high WUE in groundnut, and SCMR measures green colour intensity associated with chlorophyll density. A RIL population (280) was evaluated during 2015/16 under well-watered (WW) and water-deficit stress (WS) for yield parameters and SCMR. Pod yield is independent of SCMR ($R2=0.003$), suggesting the importance of simultaneous selection for both these traits in breeding programs. For breeding varieties suitable for water-stress conditions, measuring both pod yield under stress and WUE through its surrogate SCMR are useful. In Africa and Asia, groundnut is largely a rainfed crop. The frequency of drought is variable, and every year is not a drought year. Therefore, the commercial groundnut varieties should perform well under normal rainfall years, and have less yield penalty during drought years. The approach of measuring pod yield penalty under water-deficit stress compared to WW condition is a useful selection criterion in breeding programs, wherein the lines with minimum yield penalty are selected. Such a selection criteria enable selection of genotypes that perform well under normal seasons and have less yield penalty during drought seasons. In this paper, we discuss progress in groundnut breeding at ICRISAT using these two approaches.

Molecular breeding tools improved drought tolerant groundnut variety for resistance to foliar fungal diseases

Rathna Kumar AL[1], Thirumalaisamy PP[1], Narendrakumar[1], Lalwani HB[1], Nadaf HL[2], Nagaraju P[2], Basavaraj Yenagi[2], Sudam Patil[3], Jitendra Suryawanshi[3], DeshmukhMP[4], Kumbhar CT[4], Kathmale DK[4], Naik KSS, Prasanna Rajesh[5], VemanaK[5], PremalathaN[6],SundaravadanaS[6],Murali T Variath[7], Manish K Pandey[7], Rajeev K Varshney[7], Janila P[7].

[1]ICAR-Directorate of Groundnut Research (DGR), Junagadh-362 001, Gujarat, India
[2]University of Agricultural Sciences, Dharwad, Karnataka-580 005,India
[3]Oilseeds Research Station, MPKV, Jalgaon, Maharastra, 425 005, India
[4]Agricultural Research Station, MPKV, K. Digraj-416 305, Sangli, Maharashtra, India
[5]Agricultural Research Station, ANGRAU, Kadiri-515591, Andhra Pradesh, India
[6]Tamil Nadu Agricultural University, Aliyarnagar-604 002, Tamil Nadu, India
[7]ICRISAT, Patancheru-502 324, Telengana, India
*E-mail: rathnakumar169@gmail.com

A largely rainfed crop in India, drought tolerance, particularly mid- and end-season tolerance, is a key trait in groundnut varieties. A combination of both empirical and trait-based approaches was used in breeding programs of ICAR and ICRISAT, resulting in release of few tolerant varieties that have superior pod yield under drought stress and/or have enhanced water-use-efficiency. There is a need to breed varieties with drought tolerance, disease resistance and quality traits that suit different production ecologies as well as meet the needs of the farmers, consumers and industries. ICRISAT has released an early-maturing (90-95 d) and drought- tolerant variety ICGV 91114 for the drought-prone Ananthapur district of Andhra Pradesh, India, where about 0.7 m ha area is under groundnut cultivation and has low (300 mm) and erratic (30-40 rainy days) rainfall. On-farm studies conducted with ICGV 91114 during 2008-10 showed 30% reduction in yield variability over the years. Following screening in hot-spots of both rust and LLS disease during 2014 rainy season, a total of 27 introgression lines derived from ICGV 91114 were selected and advanced for evaluation in multi-location trials at six locations in 2015 under rainfed conditions. Based on the pod yield under rainfed conditions and disease resistance, three superior introgression lines (ICGV 14410, ICGV 13189, ICGV 14421) were proposed for the first-ever NILs trial (near-isogenic lines trial) along with eight others conducted under All India Coordinated Research Project on Groundnut (AICRP-G) at national level.

Workshop VII

IPPN Workshop on Precision Phenotyping for Improved Stress Tolerance

Co-organizers

Dr. Roland Pieruschka

Senior Researcher
Institute of Bio- and Geosciences
Plant Sciences (IBG-2)
Germany

Dr. Pervez Haider Zaidi

Senior Maize Physiologist
International Maize and Wheat
Improvement Center (CIMMYT)
India

Field-based phenotyping for drought tolerance in maize – focus on breeder's wish-list

P.H. Zaidi[1]*, M.T. Vinayan[1], K. Seetharam[1], Ramesh Kumar[2], Salahuddin Ahmed[3], Do Van Dung[4], Dang Ngoc Ha[4], R.B. Dubey[5], B.S. Vivek[1]

[1]CIMMYT-Asia Maize Program, ICRISAT Campus, Hyderabad, India.
[2]Indian Institute of Maize Research, PAU Campus, Ludhiana (Punjab), India
[3]Bangladesh Agricultural Research Institute, Gazipur, Bangladesh
[4]National Maize Research Program, Ha Noi\s, Vietnam
[5]Maharana Pratap University of Agriculture & Technology, Udaipur, Rajasthan, India
*E-mail: phzaidi@cgair.org

High-quality phenotyping data is the key to success in genetic improvement for targeted traits, irrespective of the breeding approach, whether conventional or molecular breeding. Breeders generate different types of breeding populations, screen for the targeted traits, and select among a large number of segregating progenies the top-ranking progenies for use in their breeding program. In molecular breeding approach, progenies are genotyped and phenotyped, and selections are done on the basis of genotype-phenotype association, and favourable alleles are taken forward for use in breeding program. However, the key to success remains dependent on high-quality phenotyping data support. In CIMMYT-Asia maize program, we focus on precision in field-based phenotyping, including selection of appropriate phenotyping location and field, suitable cropping season in order to achieve targeted stress, managed stress phenotyping under field (or field-type) conditions to simulate drought stress relevant in target potential environment (TPE), and use of tools to keep track with stress intensity with uniformity within phenotyping site. By following the standardized protocol, we are able achieve good broad-sense heritability at each site in multi-location managed stress trials for drought tolerance phenotyping. In terms of plant traits for phenotyping and selection criteria, more emphasis is given on breeder's wish-list in selecting genotypes, which could eventually be used in developing the final product with agronomically desirable traits in TPE. In the case of molecular breeding projects, traits are further dissected into its components, which helps identify favourable gene/alleles associated with desirable components traits, and that could be taken forward on introgression into elite genetic background but lack tolerance to a targeted abiotic stress.

Phenotyping for the response to drought and high temperatures in a diversity of scenarios

François Tardieu[1], Emilie J. Millet[1], Santiago Alvarez Prado[1], Aude Coupel-Ledru[1], LlorençCabrera-Bosquet[1], Sébastien Lacube[1], Boris Parent[1], Claude Welcker[1]

[1] INRA LEPSE, Montpellier, France
*E-mail: francois.tardieu@supagro.inra.fr

The plant science community has to design new genotypes that are able to cope with the diversity of environmental conditions linked to climate change. A major issue is to combine genomic selection with knowledge originating from phenotyping. We have adopted for that a multi-scale multi-environment approach. In the field, it consisted of clustering time courses of environmental variables over Europe into six scenarios of temperature and water deficit experienced by plants; of performing field experiments in 29 contrasting environmental conditions across Europe with a panel of 250 maize hybrids; assigning individual experiments to previously defined scenarios, and finally analysing the genetic variation of plant performance for each environmental scenario via genome wide association studies (GWAS). Large variations of QTL effects depending on environmental scenarios resulted in a pattern associated with each QTL. In a phenotyping platform (Phenoarch), we have estimated intercepted light and radiation use efficiency of each hybrid of the same panel via a functional-structural model using 3D reconstructions of each plant, and the sensitivity of growth to water deficit of each hybrid via a joint analysis of several experiments with contrasting light, evaporative demand and soil water potential. As a whole, the combination of field and platform approaches results in a dataset that allows one to identify genomic regions associated with tolerance in specific scenarios of heat and drought, and with traits associated to these genomic regions. Finally, models allow identifying geographical regions in which a given combination of alleles is likely to have comparative advantages.

LeasyScan: 3D scanning of crop canopy plus seamless monitoring of water use to harness the genetics of key traits for drought adaptation

Vadez V[1], Kholova J[1], Srikanth M[1], Rekha B[1], Tharanya M[1], Sivasakthi K[1], Alimagham M[1], Karthika G[1], Keerthi C[1]

ICRISAT – Crop Physiology Laboratory, Greater Hyderabad, Patancheru 502324, Telangana, India
*E-mail: v.vadez@cgiar.org

With the genomics revolution in full swing, relevant phenotyping is now a main bottleneck. New imaging technologies provide opportunities for easier, faster and more informative phenotyping of many plant parameters. However, it is critical that the development of automated phenotyping be driven by a clear framing of target phenotypes rather than by a technological push, especially for complex constraints. Previous studies on drought adaptation shows the importance of water availability during the grain filling period, which depends on traits controlling the plant water budget at earlier stages. We will then discuss "cause" and "consequence" in phenotypes. Drawing on this, a phenotyping platform (LeasyScan) was developed to target canopy development and conductance traits. Based on a novel 3D scanning technique to capture leaf area development continuously and a scanner-to-plant concept to increase imaging throughput, LeasyScan is also equipped with 1488 analytical scales to measure transpiration seamlessly. Examples of the first applications are presented: (i) to compare the leaf area development pattern of pearl millet breeding material targeted to different agro-ecological zones, (ii) for the mapping of QTLs for vigour traits in chickpea, shown to co-map with an earlier reported "drought tolerance" QTL; (iii) for the mapping of leaf area development in pearl millet; (iv) for assessing the transpiration response to high vapour pressure deficit in different crops. This new platform has the potential to phenotype traits controlling plant water use at a high rate and precision, opening the opportunity to harness their genetics towards breeding improved varieties.

Drought acclimation during multiple vegetative growth stages in wheat improves drought tolerance during generative growth: insights from proteomics and physiology

Wang X[1], Jiang D[1]*

[1]Key Laboratory of Crop Physiology and Ecology in Southern China, Ministry of Agriculture/Hi-Tech Key Laboratory of Information Agriculture of Jiangsu Province, Nanjing Agricultural University, P. R. China
*E-mail: xiaowang@njau.edu.cn, jiangd@njau.edu.cn

Wheat is one of the major crops grown throughout the world, with primary use in human nutrition. Anticipated changes in global climatic variability leading to more frequent extreme conditions will require adaptation of crop species on an unprecedented magnitude in order to sustain agricultural production. Drought stress is one of the most severe abiotic stress forms, constraining both plant growth and productivity. The response of plants to stress involves both short-term molecular and physiological responses as well as long-term structural and morphological modifications. Little is known on the impact of the increased frequency of extreme climate events and the implications of environmental variability on quality parameters in wheat. We tested the hypothesis that acclimation to drought-stress during vegetative growth could be "memorized" by the plants and could lead to tolerance against a stress event during reproductive growth. In order to investigate the effect and mechanisms of drought acclimation, the responses of the physiological (photosynthesis rate and activities of antioxidant enzymes) and proteomic parameters (protein expression in leaves) were analyzed and identified. The results indicate changes to both enzyme synthesis and enzyme activity which may contribute to drought tolerance mechanisms in wheat.

Precise monitoring of stress response and high throughput phenotyping for stress adaptive traits – use of stable isotopes and gravimetric approaches.

MS. Sheshshayee[1]*

[1]Professor, Crop Physiology, University of Agricultural Sciences, Bengaluru, INDIA
*E-mail: msshesh1@uasbangalore.edu.in

Future agriculture would have to produce more with less water! Global initiatives are being taken up to enhance crop drought adaptation. Although drought adaptation is projected as a complex phenomenon, identification and dissection of stress adaptive "traits" have considerably simplified this so-called complexity. These drought adaptive traits are generally classified into those necessary for maintenance of tissue water relations and those essential for maintaining metabolism under decreasing turgor. These traits are often referred to as "constitutive" or "integral" traits. Plants also have evolved a propensity to cope with stress through a set of physiological and biochemical mechanisms collectively referred to as "acquired" tolerance traits. For a comprehensive improvement in drought adaptation, both constitutive and acquired tolerance traits must be introgressed onto a single elite genetic background. Acceleration and accurate trait introgression can only be achieved with the adoption of marker assisted breeding strategy. Accurate phenotyping of these traits is, therefore, the most crucial aspect for the discovery of QTL. Thus, improving drought adaptation is phenotyping centric.

Stable isotope ratios are powerful surrogates for important constitutive adaptive traits. Maintenance and monitoring soil and plant water status is crucial for acquired tolerance traits. We developed a novel real-time gravimetry-based approach for creation of specific stress level to capture genetic variability in acquired tolerance traits. Principles of these approaches and their practical application will be discussed. This approach is expected to significantly enhance the accuracy of QTL discovery and subsequent molecular breeding.

Workshop VIII

Next Generation Genomics & Molecular Breeding Platforms

Co-organizers

Prof. Dave Edwards

Professor
The University of Western
Australia (UWA)
Australia

Dr. Rajeev K Varshney

Research Program Director - Genetic Gains
International Crops Research Institute for the
Semi-Arid Tropics (ICRISAT)
India

The BGISEQ-500 sequencing platform for multiple research applications

Xin Liu

BGI Research, Beijing, China
E-mail: liuxin@genomics.cn

BGISEQ-500 is a new second-generation desktop sequencer developed by BGI, based on the sequencing technologies from Complete GenomicsTM. Since the release of BGISEQ-500 in 2015, different sequencing library construction methods have been developed for different sequencing purposes, including whole genome sequencing, exome capture sequencing, transcriptome sequencing, small RNA sequencing, microRNA sequencing, epigenetic sequencing and meta-genomic sequencing. For now, the sequencing throughput can reach up to 200 Gb per sequencing run, and the sequencing data can be single end 50/100/150 bp and pair end 50/100 bp, with further improving in progress. Analysis of the whole genome sequencing data of a standard human cell line has illustrated similar data quality and variation identification performance. Sequencing data of both human and several model species with different insert sizes has enabled good *de novo* genome assembly for these species. Similarly, we have conducted comprehensive comparisons of all the sequencing applications based on BGISEQ-500 to those on other sequencing platforms, to illustrate the feasibility of BGISEQ-500 data, which reflected availability of applying BGISEQ-500 sequencing platform for multiple researches in a more cost-effective manner.

Using genomics to breed for the future: sequencing and genotyping platforms

Ryan Rapp

Illumina, Inc., San Diego, USA
E-mail: rrapp@illumina.com

Global sourcing of food presents unique resource management and environmental challenges from land allocation to water use to plant disease resistance. Here, I make a case for the widespread use of genomic selection and demonstrate how genomic selection can provide a rapid means to improving the sustainability of food supplies, while reducing the consumption of natural resources -- with particular attention to water use and water use efficiency. Illumina's technology systems have been honed over the last decade to help plant breeders achieve these goals.

Delivering higher rates of genetic gain to farmers in drought-prone environments

Gary Atlin[1]

[1]Bill & Melinda Gates Foundation (BMGF), Seattle, USA
E-mail: Gary.Atlin@gatesfoundation.org

Significant progress has been made over the last 15 years in several species in identifying parents, haplotypes, and alleles associated with higher yields under particular types of drought stress, but there has been limited impact of this work in farmers' fields in South Asia and Sub Saharan Africa, the world's poorest regions. Most farmers in the developing world are growing varieties that are between 15 and 50 years old, and genetic gains delivered by most breeding programs serving Africa and South Asia are well under 1% annually. Cropping systems in these regions are commercialising rapidly, and smallholder farmers rarely adopt new varieties on the basis of a stress-tolerance trait. Abiotic stress tolerance must be delivered in the form of cultivars that also have high yield potential in favorable seasons, and that have the quality traits needed for rapid market acceptance. Integrating these traits, as well as the nutritional enhancements increasing requested by governments and donors, will require a much more effective and aggressive international public crop improvement system that adapts many of the tools and approaches of multinational seed companies to the problem of raising crop yields for smallholder farmers. Breeding programs that effectively deliver usable genetic gains in stress-prone environments will require substantially increased population sizes and concomitantly increased phenotyping, genotyping, and information management capacity. Effective programs also need clear and formal product profiles, institutionally managed advancement systems, and new approaches to dissemination wherein the breeding organization takes full responsibility for making the case for replacing currently grown varieties with new products. Most public breeding programs and institutions will require extensive redesign to deliver the gains needed by African and South Asian farmers. The CGIAR will support this redesign through the newly-established Excellence in Breeding Platform.

The assembly, analysis and application of pangenomes

Edwards D[1]

[1]The University of Western Australia, Perth, 6009, Australia
E-mail: dave.edwards@uwa.edu.au

As an increasing number of genome sequences become available, there is a growing understanding that there is significant gene presence absence variation between individuals within a species and so the genome of a single individual is insufficient to represent the gene diversity of a whole species. The sum of the genes for a species is termed the pangenome and the determination and characterisation of the pangenome is a requirement to understand variation within a species. In this presentation, I will discuss the current progress in pangenomics as well as methods and approaches for the characterisation of pangenomes for a range of plant species. The impact of this gene variation on traits is only now being studied in detail, but knowledge of gene presence/absence variation is valuable for both traditional breeding and as a foundation for genome editing.

Genotyping by sequencing: which application is right for me?

Batley J[1]

[1]School of Biological Sciences, The University of Western Australia, Crawley, WA 6009, Australia
E-mail: jacqueline.batley@uwa.edu.au

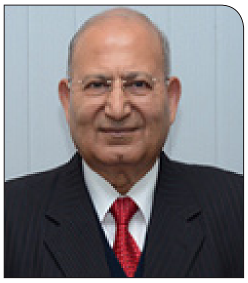
In the last decade, the revolution in sequencing technologies has enabled rapid advances in crop genotyping for advancing breeding, allowing rapid, high-throughput genotyping of the entire crop populations. There are many new genotyping by sequencing (GBS) methods comprising reduced representation sequencing (RRS) and whole genome resequencing (WGR) approaches. The diversity of methods available, each often producing different types of data at different cost, can make selection of the best-suited method seem a daunting task. I will present a comparison of commonly used genotyping methods and compare their suitability for different applications, such as linkage mapping, genome wide association studies (GWAS), marker-assisted and genomic selection and genome assembly. Consideration will be taken about method development, bioinformatics analysis and population structure in a complex polyploid species.

Panel Discussions on Climate Smart Agriculture

Co-chairs

David Bergvinson

Director General
International Crops Research
Institute for the Semi-Arid
Tropics (ICRISAT)
India



Dr Rajendra Singh Paroda

Chairman-TAAS & President
Indian Society of Plant Genetic Resources
(ISPGR)
India

Panelists

Dr David Bergvinson

Director General
International Crops Research Institute
for the Semi-Arid Tropics (ICRISAT)
India

Dr Rajendra Singh Paroda

Chairman-TAAS & President
Indian Society of Plant Genetic Resources
India

Dr William Dollente Dar
Former DG, ICRISAT & President
Inanglupa Movement Inc.
Philippines

Dr Swapan Kumar Datta

Former DDG-CS, ICAR &
Pro-Vice-Chancellor
Visva - Bharati University, Santiniketan
India

Dr Jeff Ehlers

Senior Program Officer
Bill and Melinda Gates Foundation
(BMGF)
USA

Usha Barwale

Joint Director
Maharashtra Hybrid Seeds Company
Limited (MAHYCO)
India

Dr Shadrack Moephuli

President and CEO
Agricultural Research Council
South Africa

Prof. Kadambot Siddique

Hackett Professor of Agriculture Chair and Director
UWA Institute of Agriculture
Australia

Arabinda Kumar Padhee

Director
Country Relations and Business Affairs
International Crops Research Institute
for the Semi-Arid Tropics (ICRISAT)
India

List of Posters

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
Theme 1: Setting the Biophysical Context: Climatic/Soil Constraints (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
1	Badolo, Felix	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	Economic analysis of alternative systems for sorghum production in Southern Mali	f.badolo@cgiar.org	IDT1-001
2	Dippold, Michaela	University of Goettingen, Goettingen, Germany	Mucilage secretion: Do plants protect their rhizosphere community from drought effects to maintain their beneficial functions?	dippold@gwdg.de	IDT1-002
3	Eskinder, Gidey Sintayehu	Mekelle University, Mekelle, Ethiopia	Modeling the spatio-temporal meteorological drought variability, extent, and severity using the standardized precipitation index (SPI) in raya and its environs, northern Ethiopia	eskinder14@yahoo.com	IDT1-003
4	Hella, Joseph P	Sokoine University of Agriculture, Morogoro, Tanzania	Climate change, commercialization and gender divides: Alternative pathways for groundnut breeding in semi-arid Tanzania	jp_hella@yahoo.co.uk	IDT1-004
5	Holz, Maire	University of Goettingen, Goettingen, Germany	The critical role of root growth and water content in controlling rhizosphere extension during drought	maire.holz@forst.uni-goettingen.de	IDT1-005
6	Ige, Adenike Damilola	Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana	Responses of tropical maize genotypes to maize streak virus disease	niccollo4real@yahoo.com	IDT1-006
7	Kailappan, Amudha	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Identification of QTLs for zinc deficiency tolerance in aerobic rice (*Oryza sativa* L.)	amudha_pbg@yahoo.com	IDT1-007
8	Kandula, Naga Madhuri	Regional Agricultural Research Station (RARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Tirupati, India	Evaluation of groundnut genotypes for phosphorous efficiency through acid phosphatase content in leaves	nagamadhurikv@gmail.com	IDT1-008
9	Kotyal, Kavita	University of Agricultural Sciences (UAS), Bangalore, India	Effect of sodium nitroprusside and ferrous sulphate on the performance of groundnut genotypes in calcareous soil	kavitakotyal@gmail.com	IDT1-009
10	Muktha, J	University of Agricultural Sciences (UAS), Bangalore, India	Zinc intervention for drought tolerance	muktha.j@gmail.com	IDT1-010
11	Naik, Shilpa Mahadeva	International Rice Research Institute (IRRI), Patancheru, India	High zinc rice lines for drought prone eastern India: Genotype x environment interaction and stability	s.naik@irri.org	IDT1-011
12	Padma Latha, Y	Agricultural Research Station (ARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Reddipalli, India	Experiences with rainwater harvesting and recycling – the best climate resilient technology for higher yields of rainfed groundnut (*Arachis hypogaea* L.)	sahadevardd@gmail.com	IDT1-012
13	Rana, Jyoti	Murdoch University, Murdoch, Australia	Root lesion nematodes:'drought in disguise'	rana.om.jyoti@gmail.com	IDT1-013
14	Schwartz, Nimrod	Hebrew University of Jerusalem, Rehovot, Israel	Modelling the impact of rhizosphere processes on root water uptake	nimrod.schwartz@mail.huji.ac.il	IDT1-014

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
15	Sudini, Hari Kishan	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Investigations on prevalence of aflatoxin contamination in major groundnut growing states of India, influence of soil characteristics and farmers' level of awareness	h.sudini@cgiar.org	IDT1-015
16	Swarnalakshmi, K	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Evaluation of symbiotic potential, nutrient uptake and yield of chickpea cultivars under field conditions	swarna_bga@yahoo.com	IDT1-016
Theme 2: Maximising Dryland Crop Production: Crop Design (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
17	Adu, Gloria Boakyewaa	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	Identification of locally adapted drought tolerant maize varieties using local preferences and selection of farmers in northern savannah zones of Ghana	gloriaboakyewaa@yahoo.com	IDT2-001
18	Batieno, Joseph Benoît	Institut de l'Environnement et des Recherches Agricoles (INERA), Ouagadougou, Burkina Faso	Progress in cowpea cultivation, improvement, and storage in Burkina Faso from 1978 to date	batieno52@gmail.com	IDT2-002
19	Beena, R	Kerala Agricultural University, Thiruvananthapuram, India	Screening of rice varieties to identify a thermo-tolerant variety using Temperature Induction Response (TIR) technique	beenaajithkumar@gmail.com	IDT2-003
20	Gadri, Yaron	Hebrew University of Jerusalem, Rehovot, Israel	Effect of water deficit on yield components in sesame (*Sesamum indicum* L.)	ygadri@gmail.com	IDT2-004
21	H Rao, Bindumadhava	AVRDC - The World Vegetable Center South Asia, Hyderabad, India	Heat tolerant mungbeans – Hope for harsh climates	bindu.madhava@worldveg.org	IDT2-005
22	Muddarsu, Venkata Ramana	Sikkim University, Gangtok, India	Screening and multi elemental profiling of chilli germplasm against drought tolerance under controlled condition	venkat.muddarsu@gmail.com	IDT2-006
23	Nalina, M	Upasi Tea Research Institute, Coimbatore, India	Exogenous application of trehalose to mitigate drought stress in tea	nalinam08@gmail.com	IDT2-007
24	Nasirzadeh, Leila	Seed and Plant Improvement Institute (SPII), Karaj, Iran	Comparison of Iranian National Genebank Wheat landraces Tolerant to Drought and Commercial Cultivars for Maximising Crop Production in Iran	l.nasirzadeh@gmail.com	IDT2-008
25	Nkalubo, Stanley T	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	Multi-locational evaluation and release of micronutrient dense bean varieties in Uganda	tamusange@yahoo.com	IDT2-009
26	Pasala, Ratna Kumar	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	Yield enhancement through bio-fertilizer priming and effect of bio-regulators in soybean under soil moisture stress	ratna.pasala@icar.gov.in	IDT2-010
27	Pradeep, CM	University of Agricultural Sciences (UAS), Raichur, India	Rainfall probability analysis for drought occurrence and crop planning at Raichur	pradeep0393@gmail.com	IDT2-011
28	Putta, Latha	Regional Agricultural Research Station (RARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Tirupati, India	Phenotyping pre release groundnut (*Arachis hypogaea* L.) Genotypes for drought adaptive traits under simulated mid season stress conditions	latha_damu@yahoo.com	IDT2-012

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
29	Sekhar, Kalva M	University of Hyderabad, Hyderabad, India	Elevated CO_2 alleviates drought induced negative effects in short rotation coppice mulberry (Morus spp.), a potential bio-energy tree crop	madhansekhar@gmail.com	IDT2-013
30	Shashibhushan, NB	University of Agricultural Sciences (UAS), Bangalore, India	Identification of a rice genotype with reasonable adaptation to aerobic cultivation	shashibhushannb@gmail.com	IDT2-014
31	Singh, Naresh Pratap	Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, India	Stay green wheat for drought and heat stress	naresh.singh55@yahoo.com	IDT2-015
32	Sridevi, R	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Influence of seed priming on growth and yield of foxtail millet	agrirose.28@gmail.com	IDT2-016
Theme 3: Plant Productivity Under Drought I: Effective Capture Of Water (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
33	Bhat, Muhammad	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Kashmir, India	Relative water content, cell membrane stability and DAB assay in relation to reduction in yield components and resource remobilisation under drought in common bean (*Phaseolus vulgaris* L.)	mashrafbhat@skuastkashmir.ac.in	IDT3-002
34	Bheemanahalli, Raju	Kansas State University, Manhattan, USA	Exploring root-leaf continuum between wild rices and sorghum to enhance drought stress resilience in rice	rajubr@ksu.edu	IDT3-003
35	Choudhary, Sunita	Dupont Pioneer, Wargal, India	Comparison of three C4 cereals for transpirational sensitivity to elevated evaporative demand	sunita963@gmail.com	IDT3-004
36	Dewanjee, Sujaya	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	Ideal root types in drought resistant rice (*Oryza sativa* L.)	sujaya2009@gmail.com	IDT3-005
37	Dhanyalakshmi, KH	University of Agricultural Sciences (UAS), Bangalore, India	Understanding drought adaptive mechanisms: Can stress responsive Proteins of Unknown Function (PUFs) be a missing link?	hemaadhanya@gmail.com	IDT3-006
38	Dockx, Adrien	UCL - Earth & Life Institute, Louvain-la-Neuve, Belgium	Field evaluation of deep water capture using thermal imaging	adrien.dockx@uclouvain.be	IDT3-007
39	Falalou, Hamidou	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger	Drought (WS) and low phosphorus (LP) stress in groundnut: Water extraction pattern and tolerance related traits for breeding program	f.hamidou@cgiar.org	IDT3-008
40	Haddadi, Shaghayegh H	University of Tehran, Tehran, Iran	Effects of drought stress on water relationships and osmotic adjustment in pasture annual medic ecotype	sh_haddadi@ut.ac.ir	IDT3-009
41	Kamalnath Reddy, KR	ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, India	Evaluation of root system in aerobic rice (*Oryza sativa* L.) hybrids & CMS lines	kamalnath.reddy@gmail.com	IDT3-010
42	Mahatma, Mahesh	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Diurnal variation in accumulation of different metabolites in drought-stressed peanut	maheshmahatma@gmail.com	IDT3-011
43	Passot, Sixtine	Universite Catholique de Louvain, Louvain-la-Neuve, Belgium	Impact of three lateral root types identified in pearl millet on water uptake	sixtine.passot@uclouvain.be	IDT3-012

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
44	Raghavendra, T	Acharya N.G. Ranga Agricultural University (ANGRAU), Nandyal, India	Temperature Induction Response (TIR)-A Novel physiological approach for thermotolerant genotypes in chickpea (*Cicer arietinum* L.)	raghavendraagrico@gmail.com	IDT3-013
45	Rashmi, K	University of Agricultural Sciences (UAS), Bangalore, India	Identification and evaluation of selected tomato (*Lycopersicum esculentum* L) rootstock donors under drought stress condition	rashmipalb1190@gmail.com	IDT3-014
46	Sampangi-Ramaiah, Megha H	ICAR-Indian Institute of Horticultural Research (IIHR), Bangalore, India	Computational mining of miRNAs and their targets involved in root development in banana	megha.hs28@gmail.com	IDT3-015
47	Sowmya, HC	University of Agricultural Sciences (UAS), Raichur, India	Genetic analysis of F2 generation of four derived crosses for yield and water use efficiency related traits in groundnut (*Arachis hypogaea* L.)	hc.sowmya@gmail.com	IDT3-016
48	Srivastava, Rakesh K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Fine mapping of the linkage group 2 drought tolerance QTL in pearl millet [*Pennisetum glaucum* (L.) R. Br.]	r.k.srivastava@cgiar.org	IDT3-017
49	Thangthong, Nuengsap	Khon Kaen University, Khon Kaen, Thailand	Root distribution of drought resistant peanut genotypes in response to early season drought stress	nuengsap.th@gmail.com	IDT3-018
50	Tuberosa, Roberto	University of Bologna, Bologna, Italy	Root system architecture phenotyping of durum wheat reveals differential selection for a major QTL in contrasting environments & Vegetative growth and water use characterization of a maize introgression library	roberto.tuberosa@unibo.it	IDT3-019 ,020
51	Wallach, Rony	Hebrew University of Jerusalem, Rehovot, Israel	The whole-plant response to soil water availability as a mean for drought-resistance phenotyping	rony.wallach@mail.huji.ac.il	IDT3-021
52	Xie, Xiaobing	International Rice Research Institute (IRRI), Los Banos, The Philippines	Approaches to relating rice root plasticity with yield stability across different drought stress and establishment conditions	X.Xiaobing@irri.org	IDT3-022
53	Yamanura, M	University of Agricultural Sciences (UAS), Dharwad, India	Identification of drought tolerant Pigeonpea [*Cajanus cajan* (l.) Millsp.] genotypes and their stability analysis	yaman_gpb4357@rediffmail.com	IDT3-023
54	Yildirim, Mehmet	Dicle University, Diyarbakir, Turkey	Water use efficiency of Turkish maize landrace for drought tolerance at filed conditions	mehmety@dicle.edu.tr	IDT3-024
Theme 4: Plant Productivity Under Drought II: Transpiration Efficiency (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
55	Alvarez Prado, Santiago	French National Institute for Agricultural Research (INRA), Montpellier, France	Physiological mechanisms controlling plant water use in maize	santiago.alvarez-prado@inra.fr	IDT4-001
56	Basdemir, Fatma	Dicle University, Diyarbakir, Turkey	Transpiration rate of chickpea wild accessions and cultivars in Turkey	ftmbsdmr87@hotmail.com	IDT4-002
57	Batlang, Utlwang	Botswana University of Agriculture and Natural Resources, Gaborone, Botswana	Drivers of water use efficiency of cowpea under contrasting environment and water deficit conditions	ubatlang@bca.bw	IDT4-003

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
58	Chaudhari, Gaurav	College of Horticulture, Bangalore, India	Ab initio candidate genes mining and transcript abundance carrying water use efficiency quantitative trait loci in sorghum (*Sorghum bicolor* L.)	CHAUDHARIGAURAV11@gmail.com	IDT4-004
59	Christopher, Jack T	The University of Queensland, Toowoomba, Australia	Historical improvement in drought adaptation of Australian wheat has coincided with changes in transpiration efficiency and other traits	j.christopher@uq.edu.au	IDT4-005
60	Dash, Goutam Kumar	ICAR-National Rice Research Institute (NRRI), Cuttack, India	Transpiration efficiency of rice (*Oryza sativa* L.) under drought: A physiological determinant for tolerance	gkdash.bot@gmail.com	IDT4-007
61	George, Suja	M S Swaminathan Research Foundation (MSSRF), Chennai, India	Drought and salt stress in *Chrysopogon zizanioides* leads to common and specific transcriptomic responses and may affect essential oil composition and benzylisoquinoline alkaloids metabolism	sujageorge@mssrf.res.in	IDT4-008
62	Gobu, R	Banaras Hindu University (BHU), Varanasi, India	Evaluation of eggplant (*Solanum melongena* L.) cultivars under moisture stress condition	gobu.agri@gmail.com	IDT4-009
63	Grieu, Philippe	Université de Toulouse/ INP-ENSAT, Castanet Tolosan, France	Genetic analysis of the transpiration control in sunflower (*Helianthus annuus* L.) subjected to drought	grieu@ensat.fr	IDT4-010
64	Hasanuzzaman, Md	University of Tasmania, Tasmania, Australia	Assessing suitability of various screening methods as a proxy for drought tolerance in barley	md.hasanuzzaman@utas.edu.au	IDT4-011
65	Kumar, Sudhir	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	High throughput phenotyping for drought tolerance in rice at reproductive stage	sudhirnpf@gmail.com	IDT4-012
66	Muktadir, MD Abdul	University of Sydney, Narrabri, Australia	Characterizing leaf gas exchange and carbon isotope discrimination responses of diverse faba bean genotypes during reproductive stage in irrigated and rainfed condition	md.muktadir@sydney.edu.au	IDT4-013
67	Natarajan, Sijesh	The University of Queensland, Queensland, Australia	Effect of vapour pressure deficit on sugarcane transpiration efficiency in a drying soil	s.natarajan@uq.edu.au	IDT4-014
68	Palakolanu, Sudhakar Reddy	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Role of the pearl millet Aquaporin genes in abiotic stress response	p.sudhakarreddy@cgiar.org	IDT4-015
69	Rachapudi, Sreeharsha	University of Hyderabad, Hyderabad, India	Photosynthetic efficiency is well coordinated with Nitrogen assimilation in drought stressed pigeonpea grown under elevated CO_2	rvsreeharsha@gmail.com	IDT4-016
70	Rachaputi, C N Rao	The University of Queensland, Gatton, Australia	Physiological mechanisms underpinning genotypic variation for heat tolerance in mungbean (*Vigna radiata* L.)	rao.rachaputi@uq.edu.au	IDT4-017
71	Raju, Dhandapani	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	High throughput screening for differential nocturnal transpiration in rice genotypes under moisture-deficit stress	dandyman2k3@yahoo.co.in	IDT4-018
72	Romana, Kirandeep K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Determining transpiration efficiency of bmr sorghum genotypes for progressive drought tolerance	k.romana@cgiar.org	IDT4-019

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
73	Sankaranarayanan, Kavitha	Anna University K B Chandrashekar Research Centre (AU-KBC), Chennai, India	Ion channels in rice – Development of a novel rapid screen for drought tolerance	skavitham@yahoo.com	IDT4-020
74	Sengupta, Debashree	University of Hyderabad, Hyderabad, India	Carbon allocation efficiency under drought: Targeting the hexose/sucrose ratio based signaling mechanism	debashreehcu@gmail.com	IDT4-021
75	Shekoofa, Avat	University of Tennessee, Knoxville, USA	High temperature influence on limited transpiration response at elevated vapor pressure deficit in maize	ashekoof@utk.edu	IDT4-022
76	Vadez, Vincent	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Transpiration Efficiency: Further insights from species, sink strength, and soil comparisons & LeasyScan: 3D scanning of crop canopy plus seamless monitoring of water use to harness the genetics of key traits for drought adaptation	V.VADEZ@CGIAR.ORG	IDT4-023
77	van Oosterom, Erik J	The University of Queensland, Brisbane, Australia	The role of leaf conductance and photosynthesis in genotypic differences in transpiration efficiency in sorghum	erik.van.oosterom@uq.edu.au	IDT4-024
78	Yattara Inamoud Ibny, Fadimata	Tshwane University of Technology (TUT), Pretoria, South Africa	Evaluation of plant growth, photosynthesis and intrinsic water-use efficiency of 25 Bambara groundnut landraces at Marapyane, South Africa	fad_yatt2007@yahoo.fr	IDT4-025
Theme 5: Plant Productivity Under Drought III: Vegetative Growth (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
79	Banu, Afsana	University of Agricultural Sciences (UAS), Bangalore, India	Phenotypic Variation under moisture stress is regulated by variation in photosynthetic ability in finger millet	afsanabanu.manik@gmail.com	IDT5-001
80	Biju, Sajitha	University of Melbourne, Victoria, Australia	Screening for drought tolerance in lentil genotypes using thermal Imaging and multivariate data analysis	sbiju@student.unimelb.edu.au	IDT5-002
81	Chadalavada, Keerthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Sorghum early vigor increases grain size, striga resistance and has linkages with some stay-green phenotype	keerthichadalawada@gmail.com	IDT5-003
82	Dey, Narottam	Visva-Bharati University, Santiniketan, India	Exploration of rice (*Oryza sativa*. L) land races for drought tolerance	narottam.dey@visva-bharati.ac.in	IDT5-004
83	Iwuala, Emmanuel Nkmakolam	University of Lagos, Lagos, Nigeria	Differential responses of maize (*Zea mays* L.) and pearl millet [*Pennisetum glaucum* (L.) R. Br under augmenting drought stress.	iwuala097@gmail.com	IDT5-006
84	Kanubothula, Sitaramireddy	University of Hyderabad, Hyderabad, India	Interdependence of plant photosynthesis with hydraulic efficiency in field grown mulberry (Morus spp.) under water deficit and recovery	krsitaram1@gmail.com	IDT5-007
85	Kulwal, Pawan	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India	Multi-stage phenotyping of dynamic traits for increased efficiency of breeding experiments: A case study of plant height in chickpea	pawankulwal@gmail.com	IDT5-008
86	Lake, Lachlan	University of Adelaide, Adelaide, Australia	Screening chickpea for adaptation to water stress: Associations between yield and crop growth rate	lachlan.lake@sa.gov.au	IDT5-009

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
87	Ramalingam, Poornima	Tamil Nadu Agricultural University (TNAU), Sivagangai, India	Eco-physiological and genetic characterization of drought response index of rice (*Oryza sativa* L.) under upland conditions in temperate monsoon climate in Japan	poornimabio18@yahoo.com	IDT5-010
88	Rathnathunga, Elpitiya Udari Uvindhya	University of Ruhuna, Matara, Sri Lanka	Sri Lankan rice is sensitive to photoperiod and temperature at early vegetative growth	uvindhyaru@gmail.com	IDT5-011
89	Sowmya, HR	University of Agricultural Sciences (UAS), Bangalore, India	Physiological and genetic insights towards understanding the canopy architecture in contrasting leaf size mutants of an upland size-Nagina 22 (N22)	sowmyahreddy@yahoo.co.in	IDT5-012
90	Tuberosa, Roberto	University of Bologna, Bologna, Italy	QTL mapping for root architecture and transpiration efficiency in a maize introgression library	roberto.tuberosa@unibo.it	IDT5-013
91	Vinutha, DN	University of Agricultural Sciences (UAS), Bangalore, India	Museum of whole- plant across crops	vinuthagpb@gmail.com	IDT5-014
Theme 6: Reproductive Development, Yield, Yield Quality (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
92	Adeboye, Kehinde Adewole	The Federal University of Agriculture, Abeokuta (FUNAAB), Abeokuta, Nigeria	Identification and characterization of flowering-delay rice lines under reproductive stage drought stress	kaadeboye@yahoo.com	IDT6-001
93	Akuja, Thomas E	South Eastern Kenya University, Kitui, Kenya	Adaptability of pearl millet (*Pennisetum glaucum* (L.) R.Br)varieties in the semi- arid Kitui County of Kenya	akuja05@gmail.com	IDT6-002
94	Ali, Mohammed Anwar	Acharya N.G. Ranga Agricultural University (ANGRAU), Bapatla, India	Influence of pollen germination and pollen tube length on pod setting and yield in groundnut (*Arachis hypogaea*. L).	anwar.mohammed225@gmail.com	IDT6-003
95	Amongi, Winnyfred	International Center for Tropical Agriculture (CIAT), Kampala, Uganda	Yield stability and response of common bean drought tolerance breeding lines to field disease in Uganda	w.amongi@cgiar.org	IDT6-004
96	Angarawai, Ignatius	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria	Performance of some sorghum varieties as affected by heat stress under irrigation in northern Nigeria	I.Angarawai@cgiar.org	IDT6-005
97	Anjani, K	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	Influence of severe drought on oleic acid content and seed yield of high oleic Indian safflower varieties	k.anjani@icar.gov.in	IDT6-006
98	Antur, Veeresha B	University of Agricultural Sciences (UAS), Dharwad, India	The influence of drought on the expression of quality parameters in bread wheat	ambavee@gmail.com	IDT6-007
99	Anumalla, Mahender	ICAR-National Rice Research Institute (NRRI), Cuttack, India	Genetic diversity and population structure among assorted group of genotypes pertinent to reproductive stage drought stress in rice (*Oryza sativa* L.)	mahenderbio@gmail.com	IDT6-008
100	Attamah, Patrick	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	Screening for drought tolerance among elite cowpea (*Vigna unguiculata* (L.) Walp) lines	attamahpat@yahoo.com	IDT6-009
101	Bansal, Ruchi	National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India	Evaluation of wheat (*Triticum aestivum* L.) genotypes for post anthesis drought tolerance	Ruchi.Bansal@icar.gov.in	IDT6-010

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
102	Belliappa, Shruthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Super early pigeonpea varities and hybrids: New intervener for maximized, time specific dry land production	shruthibelliappa155@gmail.com	IDT6-011
103	Bharathi, A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Fine mapping of QTL for grain yield under drought using rice lines adapted to target populations of environment	reenmvel@gmail.com	IDT6-012
104	Bohare, Tinkeshwari	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India	Correlated response of various morpho-physiological and biochemical traits with yield under heat stress condition in chickpea (*Cicer arietinum* L.)	tinabohare@gmail.com	IDT6-013
105	Cabrera-Bosquet, Llorenc	French National Institute for Agricultural Research (INRA), Montpellier, France	An image-based automated pipeline for maize ear and silk detection in a high-throughput phenotyping platform	llorenc.cabrera-bosquet@inra.fr	IDT6-014
106	Challa, Venkateswarlu	International Rice Research Institute (IRRI), Patancheru, India	Yield stability under reproductive-stage drought stress in Swarna/Moroberekan advanced backcross introgression lines (BILs) of rice	c.venkateshwarlu@irri.org	IDT6-015
107	Chen, Hua	Fujian Agriculture and Forestry University (FAFU), Fuzhou, China	Characterization of low Ca2+ stress-induced embryo apoptosis response genes and their regulation of embryo development	hchen2013@163.com	IDT6-016
108	Danful, Rukiya	Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana	Variation in shoot biomass, δ13C and pod yield in an advanced breeding groundnut lines	danfulrukiya@ymail.com	IDT6-017
109	Dar, Zahoor	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Kashmir, India	Comprehensive assessment of drought tolerance related traits in temperate maize inbred lines	zahoorpbg@gmail.com	IDT6-018
110	DeBruin, Jason	Dupont Pioneer, Illinois, USA	Male sterility (Ms44) increases reproductive resilience under abiotic (drought and nitrogen) stress for maize hybrids	"jason.debruin@pioneer.com "	IDT6-019
111	Deosarkar , DB	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	Studies on physiological and biochemical parameters in hirsutum cotton genotypes for drought tolerance	dbdeosarkar@gmail.com	IDT6-020
112	Devnarain, Natrisha	University of Pretoria, Pretoria, South Africa	Transcriptomics of drought tolerant sorghum landraces	natrisha.devnarain@gmail.com	IDT6-021
113	Doddagoudar, Shivanagouda R	University of Agricultural Sciences (UAS), Raichur, India	Yield and lint quality of Bt –cotton (*Gossypium hirsutum* L.) as influenced by seed polymer coating and foliar spray with micronutrients	srdsst@gmail.com	IDT6-022
114	Dodig, Dejan	Maize Research Institute Zemun Polje, Zemun-Belgrade, Serbia	Morpho-anatomical and productive traits in wheat genotypes contrasting for peduncle water-soluble carbohydrates content	ddodig@mrizp.rs	IDT6-023
115	Flohr, Bonnie	Commonwealth Scientific and Industrial Research Organisation (CSIRO), Canberra, Australia	Cultivars for flowering date and yield stability	bonnie.flohr@csiro.au	IDT6-024

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
116	Gayatonde, Varsha Vinayak	Banaras Hindu University (BHU), Varanasi, India	High throughput phenotyping (HTP) of root architecture to enhance the drought tolerance in maize (*Zea mays* L.)	varshapanchu@gmail.com	IDT6-025
117	Issa Zakari, Mahaman Mourtala	Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana	Inheritance and combining ability studies on drought tolerance and grain yield among early maturing inbred lines of maize (*Zea mays* L.)	issazakarym@yahoo.fr	IDT6-026
118	Jiang, Dong	Nanjing Agricultural University, Nanjing, China	Drought priming induces thermo-tolerance to post-anthesis high-temperature in offspring of winter wheat	jiangd@njau.edu.cn	IDT6-027
119	Kaoneka, Seleman	Agricultural Research Institute-Ilonga, Morogoro, Tanzania	Identification of genomic regions associated with the yield and related –traits in pigeonpea (*Cajanus cajan* L. Millsp.)	s_kaoneka@yahoo.com	IDT6-028
120	Kavya, HP	University of Agricultural Sciences (UAS), Bangalore, India	Less water better rice G(r)ains	kavya.horantur@gmail.com	IDT6-029
121	Khan, Mohd Shahanbaj	B.S.Abdur Rahman University, Chennai, India	Autophagy is critical to cope up with drought tolerance in rice (*O. sativa* L.)	shahnawazkhandrr@gmail.com	IDT6-030
122	Khan, Jameel	University of Agricultural Sciences (UAS), Bangalore, India	Does bran drain the grain?	jameelbiotec@gmail.com	IDT6-031
123	Kirioukhova, Olga	Heidelberg University, Heidelberg, Germany	Constitutive stress response confers tolerance to osmotic stress and is linked to successful asexual reproduction in a crucifer	olga.kirioukhova@cos.uni-heidelberg.de	IDT6-032
124	Kokkanti, Rekha	Sri Padmavati Mahila Visvavidyalayam, Tirupati, India	Screening groundnut genotypes using TIR (Temperature Induction Response) technique for thermotolerance	kokknatirekha@gmail.com	IDT6-033
125	Kolawole, Adesike Oladoyin	West Africa Centre for Crop Improvement (WACCI), University of Ghana, Accra, Ghana	Genetic gain in heterosis of maize reciprocal composites	adesike@yahoo.com	IDT6-034
126	Kumar, MV Nagesh	Regional Agricultural Research Station (RARS), Professor Jayashankar Telangana State Agricultural University (PJTSAU), Palem, India	Enhancement of pigeonpea productivity through adoption of drought mitigating strategies	psoilseeds@gmail.com	IDT6-035
127	Kwon, TR	National Institute of Agricultural Sciences, Jeonju, Korea	Phenotyping of plants for drought and salt tolerance using infra-red thermography	trkwon@korea.kr	IDT6-036
128	Mallikarjuna, BP	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Molecular mapping of flowering time genes in chickpea (*Cicer arietinum* L.)	B.Mallikarjuna@cgiar.org	IDT6-037
129	Manasa, R	University of Agricultural Sciences (UAS), Bangalore, India	Screening mungbean lines for salinity tolerance using Salinity Induction Response (SIR) technique	manasaraju23@gmail.com	IDT6-038
130	Meshram, Jayant	ICAR-Central Institute for Cotton Research, Nagpur, India	Screening of cotton (*Gossypium hirsutum* L.) germplasm for drought stress under field condition	j.h.meshram@gmail.com	IDT6-039
131	Messina, Carlos	DuPont Pioneer, Johnston, Iowa, USA	Silk elongation rate response to water deficit mediated by ARGOS influence on ethylene sensitivity in maize (*Zea mays.*)	charlie.messina@pioneer.com	IDT6-040

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
132	Parveda, Maheshwari	Osmania University, Hyderabad, India	Overexpression of transcription factor SbAP37 improves grain yield in rice undersalt and drought stress and modulates the proteome as revealed by Q-TOF analysis	maheshwariraop@gmail.com	IDT6-041
133	Patil, BC	University of Agricultural Sciences (UAS), Dharwad, India	Drought tolerance studies in *Gossypium hirsutum* cotton genotypes	patilbc10195@uasd.in	IDT6-042
134	Pervin, Salma	Bangladesh Agricultural University (BAU), Mymensingh/Bangladesh Rice Research Institute (BRRI), Gazipur, Bangladesh	Effect of drought stress on growth, yield and assimilates partitioning in rice (*Oryza sativa*) genotypes at reproductive phase	pervinsalma@yahoo.com	IDT6-043
135	Phukon, Munmi	University of Aberdeen, Aberdeen, UK	Alternate wetting and drying enhances photosynthesis in rice	munmiphukan@gmail.com	IDT6-044
136	Prayaga, Lakshmi	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	Drought tolerance of sunflower genotypes with contrasting root traits	lprayaga@rediffmail.com	IDT6-045
137	Purushothaman, R	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Traits that confer post-flowering drought tolerance in short duration pigeonpea	purushothmurthy@gmail.com	IDT6-046
138	Pushpa, BN	University of Agricultural Sciences (UAS), Bangalore, India	Overexpression of plasma membrane Na+/H+ antiporter gene NHX7 : strategy for imparts salinity tolerance in rice	pushpalatha0001@gmail.com	IDT6-047
139	Rakhmanov, Bakhtiyor	Center of Genomics and Bioinformatics, Tashkent, Uzbekistan	Influence of epigenetic regulations on cotton	bakhtiyor.rakhmanov@gmail.com	IDT6-048
140	Saeed, Bushra	University of Delhi-South Campus, New Delhi, India	Isolation and characterization of a drought inducible transcription factor, ERD15 from mulberry	bushra.saeed1@gmail.com	IDT6-049
141	Sako, Dramane	Institut d'Economie Rurale (IER), Kayes, Mali	Development of high yielding medium duration groundnut tolerant to early leaf spots in mali	dramanesako@yahoo.fr	IDT6-050
142	Sanasam, Debina	University of Agricultural Sciences (UAS), Bangalore, India	Development and identification of high productive doubled haploid rice lines	debina01@gmail.com	IDT6-051
143	Sathishraj, Rajendran	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Interaction effect of heat and drought stress at reproductive phase in rice	r.sathishrajbiotech@gmail.com	IDT6-052
144	Sebastian, Anil	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	ABA induced seed dormancy and climate resilience in proso millet	sebastiananil.151@gmail.com	IDT6-053
145	Sharma, Sushma	Chaudhary Charan Singh University, Meerut, India	Impact of drought stress on floral biology of two species of *Dianthus* (Caryophllaceae)	sushma_sharma130@yahoo.co.in	IDT6-054
146	Tardieu, Francois	French National Institute for Agricultural Research (INRA), Montpellier, France	Phenotyping for the response to drought and high temperatures in a diversity of scenarios &Yield maintenance under drought: expansive growth and hydraulics also matter in reproductive organs	francois.tardieu@supagro.inra.fr	IDT6-055
147	Vanishri, BR	University of Agricultural Sciences (UAS), Bangalore, India	An aromatic twist in the quest of biofortification	vanishribr41@gmail.com	IDT6-056

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
148	Vinutha, KS	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Genetic variability for fodder quality traits in sorghum under different water regimes	vinuthaks.mysore@gmail.com	IDT6-057
149	Wehner, Gwendolin	Julius Kühn-Institut (JKI), Quedlinburg, Germany	Identification of QTL and eQTL for drought stress tolerance and leaf senescence in juvenile barley	gwendolin.wehner@julius-kuehn.de	IDT6-058
150	Zhang, Xia	Biotechnology Research Institute (BRI), CAAS, Beijing, China	Identification of maize mutants with enhanced drought tolerance and increased grain yield	zhangxia@caas.cn	IDT6-059
Theme 7: Breeding for Water-Limited Environments (Presentation on Feb 24, 2017, 16:00 - 18:00 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
151	Abdulmaliki, Rekiya Otuchu	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	Testcross performance and screening for drought tolerance in a bi-parental maize cross improved through marker assisted recurrent selection	rekimalik83@yahoo.com	IDT7-001
152	Abraha, Mizan Tesfay	University of KwaZulu-Natal (UKZN) and Tigray Agricultural Research Institute (TARI), Axum, Ethiopia	Breeding tef [Eragrostis tef (Zucc.) trotter] for drought tolerance in northern Ethiopia	mizantesfay90@gmail.com	IDT7-002
153	Adediran, Olaotan	Federal University of Technology Minna, Minna, Nigeria	Improved productivity of *Corchorus olitorius* L. varieties under moisture stress through nutrient management	o.adediran@futminna.edu.ng	IDT7-003
154	Adegbehingbe, Felix Taiwo	University of Ibadan, Ibadan, Nigeria	Identification of large-effect QTL for drought tolerance in rice in West African conditions	felix_taiwo@yahoo.co.uk	IDT7-004
155	Adejumobi, Idris Ishola	Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana	Breeding for water-limited environment: Performance of extra early tropical maize (*Zea mays* L.) genotypes under artificial drought stress using secondary traits	adejumobiidris@yahoo.com	IDT7-005
156	Ahmed, Hauwa Oziohu	Ahmadu Bello University (ABU), Zaria, Nigeria	Drought tolerance traits: indices of resistance to pre-harvest aflatoxin contamination in groundnut (*Arachis hypogaea* L.)	hauwaahmed21@gmail.com	IDT7-006
157	Ajay, BC	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	GGE biplot to analyse the response of recombinant inbred lines (RILs) of peanut to water stress	ajaygpb@yahoo.co.in	IDT7-007
158	Akinseye, Folorunso Mathew	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria	Simulating the effects of plant traits for increasing grain sorghum in water- limited environments: A case study of West Africa Sudano-sahelian region	f.akinseye@cgiar.org	IDT7-008
159	Alam, Ashraful	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	Genotype x environment interactions and identification of trait donors for reproductive stage drought stress in maize (*Zea mays* L.)	a.ashraful@cgiar.org	IDT7-009
160	Albayrak, Onder	Dicle University, Diyarbakir, Turkey	Determination of agronomic traits and drought susceptibility index (DSI) of drip irrigated maize landraces	onderalb@hotmail.com	IDT7-010
161	Aliche, Ernest	Wageningen University & Research, Wageningen, The Netherlands	Drought response of field cultivated potatoes: the interaction between canopy growth and yield	ernest.aliche@wur.nl	IDT7-011

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
162	Anaya, Fatima	Cadi Ayyad University, Marrakech, Morocco	Salicylic acid exogenous application boosts biochemical, physiological and chlorophyll a fluorescence transient of *Vicia faba* L. under irrigation with salt water	anaya.fatima@gmail.com	IDT7-012
163	Baig, Khizer	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Nanded, India	NH 635: A new high yielding variety of American cotton suitable for rainfed ecosystem of Maharashtra	khizerbaig1@rediffmail.com	IDT7-013
164	Bantte, Kassahun	Jimma University, Jimma, Ethiopia	Characterization of Ethiopian sorghum [*Sorghum bicolor* (L) Moench] germplasm collection for drought adaptation traits associated with roots	kassahunb@gmail.com	IDT7-014
165	Barurkar, Praveen Kumar	Agricultural Research Station (ARS), Kalaburagi, India	Breeding investigations for improving drought tolerance in maize (*Zea mays* L.)	praveenbarurkar@gmail.com	IDT7-015
166	Barutcular, Celaleddin	Cukurova University, Adana, Turkey	Canopy temperature and flag leaf greenness association with yield traits under heat stress in spring bread wheat	cebar@cu.edu.tr	IDT7-016
167	Bharti, Pooja	University of Agricultural Sciences (UAS), Bangalore, India	Physiological characterization of trait introgressed lines of rice (*Oryza sativa* L.) under drought	poojapb62@gmail.com	IDT7-017
168	Bora, Lokesh	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	In vitro polyploidization a novel approach for producing polyploids and screening for drought tolerance in acid lime (*Citrus aurantifolia* Swingle)	lokeshbora36099@gmail.com	IDT7-018
169	Borna, Fatemeh	The University of Tehran, Karaj, Iran	The influence of water stress on yield, some physiological characteristics and Leonurine contents of some ecotypes of *Leonurus cardiaca* in Iran	fatemehborna@gmail.com	IDT7-019
170	Brunel, Nidia	Universidad de Talca, Talca, Chile	Relationships between morpho-physiological root traits and the performance of spring wheat genotypes under water-stress in Mediterranean environments	nidiabrunel@gmail.com	IDT7-020
171	Caguiat, Joanne Domingo	Philippine Rice Research Institute (Philrice), Nueva Ecija, The Philippines	Evaluation of Drought Tolerance QTL effect in adapted genetic background	"jm.domingo@philrice.gov.ph "	IDT7-021
172	Cazenave, Alexandre-Brice	The Samuel Roberts Noble Foundation, Ardmore, USA	Discovering adaptive responses of alfalfa (*Medicago sativa* L.) to drought stress	abcazenave@noble.org	IDT7-022
173	Chukwudi, Uchechukwu Paschal	University of Nigeria Nsukka, Nsukka, Nigeria	Analysis of leaf yield components in fluted pumpkin (*Telfairia occidentalis* Hook F.) using path coefficient and GGE Biplot in derived savannah agro-ecology	uchechukwu.chukwudi@unn.edu.ng	IDT7-023
174	Deshpande, Sanjeev	University of Agricultural Sciences (UAS), Dharwad, India	Genetics of important traits for moisture stress tolerance in derived test cross hybrids of maize (*Zea mays.* L)	sanjeevgpb@gmail.com	IDT7-024
175	Desmae, Haile	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	Advances in groundnut breeding for drought prone West and Central Africa	h.desmae@cgiar.org	IDT7-025
176	Dhivyapriya, D	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Pyramiding of mega effect multiple QTLs and Development of "Climate Resilient rice"	dhivyaraj.89@gmail.com	IDT7-026

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
177	Dixit, Shilpi	International Rice Research Institute (IRRI), Patancheru, India	Pyramiding genes to develop multiple stress-tolerant rice lines	shilpi.dixit@irri.org	IDT7-027
178	Dowla, Mirza Nazim Ud	Murdoch University, Perth, Australia	Fine tuning phenology genes to safeguard wheat (*Triticum aestivum* l.) yield in water limited environments	m.dowla@murdoch.edu.au	IDT7-028
179	Drabo, Inoussa	West Africa Centre for Crop Improvement (WACCI), University of Ghana, Accra, Ghana	Landrace based top-cross pearl millet hybrid development for the sahel zone in burkina faso	idrabo@wacci.edu.gh	IDT7-029
180	Fellahi, Zine El Abidine	Ferhat Abbas University of Sétif, Sétif, Algeria	Genome-Wide Association analysis for yield and yield-related traits in bread wheat (*Triticum aestivum* L.) under contrasting moisture regimes	zinou.agro@gmail.com	IDT7-030
181	Gazal, Asima	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Kashmir, India	Studies on Drought Tolerance in Maize (*Zea mays* L.) Inbred Lines Using Morphological and Molecular Approaches	asimagazal@gmail.com	IDT7-031
182	Gorim, Linda	University of Saskatchewan, Saskatoon, Canada	Wild lentils as genetic resources to drought proof cultivated lentil	linda.gorim@usask.ca	IDT7-032
183	Hassan, Lateefat Bolanle	Ahmadu Bello University (ABU), Zaria, Nigeria	Potential of *in vitro* screening for drought tolerance in crops	lbhassan@abu.edu.ng	IDT7-033
184	Hotti, Avinalappa	University of Milan, Lodi, Italy	Identification and evaluation of chickpea genotypes for tolerance to heat stress under normal and heat stress environments for rice fallow condition in West Bengal	avihotti@gmail.com	IDT7-034
185	Hussain, Muhammad Mubashar	University of Sargodha, Sargodha, Pakistan	Screening of some functional markers in *Helianthus argophyllus*, *Helianthus annuus* and it derived population for adaptabilty under abiotic stress conditions	mubashar_uca@yahoo.com	IDT7-035
186	Ibitoye, Dorcus Olubunmi	National Horticultural Research Institute (NIHORT), Ibadan, Nigeria	Combining ability of cowpea [*Vigna unguiculata* (L.) Walp] lines for grain yield and drought tolerance under managed moisture condition.	bunmiajisafe@yahoo.com	IDT7-036
187	Indriatama, Wijaya Murti	Center for Isotope and Radiation Application, Jakarta, Indonesia	Evaluating for drought stress tolerance of some soybean promising mutant lines	wijaya@batan.go.id	IDT7-037
188	Issaharou Matchi, Issiaka	University of Diffa, Diffa, Niger	Evapotranspiration rates influence biogenic silica concentration in the shoots of *Pennisetum pedicellatum* Trin. at intraspecific level in semi-arid environment, West Africa	issakissaharou@gmail.com	IDT7-038
189	Jain, Abhinav	International Rice Research Institute (IRRI), Hyderabad, India	Combining ability analysis for yield and its contributing traits in rice (*Oryza sativa* L.) under water limited condition	a.jain@irri.org	IDT7-039
190	Jangra, Sumit	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	Molecular breeding for drought tolerance in pearl millet [*Pennisetum glaucum* (L.) R. Br.] using microsatellite markers	sumit.jangra712@gmail.com	IDT7-040
191	Jhang, Tripta	CSIR-Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow, India	Evaluation of selected lines of *Withania somnifera* for their root quality and yield performance	t.jhang@cimap.res.in	IDT7-041

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
192	Jukanti, Aravind Kumar	ICAR-Central Arid Zone Research Institute (CAZRI), Jodhpur, India	Development of hybrid parents and hybrids in pearl millet (pennisetum glaucum l.) For the arid north-western india (a1 zone)	aravindjukanti@gmail.com	IDT7-042
193	Kalpande, Hirakant V	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	Genetic Variability in post rainy sorghum (*Sorghum biocolor* (l.) Monech) genotypes for drought tolerant parameters & evaluation of chickpea genotypes in state multilocation varietal trial in rainfed condition	hvkalpande@rediffmail.com	IDT7-043, 044
194	Khan, Nadia	University of Karachi, Karachi, Pakistan	Genetic dissection of stem water-soluble carbohydrates and agronomic traits in wheat under different water regimes	nadiakhan@uok.edu.pk	IDT7-045
195	Kilango, Michael	Agricultural Research Institute- Uyole (ARI-U), Mbeya, Tanzania	Identification of selection indices for drought tolerance and drought tolerant common bean (*Phaseolus vulgaris*) genotypes in the southern highlands of tanzania	michaelkilango@yahoo.com	IDT7-046
196	Kovi, Basavaraj	University of Agricultural Sciences (UAS), Raichur, India	Studies on rice genotypes suitable for direct Seeded Condition (DSR)	basurajk7@gmail.com	IDT7-047
197	Kumar, Rahul	DAV university, Jalandhar, India	Development and characterization of sequence based markers in highly draught tolerant legume Horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] for various genomic applications	rahulihbt@gmail.com	IDT7-048
198	Kumar, Narendra	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Alternaria leaf blight of groundnut influenced by moisture deficit stress	narendrapb09@gmail.com	IDT7-049
199	Lakshmanan, Prakash	Sugar Research Australia (SRA), Brisbane, Australia	Breeding sugarcane for water-limited environments: integration of phenomics to improve clone selection	plakshmanan@sugarresearch.com.au	IDT7-050
200	Linden, Gerard	Wageningen University & Research, Wageningen, The Netherlands	Drought response of field cultivated potatoes: the interaction between canopy growth and yield	gerard.vanderlinden@wur.nl	IDT7-051
201	Lokhande, Prakash	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India	Physio-biochemical evaluation of F2 population of chickpea (*Cicer arietinum* L.) for drought tolerance	pklokhande@gmail.com	IDT7-052
202	Mallana Gowdra, Mallikarjuna	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Comparative and evolutionary analysis of drought-responsive transcription factor families in maize	mg.mallikarjuna@icar.gov.in	IDT7-053
203	Manasa, KG	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Utilizing genomic resources for understanding the stay-green QTLs interactions in sorghum	g.manasa@cgiar.org	IDT7-054
204	Mangrauthia, Satendra	ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, India	A multi-dimensional approach from seed-to-seed to understand and improve heat stress tolerance in rice	skmdrr@gmail.com	IDT7-055
205	Mani, BR	University of Agricultural Sciences (UAS), Dharwad, India	Selection of superior parents to derive single cross hybrids of maize for water limited and well watered conditions through development of new heterotic pools	mbreddys8102014@gmail.com	IDT7-056

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
206	Marriboina, Sureshbabu	University of Hyderabad, Hyderabad, India	Physiological and molecular insights into the high salinity tolerance of *Pongamia pinnata* (l.) pierre, a potential biofuel tree species	msuresh.biochem@gmail.com	IDT7-057
207	Mazaengo, Karantin D	Ministry of Agriculture Training Institute - Uyole, Mbeya, Tanzania	Response of common bean genotypes (*Phaseolus vulgaris* l.) To drought in relation to growth and yield characteristics in the southern highlands of tanzania	mkarantin@yahoo.co.uk	IDT7-058
208	Minnuru, Nagamallika Devi	International Rice Research Institute (IRRI), Patancheru, India	Evaluation of rice near isogenic lines for drought tolerance under aerobic condition	m.nagamallikadevi@irri.org	IDT7-059
209	Mittal, Shikha	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Comparison of genomic selection models for drought tolerance in sub-tropical maize	shikhamittal259@gmail.com	IDT7-060
210	Mohammed, Haruna	Savanna Agricultural Research Institute (SARI)/Tshwane University of Technology (TUT), Tamale, Ghana	Physiological and genetic diversity among cowpea (*Vigna unguiculata* L. Walp) landraces from Northern Ghana, determined by δ15N, gas exchange, RAPD and SSR markers	Haruna_mohammed67@yahoo.com	IDT7-061
211	Mohanraj, K	ICAR-Sugarcane Breeding Institute, Coimbatore, India	Potential of Erianthus procerus introgressed sugarcane clones under water deficit stress	mohangene@yahoo.com	IDT7-062
212	More, Ambika	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	Combining Ability and Heterosis in Rabi Sorghum (*Sorghum biocolor* (L.) Monech) Hybrids for Yield and Drought Parameters	ambikamore@rediffmail.com	IDT7-063
213	Mponda, Omari	Naliendele Agricultural Research Institute (NARI), Mtwara, Tanzania	Advances of groundnut breeding and seed systems in Tanzania	kalanjekanduru@gmail.com	IDT7-064
214	Muniswamy, S	Agricultural Research Station (ARS), Gulbarga, India	Identification of climate reisilient pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes	muniswamygpb@gmail.com	IDT7-065
215	Murugesan, Tharanya	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Phenotypic and genetic dissection of water stress adaptations in pearl millet (*Pennisetum glaucum*)	m.tharanya@gmail.com	IDT7-066
216	Muthuramu, S	Tamil Nadu Agricultural University (TNAU), Paramakudi, India	Variability studies for quantitative traits in upland rice (*Oryza sativa* L.)	smuthuramu@gmail.com	IDT7-067
217	Nabateregga, Mabel	Makerere University, Kampala, Uganda	Discovery of Quantitative Trait Loci (QTL) underlying drought tolerance in a F5 RIL Andean intragene cross population (BRB191/SEQ1027) of common bean (*Phaseolus Vulgaris* L.)	mnabateregga@gmail.com	IDT7-068
218	Naga, Supreetha	University of Agricultural Sciences (UAS), Bangalore, India	Mutation in *Zeaxanthin epoxidase* enhanced excess enenrgy dissipation and improved drought tolerance in rice - study using mutants.	supreetasharaff@gmail.com	IDT7-069
219	Namugga, Prossy	University of KwaZulu-Natal (UKZN) and National Agricultural Research Organisation (NARO), Kabale, Uganda	Performance of elite potato clones for drought tolerance in Uganda	namuggak@gmail.com	IDT7-070

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
220	Natarajan, Kumari	Maize Reasearch Station TNAU, Palani, India	Evaluation of combining ability and heterotic responses in maize (*Zea mays* L.) for drought tolerance	soundhini@yahoo.co.in	IDT7-071
221	Nichols, Shirley	AgResearch, Hamilton, New Zealand	Variation among white clover interspecific hybrid families for traits associated with improved drought resistance	shirley.nichols@agresearch.co.nz	IDT7-072
222	Nouhoun, Belko	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	Phenotypic variability of drought-avoidance shoot and root phenes and their relationships with yield under drought and low P conditions in cowpea	N.Belko@cgiar.org	IDT7-073
223	Obala, Jimmy	University of KwaZulu-Natal (UKZN), Pietermaritzburg, South Africa	Molecular mapping of seed protein content in pigeonpea – a drought tolerant crop of the semi-arid tropics	jimmyobala@gmail.com	IDT7-074
224	Ogunkanmi, Adebayo	University of Lagos, Lagos, Nigeria	QTL mapping for drought resistant in cowpea	logunkanmi@unilag.edu.ng	IDT7-075
225	Ojiewo, Chris	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Addis Ababa, Ethiopia	Breeding tropical legume crops for resilient cropping systems in Sub-Saharan Africa	C.Ojiewo@cgiar.org	IDT7-076
226	Ojulong, Henry	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	Field screening finger millet germplasm for drought tolerance	H.Ojulong@CGIAR.ORG	IDT7-077
227	Okello, David Kalule	National Semi Arid Resources Research Institute (NaSARRI), Soroti, Uganda	Current status of groundnut improvement in Uganda	kod143@gmail.com	IDT7-078
228	Olufajo, Olusoji	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	Increasing cowpea (*Vigna unguiculata* (L.) Walp) production and productivity in drought prone agro-ecologies of Nigeria	sojiolufajo@yahoo.com	IDT7-079
229	Oteng-Frimpong, Richard	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	Performance and yield stability of groundnut (*Arachis hypogaea* L.) in the guinea savanna zone of Ghana	kotengfrimpong@gmail.com	IDT7-080
230	Palta, Jairo	The University of Western Australia, Perth, Australia	Towards the improvement of tolerance to early-season-drought in wheat – assessment of candidate traits	jario.palta@uwa.edu.au	IDT7-081
231	Parvathaneni, Lakshmamma	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	Performance of good root and drought tolerant castor (*Ricinus communis* L.) germplasm in kharif under rainfed conditions	lakshmiparvathaneni@rediffmail.com	IDT7-082
232	Person, Taylor	Colorado State University, Colorado, USA	Characterization of drought adapted grain sorghum varieties and favorable root phenotypes in BTx623 X IS3620C recombinant isogenic line population.	tperson47@gmail.com	IDT7-083
233	Pettam, Mamatha	International Rice Research Institute (IRRI), Patancheru, India	Identification of stable grain Yield QTLs under reproductive-stage drought stress in rice (*Oryza sativa* L.)	pettemmamatha23@gmail.com	IDT7-084
234	Pokharel, Bhanu Bhakta	Agriculture and Forestry University, Bharatpur, Nepal	Molecular approaches to improve performance of barley under water limited environments	bhanu.pokharel@gmail.com	IDT7-085
235	Pranesh, K Jayadevappa	International Rice Research Institute (IRRI), Patancheru, India	Identification of rice genotypes under different water-limiting practices	praneshkj@gmail.com	IDT7-086

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
236	Preethi, NV	University of Agricultural Sciences (UAS), Bangalore, India	Comparative assessment of drought adaptation in rice and wheat	reddypreethi.reddy@gmail.com	IDT7-087
237	Priyadarshi, Rahul	International Rice Research Institute (IRRI), Patancheru, India	Identification of QTLs for reproductive stage drought and high-temperature stress in rice (*Oryza sativa* L.)	r.priyadarshi@irri.org	IDT7-088
238	Ragimasalawada, Madhusudhana	Indian Institute of Millets Research (IIMR), Hyderabad, India	Evaluation of partial stay-green QTL introgression lines of Indian post-rainy sorghum lines	madhu@millets.res.in	IDT7-089
239	Rahman, Hifzur	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Exploiting finger millet as a source for isolating novel genes controlling abiotic stress tolerance	rahman.biotech@gmail.com	IDT7-090
240	Rahman, A K M Mahbub	Bangladesh Agricultural University (BAU), Gazipur, Bangladesh	Characterization of lentil germplasm and identification of potential morphological marker(s) linked to drought tolerance	kbdbabu@gmail.com	IDT7-091
241	Rai, Pooja	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	Identification of superior alleles of known rice genes for high yield-potential under drought	poojarai140@gmail.com	IDT7-092
242	Rajurkar, Ashish Balkrishna	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Breeding for drought resilience in rice: Root growth and yield under drought in managed stress and target populations of environments	ashu.raj123@gmail.com	IDT7-093
243	Rana, Maneet	ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi, India	Molecular mapping of quantitative trait loci for drought tolerance and yield traits in lentil	rana.maneet@gmail.com	IDT7-094
244	Rana, Vijay	CSK Himachal Pradesh Agricultural University, Palampur, India	Studies on drought tolerance using some morpho-physiological parameters in wheat (*Triticum aestivum* l.)	vijayrana_2005@rediffmail.com	IDT7-095
245	Rane, Jagadish	ICAR-National Institute of Abiotic Stress Management (NIASM), Pune, India	Optimizing high throughput phenotyping for productive use of water in mungbean and chickpea	jagrane@hotmail.com	IDT7-096
246	Ranganathan, Chandrababu	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Breeding for drought resilience in rice: mapping QTLs for yield under drought in TPE using local landraces, development and testing of QTL lines for drought physiology, root growth and transcriptome	chandrarc2000@yahoo.com	IDT7-097
247	Rao, SS	Indian Institute of Millets Research (IIMR), Hyderabad, India	Phenotyping dryland sorghum (*Sorghum bicolor* (L.) Moench) for drought tolerance across semiarid tropical climates- an overview of research progress	ssrao@millets.res.in	IDT7-098
248	Rohila, Jai	USDA-Agricultural Research Service, Stuttgart, USA	Agronomic and physiological performance of Teqing x Lemont introgression rice (*Oryza sativa* L.) lines under limited irrigation system	jai.rohila@ars.usda.gov	IDT7-099
249	Sallam, Ahmad	Assiut University, Assiut, Egypt	Genetic molecular dissection of drought tolerance in winter wheat (*Triticum aestivum* l.) using QTL mapping	amsallam@aun.edu.eg	IDT7-100
250	Sanka, Thippeswamy	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Jagtial, India	Development of rice (*Oryza sativa* L.) varieties and hybrids for aerobic conditions	thippeswamys@gmail.com	IDT7-101
251	Seetharam, K	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	Genomic regions associated with drought tolerance in maize in Asian tropics	k.seetharam@cgiar.org	IDT7-102

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
252	Sellamuthu, Reena	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Improving drought resilience of a mega rice variety by pyramiding QTLs for root traits and yield under drought	reenasen23@gmail.com	IDT7-103
253	Selvaraj, Gopalan	National Research Council of Canada, Saskatoon, Canada	Identification of drought tolerance traits for addressing yield protection in western Canadian conditions	gopalan.selvaraj@nrc-cnrc.gc.ca	IDT7-104
254	Sen, Poulomi	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	Pyramiding of drought tolerance QTLs and P-deficiency tolerance genes in rice.	poulomisen6121991@gmail.com	IDT7-105
255	Shah, Asif Ashraf	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Jammu, India	Breeding for water-limited environments	ashu.ashraf@gmail.com	IDT7-106
256	Shandu, Siphiwokuhle	ARC-Grain Crops Institute, Potchefstroom, South Africa	Selection for improved maize (*Zea mays* L.) variety performance under drought stress conditions in South Africa	ShanduS@arc.agric.za	IDT7-107
257	Shashidhara, N	Pandit Jawaharlal Nehru College of Agriculture and Research Institute (PAJANCOA) & RI, Karaikal, India	Development of HP-RILs in rice (*Oryza sativa* L.) through MAS suitable for aerobic cultivation	shashidhara.gpb@gmail.com	IDT7-108
258	Shimelis, Hussien	University of KwaZulu-Natal (UKZN), Pietermaritzburg, South Africa	Population structure and genome-wide marker-trait association of key agronomic traits in wheat under drought-stressed and non-stressed conditions	Shimelish@ukzn.ac.za	IDT7-109
259	Singh, Jang Bahadur	ICAR-Indian Agricultural Research Institute (IARI), Indore, India	Genetic analysis of yield and other important traits in wheat under moisture stress conditions	jangbsingh@gmail.com	IDT7-110
260	Singh, Amrit Lal	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Elasticity of drought tolerance among Indian peanut cultivars during rainy season	alsingh16@gmail.com	IDT7-111
261	Singh, Sukhwinder	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	Wheat pre breeding for drought prone environments	Suk.Singh@cgiar.org	IDT7-112
262	Smitha Rani, JA	University of Agricultural Sciences (UAS), Bangalore, India	Phenotypic diversity of trait specific mapping populations to determine QTL allelic effect in rice (*Oryza sativa* L.)	smirja.arakesh@gmail.com	IDT7-113
263	Sserumaga, Julius Pyton	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	Grain yield stability, heritability and genotype by environment interaction among double haploid maize hybrids under drought stress and optimum conditions	j.serumaga@gmail.com	IDT7-114
264	Stephen, Roy	Kerala Agricultural University, Thiruvananthapuram, India	Selective fertilization for inducing water stress tolerance in coconut (*Cocos nucifera* L)	roykau@gmail.com	IDT7-115
265	Tengli, Srikant	University of Agricultural Sciences (UAS), Bangalore, India	Temperature induction response technique: A physiological approach to identify thermotolerant genotypes in mungbean	srikanttengli@gmail.com	IDT7-117
266	Thakur, Padma	Banaras Hindu University (BHU), Varanasi, India	Assessment of rice (*Oryza sativa* L.) for drought tolerance with SSR markers	padma.13291@gmail.com	IDT7-118
267	Thakur, Vidisha	Banasthali Vidyapith, Jaipur, India	Effect of drought stress on antioxidant enzymes activity and gene expression and physiological response in wheat (*Triticum aestivum* L.)	vidisha.thakur30@gmail.com	IDT7-119

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
268	Thirunavukkarasu, Nepolean	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Deciphering the genetics of drought tolerance through comprehensive genomic approaches in maize	tnepolean@gmail.com	IDT7-120
269	Torres, Rolando	International Rice Research Institute (IRRI), Los Banos, The Philippines	Selection of donor cultivars for breeding drought resistant rice (Oryza sativa L.)	r.torres@irri.org	IDT7-121
270	Tripathi, Pramila	ICAR-Indian Institute of Sugarcane Research (IISR), Lucknow, India	Expression analysis of genes associated with drought tolerance vis a vis impact of GA3 in sugarcane (Saccharum spp. hybrids)	pramila.t.21@gmail.com	IDT7-122
271	Tura, Habtamu	University of Adelaide, Adelaide, Australia	Growth and transpiration rates as a potential proxy traits to track yield QTL in wheat under drought	habtamu.tura@acpfg.com.au	IDT7-123
272	Uba, Charles Uwazuruike	University of Nigeria Nsukka, Nsukka, Nigeria	Field evaluation of yield and yield component traits of breeding lines of maize over two seasons in a derived savannah agro-ecology.	Charlesuba192@gmail.com	IDT7-124
273	Vaithiyalingan, M	Tamil Nadu Agricultural University (TNAU), Tindivanam, India	Combining ability studies in drought tolerant groundnut (*Arachis hypogaea* L.) genotypes	mvaithiyalingan@gmail.com	IDT7-125
274	Vanitha, A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Evaluation of chilli (*Capsicum annuum var annuum* L.) genotypes for pod yield and quality under rainfed conditions of Tamil Nadu	ajjanvanitha@gmail.com	IDT7-126
275	VenuPrasad, R	Africa Rice Centre (AfricaRice), Ibadan, Nigeria	Exploiting African rice germplasm to breed for drought tolerance	R.Venuprasad@cgiar.org	IDT7-127
276	Vikram, Prashant	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	Exploration of landraces for future climate resilient wheat improvement	p.vikram@cgiar.org	IDT7-128
277	Vinayan, MT	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	Genotype x environment interactions and trait donors for drought stress among Asia-adapted maize inbred lines	m.vinayan@cgiar.org	IDT7-129
278	Vipparla, Abhilash Kumar	International Rice Research Institute (IRRI), Patancheru, India	Development of high-yielding varieties for dry, direct seeded aerobic conditions utilizing marker-assisted breeding	abhilash.kumar@irri.org	IDT7-130
279	Wang, Feiming	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	A new water-saving and drought-resistant rice variety Huhan61	wfm@sagc.org.cn	IDT7-131
280	Wang, Shiwen	Northwest A&F University, Yangling, China	Glycolipids remodeling involved in the drought-induced leaf senescence in maize	shiwenwang@nwsuaf.edu.cn	IDT7-132
281	Xu, Jianlong	Agricultural Genomics Institute/Chinese Academy of Agricultural Sciences (CAAS), Shenzhen, China	Harnessing the Hidden Genetic Diversity for Improving Multiple Abiotic Stress Tolerances in Rce (*Oryza sativa* L.)	xujlcaas@126.com	IDT7-133
282	Yadav, Arun	Australian National University (ANU), Canberra, Australia	Translational research to develop drought tolerant wheat cultivar	arun.yadav@anu.edu.au	IDT7-134
283	Zaidi, Pervez Haider	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	Drought tolerant maize for Asian tropics - What worked and what is challenging?	phzaidi@cgiar.org	IDT7-135

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
284	Zargar, Sajad Majeed	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Srinagar, India	Agro-morphological and physiological evaluation of common bean (*Phaseolus vulgaris* l.) Germplasm under water stress	smzargar@gmail.com	IDT7-136
Theme 8: Agronomic Management/Cropping Systems for Water-Limited Environments, Broad Approaches (Presentation on Feb 22, 2017, 16:45 - 18:30 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
285	Abubakar, Zainab Adamu	Gombe State University, Gombe, Nigeria	Contribution to the interaction between *Arbuscular Mycorrhiza* Fungi (AMF) (*Rhizophagus irregularis*) NPK and drought tolerance to yield of NERICA in Northern Nigeria	zeepha22@gmail.com	IDT8-001
286	Ajilogba, Caroline	North-West University, Mafikeng, South Africa	EFFECT of growth stages on community dynamics of Bambara Groundnut (Drought-tolerant crop) Rhizospheric bacteria	carolfad@yahoo.com	IDT8-002
287	Ashoka, P	University of Agricultural Sciences (UAS), Dharwad, India	In situ rainwater conservation for enhancement Productivity of maize (*Zea Mays* L) -chick pea (*Cicer arietinum*) cropping system on Vertisol region	ashokapuas@gmail.com	IDT8-003
288	Balasubramanian, P	Tamil Nadu Agricultural University (TNAU), Madurai, India	Charred rice husk to improve the soil moisture retention and nutrient management in rainfed groundnut (*Arachis hypogaea* L.)	agribalatnau1991@gmail.com	IDT8-004
289	Betaw, Hirut Getinut	International Livestock Research Centre (ILRI), Addis Ababa, Ethiopia	Combining ability for drought tolerance and yield components of highland tropic adapted potato in Ethiopia	H.Getinet@cgiar.org	IDT8-005
290	Bharath, CT	University of Agricultural Sciences (UAS), Bangalore, India	Microbes bio-fortify rice	bharath7015@gmail.com	IDT8-006
291	Binagwa, Papias	Selian Agricultural Research Institute (SARI), Arusha, Tanzania	Assessment of common bean (*Phaseolus vulgaris*) genotypes for farmers' preferences and acceptance through participatory bean breeding approaches	hongera1984@yahoo.com	IDT8-007
292	Buchupalli, Ravindranatha Reddy	Agricultural Research Station (ARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Anantapur, India	Higher productivity in pearlmillet (*Pennisetum glaucum* L.) with conservation furrow and supplemental irrigation	b.ravindranathareddy@gmail.com	IDT8-008
293	Bustos-Korts, Daniela	Wageningen University & Research, Wageningen, The Netherlands	A protocol combining statistical and crop growth modelling to evaluate phenotyping strategies useful for selection under different drought patterns	daniela.bustoskorts@wur.nl	IDT8-009
294	Chaudhary, Suman	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	Promising sulphur oxidizing bacteria as a remedy for unavailable sulphur in dryland areas of india	kesarsuman21@gmail.com	IDT8-010
295	Chichaybelu, Mekasha	Ethiopian Institute of Agricultural Research (EIAR), DebreZeit, Ethiopia	Advances in Chickpea Crop Improvement forImproved Productivity and Resilient Cropping Systems in Ethiopia	chichemekasha@gmail.com	IDT8-011
296	Datta, Avishek	Asian Institute of Technology, PathumThani, Thailand	The effects of cultivation methods and water regimes on root systems of one drought-tolerant (RD6) and one drought-sensitive (RD10) rice varieties of Thailand	datta@ait.asia	IDT8-012
297	Dhanker, Rinku	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	Impact of municipal sewage sludge on physicochemical characteristics and heavy metal accumulation in soil in accordance to its agricultural uses	rinku1989d@gmail.com	IDT8-013

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
298	Dick, Richard	Ohio State University, Columbus, USA	Intercropped woody species in the sahel to resist drought: hydraulic lift and crop water relations & intercropped woody species in the sahel to resist drought: Beneficial microorganisms and common mycorrhizal hyphal networks to reduce water stress	dick.78@osu.edu	IDT8-014, 015
299	Dubey, Rama Kant	Banaras Hindu University (BHU), Varanasi, India	Synergistic agronomic practices for improving soil functions and agricultural sustainability	ramakant.sls@gmail.com	IDT8-016
300	Echekwu, Candidus A	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	Tropical legume project impact on groundnut improvement research outputs in Nigeria	candyechekwu@gmail.com	IDT8-017
301	Ekwomadu, Theodora	North-West University, Mmabatho, South Africa	Drought impacts on fungal and mycotoxin contamination of small-scale maize from the North-West province of South Africa	23115394@nwu.ac.za	IDT8-018
302	Etim, NseAbasi NsikakAbasi	Akwa Ibom State University, Uyo, Nigeria	Animal manure: A remedy for dry land crop production	etimbobo@yahoo.com	IDT8-019
303	Fenta, Berhanu Amsalu	Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia	Innovative approach on common bean based technology generation and promotion for improvement of the livelihood at lowland areas of Ethiopia	berhanufenta@gmail.com	IDT8-020
304	Ferdous, Md Zannatul	Asian Institute of Technology, PathumThani, Thailand	Effect of plastic mulch on yield and yield attributes of cauliflower and tomato in inland and coastal regions of Bangladesh	manikbau80@gmail.com	IDT8-021
305	Fghire, Rachid	Cadi Ayyad University, Marrakech, Morocco	Response of quinoa to different water management strategies: Field experiments and SALTMED model application results	r.fghire@gmail.com	IDT8-022
306	Govindasamy, V	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Rhizobacterial endophytes contribute to moisture stress tolerance in senescent genotype of sorghum [*Sorghum bicolor* (L.) Moench]	" govindasamy@iari.res.in"	IDT8-023
307	Gurikar, Chennappa	University of Mysore, Mysore, India	Bio protectant potential, abiotic stress tolerance and phytopathogenic properties of Azotobacter tropicalis KOP-11 strain isolated from paddy soils	chinnagurikar@gmail.com	IDT8-024
308	Hanumanthu, Nagaraja	University of Mysore, Mysore, India	Seed bioprotectant efficacy of *Azotobacter salinestris* and Azotobacter species (JX 262164) against phyto pathogenic Fusarium associated with cereal grains	nagarajh82@gmail.com	IDT8-025
309	Hegde, Shridhar	Pioneer Hi-Bred Private Limited, Hyderabad, India	Applications of Enclass® system and managed stress environment for characterizing and developing drought tolerant products in CORN	shridhar.hegde@pioneer.com	IDT8-026
310	Jabborova, Dilfuza	Institute of Genetics and Plant Experimental Biology, Тошкент, Uzbekistan	Coinoculated with *Bradyrhizobium* japonicum NU1 and *Pseudomonas* putida NUU8 to improve growth and nodulation of soybean under drought condition	dilfuzajabborova@yahoo.com	IDT8-027
311	Jat, Ram	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Evaluating response of groundnut to crop geometries and growth promoting substances	rajatagron@gmail.com	IDT8-028
312	Javid, Majid Ghorbani	University of Tehran, Tehran, Iran	Improvement of flower yield and physiological traits of saffron (*Crocus sativus* L.) under drought stress via different planting dates and corm sizes	mjavid@ut.ac.ir	IDT8-029

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
313	Jinbaani, Alhassan Nuhu	CSIR-Savanna Agricultural Research Institute, Tamale, Ghana	SWOT analytical framework of innovation platforms (IPS) for promoting the adoption of improved groundnut seed in northern Ghana	jinbaani@yahoo.com	IDT8-030
314	Ka, Sambalaha	Senegalese Institute of Agricultural Research, Kolda, Senegal	The weeds flora of grain Sorghum (*Sorghum bicolor* (L.) Moench) in Senegal (West Africa): Characterization of flora and species harmfulness	kasam74@gmail.com	IDT8-031
315	Kamoshita, Akihiko	University of Tokyo, Tokyo, Japan	Water-saving irrigation to maximize rice production in Colombia	akamoshita@anesc.u-tokyo.ac.jp	IDT8-032
316	Kiboi, Milka	Embu University College, Embu, Kenya	Soil water conservation strategies effects on maize yields in farmer managed trials in the Central Highlands of Kenya	milka.kiboi@gmail.com	IDT8-033
317	Kimurto, Paul K	Egerton University, Egerton, Kenya	Performance of marker assisted backcross breeding (MABC) elite chickpea lines under drought conditions in Kenya	kimurtopk@gmail.com	IDT8-034
318	Kumar, GD Satish	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	Best Management Practices in sunflower for maximizing yield in dry lands	gd.satishkumar@icar.gov.in	IDT8-035
319	Kumar, Ashish	Jawaharlal Nehru Agricultural University (JNKVV), Rewa, India	Selection of *Trichoderma* spp. for plant growth promotion and abiotic stress tolerance	ashishashish2612@gmail.com	IDT8-036
320	Kumar, Deepak	Central University of Jammu, Jammu, India	Potential application of aldose reductase homolog from a resurrection plant for abiotic stress tolerance	deepakinjnu@gmail.com	IDT8-037
321	Kumar, Sumit	University of Hyderabad, Hyderabad, India	Efficacy of Jatropha seedcake on growth, photosynthesis and yield of *Camelina sativa* under water-limited conditions	sumit.gre@gmail.com	IDT8-038
322	Lutonadio, Genie Spirou	University of Kinshasa, Kinshasa, Democratic Republic of the Congo	Adaptation of seven quinoa (*Chenopodium quinoa* Willd.) cultivars to agroecological conditions of Kinshasa (DRC)	geniespiroulutonadio01@gmail.com	IDT8-039
323	Macharia, Joseph Maina	Kenyatta University, Nairobi, Kenya	Potential contribution of maize (*Zea mays*) in the estimation of croplands' carbon fluxes under climate variability using static chambers in Kenya	machariamjoseph@gmail.com	IDT8-040
324	Madireddi, Sai Kiran	University of Hyderabad, Hyderabad, India	LHCSR3 impairs photosynthetic membrane complex assembly of Chlamydomonas reinhardtii under drought stress	saimadireddi@gmail.com	IDT8-041
325	Malamasuri, Kadasiddappa	University of Agricultural Sciences (UAS), Dharwad, India	Determination of suboptimal irrigation rates through drip for maize (*Zea mays* L.) under southern peninsular region of India	kadasiddappa.m@gmail.com	IDT8-042
326	Manonmani, V	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Efficacy of polymer coated cotton seeds on crop productivity under moisture stress conditions	vmano_2004@yahoo.com	IDT8-043
327	Masuka, Benhidah Pamhidzai	University of Zimbabwe, Marondera, Zimbabwe	Dissemination and adoption of drip irrigation among smallholder farmers in Svosve-Wenimbi, Marondera, Zimbabwe	trimasuka@gmail.com	IDT8-044
328	Mathews, Cherian	Tshwane University of Technology (TUT), Pretoria, South Africa	Intercropping pigeonpea [*Cajanus cajan* (L.) Millspaugh] with maize (*Zea mays* L.) to enhance food security, sustainability and profitability of smallholder farmers in semi-arid South Africa	cherianm47@gmail.com	IDT8-045
329	Miningou, Amos	Institut de l'Environnement et des Recherches Agricoles (INERA), Ouagadougou, Burkina Faso	Advances in groundnut (*Arachis hypogaea*) breeding for resilient cropping systems in Burkina Faso	miningou_amos@yahoo.fr	IDT8-046

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
330	Mofokeng, Maletsema Alina	ARC-Grain Crops Institute, Potchefstroom, South Africa	The potential of cowpea in marginal cropping areas of South Africa	MofokengA@arc.agric.za	IDT8-047
331	Mubuka, Amina Subira	Makerere University, Kampala, Uganda	Gender and climate change adaptation among bean farming systems in Uganda	asmubuka@gmail.com	IDT8-048
332	Mugisha, Johnny	Makerere University, Kampala, Uganda	Women's production capacities enhancement and gender yield gap reduction in groundnuts in Uganda	jomugisha@agric.mak.ac.ug	IDT8-049
333	Mwakimata, Romanus	Sokoine University of Agriculture, Morogoro, Tanzania	Groundnut gendered yield gap analysis in tanzania: Social and economics implication	mwakimata@gmail.com	IDT8-050
334	Mwenda, Emmanuel Thomas	Agricultural Research Institute-Ilonga, Morogoro, Tanzania	Agronomic options in sorghum for improved water use efficiency across semi arid areas of Tanzania	emmamwenda@yahoo.com	IDT8-051
335	Neog, Prasanta	Assam agricultural University, Jorhat, India	Resilient agronomic practices to cope with seasonal drought in Sali rice grown in North Bank Plain Zone of Assam, India	neogprasanta@rediffmail.com	IDT8-052
336	Nzungize, John	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	Research and development partnerships for a large-scale diffusion of technologies for sorghum and millet systems in Mali	j.nzungize@cgiar.org	IDT8-053
337	Oloyede, Funmilayo Mary	Osun State University (UNIOSUN), Osogbo, Nigeria	Sowing dates affect pumpkin fruit yield and quality	funmilayooloyede@yahoo.co.uk	IDT8-054
338	Omari, Mikidadi Abubakar	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	Flowering responses of selected cassava genotypes to plant growth regulator application under screen house and field conditions in Uganda	mikisb2340@yahoo.com	IDT8-055
339	Onzima, Benard	Makerere University, Kampala, Uganda	Market access and the impact of adaptation to climate change among bean farmers in Uganda	benardonzima@yahoo.com	IDT8-056
340	Pal, Kamal	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Endophytic bacteria endow solace to drought-stressed peanut	kkpal9426476749@gmail.com	IDT8-057
341	Pandagale, Arvind	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Nanded, India	Soil moisture conservation measures in cotton (*Gossypium hirsutum*) under high density planting system to sustain drought condition	arvindpandagale@yahoo.co.in	IDT8-058
342	Praharaj, Subhashisa	G B Pant University of Agriculture and Technology, Pantnagar, India	Effect of ethephon and gibberellic acid on productivity and juice quality of Sugarcane (*Saccharum officiarum* L.)	praharaj93@gmail.com	IDT8-059
343	Radhajeyalakshmi, Raju	Tamil Nadu Agricultural University (TNAU), Vagarai, India	Identification and characterization of drought tolerant CLP producing fluorescent Pseudomonads in maize (*Zea mays* L.)	radhajeyalakshmi@hotmail.com	IDT8-060
344	Rahman, Shah Moinur	Hajee Mohammad Danesh Science & Technology University, Dinajpur, Bangladesh	Comparison of water use, growth and 15N recovery among Flooding, SWD and Non-flooding water-saving irrigation practices under lowland paddy field	nurhstu@gmail.com	IDT8-061
345	Rangappa, Krishnappa	ICAR, Research Complex for NEH region, Umiam, India	Physiological efficiency and drought tolerance ability of Buckwheat (*Fagopyrum esculantum* L.) under hill slopes of North Eastern Himalayan region of India	Krishphysiology@gmail.com	IDT8-062
346	Rao, Poornachandra	University of Mysore, Mysore, India	*Lactobacillus plantarum* MYS44 as potential biological tool to control aflatoxigenic *Aspergillus parasiticus*	pckrao.06@gmail.com	IDT8-063

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
347	Ressaissi, Yosra	National Agricultural Research Institute of Tunisia (INRAT), Tunis, Tunisia	Genotype and environment interaction in the tunisian dairy flocks	yos.re@hotmail.fr	IDT8-064
348	Saha, Saurav	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Evaluating the potential of increasing atmospheric CO_2 to promote chickpea (*Cicer arittinum* L.) production in semi-arid region of northern india	sauravs.saha@gmail.com	IDT8-065
349	Sahadeva Reddy, B	Agricultural Research Station (ARS), Acharya N.G. Ranga Agriciultural University (ANGRAU), Anantapur, India	Innovative rainwater management technology to cope with climate variability and sustainable productivity of rainfed groundnut (*Arachis hypogaea* L.)	sahadevardd@gmail.com	IDT8-066
350	Samaila, Jeremiah	Harper Adams University, England, UK	Response of sorghum drought tolerance to application of film-forming antitranspirants over the reproductive stage	jsamaila@harper-adams.ac.uk	IDT8-067
351	Sangwan, Pooja	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	Variation in total soluble sugars and protein content in the leaves of downy mildew resistant and susceptible pearl millet genotypes	choudhary.shweta737@gmail.com	IDT8-068
352	Satpute, Gyanesh	ICAR-Indian Institute of Soybean Research (IISR), Indore, India	Plant ideotype suitable for adaptation to water limited environment and per se yield enhancement in rainy season in soybean (*Glycine max* L. Merill)	gksatpute@yahoo.co.in	IDT8-069
353	Satturu, Vanisri	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	Effect of mannitol mediated water stress on chlorophyll content and scavenging enzyme actitivity in rice genotypes	vanisree_dhar@yahoo.com	IDT8-070
354	Sharma, Seema	KSKV Kachchh University, Bhuj, India	Building drought resilient agri-systems in semi arid tropics through the intervention of TEK (Traditional Ecological Knowledge): The Kachchh case study	seemabhargavsharma@gmail.com	IDT8-071
355	Sheeba, A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Identifying suitable rice hybrids for rainfed ecosystem using AMMI analysis	sheebateddy@gmail.com	IDT8-072
356	Silambarasan, M	Agricultural College and Research Institute, Madurai, India	Crop geometry and nitrogen management to combat water scarcity and yield maximization in extra early rice	silambutnau@gmail.com	IDT8-073
357	Singaram, Ambika	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Performance of polymer coated CORH 3 hybrid rice seed on productivity under moisture stress conditions	ambikasingaram@gmail.com	IDT8-074
358	Sunkalikar, Laxman	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Jagtial, India	Effect of spacing and fertiliser dose on dry and sprouted seed sown aerobic rice (*Oryza sativa* L.)	adr_rarsjgl@yahoo.com	IDT8-075
359	Suvarna, Praneeth	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	Enhanced root activity and nitrification under SRI system improves nitrogen nutrition of rice	suvarnapraneeth@gmail.com	IDT8-076
360	Swain, Sabyasachi	IIT Bombay, Mumbai, India	Development of an index to characterize and monitor agricultural droughts	sabyasachiswain16@gmail.com	IDT8-077

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
361	Thatikunta, Ramesh	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	Evaluation of cotton genotypes and standardization of agrotechniques for high density planting in rainfed alfisols of Telangana	thatikuntaramesh@gmail.com	IDT8-078
362	Tiwari, Shalini	CSIR-National Botanical Research Institute (NBRI), Lucknow, India	*Pseudomonas* putida modulates morphophysiological, biochemical and molecular responses in chickpea (*Cicer arietinum* L.) during drought stress and recovery	shalini8apr@gmail.com	IDT8-079
363	Tram, Nguyen Thi Hoai	Hue University, Hue, Vietnam	New drought-tolerant groundnut varieties for Bac Binh district, Binh Thuan province, Vietnam	hoaitramnt@gmail.com	IDT8-080
364	Tyagi, Jaagriti	Amity University, Noida, India	Differential effect of AMF (Glomus intraradices) and endophytic fungus (*Piriformospora indica*) on *Finger millet* [*Eleusine coracana* (L.) Gaertn] under the drought stress	jaagriti.tyagi13@gmail.com	IDT8-081
365	Veera, Jayalakshmi	Regional Agicultural Research Station (RARS), Nandyal, India	Prospects of new chickpea varieties in Andhra Pradesh	veera.jayalakshmi@gmail.com	IDT8-082
366	Vijaya Prabhakar, A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Strip intercropping system for sustainable crop production under rainfed ecosystem	a.vijayp@ymail.com	IDT8-083
367	Wekha, Nelson Wafula	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	Phosphorus influence on nitrogen uptake, nutrient and yield attributes of finger millet in semi-arid region of Kenya	nelwaf@gmail.com	IDT8-084
368	Yadav, Vijay	ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi, India	Exploitation of grasspea (*Lathyrus sativus* L.) potential for food and fodder security in dry areas of central India	vijayyadav777@gmail.com	IDT8-085
Theme 9: Genomics, Biotechnology and Molecular Breeding (Presentation on Feb 24, 2017, 16:00 - 18:00 hrs, Hall 1, 2 & 3, HICC, Hyderabad)					
369	Al-Shafeay, Amal F	Agricultural Genetic Engineering Research Institute (AGERI), Cairo, Egypt	Engineering dehydration stress tolerance in Sesame: use of sodium tungstate, as ABA inhibitor, to overcome problems associated with overexpressing of LOS5/ABA3 gene in sesame	amal.alshafeay@gmail.com	IDT9-001
370	Amareshwari, P	Osmania University, Hyderabad, India	Overexpression of Sorghum bicolor vacuolar H+- pyrophosphatase (SbV-PPase) to improve salt and drought stress tolerance in peanut (*Arachis hypogaea* L.)	puduthaamareshwari@gmail.com	IDT9-002
371	Anjali, N	Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI), Trivandrum, India	Identification and characterisation of drought responsive microRNAs in cardamom	anjalinair20@gmail.com	IDT9-003
372	Anuradha, Ch	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	Studies on Genetic Relationship in Pigeon Pea under Drought Stress using SSR Markers	anu_dna@rediffmail.com	IDT9-004

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
373	Arora, Vivek	Bose Institute, Kolkata, India	Development of chalcone synthase locus specific CAPS marker to screen abiotic stress tolerant mulberry genotypes from a recombinant population	vikarora.arora@gmail.com	IDT9-005
374	Arya, Mamta	ICAR-Indian Institute of Soybean Research (IISR), Indore, India	Metabolic activity in breeding lines favoring drought tolerance in soybean (*Glycine max* (L.) Merrill)	mamta.gpb@gmail.com	IDT9-006
375	Audebert, Alain	Cirad UMR AGAP - Equipe PAM/CERAAS-ISRA, Thiès Senegal, Senegal	Rhizoscope phenotyping tools: Validation under natural condition	alain.audebert@cirad.fr	IDT9-007
376	Balcha, Lijalem Korbu	Ethiopian Institute of Agricultural Research (EIAR) -Debre Zeit Agricultural Research Center (DZRC), Addis Ababa, Ethiopia	Developing a resource of wild x cultivated chickpea introgression lines for climate resilience	lijupeace@gmail.com	IDT9-008
377	Baniekal Hiremath, Gangadhar	University of Horticultural Sciences, Bagalkot, India	Over-expression of gene encoding hydrogen peroxide generating germin-like protein induces thermo-tolerance in potato	gangubhm@gmail.com	IDT9-009
378	Batra, Ritu	Chaudhary Charan Singh University, Meerut, India	Genome wide analysis of the family of genes encoding SET-domain containing proteins in *Triticum aestivum*	ritu.biotech24@gmail.com	IDT9-010
379	Bensen, Robert	Syngenta Crop Protection, LLC, Minnesota, USA	Using the allelic diversity platform at Syngenta for identifying optimized alleles of drought tolerant loci	robert.bensen@syngenta.com	IDT9-011
380	Bishi, Sujit Kumar	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Heat tolerance in groundnut is associated with efficient strategies of physiological adaptation and early induction of small HSPs	sujitbishi@gmail.com	IDT9-012
381	BoghiReddy, Sailaja	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Comprehensive expression study on microRNAs and their targets transcripts under different heat stress treatments in contrasting rice cultivars	B.Sailaja@cgiar.org	IDT9-013
382	Boranayaka, MB	University of Agricultural Sciences (UAS), Raichur, India	Genetic variation, marker validation and water use efficient lines identification in recombinant inbred lines of rice (*Oryza sativa* L.)	mbboranayak@gmail.com	IDT9-014
383	Breria, Caleb Manamik	World Vegetable Centre and National Pingtung University of Science and Technology (NPUST), Pingtung, Taiwan	Enhancing stress tolerance of mungbean (*Vigna radiata*) through the use of genetic diversity and molecular breeding	caleb.breria@worldveg.org	IDT9-015
384	Chakraborty, Niranjan	National Institute of Plant Genome Research (NIPGR), New Delhi, India	Chickpea transcription factor, CaTLP1, modulates ROS accumulation and promotes ABA-mediated stomatal closure	nchakraborty@nipgr.ac.in	IDT9-016
385	Chakraborty, Koushik	ICAR-National Rice Research Institute (NRRI), Cuttack, India	A transcriptomic study to understand the combined effect of waterlogging and salinity stress in rice	koushikiari@gmail.com	IDT9-017
386	Chamarthi, Sivakumar	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	Maker-assisted recurrent selection (MARS) and genome-wide association study (GWAS) for enhanced drought tolerance in cowpea	s.chamarthi@cgiar.org	IDT9-018

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
387	Chandrashekara, KN	Upasi Tea Research Institute, Coimbatore, India	Transcriptomic analysis of tolerant and susceptible tea cultivars during drought stress	knchandu1@gmail.com	IDT9-019
388	Chaudhary, Saurabh	ICAR-National Research Centre on Plant Biotechnology (NRCPB), New Delhi, India	NGS-based identification of heat stress responsive genes in seabuckthorn (Hippophae sp.)	saurabh.biozone@gmail.com	IDT9-020
389	Chauhan, Shubhendra	Sam Higginbottom Institute of Agriculture, Technology and Sciences (SHIATS), Allahabad, India	*In silico* comparison of HSF family genes in *Solanum tuberosum* and *Solanum lycopersicum*	shubhendra.schauhan@shiats.edu.in	IDT9-021
390	Chinnaswamy, Appunu	ICAR-Sugarcane Breeding Institute, Coimbatore, India	Engineering of sugarcane for enhanced water deficit stress tolerance	cappunu@gmail.com	IDT9-022
391	Das, Alok	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	Genetically transformed chickpea (*Cicer arietinum* L.) carrying transcription factor, AtDREB1a improves drought tolerance through modifying water relation and photosynthesis	alokbio@gmail.com	IDT9-023
392	Divya, K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Isolation and characterization of stress inducible promoters from Pennisetumglaucum and their role in abiotic stress adaptation	divyanu.k@gmail.com	IDT9-024
393	Dossa, Komivi	Oil Crops Research Institute -Chinese Academy of Agricultural Sciences (OCRI-CAAS), Wuhan, China	Identification and expression profiling of stress-related transcription factors involved in drought stress response in sesame: Case of DREB, HSF and WRKY	dossakomivi@gmail.com	IDT9-025
394	Dutta, Debabrata	Bose Institute, Kolkata, India	Marker assisted selection and phenotyping of an inter-specific hybridization derived population towards development of sesame with synchrony in pod maturation for drought avoidance	debabratadutta6@gmail.com	IDT9-026
395	Dwivedi, Priyanka	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Marker assisted introgression of a major QTL, qDTY3.1 governing reproductive stage drought tolerance into a popular rice variety Pusa 44 and their phenotypic assessment	priyankam28@gmail.com	IDT9-027
396	Feng, Fangjun	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	de novo genome assembly and high dense SNP linkage map facilitate genetic dissection of drought avoidance possessed by the upland rice variety IRAT109	ffj@sagc.org.cn	IDT9-028
397	Gahlaut, Vijay	Chaudhary Charan Singh University, Meerut, India	Genome wide association mapping of four agronomic traits in wheat (*Triticum aestivum* L.) under irrigated and rain-fed environments using 18K SNP	zone4vijay@gmail.com	IDT9-029
398	Gaikwad, Priyanka	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	Detection of stay-green QTL in a sorghum recombinant inbred population based on cross (N13 × E36-1)	priyankagaikwad00@gmail.com	IDT9-030
399	Garladinne, Mallikarjuna	Agri Biotech Foundation, Hyderabad, India	Expression of *Pennisetum glaucum* translational initiation factor for enhancing drought and salinity tolerance in groundnut	garladinnemarjun@gmail.com	IDT9-031

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
400	Gautam, Tinku	Chaudhary Charan Singh University, Meerut, India	Marker-assisted introgression of a major QTL for yield related traits to improve grain yield in wheat under drought	tinkugoutam@gmail.com	IDT9-032
401	Girsil, Tigist Shiferaw	Ethiopian Institute of Agricultural Research (EIAR), Adama, Ethiopia	Introgression of arcelin gene in to advanced line of common bean and validation using marker assisted selection	tshiferaw2006@gmail.com	IDT9-033
402	Gopala Krishnan, S	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Marker assisted transfer of QTLs, qDTY1.1 into Basmati rice variety "Pusa Basmati 1" and qDTY3.1 into elite rice variety "Pusa 44" for enhancing grain yield under reproductive stage drought stress	gopal_icar@yahoo.co.in	IDT9-034
403	Gowda, Manje	International Maize and Wheat Improvement Center (CIMMYT), Nairobi, Kenya	Discovery and validation of genomic regions associated with drought tolerance in tropical maize germplasm	M.Gowda@cgiar.org	IDT9-035
404	Gupta, Saurabh	Indian Institute of Information Technology (IIIT), Allahabad, India	Draft Genome based analysis of WRKY gene family in *Triticum* aestivum and their role in different abiotic stress	rs159@iiita.ac.in	IDT9-036
405	Hake, Anil Arjun	University of Agricultural Sciences (UAS), Dharwad, India	Mapping the genomic regions governing chlorophyll content as a component trait of drought tolerance in peanut (*Arachis hypogaea* L.)	anilhake30@gmail.com	IDT9-037
406	Jha, Uday Chand	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	Evaluation of drought tolerance selection indices in chickpea genotypes	u9811981@gmail.com	IDT9-038
407	Kadam, Sandeep	College of Horticulture, Bagalkot, India	Elucidation of differentially expressing genes in roots experiencing different levels of moisture stress using NGS in sorghum (*Sorghum bicolor* L.)	sandeepkadam15@gmail.com	IDT9-039
408	Kakkera, Aparna	Jawaharlal Nehru Technological University (JNTU), Hyderabad, India	Mapping of quantitative trait loci in pearl millet (*Pennisetum glaucum* (L.) R. Br.) and relating to the water stress environments	aparna_jgd@rediffmail.com	IDT9-040
409	Kale, Sandip	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Fine mapping studies identified a 113 kb region within "QTL-hotspot_a" for seed weight and drought related traits in chickpea	S.Kale@cgiar.org	IDT9-041
410	Kaliamoorthy, Sivasakthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	High throughput phenotyping and advanced genotyping reveals QTLs for plant vigor and water saving traits in a "QTL-hotspot": New opportunities for enhancing drought tolerance in chickpea	sakthibiotechbdu@gmail.com	IDT9-042
411	Kaur, Navneet	IIT Roorkee, Roorkee, India	Optimization of sand hydroponics system and transcriptional studies on the putative high affinity nitrate transporter gene in guar	navneetkaursekhon88@gmail.com	IDT9-043
412	Koehl, Karin	Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany	Phenotypic and marker-assisted selection for drought tolerance in potato	koehl@mpimp-golm.mpg.de	IDT9-044
413	Lou, Qiaojun	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	Root transcriptom analysis to reveal the genetic mechanism of deep rooting in rice	lqj@sagc.org.cn	IDT9-045
414	Mamidala , Praveen	Telangana University, Nizamabad, India	Development of salt tolerant transgenic cultivated tomato by constitutive over expression of HSP24.4 gene	pmamidala@gmail.com	IDT9-046

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
415	Manimekalai, R	Sugarcane Breeding Institute, Coimbatore, India	Comparative analysis of miRNA in oxidative stress response in cultivated sugarcane and its wild species	rmanimekalaiicar@gmail.com	IDT9-047
416	Manuka, Rakesh	BITS PILANI K K Birla Goa campus, Goa, India	Functional characterization of With No Lysine (WNK) kinase in rice under abiotic stress condition	rakesh_manuka@yahoo.com	IDT9-048
417	Mishra, Nilesh	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Harnessing the power of social media to reach the unreached: knowledge dissemination for greater impact of tropical legumes	m.nilesh@cgiar.org	IDT9-049
418	Mohan, Nidhi	Banaras Hindu University (BHU), Varanasi, India	Extent of heterosis in CMS based hybrids of Pigeonpea [*Cajanus cajan* (L.) Millsp.]	nidhimohan91@gmail.com	IDT9-050
419	Moukoumbi, Yonnelle Dea	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	MAGIC population in cowpea for facilitating gene discovery for drought tolerance related traits	Y.Moukoumbi@cgiar.org	IDT9-051
420	Mudalkar, Shalini	University of Hyderabad, Hyderabad, India	JcAKR, an aldo-keto reductase from *Jatropha curcas* L. and its role in drought and salt tolerance	mudalkar.shalini@gmail.com	IDT9-052
421	Murugesan, Ashok Kumar	M S Swaminathan Research Foundation (MSSRF), Chennai, India	Regulated expression of AmNAC1 transcription factor by biotic and abiotic stresses in the mangrove plant *Avicennia marina* (Forsk.) Vierh	ashokkumar.mb@gmail.com	IDT9-053
422	Nachimuthu, Vishnu Varthini	International Rice Research Institute (IRRI), Patancheru, India	Marker-assisted introgression of different traits in drought-tolerant rice variety Sahbhagi Dhan	v.varthini@irri.org	IDT9-054
423	Nayak, Spurthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Insights on host-pathogen interaction between groundnut (*Arachis hypogaea*) and *Aspergillus flavus*	S.Nayak@cgiar.org	IDT9-055
424	Nisarga, KN	University of Agricultural Sciences (UAS), Bangalore, India	Iron acquisition and transport under aerobic and alkaline soil pH condition in rice (*Oryza sativa* L.)	nishukgowda@gmail.com	IDT9-056
425	Noble, Tom	Queensland University of Technology (QUT), Brisbane, Australia	Development of the mungbean Nested Association Mapping (NAM) resource: transformation from opportunity crop into Queensland's most dynamic pulse	tj.noble@hdr.qut.edu.au	IDT9-057
426	Palavalasa, Hima Kumari	Osmania University, Hyderabad, India	Genome wide analysis of sodium transporters and expression of Na+/H+-antiporter-like protein (SbNHXLP) gene in tomato for salt tolerance	phimakumari@gmail.com	IDT9-058
427	Parankusam, Santisree	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Heat induced differential proteomic changes reveal molecular mechanisms responsible for heat tolerance in chickpea	S.Parankusam@cgiar.org	IDT9-059
428	Patil, Sucheta	CSIR-National Chemical Laboratory (NCL), Pune, India	Exploring the behavior of transporter proteins in response to abiotic stress through genomics and microarray analyses	suchetap001@gmail.com	IDT9-060
429	Pazhamala, Lekha	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Next generation sequencing based transcriptomic studies for crop improvement in pigeonpea	L.Pazhamala@cgiar.org	IDT9-061

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
430	Phuke, Rahul Madhavarao	ICAR-Indian Agricultural Research Institute (IARI), Indore, India	*In Silico* analysis of candidate gene from identified QTL regions for Drought stress tolerance in wheat	rahulphuke18@gmail.com	IDT9-062
431	Punna, Jayamma	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	Improvement of Brinjal germplasm for root knot - nematode resistance using molecular markers	jayapunna@gmail.com	IDT9-063
432	Puppala, Naveen	New Mexico State University, Clovis, USA	Next generation sequencing approaches for understanding genetic mechanism of drought tolerance in valencia peanut	npuppala@nmsu.edu	IDT9-064
433	Rafique, Suphia	Department of Biotechnology/Jamia Hamdard University, New Delhi, India	A system biology approach to elucidate the network of proteins involved in NO-3 signalling and transport under multiple abiotic stresses in shoot and root of maize genotype (*Zea mays* L.)	suphia123@gmail.com	IDT9-065
434	Rajasheker, G	Osmania University, Hyderabad, India	Cloning and characterization of bacterial RNA chaperone genes (CspA and CspB) and their heterologous expression in rice confers drought and saltstress tolerance	grajashekharou@gmail.com	IDT9-066
435	Rakshitha, HC	University of Agricultural Sciences (UAS), Bangalore, India	Expression analysis of basal transcriptional regulators (TBP Associated Factors) under different stress conditions in finger millet	rakshithahc42.rr@gmail.com	IDT9-067
436	Ramayya, Perumalla Janaki	International Rice Research Institute (IRRI), Patancheru, India	Marker-assisted breeding for introgression of multiple QTLs/genes for drought and disease resistance in rice variety Naveen	p.ramayya@irri.org	IDT9-068
437	Ramchander, S	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Whole genome recovery and development of drought tolerant rice (*Oryza sativa* L.) through marker assisted backcross – inbreeding method	rubulochander_009@yahoo.co.in	IDT9-069
438	Ramsankar, C	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	Functional validation of drought responsive genes in rice	cramsankar007@gmail.com	IDT9-070
439	Rasool, Souliha	Punjab Agriculture University (PAU), Ludhiana, India	A novel strategy to tap the drought tolerance genes of *Aegilops tauschii* for bread wheat improvement.	souliha.rasool@gmail.com	IDT9-071
440	Ratnaparkhe, Milind	ICAR-Indian Institute of Soybean Research (IISR), Indore, India	Molecular and evolutionary studies of genes associated with drought tolerance in soybean	milind.ratnaparkhe@gmail.com	IDT9-072
441	Roy, Anirban	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	Comparision of expression and sequence of SnfK and DREB2A transcript in heat tolerant lentil genotypes	anirbanneelroy@gmail.com	IDT9-073
442	Ruperao, Pradeep	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Constructing improved chickpea genome assemblies using skimGBS	p.ruperao@uq.edu.au	IDT9-074
443	Salam, Shaheen A	Regional Agricultural Research Station (RARS), Pattambi, India	Molecular characterisation of rice genotypes for drought tolerance using microsatellite markers	shaheensalam121@gmail.com	IDT9-075
444	Sarsu, Fatma	International Atomic Energy Agency (IAEA), Vienna, Austria	Pre-field screening protocols for heat tolerant mutants in rice	F.sarsu@iaea.org	IDT9-076

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
445	Saxena, Rachit	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Towards defining heterotic pools for accelerating hybrid breeding in pigeonpea	r.saxena@cgiar.org	IDT9-077
446	Shanker, Arun K	ICAR-Central Research Institute for Dryland Agriculture (CRIDA), Hyderabad, India	Targeted genome mining, comparative modelling and protein structural motifs studies of Δ1-pyrroline-5-carboxylate synthetase (P5CS) in Zea maize	arunshank@gmail.com	IDT9-078
447	Sharma, Ram	CSIR-Institute of Himalayan Bioresource Technology (IHBT), Palampur, India	Global transcriptome analysis of multiple genotypes to identify key regulator(s) involved in drought tolerance and genomic resource creation in tea [*Camellia sinensis* (L) O. Kuntze]	rksharma.ihbt@gmail.com	IDT9-079
448	Sharma, Ambika	Eternal University, Baru Sahib, India	Marker assisted backcross breeding (MABB) of recombinant 1BL.1RS chromosome for better root traits and bread making quality in wheat (*Triticum aestivum* L.)	pritesh2010@gmail.com	IDT9-080
449	Shivhare, Radha	CSIR-National Botanical Research Institute (NBRI), Lucknow, India	Selection of suitable reference genes for assessing gene expression in pearl millet under different abiotic stresses and their combinations	radha.shivhare09@gmail.com	IDT9-081
450	Singh, Sadhana	Defence Institute of Bio-Energy Research, Nainital, India	NAC gene from Lepidium Latifolium confers drought tolerance in transgenic tobacco plants	sadhnasingh1986@gmail.com	IDT9-082
451	Singh, Uma Maheshwar	International Rice Research Institute (IRRI), Patancheru, India	Marker-assisted stacking of QTLs/genes for drought, blast and BLB into popular rice variety – Lalat	uma.singh@irri.org	IDT9-083
452	Singh, Vikas Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Identification and validation of insertion-deletion polymorphisms in pigeonpea	Vikas.Singh@cgiar.org	IDT9-084
453	Singh, Rakshita	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	Development and characterization of transgenic pigeon pea plants carrying OsRuvB gene for drought and salinity tolerance	singhrakshita19@gmail.com	IDT9-085
454	Singh, Anil	ICAR-Indian Institute of Agricultural Biotechnology (IIAB), Palampur, India	Identification of drought-responsive genes in Cicer microphyllum using high-throughput sequencing	anils13@gmail.com	IDT9-086
455	Sinha, Pallavi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Haplotype for drought responsive genes in pigeonpea	P.Sinha@cgiar.org	IDT9-087
456	Somanaboina, Anil Kumar	Osmania University, Hyderabad, India	Development of transgenic tomato (*Solanum lycoperscicum* L.) by heterologous expression of osmotin-like protein (OLP) and chitinase (Chi11) genes for salt and drought stress tolerance	anilkumarou@gmail.com	IDT9-088
457	Soregaon, Chandrakant D	College of Agriculture, Vijayapur, India	Molecular mapping and tagging of fusarium wilt resistance in chickpea (*Cicer arietinum*)	soregaoncd@uasd.in	IDT9-089

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
458	Suresh, R	Tamil Nadu Rice Research Institute, Aduthurai, India	Marker assisted pyramiding of QTLs for yield under drought and root morphology into a popular rice cultivar ADT 45	sureshpbg@gmail.com	IDT9-090
459	Usha Kiranmayee, KNS	Osmania University, Hyderabad, India	Fine mapping of stay-green QTLs on sorghum chromosome SBI-10L – An approach from genome to phenome	knskira@gmail.com	IDT9-091
460	Vemuri, Hindu	Sri Padmavati Mahila Visvavidyalayam, Tirupati, India	Identification and validation of genomic loci associated with Kernel-Fe and Kernel-Zn concentrations in maize	hinduvemuri@gmail.com	IDT9-092
461	Venkataraman, Gayatri	M S Swaminathan Research Foundation (MSSRF), Chennai, India	The sodium transporter OcHKT1;5 from the halophytic wild rice *Oryza coarctata* Roxb. Tateoka shows distinct transport and structural determinants compared to rice OsHKT1;5	gayatri@mssrf.res.in	IDT9-093
462	Venkatesh, K	Osmania University, Hyderabad, India	Development of transgenic peanut (*Arachis hypogaea* L.) lines by overexpression of Na+/H+ antiporter gene for enhanced salt tolerance	kvenkatesh111@gmail.com	IDT9-094
463	Vennela, Prudhvi Raj	Banaras Hindu University (BHU), Varanasi, India	Marker assisted selection (MAS) and introgression of Quantitative Trait Loci (QTL) for drought tolerance in Rice (*Oryza sativa* L.)	v.prudhviraj2@gmail.com	IDT9-095
464	Yadav, Richa	Lucknow University, Lucknow, India	Development of 50K Cotton SNP Chip and Construction of High Density Linkage map in *Gossypium hirsutum*	richayadav.biotech@gmail.com	IDT9-096
465	Yadav, Pooja	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Identification of genes and genomic segments for cleistogamy in Pigeonpea (*Cajanus cajan* L.)	iampoojayadav@gmail.com	IDT9-097
466	Yadav, Sagar	CSIR-National Chemical Laboratory (NCL), Pune, India	Expression studies of transcription factors under moisture stress in cotton (*Gossypium hirsutum* L.)	sagaryadav04@gmail.com	IDT9-098
467	Zaynali Nezhad, Khalil	Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran	A new reason for segregation rate distortion in genetic linkage map	khalil1381@yahoo.com	IDT9-099
468	Zhang, Chong	Fujian Agriculture and Forestry University (FAFU), Fuzhou, China	Characterization of groundnut resistance to bacterial-wilt caused by Ralstonia solanacearum by forward and reverse genetics methods	chongzhang2015@163.com	IDT9-100
469	Kuldeep, Singh	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	Molecular characterization of pigeon pea rhizobial strains for abiotic stress tolerance from arid and semi-arid zones of Haryana, India	kdssc77@gmail.com	IDT9-101
Abstract received after the deadline					
1	Shahbazi, Maryam	Agriculture Biotechnology Research Institute of Iran (ABRII), Karaj, Iran	Effects of drought stress on light-dependent reactions and photosynthetic efficiency in tolerant and susceptible Barley (*Hordeum vulgare* L.) genotypes	MShahbazi@abrii.ac.ir	IDT4-026

Poster Theme I

Setting the Biophysical Context: Climatic/Soil Constraints

IDT1-001 | Economic analysis of alternative systems for sorghum production in Southern Mali

Badolo F[1]*, Kotu B[2], Birhanu Z. B[1]

[1]International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali
[2]International Institute of Tropical Agriculture (IITA)
*E-mail: f.badolo@cgiar.org

This article aims to evaluate sorghum grain yields, cash income as well as risk-efficient choice associated with treatments of sorghum under the Africa RISING project in Mali. The analysis used the survey data related to on-farm trials covering the seasons 2014 and 2015. Four treatments have been experimented for sorghum including control treatment, treatment with only manure, treatment with mineral fertilizer, and treatment with manure and mineral fertilizer. Stochastic dominance analysis was used to evaluate the cumulative distributions of grain yields and cash income associated with each treatment. The results showed that the control treatment for sorghum is dominated by the manure and fertilizer treatments. The manure and mineral fertilizer treatment has higher yields and net returns compared to the three other treatments. The control treatment has a 50% chance of generating grain yields up to 850 kg/ha, while the manure treatment, mineral fertilizer treatment, and manure and mineral fertilizer treatment have the same probability of generating respectively 1,050 kg/ha, 1,275 kg/ha, and 1500 kg/ha. The net returns were estimated to US$ 122 for manure and mineral fertilizer treatment, US$ 87 for treatment with only mineral fertilizer, and US$ 84 for treatment with only manure. The cumulative distribution of manure and mineral fertilizer treatment was to the right of the remaining cropping treatments, indicating that manure and mineral fertilizer treatment provides higher returns to smallholder farmers than the alternative treatments for a given risk level. Risk-averse farmers will prefer treatment applying manure and mineral fertilizer if they can afford manure and chemical fertilization.

IDT1-002 | Mucilage secretion: Do plants protect their rhizosphere community from drought effects to maintain their beneficial functions?

Dippold M[1], Ahmed M[2,3], Sanaullah M[1,4], Banfield C[3], Kuzyakov Y[1,3], Carminati A[2]

[1] Agricultural Soil Science, Georg August University Goettingen, Germany
[2] Soil Hydrology, Georg August University Goettingen, Germany
[3] Department of Agricultural Engineering, University of Khartoum, Sudan
[4]Institute of Soil and Environmental Sciences, University of Agriculture, Faisalabad, Pakistan
[5] Soil Science of Temperate Ecosystems, Georg August University Goettingen, Germany
*E-mail: dippold@gwdg.de

Mucilage secretion modulates soil-plant-water dynamics but also affects microbial communities' functioning. To assess the role of mucilage as C source for microorganisms and also its effect on biotic functions under drought, C4 mucilage was added in two levels to C3 soil under two different moisture contents (80 and 30% of WHC). Mucilage decomposition, microbial biomass and PLFA incorporation and hydrolytic enzyme activity was quantified.

After 15 days, most of the mucilage was decomposed (98% and 88%) under optimum water supply, but under drought only 77% and 30% of mucilage were decomposed for low and high mucilage amendment, respectively. However, microbial biomass incorporation of mucilage C was not affected under drought, suggesting its unhindered bioavailability. Gram Negatives and fungi were those groups incorporating most of the mucilage C into their PLFA. But fungi did not suffer from drought, and instead profited from the lower competitiveness of most bacterial groups. Under drought, mucilage addition always increased the maximum enzyme activity and frequently also affinity relative to the non-amended control and, thus, compensated for the loss in enzyme activity or affinity induced by drought.

This study suggests that mucilage has, besides its function as C source for microorganisms, a highly vital role as biofilm-like gel maintaining microbial and exoenzymatic activity even under drought conditions. Especially the reduced decomposition rate of mucilage under drought suggests that mucilage exudation is a plant trait that favors the capture of water and via the promotion of microbial life presumably also nutrients when water is scarce.

IDT1-003 | Modeling the spatio-temporal meteorological drought variability, extent, and severity using the Standardized Precipitation Index (SPI) in Raya and its environs, Northern Ethiopia

G. Eskinder[1,2]*, O. Dikinya[1], R. J. Sebego[1], E. Segosebe[1], Z. Amanuel[2]

[1]University of Botswana, Private Bag UB 002, Gaborone-Botswana
[2]Mekelle University, P.o. Box 231, Mekelle-Ethiopia
*E-mail: eskinder14@yahoo.com

Drought is a devastating climatic phenomenon that affects more people than any other natural hazard. In Ethiopia, the spatial extent, magnitude, duration, and frequency of drought is severe due to the effect of El-Niño. The situation is also worse in Raya and its surrounding environs. This study is, therefore, aiming at modeling the spatial-temporal meteorological drought variability, extent, and severity. Monthly rainfall data were collected from the National Meteorological Agency of Ethiopia from 1983 to 2015. The Inverse Distance Weighting (IDW) interpolation technique was then applied to produce surface rainfall map showing the spatial extent of rainfall distribution using ArcGIS 10.4.1 geostatistical tools. Based on the World Meteorological Organization (WMO) 2009 suggestion a Standardized Precipitation Index (SPI) developed by McKee et al. (1993) was used to analyze the rainfall data at SPI-3 months time scale. The findings reveal that the study area was experiencing mild to severe meteorological drought in every 2-3 years during the last 33 years. Specially, the year 1984 and 2015 were investigated as a severe drought period. A significant statistical regression of R2 = 0.98 between SPI and rainfall at 95% of the degree of confidence interval and p-value <0.000 also examined. Hence, both governmental and non-governmental institutions should work closely on introducing drought tolerant crop varieties in mass, and climate based crop insurance schemes into the frequent drought affected areas. This may help the smallholder farmers of the study area to diminish the impacts of drought significantly.

IDT1-004 | Climate change, commercialization and gender divides: Alternative pathways for groundnut breeding in semi-arid Tanzania

Hella JP[1]*, Pato I[1], Mponda O[2]

[1]School of Agricultural Economics and Business Studies, Sokoine University of Agriculture, P.O. Box 3007, Morogoro, Tanzania
[2]Naliendele Agricultural Research Institute, Ministry of Agriculture, Livestock and Fisheries, Newala Road P.O. Box 509 Mtwara, Tanzania
*E-mail: jp_hella@yahoo.co.uk

Increasingly groundnut is becoming an important crop in semi-arid Tanzania for food and nutrition security and as a commercial crop for household income generation. However in recent years crop development program (breeding) has been caught in paradox of climate change, food and nutrition needs, commercialization and gendered participation in production. This paper explores the challenges of breeding programs to solve the paradox. The paper is based on secondary data coupled with basic study conducted in four regions of Mtwara, Songwe, Dodoma and Shinyanga. The local landraces and improved groundnut varieties were benchmarked to establish the fit on challenges listed. Using multi-criteria analysis, the results revealed huge diversity of groundnut varieties by locations, food and nutritional use, market requirement, the need to accommodate equality in gender participation for increased groundnut production and the climate change impacts. The paper concludes that location-specific breeding to accommodate the realized challenges in necessary for sustainable groundnuts production in Tanzania.

IDT1-005 | The critical role of root growth and water content in controlling rhizosphere extension during drought

Holz, M.[1]*, Zarebanadkouki, M.[1], Kaestner, A.[2], Kuzyakov, Y.[1], Carminati, A.[1]

[1] University of Goettingen, Göttingen, 37077, Lower Saxony, Germany
[2]Paul Scherrer Institute, Villilgen, 5232, Aargau, Switzerland
*E-mail: maire.holz@forst.uni-goettingen.de

Root exudates are one important energy source for soil microorganisms. It is therefore crucial to estimate the distribution of root derived carbon in soil. We tested how drought affects exudate distribution in the rhizosphere. Maize plants were grown in rhizoboxes at 6% (dry) or 20% (wet) soil water content. Plants were labelled with 14CO2 to estimate C allocation into roots and rhizosphere. 14C imaging was used to identify those root parts were 14C was released. Rhizosphere water content was visualized using neutron radiography. A numerical model was employed to predict the distribution of root exudates.

Dry and wet plants allocated similar amounts of 14C into roots (0.28 ng 14C g-1) but root elongation decreased by 48% in dry soil. This caused a reduced longitudinal exudate distribution and a reduction of total C allocation. Soil water content close to the root was identical (31%) in both treatments, presumably because of the high water retention by mucilage. This caused a similar diffusion of exudates in the vicinity of the roots in both treatments. The increase of water content close to the root compared to bulk soil enhanced microbial degradation which again increased diffusion of substances out of the root and increased total exudation.

Root growth and rhizosphere hydraulic properties play an important role in C release by roots and in shaping the profiles of root exudates in the rhizosphere. The release of mucilage may be a strategy by plants to maintain the microbial activity and diffusion of exudates even under water limitation.

IDT1-006 | Responses of tropical maize genotypes to maize streak virus disease

Ige, A. D.[1*], Akromah R.[1], Oppong, A.[2], Adejumobi I. I.[1]

[1] Kwame Nkrumah University of Science and Technology, Kumasi, Ghana
[2] Crops Research Institute, Kumasi, Ghana
*E-mail: niccollo4real@yahoo.com

Maize streak virus disease (MSVD) is an economically important foliar disease limiting maize production and causing significant yield loss in farmers' fields in Sub-Saharan Africa (SSA). In several regions of Ghana, drought has been reported to enhance the occurrence of MSVD. The development and commercialization of MSVD-resistant genotypes is the most economically sustainable management option to mitigate the effect of MSVD. The objective of the study was to determine the responses of some maize hybrids to MSVD under natural and artificial infestations. Twenty maize hybrids plus two commercial checks (*Omankwa and Aburohemaa*) were evaluated under natural infestation at Wenchi and artificial infestation at Kwadaso during the minor and major seasons of 2015 and 2016 respectively. A 9 x 3 alpha-lattice design with three replications was used. Plants were visually scored for MSVD at 3, 6 and 9 WAP on a scale of 1 (resistant) to 5 (highly susceptible). The combined analyses of variance showed significant variation ($P<0.001$) among the hybrids for AUDPC, severity mean score and incidence. Genotype by environment interaction was significant ($P<0.01$) for the traits studied, suggesting that the responses of maize hybrids varied in the different environments possibly due to higher disease pressure at the artificial infestation site. Across environments, fifteen maize hybrids were moderately resistant while the others were susceptible. Only one hybrid, TZEI-22*TZEI-7 had a severity score significantly ($P<0.05$) lesser than that of *Omankwa.* These outstanding hybrids should be further tested for stability of performance and commercialized to combat food insecurity in SSA.

IDT1-007 | Identification of QTLs for zinc deficiency tolerance in aerobic rice (*Oryza sativa* L.)

Vanitha J[1], Amudha K[2,*], Usha Kumari R[3]

[1,2,3]Tamil Nadu Agricultural University, Coimbatore – 641003, Tamil Nadu, India
*E-mail: amudha_pbg@yahoo.com

Rice is the "Global Grain" because of its use as prime staple food in about 100 countries of the world. Aerobic rice provides for effective use of water as the concept of flooding paddy fields is abandoned in this ecosystem. But due to the transition from flooding of paddy fields to aerobic system of rice cultivation many factors that determine nutrient (Zn) bioavailability changes in addition to water deficit. Achieving high yields under aerobic conditions requires new varieties of "aerobic rice" combining both the water stress tolerance and nutrient (especially Zn) deficiency tolerance traits. So the goal of present study was undertaken to know the genetic and molecular basis of zinc deficiency tolerance using an *indica/ indica* F_4 RIL population of CO51 (A high yielding low land variety with low zinc efficiency) and CB-06-803-2 (An improved upland culture with high zinc efficiency) comprising of 246 RILs. These RILs were phenotyped under aerobic system in control (+Zn) and stress (-Zn) plots and genotyped using 80 SSR markers specific to zinc transporter genes (*ZIP* family) and root related traits. The parental polymorphism was 27.50 per cent. The reported map position of gramene database was used to estimate the QTLs following the ICIM-ADD method. The QTL analysis resulted in the identification of QTLs *viz*., zinc efficiency in shoot (ZES) in chromosome 1 with flanking markers RM 3694 and RM 8136 and a LOD value of 2.50 explaining 13.19 per cent of phenotypic variation; shoot zinc content in stress (SZCS) condition in chromosome 5 with flanking markers RM 1187 and RM 87 and a LOD value of 2.58 explaining 11.95 per cent of phenotypic variation. The marker RM 1187 was specific to ZIP family and RM 87 was related to root traits.

IDT1-008 | Evaluation of groundnut genotypes for phosphorous efficiency through acid phosphatase content in leaves

Naga Madhuri K.V*, Lata P, Vasanthi RP, John K, Reddy PVRM, Lavanya Kumari P, Murali G, Giridhara Krishna T, Naidu TCM and Naidu NV

Institute of Frontier Technology, Regional Agricultural Research Station, Acharya N.G Ranga Agricultural University, Andhra Pradesh, India 517 502
*E-mail: nagamadhurikv@gmail.com

Phosphorous (P) sources are limited around the globe making it unsustainable with present farming practices. This necessitates the development of more Phosphorus efficient crops while monitoring P status. Groundnut *(Arachis hypogea)* is a major crop in Southern Andhra Pradesh, India where soils are light textured and less fertile. Twenty pre-release groundnut genotypes were evaluated under a pot culture experiment conducted at Regional Agricultural Research Station, Tirupati, Andhra Pradesh, India during *kharif*, 2015. Crops were grown using standard recommended practices in P sufficient (control) and in P deficient conditions. Acid phosphatase and leaf P were monitored after 60 days of sowing using standard protocols. Results show that under P deficient conditions, genotypes TCGS1275, TCGS1157 and TCGS1398 had higher leaf P content (range between 0.27 to 0.24 %) in comparison to others. Likewise under deficient soil P conditions only TCGS1273, TCGS1157 and TCGS1398 demonstrated having lower leaf acid phosphatase content in leaves (range between 2.20-2.64 μ moles hr^{-1} gm-1) when compared to other genotypes. Only TCGS 1157 and TCGS 1398 had lower leaf acid phosphatase while at the same time having higher accumulation of leaf P suggesting that P starvation was better coped by these genotypes and hence can be recommended in soils deficient in P. Leaf acid phosphatase activity correlated negatively with P content in leaves (r = -0.67) similar to those reported for soybean cultivars in Brazil. It will be interesting to further the study in identifying groundnut genotypes combining P efficiency with drought. There is potential for breeders in accelerating identification of markers to specific traits that would be suitable for monitoring P status and manage nutrient application.

IDT1-009 | Effect of sodium nitroprusside and ferrous sulphate on the performance of groundnut (*Arachis hypogaea* L.) genotypes in calcareous soil

Kotyal SK[1]*, Koti VR[1], Ramya V[1].

[1]University of agricultural sciences, Dharwad-580085, Karnataka, India
*E-mail: kavitakotyal@gmail.com

In order to assess whether application of nitric oxide and ferrous sulphate could modulate the physiology of three groundnut cultivars (GPBD-4,GPBD-6 & TMV-2) differing in iron deficiency tolerance, a field experiment was conducted in calcareous soil of MARS, Dharwad during *Kharif* 2014. The lime induced iron chlorosis (LIIC) differed significantly among the genotypes. Genotype TMV-2 recorded the highest chlorosis and the least was observed in GPBD-4. Spraying of SNP (sodium nitroprusside) and ferrous sulphate at 15 days interval reduced the incidence of iron deficiency in all the genotypes and recovery from chlorosis was higher in susceptible genotype TMV-2. Among the treatments, foliar application of SNP and FeSO4 showed better performance compared to other treatments and control. The physiological parameters *viz*., TDM, photosynthetic rate and SPAD; and the biochemical parameters, *viz*., leaf chlorophyll and ferrous contents; were significantly influenced by treatments. Application of SNP and FeSO4 helped to maintain more chlorophyll and ferrous iron content and, in turn, increased all the physiological parameters and pod yield in groundnut. Thus, exogenous application of SNP countered iron deficiency stress-induced growth inhibition in groundnut. Effect of this treatment was more pronounced in iron stress tolerant GPBD 4 and as well in TMV-2 than in GPBD-6 where there was no improvement in growth or pod yield with SNP application. Thus, interaction effect of SNP and genotypes existed. From the results, it is confirmed that the improvement in growth and grain yield of groundnut due to SNP application was associated with decreased chlorosis, improved photosynthetic capacity and growth.

IDT1-010 | Zinc intervention for drought tolerance

Muktha J.*, Srikant, Preethi N. V. and Shankar A.G

University of Agricultural Sciences, GKVK, Bangalore, Karnataka, India
*E-mail: muktha.j@gmail.com

Drought is one of the most important factors responsible for decreasing crop yields. The stage at which drought occurs determines its effect on plant growth and development. One of the most significant effects of moisture stress at any growth stage is the non-availability of the nutrients to the plants from the dry soil. This makes the crop plants deficient in nutrients and impede their growth and development. Zinc is one which is hindered more severely by drought stress. Several reports have suggested that use of fertilizers such as zinc sulfate should be especially considered under water stress (Baybordi, 2006; Babaeian *et al*., 2010). Considering these reports, a study was conducted to evaluate the effect of drought stress in pigeonpea germplasms contrasting for seed zinc content (high and low) with and without external foliar zinc spray. Drought was imposed at 30% field capacity and assessed using gravimetric approach. Drought reduced plant height, number of leaves, leaf expansion rate, chlorophyll content, photosynthetic rate, relative water content and increased lipid peroxidation in both types, but the effect was striking in low zinc types. The stress effect in low types was effectively alleviated by zinc foliar spray. Similarly, root length increased significantly in high types under drought and low types performed similarly only with foliar application. These showed that control high types performed on par with foliar sprayed low types. Thus, high zinc genotypes could be preferred over low zinc types and foliar treatment to mitigate the effect of drought on nutrient acquisition.

IDT1-011 | High zinc rice lines for drought prone eastern India: Genotype x environment interaction and stability

Naik SM[1], NagamallikadeviM[1],Yadav S[2], Singh UM[1],Janaki RamayyaP[1], Venkateshwarlu Ch[1], Dixit S[1], Vipparla AK[1], Nachimuthu VV[1], Jain A[1], Priyadarshi R[1], Mamatha P[1], Alam S[1], Raman A[1], Virk P[3], Kumar A[2]*

[1]International Rice Research Institute, South Asia Hub, ICRISAT, Hyderabad, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
[3]HarvestPlus, ICRISAT, Hyderabad, India
*E-mail: a.kumar@irri.org

Zinc (Zn) is an essential micronutrient that serves as a co-factor for more than 300 enzymes involved in the metabolism of carbohydrates, lipids, proteins and nucleic acids in plants, animals and humans. Development of rice varieties with high zinc content and high-yield has been the focus of breeding programs for rainfed drought prone eastern India regions. Achieving grain high Zn content with stability across environments essentially requires the understanding of genotype×environment interaction (G×E). When assessing the differential performances of genotypes across environments, stability is an important factor to consider. To investigate the effect of G × E interaction on grain Zn content in rice, 63 genotypes were evaluated across five locations during 2014-2015. Phenotypic observations were made on grain zinc content in brown rice, yield and agronomic traits. Based on the stability analysis of zinc content, four genotypes (IR 91167-31-3-1-33, TARAMON, TEINEM RUISHENG MAA and IR 92960-75-1-3) with a regression coefficient (b) close to zero were identified as stable lines, of which two - TEINEM RUISHENG MAA (22.49ppm) and IR 92960-75-1-3 (26.28 ppm) - were high in Zn content as compared to check and moderately-yielding. Four genotypes (HAZOR KECHO, SAPONYO, AMKER and R-RHZIH-7) had increasing sensitivity to environmental changes (b>1), of which AMKER (22.6ppm) and R-RHZIH-7(23.86ppm) had considerable good Zn content and four genotypes (IR 80463-B39-3/IR 81421-B-B-66, IR-64, MINIL GISIM and PORA MEUNYA were identified as lines resistant to environmental changes (b<0), of which PORA MEUNYA had high zinc content (25.67ppm) and high yield.

IDT1-012 | Experiences with rainwater harvesting and recycling – the best climate resilient technology for higher yields of rainfed groundnut (*Arachis hypogaea* L.)

Padmalatha Y[1]*, Narayana Swamy G[2], Bhargavi K[1], Sahadeva Reddy B[2], Madhusudhan Reddy K[2], Ravindranatha Reddy[2]

[1]Agricultural Research Station,Reddipalli-515701, Acharya N.G.Ranga Agricultural University, Andhra Pradesh, India
[2]Agricultural Research Station, Anantapuramu-515001, Acharya N.G.Ranga Agricultural University, Andhra Pradesh, India
*E-mail: ply1986@gmail.com

It is clearly understood that rainfall is a crucial component of all weather elements determining the productivity of rainfed crops, and it remains a potential source for increasing the productivity of rainfed crops if managed properly. In the context of climatic variability, to enhance the resilience of rainfed crops, rainwater harvesting and recycling techniques are better options. Supplemental irrigation given to rainfed crops may serve as life-saving irrigation during deficit rainfall periods or as a productivity-enhancement measure during normal rainfall seasons with intermittent dry spells. In this context, farmers' participatory research was conducted, in which a 250-m3 farm pond was dug and lined with soil:cement (8:1) mixture to study the influence of one supplemental irrigation of 10 mm on rainfed groundnut. During pod development stage, groundnut recorded 1010 kg/ha pod yield as against only 842 kg/ha in without supplemental irrigation plot. On-farm research was carried out to find out a suitable method of micro irrigation for supplemental irrigation, using rain gun and sprinklers for re-use of stored water obtained through seepage from nearby canals. Both methods were found to be equally feasible and increased the shelling percent by 5% and groundnut pod yield by 32-35% with supplemental irrigation (10 mm), compared to groundnut plants without supplemental irrigation. It was found that in the farm ponds lined with soil:cement (8:1) mixture, water retention could be for three months period. However, water retention was a problem due to high seepage losses in one of the farm ponds which was dug near a gully and where soil is sandy. In farm ponds lined with Cuddapah slabs also, water retention was only for five days and it was lost through seepage losses. It is suggested that there should be one farm-pond (250 m3) lined with soil:cement (8:1) mixture to provide supplemental irrigation (10 mm) to one-hectare, using either rain guns or sprinklers for sustainable productivity of rainfed groundnut.

IDT1-013 | Root lesion nematodes: Drought in disguise

Rana. J, Fosu-Nyarko. J and Jones. M.G.K

Murdoch University, Perth, WA 6150, Australia
*E-mail: rana.om.jyoti@gmail.com

Plant parasitic nematodes (PPNs) reduce crop yields and account for crop losses of an estimated US$ 125 billion worldwide. PPNs damage host plants by disrupting water and nutrient uptake in plant roots and divert nutrients for their own growth and reproduction. The damage caused by root lesion nematodes is more severe under water-limiting or drought conditions. The symptoms caused by root lesion nematodes are typical: plants suffer water stress and nutrient deficiencies, including wilting, leaf yellowing and premature senescence. Techniques used to manage nematodes are rarely effective and genetic resistance is usually lacking. This makes it difficult to manage or control nematodes using traditional breeding approaches. Plants respond to pathogen invasion in a complex manner, including changes in structure, metabolism, gene expression and/or physiological defences which can prevent invasion, development and/or reproduction of an invading organism. To combat host defences, nematodes have developed a battery of ‘effectors’ which enable them to establish successful parasitism. In this research we have identified a series of effectors of root lesion nematodes. These are being characterised using molecular tools and using RNA interference technology to understand their function. It is expected that this research will provide important new molecular and genetic information on root lesion nematode–host interactions which could be exploited to develop new forms of resistance in major staple crops such as wheat.

IDT1-014 | Modelling the impact of rhizosphere processes on root water uptake

Schwartz N[1*], Carminati A[2], Meunier F[3], Javaux M[3,4]

[1] The Hebrew university of Jerusalem, Rehovot, Israel.
[2] Georg August University of Goettingen, Goettingen, Germany.
[3] Université catholique de Louvain, Louvain-la-Neuve, Belgium.
[4]Forschungzentrum, Juelich GmbH, Germany.
*E-mail: nimrod.schwartz@mail.huji.ac.il

In recent studies, it has been shown that root exudates and especially mucilage alter the hydraulic properties of the rhizosphere, affecting water content distribution and root water uptake (RWU). Current models that integrate RWU with rhizosphere processes are limited to a simplified one root system with a homogeneous distribution of rhizosphere and root properties. In this work, we present a 3D model of water flow in the soil-plant continuum that takes in consideration root architecture and rhizosphere processes including the spatial and temporal variation in root and rhizosphere hydraulic properties. In the new model mucilage concentration is distributed along the root system according to the exudation period and the biodegradation rate of mucilage. Mucilage considered being composed of miscible and immiscible components, each with contrasted microbial degradation preferences and rate, resulting in a different distribution of each of the component. Several scenarios describing different degradation and exudation parameters were examined. The results show that the rhizosphere water content is positively related to the mucilage concentration and that the rhizosphere hydraulic conductivity is negatively related to mucilage concentration. We observed a complex relation between the concentration of the different mucilage components and the gradient required to sustain transpiration demand. In general, a higher concentration of mucilage lead to higher gradients, but as the concentration of the immiscible components was equalized, higher miscible concentration result in lower gradients. Overall, this work demonstrates that a combination of exudate rate and degradation contributes to determine the hydraulic properties of the rhizosphere and RWU.

IDT1-015 | Investigations on prevalence of aflatoxin contamination in major groundnut growing states of India, influence of soil characteristics and farmers' level of awareness

Sudini H[1]*, Thirumalaisamy PP[2], Naik MK[3], Vemana K[4], Sundravadana S[5], Mangala UN[1], Vijay Krishna Kumar K[4]

[1] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2] ICAR - Directorate of Groundnut Research, Junagadh, Gujarat, India
[3] University of Agricultural Sciences-Raichur, Karnataka, India
[4] Acharya N.G. Ranga Agricultural University, Andhra Pradesh, India
[5] Tamil Nadu Agricultural University, Tamil Nadu, India
*E-mail: h.sudini@cgiar.org

Food safety issues are of major concern in groundnut due to aflatoxin contamination by *Aspergillus flavus*. Monitoring aflatoxin prevalence and understanding the factors responsible can provide useful information for devising effective management strategies. The present study focused on mapping the pre-harvest aflatoxin contamination in India along with its determining factors. A comprehensive survey was undertaken during 2012-2014 in four major groundnut growing States such as Andhra Pradesh, Gujarat, Karnataka, and Tamil Nadu. Pod (n=2434) and rhizospheric soil samples (n=1322) were collected to ascertain *A. flavus* populations and pre-harvest aflatoxin contamination. Further, kernel aflatoxin levels were correlated with soil organic carbon, available calcium and pH levels in the fields from where the samples were collected. Farmers' awareness on aflatoxin problem was also determined using a semi-structured questionnaire. Our results indicate wide variations in the occurrence of pre-harvest aflatoxin contamination levels of kernels among different States (0 - 5486 ppb) and samples within States. Detectable levels of aflatoxins (>1ppb) were highest in Karnataka (70.5%), whereas it was lowest in Andhra Pradesh (32.9%). Correlation studies revealed that aflatoxin contents were positively associated with soil pH (r = 0.54-0.99) and *A. flavus* populations (r = 0.63 in Gujarat; r = 0.75 in Karnataka) whereas soil organic carbon and available calcium were negatively correlated with toxin levels in kernels (r = -0.99). Farmers' awareness was considerably poor in all the States under survey. Overall, our results suggest the prevalence of aflatoxin contamination in major groundnut growing areas in India, and influence of certain edaphic factors.

IDT1-016 | Evaluation of symbiotic potential, nutrient uptake and yield of chickpea cultivars under field conditions

Swarnalakshmi K[1*], Yadav V[1], Pooniya V[1]

[1]ICAR-Indian Agricultural Research Institute (IARI), New Delhi-110012, India.
*E-mail: swarna_bga@yahoo.com

In India, chickpea (*Cicer arietinum* L) is an important cool season food legume crop cultivated under rainfed conditions. It has an inherent potential to fix atmospheric nitrogen through symbiotic association with Mesorhizobia. In chickpea, Symbiotic Nitrogen Fixation (SNF) contributes 40-80% of total plant nitrogen depending upon host genotype, efficient strains of *Mesorhizobium* in nodules, and soil type. The present study aims to evaluate the chickpea cultivars for superior SNF potential associated with improved plant growth, nutrient uptake and yield. About 23 chickpea cultivars were grown under IARI field conditions without application of chemical inputs. These cultivars were assessed for *in-planta* nitrogenase activity, nodulation potential, plant growth, nutrient uptake and seed yield to study the inter-relationship of plants' physiological characters and their variance from one genotype to another. Principal Component Analysis (PCA) showed a significant positive correlation among *in-planta* nitrogenase activity, shoot weight, nodule dry weight, and N and P uptake. Additionally, genotypes were clustered, based on their performances. Eight out of 23 cultivars were categorised as high-performing group in which SNF potential correlated with plant growth and yield; whereas six genotypes were found to be relatively poor and were categorised as low performance group. A few other genotypes were accorded to mediocre performance cluster while five genotypes did not fall in any cluster as their performance was highly variable across the tested parameters. The cultivars with improved SNF associated with plant growth and yield can perform better under low nutrient conditions which are most prevalent in rainfed agriculture.

Poster Theme II

Maximising Dryland Crop Production: Crop Design

IDT2-001 | Identification of locally adapted drought-tolerant maize varieties using local preferences and selection of farmers in northern savannah zones of Ghana

Adu GB[1]*, Abdulai MS[1], Alidu H[1], Abdulai LA[1], Buah SS[1], Kombiok JM[1], Abudulai M[1], Etwere PM[1]

[1]CSIR-Savanna Agricultural Research Institute, Tamale, Ghana
*E-mail: gloriaboakyewaa@yahoo.com

Drought is a major constraint to maize production in the savanna zones of Ghana. As climate change advances, drought stress on crop production is expected to increase. The deployment of drought tolerant (DT) varieties will not only stabilize yields but also improve the productivity of maize in drought-prone areas. Participatory variety selection trials were conducted to assess the effects of some weather parameters on the yield of eight DT hybrids and to assess farmer's variety preferences to aid introduction of the hybrids in northern Ghana. Eight mother and 96 baby trials were established in four districts (Tolon, Biduri, West Gonja and Sissala East) in 2014 and 2015. In the mother trials, the two best hybrids, EH8 and EH4, out-yielded local checks by 14-37% under well-watered conditions and 42-71% under terminal drought. These hybrids were the most preferred in all the districts. EH11 was the second preferred hybrid in Sissala East district. Variety preferences varied among males and females. Generally, selection criteria used across gender included earliness, cobs per plant, ear filling, cob size, and leaf rolling and stay-green. Thermal time to anthesis and silking showed apparent effect of latitude and/or photoperiod sensitivity on phenology of the hybrids, implying appropriate timing of agronomic practices for optimum yield. Rainfall index showed that 58% of the varieties produced above average yields using less rainfall, confirming their drought tolerance. The hybrids selected by the farmers were among those identified as drought tolerant, suggesting that knowledge of farmers' preferences could increase efficiency of targeting new germplasm.

IDT2-002 | Progress in cowpea cultivation, improvement and storage in Burkina Faso from 1978 to date

Batieno J.B.[1]*, Drabo I.[1], Tignegre J.B.[2], Barro A.[1], Dabiré C.[1], Neya J.B.[1], Zida E.[1], Ilboudo D.[1], Hamadou S.[1], Hamadou Z.[1], Felicien Z.S.[1], Karidiatou G.T.[1], Ouedraogo J.T.[3]

[1]Institut de l'Environnement et de Recherches Agricoles (INERA), Burkina Faso
[2]Asian Vegetable Research and Development Center (AVRDC)
[3]African Biotechnology Network for NEPAD
*E-mail: batieno52@gmail.com

Cowpea (*Vigna unguiculata* L. Walp.) is the most important crop that provides nutritional quality, food security and cash income for the resource poor farmers of Burkina Faso. Cowpea research started in 1978 with the IITA-SAFGRAD program at Kamboinsé in order to boost the productivity of the crop in West and Central Africa. In Burkina Faso the annual production at that time was estimated at 100,000 tones with low-yielding material and mean yield in farmer field of 200 kg/ha. The low yield was attributable to poor cultivation practices, insect pest damage, diseases, low soil fertility, drought, *Striga* and cropping system.
Cowpea production of the country in 2014 was estimated at 675 000 tones. The yield with farmer practices has increased from 200kg/ha to 800 kg/ha. This progress is the result of research activities of the multidisciplinary team composed of breeders, entomologists, pathologists, virologists, sociologists, and the financial contribution of our policy makers, international agencies and donors. The breeding team was able to release farmer-preferred varieties with a yield potential of about 2000kg/ha. In our presentation we will discuss the progress made in terms of breeding methods and variety development, crop protection and storage, agronomy, seed production, capacity building and technology dissemination.

IDT2-003 | Screening of rice varieties to identify a thermo-tolerant variety using Temperature Induction Response (TIR) technique

Radha B[1]* and Narayankutty M.C.[1]

[1]Regional Agricultural Research Station, Pattambi, Palakkad, Kerala Agricultural University, Pin code- 679 306, Kerala, India.
*E-mail: beenaajithkumar@gmail.com

In this study, a screening protocol was developed based on the principle of "acquired tolerance" in which exposure of seedlings to a sublethal level of specific stress is used to induce tolerance to a subsequent lethal level of stress. After adapting this temperature induction response (TIR) technique to one variety (Jyothi), ten rice varieties were screened for thermo-tolerance. Among the varieties Njavara recorded the highest germination percentage under 50°C. Chenellu followed by Njavara recorded the highest seedling vigour index under control condition but under high temperature condition Jyothi recorded the highest seedling vigour index followed by NS-4. NS-1 and Njavara recorded the highest activity of catalase in leaves under control condition but under high temperature condition Chenellu recorded the highest activity of catalase in leaves. NS-1 and Chenellu recorded the highest activity of ascorbate peroxidase in leaves under control condition but under high temperature condition Njavara and NS-4 recorded the highest activity of ascorbate peroxidase in leaves. During induction stress, the stress signaling pathway is triggered resulting in the expression of an array of stress responsive genes whose gene products alter several physiological and biochemical processes relevant to the stress tolerance. Expression of stress responsive genes during the sub-lethal induction stress and differences in the expression of these genes is the reason for observed genetic variability for stress tolerance. Results suggested that TIR is a robust and powerful technique and can be used to screen breeding lines or germplasms to identify thermo-tolerant lines.

IDT2-004 | Effect of water deficit on yield components in sesame (*Sesamum indicum* L.)

Gadri Y[1]*, Peleg Z[1]

[1]The Hebrew University of Jerusalem, Rehovot 7610001, Israel.
*E-mail: Yaron.gadri@mail.huji.ac.il

Sesame (*Sesamum indicum* L.) is used in a large variety of food and medical industries. It is an 'orphan crop-plant', which grows mostly under rain-fed conditions, using traditional agriculture practices. Worldwide, sesame yields are relatively low (300-600 kg ha-1), due to lack of knowledge and research on sowing stands, irrigation, fertilization, herbicides and pesticides. The current study goals were to test the effect of water-limited conditions on morpho-physiological adaptations and productivity in sesame. Field experiments were conducted over two growing seasons in Israel. Morpho-physiological parameters were measured throughout the growing season in order to characterize the plants' response to water-limited (299 mm) conditions as compare with well-watered conditions (433mm).Water-limited treatment was determined based on soil water potential using tansiometers sensors. As expected, higher yield components and total seed yield (2200 kg ha-1) were observed under well-watered regime. However, under water-limited irrigation regime, plants maintained relatively high yield (1600 kg/ha). Leaf gas exchange measurements revealed the ability of sesame to acclimate to low water potential in the soil throughout the growing season, which resulted in improved water-use efficiency. Carbon isotope ratio (δ13C) analysis (-29.2 *vs.* -27.1‰, under well-watered and water-limited conditions respectively) further supports greater water-use efficiency. This ability to maintain relatively high yields under water-limited conditions might be attributed to improved osmotic adjustment. Our results serve as a basis for developing efficient irrigation regime for sesame under the climate changes of the Mediterranean environment.

IDT2-005 | Heat tolerant mungbeans: Hope for harsh climates

Bindumadhava H[1]*, Nayyar H[2], Nair R.M[1], Rane J[3], and Easdown W[1]

[1]World Vegetable Center South Asia, India.
[2]Panjab University, Chandigarh, India.
[3]NIASM, Baramati, India.
* E-mail: bindu.madhava@worldveg.org

Mungbean is one of the world's most important fast maturing warm season legumes, and it is a major crop in the spring/summer season in northern India. Increasing temperatures in this region will impact mungbean productivity. Temperatures over 45°C that often occur at flowering can lead to flower abortion and yield losses. The adaption of mungbean to heat stress needs to be broadened, and so we evaluated the effect of high temperatures on the vegetative and reproductive performances of different top performing commercial and research mungbean lines. Firstly, these lines were screened at the seedling stage using the temperature induction response (TIR) technique, and putative tolerant lines were shortlisted for validation at the whole plant level. These were grown outdoors in containers under full irrigation, and screened for growth and yield traits at two sowings: (1) Normal sowing (NS) in March, so that the day/night temperatures during the reproductive stage were <40/28°C, and (2) Late-sown (LS) in April, so that temperatures were higher (>40/28°C). In the LS plants, leaves showed symptoms of rolling & chlorosis and phenology was accelerated, leading to a sizable reduction in leaf area, biomass, flowers and pods. Interestingly, the shortening of flowering and podding duration was also evident. In LS plants, the reproductive function was distinctly condensed in most of the lines, along with increased flower and pod abortions. These lines were further subjected to specific high temperature regimes (flowering phase) for assessing effects on the reproductive cycle and relative yield using a phenomics facility. The results showed that heat stress during the reproductive phase (flowering to pod set) was very detrimental and our study shows considerable variation in heat tolerance among lines. We identify a few heat tolerant types (EC693357, 58, 69, PDM139, Harsha and ML 1299) using agronomic and physiological interventions at the seedling and whole plant stages and they have potential for use in breeding new lines better adapted to harsh arid and semi-arid environments.

IDT2-006 | Screening and multi-elemental profiling of chilli germplasm against drought tolerance under controlled conditions

Venkata Ramana Muddarsu[1]*, S. Manivannan[1], S. Upadhayay[1]

[1]Department of Horticulture, Sikkim University, Sikkim, Gangtok, India, 737102
*E-mail: venkat.muddarsu@gmail.com

Drought is a major abiotic factor that limits plant growth and productivity. Chilli (*capsicum annuum*) is an important vegetable crop and area under production is limited by irrigation water scarcity. Effort was made to screen seven germplasms of *Capsicum annuum* through hydroponics under controlled conditions using polyethylene glycol (PEG) at four concentrations (0, 20, 40 and 60 g/l) with three replications in factorial CRD. Important growth parameters like shoot length, root length, number of leaves, number of internodes, leaf area, shoot dry weight, root dry weight and root to shoot dry weight were observed. In addition, multi elemental profiling of each genotype grown under different treatments were analyzed using ICP-MS. Significant differences were observed among the genotypes, treatments and their interactions for evaluated growth parameters and elemental concentrations suggesting that variability has found for drought tolerance in chilli. Based on the phenotypic characters analysis, *Arka Lohit* and *Arka Mohini* were found to be drought tolerant and susceptible genotypes respectively. Further, the interaction of different elements with growth parameters and contribution of these elements, especially essential elements of plants and some non essential trace elements for drought tolerance were ascertained.

IDT2-007 | Exogenous application of trehalose to mitigate drought stress in tea

Nalina M*, Chandrashekara KN, Manigandan N, Rajkumar R, Radhakrishnan B

United Planters Association of Southern India Tea Research Foundation Tea Research Institute (UPASI TRF TRI), Valparai 642 127, Tamil Nadu, India
*E-mail: nalinam08@gmail.com

Drought stress is one of the most important factors limiting the survival and growth of plants, thus affecting the yield and quality of tea. In this context, a field experiment was conducted to document the crop response to five treatments, i.e., exogenous application of trehalose at 50, 100, 200 ppm, 1% NK (Nitrogen-Potassium) and control, to mitigate the drought stress and to improve the quality of made tea. Field grown tea bushes of UPASI-9 (drought tolerant) and UPASI-3 (susceptible) plants were selected. At the onset of drought, foliar applications were implemented at fortnightly intervals till summer showers. All other cultural operations were kept constant as per the UPASI guidelines. At each commercial harvest yields were recorded, crop shoots were subjected to biochemical quantification and antioxidative enzymes assays. Black tea was manufactured and quality parameters of black tea were studied as per FSSAI guidelines. Pigments, osmotic solutes (soluble sugars and proline), cellular damages, and antioxidant enzymes (superoxide dismutase, poly phenol oxidase and peroxidase) were investigated. Drought stress significantly decreased the pigment content, but increased the ratio of carotenoids to total chlorophylls. During the prolonged drought stress, gradual decrease in the anti-oxidative enzymes were observed in control compare to trehalose and NK treated plants but significantly increased proline, glycine-betaine content and superoxide dismutase activity, ion leakage was found more in control plants. The quality parameters of black tea such as poly phenols, total catechins, reducing sugars, amino acids, theoflavins and theorubigins are higher in treated plants compared to control. These findings suggested that the treated plants showed higher tolerance to severe drought stress than the control plants due to its higher capacities of osmotic adjustment and antioxidant protection.

IDT2-008 | Comparison of Iranian national Genebank wheat landraces tolerant to drought and commercial cultivars for maximizing crop production in Iran

Leila Nasirzadeh[1,2]*, Behzad Sorkhi Lalehlu[2], Eslam Majidi Hervan[3]

[1]Department of Agronomy and Physiology, Science and Research Branch, Islamic Azad University, Tehran, Iran
[2]National Plant Gene-Bank of Iran (NPGBI), Seed and Plant Improvement Institute, Karaj, Iran
[3]Department of Plant Breeding, Science and Research Branch, Islamic Azad University, Tehran, Iran
*E-mail: l.nasirzadeh@gmail.com

Breeding under water-limited conditions has gained more attention during recent years with regard to climate change and its negative effects on increasing the temperature and decreasing available agricultural water for crop production in Iran. The Iranian National Genebank Wheat landraces are promising sources of germplasm to provide wheat breeders with genes tolerant to drought. To achieve wheat productivity under drought and to maximize crop production in Iran, both dryland and irrigated under terminal drought conditions, a subset of 10 selected/designated Wheat Genebank accessions were compared to eight commercial wheat cultivars. The objective of this study was to evaluate the wheat landraces and cultivars for their quantitative traits and to demonstrate similarities of the studied genotypes using GGEBiplot analysis. The results revealed that cultivar Star and Sirvan, and the landraces 1399 and 1998, were the top superior genotypes. Accession number TN1399 was a superior genotype, with the highest ranking for biological and seed yield. In contrast, TN4228 as an accession with the least amount of yield had high ranking for the traits such as peduncle weight, first internode weight, and single plant weight; and the lowest ranking for spike weight, spike number, and sterile spikelets number. The result of GGEBi plot configured similarities between Star and Sivran, and Roshan and TN1998, whereas dissimilarities were observed for TN1399 vs Pastor; and Star vs TN 4228.

It was concluded that Iranian landraces could be either used directly as sources of tolerant wheat genotypes in dryland cultivation or implemented in breeding programs for enriching improved dual purpose cultivars with high potential yield as well as tolerance to drought.

IDT2-009 | Multi-locational evaluation and release of micronutrient dense bean varieties in Uganda

Nkalubo S. T.[1]*, Ugen M.[1], Aogon G.[1], Ssekabembe R.[1], Sulume J.[1]

[1]National Crops Resources Research Institute-National Agriculture Research Organization. Kampala, Uganda
*E-mail: directornacrri@yahoo.com

Micronutrient malnutrition affects more than one-half of the world's population, especially pregnant women and preschool children in developing countries. In Uganda, nearly 38% of children below five years are stunted, 6% are wasted and 16% are underweight, which is among the highest global malnutrition rates. Deficiencies of micronutrients such as iron and zinc are a major component of this malnutrition and various health complications. The biofortified bean is one of the most important food sources of iron and zinc, given high production and consumption volumes of beans in Uganda. This study was conducted in six agroecologies to determine the adaptability and stability of 16 new biofortified genotypes for high micronutrients (iron and zinc) accumulation, high yield and reaction to pests and diseases. Data was analysed by the GGE (i.e. G, genotype + GEI, genotype-by-environment interaction) biplot method. Consumer and market acceptability test was conducted in terms of grain characteristic, marketability and organoleptic properties. Results indicated the presence of a genotype-by-environment interaction for different bean genotypes in micronutrient accumulation, yield and reaction to pests and diseases. Bush genotypes MORE 88002, RWR 2154 and RWR 2245 and climber genotypes MAC 44 and Nyiramuhondo were the highest yielding, most micronutrient dense, most resistant to pests and diseases, and most preferred with MORE 88002 being best-in-class. Five genotypes were recommended and released as new biofortified bean varieties for promotion and production in Uganda.

IDT2-010 | Yield enhancement through bio-fertilizer priming and effect of bio-regulators in soybean under soil moisture stress

Ratnakumar P[1,2]*, Govindasamy V [1,3], Minhas PS[1]

[1]ICAR- National Institute of Abiotic Stress Management (NIASM), Baramati, Maharashtra
[2]ICAR- Indian Institute of Oilseeds Research (IIOR), Rajendranagar, Hyderabad
[3]ICAR- Indian Institute of Agriculture Research (IARI), Pusa, New Delhi
*E-mail: ratna.pasala@icar.gov.in

Bio-fertilizer and plant bio-regulators technology is now being proposed as a key strategy to maximize the yield of crops growing in marginal lands of rainfed areas. Impact of foliar application of bio-regulators (BR) salicylic Acid (5mM) + Ortho-silicic Acid 4ml/L on the seed application of a bio-fertilizer (BF) strain *Bradyrhizobium diazoefficiens* USDA-110 was assessed in soybean cultivars known as drought tolerant (JS-335) and susceptible (NRC-37). Rainfall received during experimentation and application of basal N fertilizer was nil. Moisture stress was imposed by withholding surface irrigation from 28 days after sowing to seed maturity. The leaf area, RWC, nodule number, nodule weight and yield components enhanced in both varieties under irrigated and moisture stress with the application of BF+BR together, BF and BR exclusively. NRC-37 responded well to BF, BR and BF+BR as compared to JS-335 under soil moisture stress. The relationship between nodule numbers and nodule fresh weight was highly significant in NRC-37 (r^2: 0.78) and in JS335 (r^2: 0.98) under soil moisture stress conditions than irrigated with application of BF, BR and BF+BR. The results showed that BF together with BR had enhanced the root-nodulation and N-fixation in NCR-37 than JS-335 under soil moisture stress. The percent yield increase was varied in BF, BR and BF+ BR applications in both cultivars under stress condition. The both varieties were performed better in terms of final seed yield with the application of BF + BR, the combined/mixed application of BF+BR, be an alternate mitigation option to drought.

IDT2-011 | Rainfall probability analysis for drought occurrence and crop planning at Raichur

Pradeep CM[1]*, Yasmin[2], Balakrishnan P[3]

[1]College of Agricultural Engineering, Raichur, Karnataka, India
[2]RSK, Chandrabanda, Karnataka, India
[3]College of Agricultural Engineering, Raichur, Karnataka, India
*E-mail: pradeep0393@gmail.com

Knowledge about the amount of rainfall and its distribution is major a constraint affecting agricultural production. Hence, the quantum of rainfall and its uncertainty are a pre-requisite to determining the choice of any particular crop and agronomic practice in dryland agriculture. Therefore, a study was carried out to analyse the weekly, monthly and annual rainfall data for crop planning and drought management under semi-arid regions of Karnataka, using a time series record of 59-years (1957-2015) data. The monthly analysis showed that the rainfall is mainly confined to five months, from June to October. September was the wettest month with average rainfall of 147.78 mm and February was the driest month with average rainfall of 1.60 mm. The promptness of rainfall was observed in July month with a CV of 59.58%, followed by September, August and June months with CVs of 62.82, 66.67 and 69.62% respectively. The percentage occurrence of drought, normal and surplus months during the study period were observed to be 49.72%, 39.55% and 10.73% respectively. Similarly, the percentage occurrences of normal, surplus and drought years during the study period were found to be 67.80%, 18.60% and 13.60% respectively. The mean, SD and CV of weekly rainfall for the study area during the study period were observed to be 12.87 mm, 13.56 mm and 105.32% respectively; whereas for monthly rainfall data the mean, SD and CV was observed to be 55.71 mm, 80.24 mm and 144.04% respectively. It was observed that, within a month the weekly variations were observed which was not reflected in monthly data analysis. Therefore, monthly analysis of rainfall was found to be too long a period for crop planning, while weekly analysis could serve the purpose better.

IDT2-012 | Phenotyping pre release groundnut (*Arachis Hypogaea* L.) genotypes for drought adaptive traits under simulated mid season stress conditions

Latha P[1]*, Vasanthi R P[1], John K[1], Nirmal Kumar A R[1], Sudhakar P[2], Sujatha K[1] and Naidu T C M[1]

[1]Institute of Frontier Technology, Regional Agricultural Research station, ANGRAU, Tirupati – 517 502, A.P., India
[2]Professor and Head, SV Agricultural College, Tirupati – 517 502, A.P., India
*E-mail: latha_damu@yahoo.com

Owing to increasing water scarcity and low productivity in groundnut warrants urgent need to identify water-saving capacity or drought tolerance varieties through various physiological and biochemical approaches in groundnut which will perform better under rainfed condition. The pre release groundnut genotypes were screened for drought adaptive traits and high yield under rabi conditions of 2014-15 and 2015-15. The crop was grown both under irrigated and also subjected to simulated mid-season moisture stress conditions (50-80 DAS) using rain out shelters. The data of rabi' 2014-15 and 2015-16 were pooled and statistically analysed by SPSS. The results of pooled mean data reveal that, TCGS 1345 significantly recorded high relative water content, photosynthetic rate, stomatal conductance, chlorophyll stability index and lowest membrane injury per cent followed by TCGS 1342 and TCGS 1343 under mid season stress conditions. The genotype TCGS 1345 significantly recorded highest yields followed by TCGS 1346 and TCGS 1426 under mid season stress conditions. Hence, the results conclude that, TCGS 1345 recorded high drought adaptive traits and also high yields. Whereas, the genotypes TCGS 1342 and 1343 recorded high drought adaptive traits with moderate yields.

IDT2-013 | Elevated CO_2 alleviates drought-induced negative effects in short rotation coppice mulberry (*Morus* spp.), a potential bio-energy tree crop

Sekhar KM[1], Reddy AR[1]*

[1]University of Hyderabad, Hyderabad-500046, India
*E-mail: attipalli.reddy@gmail.com)

The present study describes the responses of short rotation coppice (SRC) mulberry, a potential bio-energy tree, grown under interactive environment of elevated CO2 (E) and water stress (WS). Growth in E stimulated photosynthetic performance in well-watered (WW) conditions as well as during WS, with significant increases in light saturated photosynthetic rates (*A*Sat), water use efficiency (WUEi) and intercellular [CO2], with concomitant reduction in stomatal conductance (gs) and transpiration (*E*) compared to ambient CO2 (A) grown plants. Reduced levels of proline, H2O2 and malondialdehyde (MDA), and higher contents of antioxidants, including ascorbic acid and total phenolics in WW and WS in E plants, clearly demonstrated lesser oxidative damage. Further, A plants showed higher transcript abundance and antioxidant enzyme activities under WW as well as during initial stages of WS (15 days). However, with increasing drought imposition (30 days), A plants showed down regulation of antioxidant systems compared to respective E plants. Analysis of OJIP chl a fluorescence kinetics revealed that D negatively affects the photosystem-II (PS-II) performance in both E as well as A plants, as manifested with prominent L and K bands. Further, significant increase in parameters including FV/FM, ET/CSm and PI(ABS) with concomitant reduction of DI0/RC and DI0/CSm in E plants under WW as well as D demonstrated more photochemical quenching. These results clearly demonstrated that future increased atmospheric CO2 could enhance the photosynthetic potential and also mitigate drought-induced oxidative stress in SRC mulberry.

IDT2-014 | Identification of a rice genotype with reasonable adaptation to aerobic cultivation

Shashibhushan N. B[1]*, Rashmi K.[1], Chethankumri C C[1], Ramachandra Y.L.[2], Udayakumar M[1]

[1]College of agricultural sciences, GKVK, Bengaluru-560065, Karnataka, India.
[2]Kuvempu University, Shankarghatta-57745, Karnataka, India.
*E-mail: shashibhushannb@gmail.com

Rice is a widely cultivated crop in India under irrigated conditions and its water requirement is very high. Due to dwindling water resources, to save irrigation water, growing rice under semi-irrigated aerobic condition has phenomenal relevance. In this ecosystem, decreased water availability, high VPD affects crop growth and productivity. In this context it is important to improve adaptation of rice under aerobic conditions by improving water relations and cellular level tolerance mechanisms. To achieve this objective, we have screened few rice genotypes (Ac39020, BPT5204, JBT36/14, KMP-153, KMP-175 and Telahamsa) to determine adaptability and survivability under aerobic conditions. Seeds of all the six genotypes were initially grown at 100% field capacity up to 21 days. Twenty one day old plants were subjected to a progressive water stress by withholding the water. Plant water status was measured at regular intervals by gravimetric method to achieve required levels of soil moisture (100, 60 and 40%FC). The plant samples were collected when soil moisture reached to 60 and 40% field capacity and analyzed for physiological and biochemical parameters such as SOD activity, (MDA) levels, ROS levels, membrane integrity with respective controls (100% soil moisture level). KMP-175 and KMP-153 showed less accumulation of cytotoxic compounds and loss in membrane integrity. In these genotypes, percent reduction in growth was significantly less compared to others, signifying the relevance of cellular level tolerance mechanisms associated with scavenging ROS and reactive carbonyl compounds (RCC's). From these morpho-physiological and biochemical assays, KMP-153 is considered as relatively superior.

IDT2-015 | Stay green wheat for drought and heat stress

Naresh Pratap Singh[1]*, Vaishali[1]

[1]Department of Biotechnology, College of Agriculture, SVPUA&T, Meerut, INDIA.
*E-mail: naresh.singh55@yahoo.com

Keeping in view the food needs of a growing population, researchers are focusing on developing better varieties, including new ideotype cultivars with a different sets of physiological and morphological traits. Mainly, water shortages and heat stress due to global warming threaten the agricultural productivity of many developing countries, especially in South Asia and Africa. It is predicted that the detrimental effect of abiotic stresses such as drought, heat, and rising soil salinity decreases the yield significantly. This can be managed by genetic improvement in terms of photosynthetic response, long green leaf duration, and delayed leaf senescence. 'Stay green' is a vital trait which is directly associated with the capacity of the plant to maintain CO_2 assimilation, photosynthesis and chlorophyll content. Wheat genotypes with the ability to maintain their green leaf area (stay green traits) throughout grain filling offer potential for adapting and improving wheat for higher yield under drought conditions. There is strong association between the duration of photosynthetically active leaf area, chlorophyll content and grain yield. Stay green trait (SG) can be considered as a defense mechanism that postpones the onset of senescence and keep leaves green (i.e in an active photosynthetic state) and is expected to give additional yield to crop plants. Therefore, stay green genotypes are expected to have a significant agronomic interest for better crop productivity under stressed environments.

IDT2-016 | Influence of seed priming on growth and yield of foxtail millet

*Sridevi. R[1], V. Manonmani[1]

[1]Tamil Nadu Agricultural University, Coimbatore – 641 003, Tamil Nadu, India.
*E-mail: agrirose.28@gmail.com

Millets are small-seeded grasses that are hardy and grow well in dry zones as rain-fed crops, under marginal conditions of soil fertility and moisture. Small millets may not appear important in terms of world food production, but are essential as food crops in their respective agro ecosystems. Seed priming is a widely recommended pre-sowing seed treatment, proven for its invigorative effect. Seed priming could advance germination; improve the initial quality characters, field emergence, better establishment, and crop stand; and increase yields in many diverse environments. Seeds of foxtail millet cv. CO7 were primed with water, KH_2PO_4 2% and *Pseudomonas fluorescens* 20% and were evaluated along with non-primed seeds for their productivity under field conditions. Seed priming with *Pseudomonas fluorescens* 20% registered higher plant growth parameters such as plant height, chlorophyll content, net assimilation rate, and dry matter efficiency; and yield parameters such as higher panicle weight per plant, panicle to seed recovery, seed yield per plant, seed yield per plot, and 1000-seed weight. Improvement in growth parameters due to *P. fluorescens* 20% could be attributed to production of plant growth regulators such as gibberellins, cytokinins and indole acetic acid; increased availability of minerals and other ions; and extensive rooting which facilitates water and nutrient uptake (Van *et al.,* 1998; Ramamoorthy *et al.,* 2001). Increase in yield parameters might be attributed to N_2-fixing and phosphate solubilizing capacity of bacteria as well as the ability of these microorganisms to produce growth promoting substances (Salantur *et al.,* 2006.)

Posters Session III

Plant Productivity under Drought I: Effective Capture of Water

IDT3-002 | Relative water content, cell membrane stability and DAB assay in relation to reduction in yield components and resource remobilisation under drought in common bean (*Phaseolus vulgaris* L.)

Sofi, P. A.[1]*, Rehman, K[1]., Bhat, M. A.[1], Dar, Z. A[1], Lone, A.A[1]

[1]Faculty of Agriculture, SKUAST-Kashmir, Wadura, 193201, J&K, India
*E-mail: mashrafbhat@skuastkashmir.ac.in

The present study reports the response of 20 genotypes of common bean for relative water content (RWC), cell membrane stability (CMS), DAB assay and yield parameters in relation to drought tolerance. The highest reduction in RWC was recorded for SR-1, followed by WB-112, while the lowest decrease was observed in the case of WB-451. Cell membrane stability values under drought were the lowest in the case of SR-1 (0.113), followed by WB-257 (0.189), whereas it was the highest in the case of WB-83 (0.814), followed by WB-401 (0.751), and WB-341 (0.735). Invariably, genotypes with better yield performance and better resource remobilisation had better values of cell membrane stability (or alternatively lower membrane injury) under stress. The largest reduction in pod length was observed in the case of SR-1 (44.52), followed by WB-1587 (26.34), while the smallest reduction was recorded for WB-341 (8.96%). WB-6 and ArkaAnoop suffered the largest reduction in seed weight while the lowest reduction was recorded in WB-1634. The largest reduction in seed yield under drought was observed in WB-6, followed by WB-1492, whereas the lowest reduction was recorded for WB-1634 (11.33%). The largest decrease under drought was recorded for seed yield per plant, followed by pods per plant, whereas lower decrease was recorded for 100-seed weight. DAB assay clearly differentiated the lines on the basis of darker staining of leaves under drought. The lines showing greater percent reductions in yield parameters show greater staining in DAB assay, underlining the reliability of using this assay as an effective supplement to phenotyping protocols for characterising large germplasm sets.

IDT3-003 | Exploring root-leaf continuum between wild rices and sorghum to enhance drought stress resilience in rice

Raju BR[1,2]*, Quinones OC[1], Anandhan T[1], Hechanova S[1], Jena KK[1], Jagadish SVK[1,2]

[1]International Rice Research Institute (IRRI), Metro Manila, Philippines
[2]Kansas State University (KSU), Department of Agronomy, Manhattan, Kansas, United States of America
*E-mail: rajubr@ksu.edu

Carbon assimilation or biomass production per unit water lost under water-deficit (WD) conditions is a dynamic process connecting rhizosphere-plant-environment continuum. Rice grown under WD conditions undergoes root and shoot traits alterations, affecting morph-physiological and anatomical characteristics. Earlier attempts to assess rice responses to WD condition have overlooked the root-leaf continuum, a dynamic approach compared to investigating either of the two components. The goal of our study was to compare *Oryza* species (*Oryza granulata*, *O. meyeriana,* IR64 and N22) and sorghum for exploring root (root and stele diameter, xylem number and diameter)-leaf (stomatal size and density) anatomical traits under non-stress (100% field capacity-FC) and WD (60%-FC)conditions coinciding with panicle initiation and anthesis stages, independently. Root anatomical traits such as proportion of stele to root diameter and xylem diameter were significantly different at both stages among the species studied. Across species, there was 10-fold variation in stomatal density (mm-2), ranging from ~115 (sorghum in control) to 1160 (in IR64 under WD). Across species, stomatal conductance and transpiration-rate were negatively correlated with stomatal size and positively with stomatal density. Interestingly, *O. granulata*, *O. meyeriana* (GG genome sps.) having small root xylem diameter, larger stomata pore size and lower number of stomata transpired ~50% less water (g.day-1) compared to IR64 (~410 g.day-1) under WD. A greater similarity between wild rice (GG genome sps.) and sorghum in water mining and water use efficiency were observed in response to WD. Yield and yield components were recorded from control and stress recovered plants and their relationship with root-leaf continuum traits was established. Promising drought adaptive traits connecting root-leaf continuum to improve adaptability of rice to WD conditions will be discussed.

IDT3-004 | Comparison of three C4 cereals for transpirational sensitivity to elevated evaporative demand

Sunita Choudhary [1,2], Vincent Vadez[1]*, P Anand[2], Charlie Messina[3] and Mark Cooper[3]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru- Telangana State-502336, India
[2]DuPont Pioneer, Multi Crop Research Center, Tunkikalsa, Wargal, Medak District, Telangana State-502336, India
[3]DuPont Pioneer, 7250NW 62nd Avenue, Johnston, IA 50131, USA
*E-mail: v.vadez@cgiar.org

Maize, sorghum and pearl-millet are leading C4 cereals for tropical regions where evaporative demand is high. The transpiration response to high VPD and leaf area of plants grown under different VPD conditions was compared among species to assess the degree of water conservation of these crops and then their potential fitness to different stress scenarios. Ten genotypes of each species were grown under moderate (2.2-2.8kPa) and high VPD (3.9-4.5kPa) conditions till early vegetative (V5-V7) stage with no water-limitation. At that stage transpiration was measured under elevating VPD (0.9-4.1kPa) in controlled conditions. All three species grown under moderate VPD conditions showed a variation in transpiration restriction above 3.0kPa, although the decrease in transpiration above 3.0kPa was high in the case of maize. Sorghum and pearl-millet grown under high VPD conditions showed significant reduction in leaf area whereas maize showed trivial differences in leaf area across VPD conditions. Therefore, under high evaporative demand when soil water was not limiting, maize saved water only by restricting water use during pre-flowering stages whereas sorghum and pearl millet bothreduced canopy sizeand transpiration under high VPD. The soil moisture thresholds where transpiration declined upon progressive water stress imposition did not differ significantly, regardless of different VPD in the growing conditions. Maize had also higher TE than sorghum and millet in the high VPD conditions. Therefore, water conserved in maize by restricted transpiration in high VPD condition, probably leading to higher TE, was sufficiently rewarded to sustain biomass accumulation in water stress period.

IDT3-005 | Ideal root types in drought resistant rice (*Oryza sativa* L.)

Dewanjee S[1]*, Sarkar KK[2]

[1]Department of Genetics and Plant Breeding, Regional Research Sub-Station, Red and Laterite Zone, Bidhan Chandra Krishi Viswavidyalaya, Raghunathpur-723133, Purulia, West Bengal, India
[2]Department of Genetics and Plant Breeding, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur -741252, Nadia, West Bengal, India
*E-mail: sujaya2009@gmail.com

Roots may promote plant growth under water stress condition, providing desirable root geometry. The present experiment was conducted to evaluate root traits in laboratory by growing them in glass plates under osmotic stress at different concentrations of PEG, and further growing them in PVC pipes. The data on 13 rice genotypes for shoot length, root length and root diameters were taken from 11 days glass plates-grown seedlings. The data for maximum root length, root volume, fresh and dry root weight, dry shoot weight and estimated root-shoot ratios were taken from 65-days-old plants grown in PVC pipes. Osmotic stress at seedling stage using PEG identified *Dular* and *Browngora* as less affected genotypes with increased root length and root diameter. *Aditya, Dular* and *Browngora* found were found to be favourable genotypes with respect to the root traits. Records from later growth phase revealed maximum heritability for root length. High genetic advance with moderately high heritability was noticed for dry root weight, followed by dry shoot weight. On the basis of two experiments, three genotypes (*Dular, Browngora, Aditya*) were found as favourable parents, while IR 64, IR 30 and *Satabdi* as poor parents under water stress conditions, and these parents were mated in diallele combinations without reciprocals. Results showed both additive and non-additive gene action in the inheritance of all the root traits, with predominance of non-additive gene action confirmed from predictability ratio. *Dular* was identified as the best general combiner for all the root traits. Maximum heterosis with high per-se performance for the root traits as well as yield was found in *Dular* x *Aditya* cross.

IDT3-006 | Understanding drought adaptive mechanisms: Can stress responsive proteins of unknown function (PUFs) be a missing link?

Dhanyalakshmi K H[1], Nataraja K N[1]*

[1]University of Agricultural Sciences, GKVK, Bangalore, Karnataka, India
*E-mail: nataraja_karaba@yahoo.com

The growth and productivity under any stressful condition like drought is dependent upon the stress acclimation mechanisms/traits owned by the plant. This ability to acclimatize to stress at whole plant level is primarily a manifestation of the cellular tolerance traits that helps the plants to achieve a homeostasis of the cellular activities. But all these traits are strictly governed at molecular level, by the coordinated expression of several known and unknown stress responsive genes and their products. Understanding the functional relevance of such unknown proteins, called as Proteins of Unknown Functions (PUFs), is quite essential for designing a targeted trait based crop improvement strategy. In this direction, a drought specific library was developed from a mulberry genotype (SRA accession SRP047446), having drought tolerance traits. The library has 17% of the transcripts falling into the category of hypothetical or uncharacterized or unknown proteins, grouped as PUFs. The PUFs primarily needed a function assignment to understand their relevance in stress acclimation. A concerted effort was made to devise a strategy for rapid and precise annotation of PUFs using computational tools (http://caps.ncbs.res.in/pufas). Using this approach, we annotated many PUFs, which belong to the predicted categories of both functional as well as regulatory genes. The expression patterns of the selected PUFs analyzed under various abiotic stress conditions indicated their stress responsiveness. Further experimental validation of these genes in model systems would be required to assign function to these novel proteins expressed under stress.

IDT3-007 | Field evaluation of deep water capture using thermal imaging

Dockx A[1]*, Faux Ph-F[1], Wuyts N[2], Canè MA[3], Tuberosa R[3], Welcker C[4], Draye X[1]

[1]Earth and Life Institute – *Agronomy*, UCLouvain, Louvain-la-Neuve, Belgium
[2]Vlaams Instituut voor Biotechnologie, Dept. of Plant Systems Biology, UGent, Gent, Belgium
[3]Dipartimento di Scienze Agrarie, Università di Bologna, Bologna, Italy
[4] Lab. d'Écophysiologie des Plantes sous Stress Environnementaux, INRA, Montpellier, France
*E-mail: adrien.dockx@uclouvain.be

Deep water extraction is an important determinant of drought tolerance, but is difficult to estimate for breeding applications. Our project evaluates the potential of high resolution thermal imaging and accurate measurements of leaf temperature combined with a controlled water table design to estimate the sensitivity of maize (*Zea mays* L.) genotypes to the depth of water table and, presumably, their ability to capture deep water.

We have replicated complete blocks of a set of genotypes at different positions along a slightly inclined field. An irrigation ditch maintained a stable water depth which, according to the position along the slope, was located 1.0 to 2.5 meters below the soil surface. Leaf temperature, water table depth and soil moisture have been monitored for each genotype during the flowering period, and yield components have been recorded at harvest. The variation of leaf temperature for the same genotype in different water conditions has been analysed using different indices. Several indices showed a good correlation with the water table depth, indicating the value of leaf temperature as a quantitative indicator of deep water extraction and, presumably, root system depth. A linear relationship was observed between the number of grains and several indices of leaf temperature. The regression slope and the range of values contrasted between genotypes. Interestingly, when indices were multiplied by predictors of leaf area, a unique regression seemed to apply to several genotypes, which suggests that remotely sensed leaf temperature should be adjusted to leaf area in order to link it with biomass accumulation and transpiration.

The use of thermal imaging systems in carefully designed fields appear therefore to be a valuable strategy to evaluate plant water relations in physiological studies and phenotyping applications.

IDT3-008 | Drought (WS) and low phosphorus (LP) stress in groundnut: Water extraction pattern and tolerance related traits for breeding program

Hamidou F[1,2]*, Heynikoye M[2], Halilou O[2], Upadhyaya HD[3], Vadez V[3]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger
[2]Department of Biology, Faculty of Sciences, University Abdou Moumouni, Niamey, Niger
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: f.hamidou@cgiar.org

Drought (WS) and low soil phosphorus (LP) are major constraints of groundnut productivity. This study aims to (i) understand the relative importance of phosphorus (P) deficiency, water stress and their interaction, (ii)investigate water extraction pattern under WS and LP, and (iii) identify field and controlled conditions measured traits related to better performance of genotypes under WS and LP. Six groundnut varieties were assessed under field and lysimetre conditions. Two water regimes (WW, WS) and 2 phosphorus treatments (HP, LP) were imposed. Leaf Area Index (LAI), roots volume (RV), length density (RLD) and roots dry matter (RDM), water extraction (WEx), transpiration efficiency (TE), soil moisture content (SMC) and yield were investigated. LP stress decreased LAI and pod weight (Pwt) (42 and 28 % respectively). ICGV 12991 and 12CS-116 varieties showed the highest LAI and Pwt. LAI, correlated to Pwt(r2 = 0.77), revealed relevant trait for LP tolerance.LP and WS decreased roots and canopy measured traits. WS and LP decreased WEx (51 and 7% respectively). Combined LP and WS (WS-LP) decreased WEx up to 60%. ICG 12991 and 12CS-116 showed the highest WEx, RLD and RDM under WS-LP; RLDcould contribute to water uptake to avoid dehydration. Significant genotypic variation observed on SMC revealed different pattern of WEx. TE increased under WS and decreased under LP; factors driving TE would be different.12CS-116, 55-437 and ICG 12991 revealed high TEand tolerant to WS-LP but showed different tolerance mechanism. This study revealed that ICG 12991 and 12CS-116 were tolerant to WS-LP and LAI, RLD, while WEx and TE revealed relevant traits for groundnut improvement.

IDT3-009 | Effects of drought stress on water relationships and osmotic adjustment in pasture annual medic ecotype

Haddadi SH[1,]*, Ghorbani Javid M[1], Yazdani S[1]

[1]University of Tehran, Tehran, Iran
*E-mail: sh_haddadi@ut.ac.ir

Drought stress is a major factor limiting growth, development and dispersal of plants in the biosphere. There are cultivated plants with increased resistance to this stress, which appears critical to keep growth and yields at a sufficient level. A tolerant ecotype of cutleaf medic [*Medicago laciniata* (L.) Mill] was recognized from arid areas that are able to sustain high productions and growth during drought. Thus, evaluation of mechanisms of drought response in tolerant ecotypes is important. In order to evaluate water relations and osmotic adjustment in sensitive and tolerant genotypes of cutleaf medic under drought stress, a factorial greenhouse experiment was conducted in a RCBD at the University of Tehran, Iran. The drought stress levels comprised -0.1, -0.2, -1 MPa as low, medium and high stress levels respectively, and normal condition (FC = -0.03 MPa). Results indicated that tolerant genotypes had a significant superiority to sensitive genotypes in most of the studied characteristics such as Relative Water Content (RWC), Water Potential (ψ_w), Osmotic Potential (ψ_s), Turgor Potential (ψ_t) and Osmotic Adjustment during medium and high water stress levels. The experiment showed that high RWC in drought-tolerant ecotypes was simultaneous with increase in OA and osmolytes in leaves of tolerant ecotypes. This experiment indicated that osmotic adjustment is one of the major concerns of tolerance. Therefore, it might be possible to use OA and RWC for selection of drought-tolerant medics or gene transfer them in alfalfa as a crop.

IDT3-010 | Evaluation of root system in aerobic rice (*Oryza sativa* L.) hybrids & CMS lines

Kamalnath Reddy KR.[1,2,*], Anantha, MS.[1,2], Devendra Payasi[1,3], Mohan Kumar Varma[1,4], Shashidhar HE.[1,5], Vinay Shenoy[1,6]

[1]Barwale Foundation, Himayat Nagar, Hyderabad, Andhra Pradesh, India
[2] ICAR-Indian Institute of Rice Research, Rajendra Nagar, Hyderabad, Telangana State, India
[3]JNKV, Regional Agricultural Research Station, Sagar, Madhya Pradesh, India
[4]Bayer Crop Science, Singapore
[5]Department of Biotechnology, University of Agricultural Sciences, GKVK, Bangalore, India
[6]Kaveri Seed Company Ltd, Hyderabad, Telangana State, India
*E-mail: kamalnath.reddy@gmail.com

Rice is a major staple food and the main source of nutrition for more than half of the world's population. One hundred and five hybrids were developed by crossing five CMS lines with 21 testers. Combining ability and heterosis were assessed for root morphology and grain yield under aerobic and wetland conditions. High magnitude of SCA variance revealed the predominance of non-additive gene action under different moisture regimes for shoot and root traits. The GCA effect of parents under aerobic condition revealed that the line IR58025B and testers KMR3, AR53, 35-08, DR15, 37-09 and DR14, were good general combiners with good *per se* performance; whereas in wetland condition, the lines IR58025B, IR79156B and the testers KMR3, AR53, 35-08, 37-09, DR15 and DR14 had good GCA and high mean performance for grain yield. In both conditions, similar parents resumed to have good GCA effect which could be utilized to improve heterosis under aerobic condition. The line IR58025B and testers KMR3, DR14, MG63, AR53, 37-09 and 35-08 had good general combining ability for maximum root length and other root-related traits which impart drought tolerance in rice. SSR markers associated with root morphological traits were validated. Single-marker analysis for fertility restoration gene revealed that RM6100, RM171 and RM258 could be used for identifying the restorers. The genotypic data with 51 SSR markers associated with root-related traits were utilized for generating dendrogram between 20 sets of CMS and maintainer lines. The results depicted three major clusters based on molecular diversity.

IDT3-011 | Diurnal variation in accumulation of different metabolites in drought-stressed peanut

Mahatma MK*, Dey R, Rathnakumar AL, Sherathia DN, Bhadania RA, Patel MB, Mehta DH, Thawait LK, Lalwani HB, Pal KK

ICAR-Directorate of Groundnut Research, Junagadh 362001, Gujarat, India
*Email: maheshmahatma@gmail.com

Attempts through conventional and biotechnological interventions for developing drought tolerant cultivars has so far yielded limited success necessitating the need for alternate strategies for developing such cultivars. Accumulation and overproduction of proline, glycine-betaines, sugar alcohols, etc. has been reported with increase in drought stress. To understand the diurnal variations in accumulation of metabolites in drought-stressed peanut, we analyzed the leaf samples of 70 days old TG37A (stressed and irrigated) and four of its drought tolerant selections (S13, S17, S19, and S31) by GC-QTOF, at 12h interval (15:00h and 03:00h), by raising the crop without supplementary irrigation after sowing, during summer months of 2015. A distinct metabolic pattern has been observed during day and night-time. Myrisitic acid, arachidonic acids, and glycyl-L-valine were observed only during day-time. While, dodecanoic acid, petanoic acid, oxalic acid, and amino acids-valine and proline were observed during night-time. During day time (15:00h), there was over-accumulation of D-ribino-1,4-lactone; 9-hexadecanoic acid; and arachidonic acid in drought stressed TG37A. In contrary, during night (03:00h), there was over-accumulation of N-formyl glycine, homoserine, D-penitol, malic acid and salicylic acid in TG37A in drought stress. The selections from TG37A (S13, S17, S19, and S31) behaved differently as compared to TG37A in drought stress and produced different metabolites and S13 seemed to be an outlier among all in drought stress. Further studies would unravel the roles of these metabolites in imparting drought tolerance in peanut.

IDT3-012 | Impact of three lateral root types identified in pearl millet on water uptake

Passot S.[1]*, Meunier F.[1], Muller B.[2], Javaux M.[1], Draye X.[1], Guédon Y.[3], Laplaze L.[4,5]

[1]Earth and Life Institute - Agronomy, UCL, Louvain-la-Neuve, Belgium
[2]LEPSE, INRA, Montpellier, France
[3]AGAP, Cirad, Montpellier, France
[4]DIADE, IRD, Montpellier, France
[5]LMI LAPSE, IRD, Dakar, Senegal
*E-mail: sixtine.passot@uclouvain.be

Pearl millet plays an important role for food security in arid regions. Improving its root system toward increased water uptake efficiency could improve pearl millet tolerance to drought and lead to a significant production rise under water-limiting conditions. The objective of this work was to provide an integrated description of root system development at early stages and to assess the consequences of these findings for water uptake. A precise description of pearl millet root system development evidenced large variability among lateral root growth profiles. To further analyze this diversity, the growth rates of many lateral roots were measured daily and a statistical model was designed to classify these roots on the basis of their growth profiles. Three categories of lateral roots were identified in this way: (i) roots with high growth rate that could keep on growing after the end of the experiment, (ii) roots with intermediate growth rates and (iii) roots with low growth rates that quickly stop growing. The different lateral root types were randomly distributed along the primary root and there was no influence of root types on the intervals between successive lateral roots. The proportions of these different types were variable between plants of the same genotype, suggesting that small environmental variations could control these proportions. Water movements between soil and roots is modeled with R-SWMS to assess (i) the benefits of the three-type structuring, (ii) the relative contribution of each type to water uptake and (iii) the impact of specific proportions on global water uptake.

IDT3-013 | Temperature induction response (TIR): A novel physiological approach for thermotolerant genotypes in chickpea (*Cicer arietinum* L.)

Raghavendra T*[1], Jayalakshmi V[1], Gopal Reddy B[1]

[1]Regional Agricultural Research Station, Nandyal-518501
Acharya NG Ranga Agricultural University, Andhra Pradesh, India.
*E-mail: Raghavendraagrico@gmail.com

Chickpea (*Cicer arietinum* L.) is an important food legume cultivated in arid and semi-arid regions of the world. Drought coupled with moisture stress and high temperature may impose several adverse affects on its growth and development. It is known that chickpea thrives well under drought-prone conditions. However, heat stress during reproductive development can cause significant yield loss and there is a greater variability for yield performance of chickpea genotypes under heat stress. It is extremely important to develop screening tools for identification of thermotolerant chickpea genotypes in view of the increase in average global temperatures. In this context, a lab experiment was conducted during *kharif* 2015-16 at RARS Nandyal to standardize the temperature induction response (TIR) protocol for chickpea seedlings using WGC-450 Programmable Plant Growth Chamber. Temperatures were standardized as sub lethal i.e. challenging temperatures as 38-500C (for 4 hours and 30 min) and lethal temperatures as 500C (for 2 hours). This technique can be used as a potential tool to identify and select temperature tolerant lines at the seedling stage from a large population. A set of diverse chickpea germplasm comprising of 57 genotypes were screened for intrinsic tolerance using the standardized Thermo Induced Response (TIR) protocol. Among the genotypes NBeG-528,NBeG-458,NBeG-511,NBeG-177,NBeG-747,NBeG-732 and VIHAR showed highest thermo tolerance in terms of higher seedling survival with no reduction in root and shoot growth. The genotypes with intrinsic heat tolerance can be explored for the development of varieties suitable for late sown conditions in Andhra Pradesh where chickpea is prone to terminal heat stress.

IDT3-014 | Identification and evaluation of selected tomato (*Lycopersicum esculentum* L.) rootstocks donors under drought stress conditions

Rashmi K[1]*, Shashibhushan N B[1], Abhilash K[2], Chandrashekara Reddy P[1], T G Prasad[1]

[1]University of Agricultural sciences (UAS), GKVK, Bengaluru-560065, Karnataka, India
[2]University of Horticultural sciences (UHS), Bagalkot- 587101, Karnataka, India
*E-mail: rashmipalb1190@gmail.com

Under arid environmental conditions, the quantity of irrigation water available is considered one of the most imperative limiting factors for plant production. Plants have evolved several adaptive mechanisms for coping with limited water availability. One way to reduce losses in production and productivity of vegetable crops from drought stress would be to graft them onto rootstocks capable of mining and supplying water to the shoot. Hence, grafting is regarded as a promising tool to reduce yield loss caused by drought stress. From this context, hundred tomato accessions were evaluated in specially constructed root structures under normal conditions to study the genetic variability for root architecture *viz*. root length (cm), root volume (cm3), root dry weight (g). As a measure of intrinsic cellular Level Tolerance (CLT), the ability of root cell survival under simulated stress condition was studied using PEG-6000 as an osmoticum. Cell survival was determined by Triphenyl Tetrazolium Chloride (TTC) test. Colour gives an indication of metabolic activity in terms of respiration. These studies indicated a wide and significant variation among the accessions for all the root traits and intrinsic CLT. Significant positive relationship was observed between root dry weight and leaf area, root dry weight and total biomass. Based on root dry weight, total biomass and intrinsic tolerance, six contrasting lines of tomato were identified and further evaluated under different levels of moisture stress (100%, 80% and 60%FC) and finally root stock donors were identified for grafting approach.

IDT3-015 | Computational mining of miRNAs and their targets involved in root development in banana

Megha. H.Sampangi-Ramaiah[1], A. Rekha[2], Laxman. R. Hunashikatti[3], Kundapura .V. Ravishankar[1]*

[1]Division of Biotechnology, ICAR - Indian Institute of Horticultural Research, Bengaluru-560089, Karnataka, India
[2]Division of Fruit Crops, ICAR - Indian Institute of Horticultural Research, -560089, Karnataka, India
[3]Division of Plant Physiology and Biochemistry, ICAR- Indian Institute of Horticultural Research, Bengaluru - 560089, Karnataka, India
*E-mail: kv_ravishankar@yahoo.com

Banana (Musa spp.) is the fourth most important crop in the world. Banana has a high leaf area index, and shallow root system, thus making it sensitive to water stress. The cultivated edible banana and plantains are derived from the progenitor species *Musa acuminata* and *Musa balbisiana*. *Musa balbisiana* (B genome) harbor many abiotic and biotic stress tolerant traits. Our initial root characteristic studies on *Musa balbisiana* and *Musa acuminata* revealed that *M.balbisiana* had a higher number of roots/plant, total root length/plant (cm), and average root diameter (cm) with 108.70, 500.67 and 2.16 respectively compared to that of *M.acuminata* which was 54.50, 250.8 and 1.84 respectively. Here in the present study, we utilize the transcriptome data generated from pooled 12 tissues of *Musa acuminata* from our previous study for the computational prediction of miRNAs and its targets involved in root development, using C-mii software. Finally, those miRNAs whose targets were involved in the root development were shortlisted. Initially we predicted six miRNAs whose targets were involved in the root development, further we shortlisted three miRNAs based on the stability of the secondary structure and number of mismatches. In the present study we report: MamiR2919, MamiR5075 and MamiR2091 with MFE values of -44.1Kcal/mol, -69.8Kcal/mol and -115.8 Kcal/mol and 2bps mismatch with that of a target which is *MGB-ARATH* , whose GO annotation revealed its probable role in root development. Further expression analysis of these targets and their miRNA will give us more insight into the phenomena of root development.

IDT3-016 | Genetic analysis of F2 generation of four derived crosses for yield and water use efficiency related traits in groundnut (*Arachis hypogaea* L.)

Sowmya HC[1]*, Savithramma DL[2], Latha HC[3]

[1] University of Agricultural Sciences, Raichur, Karnataka, India
[2] University of Agricultural Sciences, GKVK, Bengaluru, Karnataka, India
[3] University of Agricultural Sciences, Dharwad, Karnataka, India
* E-mail: hc.sowmya@gmail.com

The objective of this study is to develop high water use efficient genotypes of groundnut, which thrive well under water-limited conditions. The F2 generation of four crosses, GKVK16×KCG2, GKVK13×KCG2, GKVK6×KCG2 and GKVK16×ICGV91114, were analysed for genetic variability and correlation studies. Yield component traits and SLA exhibited high GCV and PCV whereas SCMR exhibited low GCV and PCV in all the four crosses, indicating the presence of genetic variation for yield traits and SLA. High heritability accompanied with high GAM was recorded for plant height, SLA, pods/plant, pod yield/plant, kernel yield/plant, shelling percent and SMK. This indicates that characters are under additive gene action and selection would be effective in later segregating generations for improvement of these traits. Pods/plant and kernel yield/plant had high positive correlation with pod yield/plant in all the four crosses and also exhibited high positive direct effect on pod yield/plant. High positive correlation with high direct effect indicated true relationship of these characters, and importance should be given to these traits during selection for higher yield. Positive association was found between SCMR and pod yield/plant whereas negative association was found between SLA and pod yield/plant; SLA and SCMR in all the crosses. In segregating generations of all the crosses, adoption of indirect selection based on yield components and WUE related traits, particularly kernel yield/plant, pods/plant, SLA and SCMR rather than direct selection for pod yield/plant will be highly rewarding for developing high-yielding and water-use-efficient groundnut genotypes which are suitable for drought conditions.

IDT3-017 | Fine mapping of the linkage group 2 drought tolerance QTL in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

Srivastava RK[1]*, Vadez V[1], Kholova J[1], Lachagari VBR[2], Mahendrakar MD[1], Katiyar P[1], Lekkala SP[2], Praveen M[1], Gupta R[1], Blumwald E[3]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]SciGenom Labs Pvt Ltd, Kochi, India
[3]University of California Davis, Davis, California, United States of America
*E-mail: r.k.srivastava@cgiar.org

Pearl millet is an important cereal crop capable of growing in semi-arid, arid and marginal regions of the world. Drought is a major abiotic constraint affecting pearl millet production globally. Previously identified and validated major linkage group 2 (LG2) drought tolerance (DT) QTL contributing to hybrid grain and stover yield potential to terminal drought stress is being fine mapped. The fine mapping population was generated by crossing two near-isogenic lines (NILs) differing for the LG2 DT QTL. A modified double digest restriction site associated DNA (ddRAD) technique using *Sph*I and *Mlu*CI enzyme combination was employed. A total of 290 out of 6,067 F2 mapping population of the cross (H77/833-2-P10 × ICMR 01029-P10), and parents were genotyped on Illumina HiSeq2500. Out of 52,028 SNPs that were identified from a total of 888.85 million reads at a read depth of 10 in the mapping population, a total of 6,821 SNPs were used for mapping. The genotypic data of these SNPs were used in combination with that of seven SSRs that had known linkage relationship with LG2 DT QTL interval. Linkage map was constructed using QTL IciMapping 4.1 software at a LOD threshold of 3.0. A total of 189 SNPs anchored to seven SSRs were mapped to the LG2 DT QTL. The length of linkage group (LG) was 639.72 cM (Haldane units) with an average inter-marker distance of 6.73 cM. In order to refine the fine mapping process, ddRAD technique is being further employed for genotyping rest of the fine mapping population.

IDT3-018 | Root distribution of drought resistant peanut genotypes in response to early season drought stress

Thangthong, N.[1], Jogloy, S.[1]*, Jongrungklang, N.[1], Vorasoot, N.[1]

[1]Faculty of Agriculture, Khon Kaen University, Khon Kaen 40002, Thailand
*E-mail: sanun@kku.ac.th

Drought limits peanut yield in the semi-arid tropics. Root traits are important as a selection criterion for improving the ability of crops to maximize water uptake. Peanut varieties with different drought resistance levels might be related to the difference in root responses and yield maintenance under drought. The objective of this study was to investigate the effect of early season drought on root distribution patterns of drought resistances peanut genotypes. A 2×3 factorial experiment was carried out and the treatment combinations were assigned in a completely randomized design with three replications for two years in a rainout shelter. Factor A consisted of two water regimes (well-watered and drought treatments),and factor B comprised of three peanut genotypes (ICGV 98305, ICGV 98324 and Tifton-8).The plants were grown in rhizoboxes with pin-board method. The data were recorded for root distribution pattern with a black sheet and scale bar to study whole root systems and root length was divided into 11 layers with 10 cm intervals. After water withholding, ICGV 98305 had significantly higher root length in deep soil layers under drought stress than under well-irrigated treatment. ICGV 98324 had a large reductions in root length in both upper and lower soil layers. Tifton-8 grown under drought had smaller root systems than under well-watered control for all root length in most soil layers, showing negative response to drought. The results suggested that ICGV 98305 had a high magnitude of root traits in deeper soil layer under early season drought might provide drought avoidance mechanism.

IDT3-019 | Root system architecture phenotyping of durum wheat reveals differential selection for a major QTL in contrasting environments

Giuseppe Sciara[1,]*, Kerstin A. Nagel[2], Marco Maccaferri[1], Jonas Lentz[2], Tania Gioia[2], Fabio Fiorani[2], Silvio Salvi[1], Roberto Tuberosa[1]

[1]Department of Agricultural Sciences (DiPSA) – University of Bologna, Bologna, Italy
[2]Institut für Bio- und Geowissenschaften Pflanzenwissenschaften (IBG-2) –Jülich Forschungszentrum, Jülich, Germany
*E-mail: roberto.tuberosa@unibo.it

This study reports the characterization of 183 elite durum wheat (*Triticum turgidum* ssp. *durum* Desf.) for RSA and shoot developmental traits. Plants were grown in controlled conditions up to the 7th leaf appearance (late tillering) using the phenotyping platform GROWSCREEN-Rhizo at the Institut für Bio und Geowissenschaften Pflanzenwissenschaften. The following RSA traits were measured: seminal root length, nodal root length, lateral root length, root system convex hull, root system width and depth distribution (twice per week). Measurements of leaf area, leaves number and tiller number were performed twice per week and SPAD measurements were collected twice along the experiment. Root dry biomass and shoot fresh and dry biomass were collected at the end of the experiment. A genome-wide association study (GWAS) based upon the Illumina Infinium 90K SNP assay identified many QTLs for RSA and/or shoot growth traits ($p\text{-value} < 0.0001$). GWAS confirmed a highly significant effect on adult plant root system width due to two major QTLs on chromosomes 6AL and 7Ac previously identified on seminal roots at the seedling stage (Maccaferri et al. 2016). Notably, haplotype frequency at one of the main QTL cluster on chromosome 7Ac found to be significantly associated with root depth, root system width, root specific weight and shoot/root ratio revealed a strong, contrasting selection pattern between the rainfed and the irrigated breeding programs conducted at ICARDA and CIMMYT, respectively, suggesting an indirect but major role of RSA in durum wheat breeding.

IDT3-020 | Vegetative growth and water use characterization of a maize introgression library

Sciara G.[1]*, Salvi S.[1], Canè M. A.[1], Welcker C.[2], Cabrera L.[1], Grau A[2], Bovina R.[1], Tardieu F.[2] & Tuberosa R.[1]

[1]University of Bologna, Bologna, 40127, Italy
[2]INRA, Montpellier, 34060, France
*E-mail: roberto.tuberosa@unibo.it

Previous work showed that a maize introgression library (IL) derived from the cross between Gaspé Flint (an early flowering Canadian landrace) and B73 (the reference maize line) segregated for phenology as well for seminal root architecture (SRA) traits. In this experiment, the IL was evaluated in the high-throughput phenotyping platform PhenoArch (INRA, Montpellier), a platform for large-scale automated imagery and evapotranspiration measurements of potted plants in controlled environment. Biomass accumulation for each plant was estimated by software-and model-assisted imaging analysis. Each pot was weighed daily allowing for the accurate estimation of evapo-transpiration. The maize IL lines were tested under well-watered (WW) and water-deficit (WD) conditions (soil water potential > -0.05 and ~ -0.4 MPa, respectively). The following traits were investigated: biomass accumulation, daily water use, water use efficiency, specific transpiration, early vigor and phyllochron. Significant genetic effects were detected for all traits ($P < 0.05$, Dunnet test) in WW and WD. Stepwise QTL analysis enabled us to identify the chromosomal regions underlying the phenotypic segregation for all the measured traits on chr. 1, 2, 3, 4, 7, 8 and 9 in both well-watered and water-deficit conditions. A number of QTLs for phenology and RSA traits affected vegetative growth and WUE. The data collected using the platform PhenoArch will contribute to the comprehensive multi-trait phenotypic characterization of the IL. The most interesting IL lines and corresponding QTLs are considered for fine mapping and QTL cloning

IDT3-021 | The whole-plant response to soil water availability as a mean for drought-resistance phenotyping

Wallach R,* MoshelionM

The R.H. Smith Faculty of Agriculture, Food and Environment, Hebrew University of Jerusalem, Rehovot, 761000 Israel
*E-mail: rony.wallach@mail.huji.ac.il

Soil water deficit is a major environmental stress that majorly affects plants development and functioning. Despite the enormous efforts that have been invested, the fast and accurate phenotyping to abiotic stress remains a bottleneck in efforts to enhance yields in water-limited environments. The rates of soil water withdrawal and plant transpiration are related in a non-linear manner as enhanced soil water extraction at higher transpiration rates decreases soil water availability (SWA) that decreases the transpiration rate. Since SWA availability depends in a dynamic manner on soil water energetic status, VPD, and transpiration rate, the rate of convergence of this loop, enables one to phenotype plant drought resistance. A novel high throughput experimental platform for simultaneous and continuous non-invasive monitoring of water relations in the soil-plant-atmosphere continuum of numerous plants has been used to measure the response profile for each plant in the array to gradually varying SWA. Three probes for each pot in the array and a specially designed algorithm enable detailed water-relations characterization of whole-plant transpiration, biomass gain, stomatal conductance and root flux. They also enable a quantitative determinationof plant water-use efficiency and relative water content at high resolution under varying soil and atmospheric conditions. Results for that were grown in a semi-commercial greenhouse during winter and summer months will be presented.The individual response of 65 introgression lines of a wild tomato species (*Solanum pennellii*) crossed with cultivated tomato (*S. lycopersicum*)to SWA gradual decrease was investigated. The investigation output will be presented and discussed.

IDT3-022 | Approaches to relating rice root plasticity with yield stability across different drought stress and establishment conditions

Xiaobing Xie[1], Nitika Sandhu[1], Sushil Subedi[1], Arvind Kumar[1], Amelia Henry[1] *

[1]International Rice Research Institute, Los Baños, Laguna, Philippines
*E-mail: a.henry@irri.org

Rice plants may face many different types of drought stress resulting from low rainfall or reduced availability of irrigation at some growing stages, especially at the reproductive stage, and rice root plasticity may play a vital role in yield stability across drought stress conditions. In this study, we aimed to evaluate root plasticity in rice across different types of drought stress and establishment conditions. Fifteen to 18 genotypes were established under direct seeding and transplanting methods within drought stress and well-watered treatments in a total of eight field experiments to understand the rice plants' response to these conditions. Several methods for calculating plasticity will be explored and compared with grain yield stability across the different drought stress and establishment conditions.

IDT3-023 | Identification of drought tolerant pigeonpea [*Cajanus cajan* (L.) *Millsp.*] genotypes and their stability analysis

Yamanura[1] *, Muniswamy S[2], Ramesh[2]

[1]AICRP on MULLaRP UAS, Dharwad-58005, Karnataka, India
[2] Agricultural Research Station, Aland Road, Kalaburagi-585101, Karnataka, India
*E-mail: yamanura@uasd.in

Pigeonpea is an important grain legume crop of rainfed agriculture in the semi-arid tropics. It is cultivated in varied agro climatic conditions ranging from moisture stress and input-starved conditions to irrigated conditions. An experiment was carried out to identify drought tolerance and stability among twenty genotypes of pigeonpea, including check WRP-1 during *kharif*-2012, 2013 and 2014 under rainfed conditions at the Agricultural Research Station, Kalaburagi located in north eastern dry zone (zone II) of Karnataka. Highly significant differences among genotypes were observed for all the characters except primary branches. Environmental and Genotype x Environment interaction was significant for days to maturity, primary branch, pod bearing length, and seed yield per plant. All the traits under the study except for plant height and 100 seed weight showed significant differences in different environments. The variance due to pooled deviation was highly significant for all the characters except for primary branches, pod length and number of seeds per pod which reflect the presence of sufficient genetic variability in the material. Out of 20 genotypes studied, RVK-275 and AKT-9913 were found to be a stable for seed yield and test weight, across the environments with good stability under rain fed conditions compared to local check.

IDT3-024 | Water use efficiency of Turkish maize landraces for drought tolerance in field conditions

Mehmet Yıldırım[1]*, Onder Albayrak[1], Cuma Akıncı[1], Ferhat Kızılgeçi[2], Fatma Basdemir[1]

[1]Dicle University, Agricultural Faculty, Field Crops Department, Diyarbakır 21280 TURKEY
[2]Sirnak University, Agricultural Faculty, Field Crops Department, Sırnak TURKEY
*E-mail: mehmety@dicle.edu.tr

This paper examines maize landraces which have high water use efficiency (WUE). Twenty five Turkish maize landraces that were selected from 250 landrace populations according to different agronomic traits were used to determine the WUE differences under full and deficit irrigation managements, by using pan evaporation method, at the Dicle Universitiy research station in Turkey. Full irrigation treatment was managed for high productivity at 1.50 Epan (I-150), whereas deficit irrigation treatment at 0.50 Epan (I-50) represented extreme drought conditions. Plants were irrigated equally from sowing to fifth leaf stage; and then water stress was applied until physiological maturity by using drip irrigation systems. Seasonal evapotranspiration reached 669 mm on the lysimeter and total irrigation was 555.9mm and 273.0 mm for I-150 and I-50 treatment, respectively. WUE was 1.46 kg m^{-3} in the I-50 treatment and 1.03 kg m^{-3} in the I-125. Grain yield decreased by more than %60 in the I-50 treatment.

Grain yield among landrace genotypes varied between 225 kg ha^{-1} and 9864 kg ha^{-1} at water stress conditions. Grain yield rank of genotypes was different at both irrigation treatments. The results show that some landraces can be used as pre-breeding material to obtain high WUE genotypes in maize hybrid breeding.

Poster Theme IV

Plant Productivity under Drought II: Transpiration Efficiency

IDT4-001 | Physiological mechanisms controlling plant water use in maize

Alvarez Prado S.[1]*, Cabrera-Bosquet L[1]., Coupel-Ledru A.[1], Grau A.[1], Welcker C.[1], Tardieu F.[1]

[1] INRA, UMR 759, LEPSE, Montpellier 34060, France
*E-mail: santiago.alvarez-prado@supagro.inra.fr

Plants tend to decrease transpiration under water deficit and/or high evaporative demand by closing stomata and reducing leaf growth. Identification of sources of genetic variability for underlying mechanisms is necessary to design genotypes adapted to stressing climatic scenarios. A series of four experiments was performed in the PhenoArch image-based phenotyping platform (M3P, France) with contrasting soil water status and evaporative demand. We used a diversity panel of 255 maize hybrids genotyped with 832K polymorphic SNPs. Equivalent stomatal conductance at plant level was estimated in the studied 1680 x 4 plants by inversion of the Penman Monteith equation. It changed with light intensity and vapor pressure deficit, with different thresholds and slopes between genotypes. Maximum values ranged from 52 to 76 mmol m^{-2} sec^{-1} depending on hybrids. The sensitivity of leaf expansion to soil water potential was calculated over the four experiments as the slope of the relationship of leaf expansion rate to soil water potential. For each hybrid, a common linear relationship applied to the four experiments. The x-intercepts of these relationships, which indicate the driest soil in which a plant still has an appreciable leaf growth, ranged from -0.6 to -1.6 MPa depending on hybrids. A GWAS analysis was performed on all variables presented above, suggesting interesting candidate genes related to hydraulics and other mechanisms. Surprisingly, no co-location was observed between QTLs of stomatal conductance and of sensitivity to soil water deficit, supporting the idea that the controls of stomatal opening/photosynthesis and of leaf expansion are largely independent.

IDT4-002 | Transpiration rate of chickpea wild accessions and cultivars in Turkey

Basdemir F[1]*, Yıldırım M[1], Biçer BT[1], Vadez V[2], Bükün B[1], Cook DR[3]

[1]Dicle University, Faculty of Agriculture, Diyarbakır, 21280,Turkey
[2]ICRISAT, Patencheru, 502324, India,
[3]University of California, Davis, USA.
*E-mail: ftmbsdmr87@hotmail.com

Chickpea (*Cicer arietinum L.*), like most cultivated crops, has exceedingly narrow genetic and phenotypic diversity. Thus breeding with only cultivated germplasm will have steeply diminishing returns, raising an urgent need for new sources of diversity. The focus of the research was to assess a representative set of newly collected wild accessions of *C. reticulatum* and *C. echinospermum*, for drought adaptation traits, i.e. transpiration rate (TR) response to increasing VPD and to soil drying.

These experiments were conducted during the spring season (18 March to 21 April 2016) at the Dicle University glasshouse. The experimental design was a complete randomised block design with six replications. Measurements were conducted in late April during vegetative growth and VPD changed from 2.13 to 4.35 kPa. To measure TR, potted plants were weighed at regular time intervals over the course of an entire day, and therefore, under increasing VPD. At the end of the experiment total leaf area was destructively measured, along with shoot, root and leaf dry weights. There was a 2.31-fold range of variation in the transpiration response among genotypes. The wild genotypes *Sirnak* and *Deste* had extreme TR values exceeding cultivated check cultivars, and several wild genotypes had only a moderate increase in TR under increasing VPD. These moderate TR responses provide germplasm sources with a potential to limit water losses under high evaporative demand, akin to a protection mechanism, especially under dry environments or in future climates. These screenings, therefore, open an exciting opportunity for breeding cultivars with enhanced performance under harsh climates.

IDT4-003 | Drivers of water use efficiency of cowpea under contrasting environment and water deficit conditions.

Nkomazana C, Mpuisang T, Moroke TS, Malambane G, Bagwasi G , Mashungwa G, Pule-Meulenberg F, Ngwako S, Batlang U*

Botswana University of Agriculture and Natural Resources, Gaborone, Botswana
*E-mail: batlangmodikwa@gmail.com; ubatlang@bca.bw

Climate change forecast predicts increased occurrence and severity of droughts for Sub-Saharan Africa, a situation that will increase the risk of crop failure resulting in food insecurity. Within this constraint, there is a need to document crops which can efficiently use available soil water. Variations in evapotranspiration (ET), water use efficiency (WUE), and grain yield (GY) of six cowpea in response to Kalahari (Hukuntsi) and Eastern Harveld (Sebele and Lecheng) environment and to water deficit conditions were investigated. Analysis of variance was conducted to determine genotypic differences and interactions with environment. The results showed that there were significant genotype x environment interactions. Significant genotypic differences were observed for aboveground biomass (ABM), evapotranspiration (ET), leaf area index (LAI), specific lead area (SLA), WUE and GY. The six genotypes were further evaluated for WUE under water deficit condition. Water deficit reduced ABM, ET and GY but increased WUE. Based on GY, genotypes BCA 001 and BCA 019 exhibited high WUE than the other four genotypes. Under water deficit conditions, linear regression conducted between WUE and other responses showed that the main drivers for high WUE were drought tolerance, ET, leaf area, maintenance of high relative water content (RWC), and high GY. Selection for high yielding cowpea for water limited environment could be based on lower water use and maintenance high water status and yield. Further, association of WUE with soil water and plant responses can improve our understanding of the linkages between water use and productivity, and the path to its improvement.

IDT4-004 | *Ab initio* candidate genes mining and transcript abundance carrying water use efficiency quantitative trait loci in sorghum (*sorghum bicolor* L.)

Chaudhari GN[1,2]*, Fakrudin B[1,2]

[1]College of Horticulture, (UHS) GKVK Post, Bengaluru - 560 065, Karnataka, India
[2] Institute of Agricultural Biotechnology, UAS, Dharwad – 580005, Karnataka, India
*E-mail: chaudharigaurav11@gmail.com

In sorghum [*Sorghum bicolor* (L.) Moench], 'water use efficiency' QTL have been employed to improve the post flowering drought tolerance and expressional analysis of such genes in NILs. Water use efficiency (*wue*) is an important target trait considered for improving drought tolerance in sorghum. Using *ab initio* algorithms *viz*., FGENESH, GENSCAN and GENMARK and there combinations, *qCID* QTL encompasses 2.33 mbp region predicting eight genes on chromosome No 10. Structural features and protein annotation for candidate genes were analysed based on nucleotide homology using different alignment algorithm and NCBI database. Expression profiling indicated upheavals of predicted genes at 30 and 45 DAF in leaf tissues of *qCID* QTL introgressed line when compared with control, M35-1 genotype. Results indicated the potential of QTL pyramiding for improving plant performance under adverse environmental conditions such as drought and also provided new insight for breeding programs in sorghum.

IDT4-005 | Historical improvement in drought adaptation of Australian wheat has coincided with changes in transpiration efficiency and other traits

Karine Chenu[1], Andrew Fletcher[1], Jack T. Christopher[2]

[1] The University of Queensland, Queensland Alliance for Agriculture and Food Innovation (QAAFI), 203 Tor street, Toowoomba, QLD 4350, Australia
[2] The University of Queensland, QAAFI, Leslie Research Facility, PO Box 2282, Toowoomba, QLD 4350, Australia
*E-mail: karine.chenu@uq.edu.au

Wheat productivity is commonly limited by a lack of water in rain-fed farming systems worldwide, particularly in Australia. Although wheat breeders have historically bred for increased yield, grain quality and disease resistance, indirect selection for other traits would also be anticipated. A set of elite wheat varieties with wide adoption and a relatively narrow phenological range was chosen to study breeding progress achieved in Australia between 1973 and 2012.

Experiments in field and glasshouse trials revealed changes in transpiration efficiency, biomass partitioning and leaf senescence rate in varieties released over recent decades. While plant biomass did not change significantly over time, differences in partitioning were observed. Modern cultivars tended to have a greater proportion of biomass allocated to the heads and stems, but reduced allocation to the leaves. Interestingly, a significant increase over the years was observed for whole-plant transpiration efficiency. While changes in biomass partitioning are approaching biological limits, the results of this study highlight potential for possible improvement in transpiration efficiency and stay-green.

Combining rapid phenotyping methods with speed breeding technologies could assist breeders to prepare for the future with the development of lines with better transpiration efficiency and/or stay-green.

IDT4-007 | Transpiration efficiency of rice (*Oryza sativa* L.) under drought: A physiological determinant for tolerance

Goutam Kumar Dash[1]*, Akhil Kumar Debata[1], Mirza Jaynul Baig[1], Padmini Swain[1]

[1]ICAR-National Rice Research Institute, Cuttack, Odisha, India.
*E-mail: gkdash.bot@gmail.com

In rice (*Oryza sativa* L.), the ability of the crop to produce high biomass and yield per unit of available water affect profitability and yield, in both well-watered (WW) and water-stressed (WS) conditions. The main goal of this study is to elucidate the mechanism underlying transpiration efficiency and the traits associated with it. Two genotypes, namely CR 143-2-2 (tolerant) and IR-64 (susceptible), having contrasting response towards drought were evaluated for their transpiration efficiency (TE) under WW and WS conditions by gravimetric method. Results revealed that TE was higher under stress than well-watered condition. CR 143-2-2 (3.86g biomass/kg water transpired) had much higher transpiration efficiency than IR64 (2.60 g biomass/kg water transpired). Diurnal variation in transpiration rate revealed low transpiration rate in CR 143-2-2 (0.12 kg water/hr) at 13:00 hrs even under WW condition compared to IR 64 (0.15 kg water/hr) at VPD -6.15 kPa. Low transpiration rate in CR 143-2-2 might be due to low stomatal density/unit leaf area (277.5±5.3/mm^2) compared to IR 64 (517.7±10.7/ mm^2) and low xylem sap flow rate (0.20g sap/g shoot in CR 143-2-2 and 0.30 g sap/ g shoot in IR 64) that lead to low transpiration rate per unit leaf area and hence low canopy temperature. This study concludes that genotypes contrasting in terms of drought tolerance also differ in the control of leaf water loss under well-watered as well as under water stressed condition with low xylem sap bleeding rate in tolerant genotype than susceptible genotype.

IDT4-008 | Drought and salt stress in *Chrysopogon zizanioides* leads to common and specific transcriptomic responses and may affect essential oil composition and benzylisoquinoline alkaloids metabolism

George S[1]*, Manoharan D[1], Jie L[2], Britton M[2], Parida A[1]

[1]M.S. Swaminathan Research Foundation, Chennai, India 600113
[2]University of California, Davis, CA 95616, United States
*E-mail: suja_gauri@yahoo.com

Abiotic stresses affect crop productivity worldwide. Understanding molecular mechanisms of plant abiotic stress tolerance is important for developing stress-tolerant crop plants for sustaining crop productivity in future. *Chrysopogon zizanioides* (vetiver) is a perennial C4 grass reported to be tolerant to water, salinity and submergence stress. Here, we subjected *C. zizanioides* seedlings to salt and drought stress and carried out whole transcriptome profiling of leaf and root tissues. Assessing the global transcriptome changes under drought and salt stress resulted in the identification of several genes contributing to stress response in this species. Overall, more transcriptomic changes were observed in leaf tissue compared to root tissue. The response to either stress manifested primarily as upregulation of gene expression in both leaf and root. The study identified stress responsive genes commonly and differently regulated under stress/tissue conditions. Several DEGs in our data were identified as enzymes involved in biosynthesis of essential oil components. The differential expression of these genes under drought and salt stress may affect the vetiver essential oil composition under these stresses. Similarly, several genes involved in the biosynthesis of benzylisoquinoline alkaloids including morphin were found to be differentially expressing in our data. Our data will facilitate further molecular studies on stress tolerance of *C. zizanioides*. The DEGs from our results are potential candidates for understanding and engineering abiotic stress tolerance in plants.

IDT4-009 | Evaluation of eggplant (*Solanum melongena* L.) cultivars under moisture stress condition

Gobu R[1]*, Harish Babu B.N.[2], Lal J.P.[1], Omprakash[1], Kailash Chandra[1]

[1]Banaras Hindu University, Varanasi 221005, Uttar Pradesh, India
[2]College of Horticulture, UAHS, Shivamogga 577225, Karnataka, India
*E-mail: gobu.agri@gmail.com

Eggplant is one of the most important vegetable crops, which is highly heterogeneous in India with respect to its varieties. Although, it is anticipated to be a moisture stress tolerant crop, greater yield losses have been well documented. The present investigation was carried out to know the comparative yield performance of 62 eggplant cultivars under normal and moisture stressed conditions. The seedlings raised in pro-trays were transplanted to field after 30 days of sowing in three replications each for moisture stressed and non-stressed plots in a randomized block design. Each of the 62 genotypes was planted in two rows per replication. For non-stressed plots, irrigation was given as per package of practices (once in five to six days). For moisture stressed plots, water stress was imposed by withdrawing irrigations for 15 days at two critical stages *viz*., flowering and fruit setting stage. Yield per plant was recorded from five randomly tagged plants in each replication for each genotype in moisture stressed and non-stressed plots. The maximum yield reductions were observed in the cultivars *Aruna* (88.45%), R-2584 (84.26%), R-2582 (83.99%), *Arka Nidhi* (79.33%) and *Jawahar Brinjal*-18 (78.68%) indicating their high susceptibility to moisture stress condition. Minimum yield reductions were observed in the cultivars *Jawahar Brinjal*-8 (7.75%), IC49358 (12.33%), *Pusa Upkar* (15.01%), IC90151 (15.18%) and R-2581 (21.34%), indicating their better moisture stress tolerance, which can be suggested for cultivation in drought-prone areas.

IDT4-010 | Genetic analysis of the transpiration control in sunflower (*Helianthus annuus* L.) subjected to drought.

Afifuddin Latif Adiredjo[1], Philippe Grieu[2,*]

[1]Brawijaya University, Faculty of Agriculture, Department of Agronomy, Plant Breeding Laboratory, Malang, Indonesia
[2]Université de Toulouse, INP-ENSAT, UMR1248 AGIR (INPT-INRA), Castanet-Tolosan, France
*E-mail: grieu@ensat.fr

Stomatal control of transpiration was implied in the major strategies by which plants cope with water stress. Here we investigated the genetic control of this process using the following trait: Fraction of Transpirable Soil Water threshold (FTSWt) representing the threshold of soil water content at which the stomatal control of transpiration started. This study extends a progressive water deficit experiment using recombinant inbred lines (RILs) of sunflower and we found the variation of FTSWt. Quantitative trait loci (QTL) mapping was then performed to identify the genetic control. One QTL was identified for FTSWt and the phenotypic variance explained by the QTL (*R2*) reached 6%.

This work has shown, for the first time, quantitative genetic analysis and QTL mapping for FTSWt in crops. In this work QTL mapping was made in sunflower.

IDT4-011 | Assessing suitability of various screening methods as a proxy for drought tolerance in barley

Hasanuzzaman M[1, 2], Shabala L[1], Brodribb JT[1], Zhou M[1], Shabala S[1,*]

[1]University of Tasmania, Hobart, Tasmania, Tas- 7001, Australia
[2]Sher-e-Bangla Agricultural University, Sher-e-Bangla Nagar, Dhaka-1207, Bangladesh
*E-mail: Sergey.Shabala@utas.edu.au

Plant breeders are in the need for a convenient, reproducible, reliable and rapid screening method to be used as a proxy for drought tolerance for large number of genotypes. Addressing this need, here we compare different physiological measures of stress in six barley (*Hordeum vulgare* L.) genotypes subjected to different drought treatments under glasshouse conditions. Genotypes were evaluated by measuring transpiration rate, quantum yield of PSII (chlorophyll fluorescence Fv/Fm ratio), SPAD chlorophyll meter reading, dry biomass, and shoot water content. The accuracy of different methods in quantifying water stress tolerance was evaluated by measuring the rates of survivor and death in plants, and leaves, and newly grown leaves after rewatering. In another experiment, the same genotypes were evaluated to 18% (w/v) of polyethylene glycol (PEG 6000) induced osmotic stress applied to germinating seeds grown in paper rolls, using relative root and shoot lengths as a measure of tolerance. The results suggested that transpiration measurement at recovery stage could be the most sensitive method for separating contrasting genotypes. However, the method is time consuming and laborious for a large scale screening. Chlorophyll content, dry biomass, shoot water content and stomatal density did not correlate with plant drought tolerance. At the same time, chlorophyll fluorescence Fv/Fm ratio showed a strong correlation with drought tolerance and could be recommended as suitable proxy for screening. Measuring relative root growth rate (length) using PEG-treated paper roll-grown seedlings also seems to be a highly suitable and promising method for screening a large number of genotypes in breeding programs.

IDT4-012 | High throughput phenotyping for drought tolerance in rice at reproductive stage

Kumar S*, Raju D, Sahoo R N and Chinnusamy V

ICAR-Indian Agricultural Research Institute, New Delhi-110012
*E-mail: sudhirnpf@gmail.com

Drought stress in rice grown area in India adversely affects yield by around 45%. Rice crop experiences intermittent cycles of drought stress and recovery and/or terminal drought stress in these areas. Extensive efforts are being made to improve drought tolerance and WUE of rice. Large-scale phenotyping under field conditions often led to the identification and use of the drought avoidance genotypes which mature early or genotypes with dehydration avoidance by water mining. An experiment with 50 diverse rice genotypes was conducted, at the automated plant phenomics facility of ICAR-IARI, New Delhi, to identify genotypic variation for reproductive stage water-deficit stress tolerance. Pot-grown plants were subjected to drought stress by withholding irrigation at booting stage. The evapotranspiration was measured for both well-watered and drought set plants by using automated weighing and watering station. The drought set of plants were re-watered when the available soil moisture content decreased to about 40%, and again the plants were subjected to the second cycles of stress. Plants were imaged by using visual, IR, NIR and chlorophyll fluorescence imaging platforms at regular intervals. Temporal responses in several image-based features measured by using visual, IRand NIR imaging platforms showed considerable variations among rice genotypes. The potential association of these image-based features with the component mechanisms of drought tolerance viz., cellular dehydration avoidance and cellular dehydration tolerance can be effectively exploited for breeding drought tolerant varieties in rice.

IDT4-013 | Characterizing leaf gas exchange and carbon isotope discrimination responses of diverse faba bean genotypes during reproductive stage in irrigated and rainfed condition.

M A Muktadir[1,3,4]*, K N Adhikari[1,2], T Buckley[1] and A Merchant[3]

[1] Plant Breeding Institute, The University of Sydney, Narrabri, NSW 2390, Australia
[2] Plant Breeding Institute, The University of Sydney, Cobbitty, NSW 2570, Australia
[3] Centre for Carbon Water and Food, The University of Sydney, NSW 2570 Australia
[4]Pulses Research Centre, Bangladesh Agricultural Research Institute, Gazipur 1701, Bangladesh
*E-mail: md.muktadir@sydney.edu.au

High throughput, cost effective, non-invasive tools for the rapid and reliable evaluation of field based plant health is of critical importance to plant breeder across a range of natural systems. Carbon isotope discrimination (Δ13C) at the leaf level has been proposed as a method for evaluating water use efficiency (WUE) in C3 plants and as a precise technique for screening plants with higher tolerance under water deficit conditions. In this research, we investigate the suitability of Δ13C isolated from leaves as surrogate measures of plant gas exchange in six diverse faba bean *vicia faba* L genotypes under irrigated and rain-fed condition. We used chemical and physiological adaptations to water deficit in faba bean to identify changes in carbon (C) allocation that combined with post-photosynthetic fractionation of C isotopes, influences WUE prediction. We found measured Δ13C using Isotope-ratio mass spectrometry (IRMS) to predict intrinsic WUE is proportional to predicted values based upon modelled Δ13C from gas exchange data irrespective of genotypes and treatments. We also investigated variation in leaf osmotic potential compared to measures of carbon isotope composition. In rainfed condition Δ13C measured WUE is close by 71.5 to 89.6 % WUE modelled from gas exchange and in irrigated condition it was 67.7 to 100 %. Genotypes with high tolerance level showed greater accuracy 89.6% and 86.8 % in both treatments. The results suggest that Δ13C can be used as an effective and accurate selection criterion for improving WUE in faba bean breeding programmes.

IDT4-014 | Effect of vapour pressure deficit on sugarcane transpiration efficiency in a drying soil

Natarajan S[1,2*], Basnayake J[2],Jackson P[3], Lakshmanan P[4], Stokes C[3], Fukai S[1]

[1]University of Queensland, St Lucia, QLD 4072, Australia
[2]Sugar Research Australia Limited, PO Box 117, Ayr, QLD 4807, Australia
[3]CSIRO, Aitkenvale, QLD 4814, Australia
[4]Sugar Research Australia Limited, PO Box 86, Indooroopilly, QLD 4068, Australia
*E-mail: s.natarajan@uq.edu.au

Plants with higher transpiration efficiency (TE), which can accumulate more biomass per unit amount of transpired water, could be beneficial in future climates with erratic scenarios. In this study, the impact of VPD on whole-plant and leaf-level TE of sugarcane was investigated to determine if there is genotypic variation and to determine if the differences were maintained across wet and dry soil water conditions. Four sugarcane genotypes with contrasting TE were maintained in two controlled growth chambers under high and low VPD (2.75kPa and 1.3kPa) with two soil water treatments. Growth of plants was monitored weekly using PlantScan (a combination of LiDAR and visual imaging), dry weight and water use were recorded, and leaf gas exchange measurements was carried out on several occasions. Genotypes showed significant differences in growth, water use and gas exchange attributes, but there was no interaction effect due to VPD or soil water. Plants in high VPD conditions had significantly higher water use than plants in low VPD conditions. However, there were no significant differences in growth. As a result, TE was significantly higher for plants grown in low VPD conditions than for those in high VPD conditions irrespective of soil water condition (high VPD wet/dry, 4.64/4.02gL-1; low VPD wet/dry, 8.47/7.22gL-1). Because sugarcane plants increase transpiration and water use at high VPD conditions without any significant gain in photosynthesis and growth, gains in TE can be achieved if genotypes that restrict transpiration at high VPD can be identified.

IDT4-015 | Role of pearl millet aquaporin genes in abiotic stress response

Reddy PS[1]*, Divya K[1], Sivasakthi[1], Tharanya M[1], Lale A[1], Bhatnagar-Mathur P[1], Kholova J[1], Kiran K. Sharma[1], Vincent Vadez[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: p.sudhakarreddy@cgiar.org

Pearl millet, *Pennisetum glaucum*L.), a crop of semi-arid tropics, has remarkable tolerance to a wide range of abiotic stresses, including high degree of genetic diversity for drought stress tolerance. To investigate the molecular mechanisms that possibly account for differences in drought tolerance, four recombinant inbred lines from a high resolution cross (HRC) were selected for their variability in transpiration rate (Tr) response to vapour pressure deficit (VPD) conditions. The expression of PgAQPs in contrasting genotypes varied during the day, generally decreasing in the afternoon regardless of the VPD conditions. However, under high VPD conditions (4.21kPa), both root and leaf tissues of the VPD-insensitive genotypes had higher transcript abundance than the VPD-sensitive genotypes. Three PIP2 subfamily genes (*PIP2;1*, *PIP2;3* and *PIP2;6*) particularly *PIP2;6* gene, showed an increase in transcript abundance under high VPD conditions. Transgenic tobacco plants constitutively expressing *PgPIP2;6* gene were developed for functional validation studies in homozygous T2 transgenic tobacco plants. The transgenic plants showed better tolerance under drought stress, VPD and salinity compared to wild type plants as seen from biochemical, physiological and molecular studies. The transgenic plants also showed increased soluble sugar, membrane stability, reduced electrolyte leakage and other photosynthetic parameters as compared to the wild type (WT). Taken together, our studies suggest that, *PgPIP2;6*gene can be deployed to engineer stress tolerant transgenic crops for sustained growth and productivity under unfavourable conditions.

IDT4-016 | Photosynthetic efficiency is well coordinated with nitrogen assimilation in drought stressed pigeonpea grown under elevated CO_2

Sreeharsha R.V.[1], Reddy A.R.[1]*

[1]University of Hyderabad, Hyderabad, Telangana state, India – 500046.
*E-mail: arrsl@uohyd.ernet.in

Elevated CO_2 enhances photosynthesis in many crops during early stages of growth but long-term growth leads to photosynthetic acclimation due to nitrogen limitation. Legumes are believed to overcome photosynthetic acclimation by virtue of their N fixation. Elevated CO_2 also have a protective role against the oxidative damage caused by drought stress. To understand legume responses to interactive elevated CO_2 and drought in terms of C and N assimilation, pigeonpea (short duration cultivar - ICPL 15011) was grown under elevated CO_2 (550 ppm) and treated with progressive drought stress. When grown under elevated CO_2, pigeonpea showed significantly high net photosynthetic rates and foliar carbohydrate content which further manifested in dry biomass at harvest. Mass and number of nodules exhibited prodigious accretion under elevated CO_2 thereby overcoming the N limitation and resulting lack of photosynthetic acclimation. Under drought stress, elevated CO_2 grown plants showed less leaf relative water content compared to ambient grown plants, while showing significant correlation between nodule mass and photosynthesis. The high levels of N and amino acids in leaf and root tissues of plants grown under elevated CO_2 can be attributed to increased levels and activities of glutamine synthetase (GS) as evidenced by our western blotting and qPCR studies. To understand the transcriptional regulation of GS, the ORF sequence was characterized by cloning into *E. Coli* BL21 cells. In conclusion, our data revealed the lack of photosynthetic acclimation in pigeonpea under elevated CO_2 which can be attributed to the effective metabolism of sink tissues including nodules.

IDT4-017 | Physiological mechanisms underpinning genotypic variation for heat tolerance in mungbean (*Vigna radiata* L.).

Rachaputi C.N Rao[1] and Nia Patriyawaty[1]

[1] Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Australia.
*E-mail: rao.rachaputi@uq.edu.au

Temperature above 35oC during reproductive phase could cause significant yield losses in mungbean. The study investigated genotypic diversity in response to temperature treatments i.e. normal (28/24oC, CON), acclimation to high temperature (35/28oC, AT) before transfer to a heat shock treatment (45oC/30oC), and direct exposure to heat shock (45/30oC, HS), in 28 diverse mungbean genotypes. Environmentally controlled growth chambers were used to provide the required temperature regimes. The initial study resulted in identification of five tolerant and five susceptible genotypes for further studies on physiological mechanisms underpinning tolerance to high temperature stress imposed at reproductive phase. The study confirmed relationship between viable pollen number/mm2 and pod number (r2=0.40**) and grain yield (r2=0.45**) on per plant basis. Plants subjected to AT showed a better performance in heat shock treatment compared to non-acclimated plants. The SPAD meter readings decreased significantly (P<0.001) in AT and HS treatments compared to control. The SPAD value was positively related to biomass (r2=0.73). The membrane damage measured as electrolyte leakage was 40.8% and 64.4% AT and HS respectively, compared to control. Most interestingly, root weight was significantly affected by temperature (P<0.05).The mean root weight of tolerant group was 48%, 180% and 130% greater than susceptible group, in CON, AT and HS treatments respectively. There was a significantly positive relationship (r2=0.54**) between shoot and root weight per plant suggesting plants with higher root weight also produced higher shoot biomass. It is concluded that roots, in addition to other traits play a significant role in enhancing heat tolerance in mungbean.

IDT4-018 | High throughput screening for differential nocturnal transpiration in rice genotypes under moisture-deficit stress

Raju D[1*], Kumar S[1], Sahoo R. N[2], Chinnusamy V[1]

[1]Division of Plant Physiology, [2]Division of Agricultural Physics,
[2]ICAR-Indian Agricultural Research Institute, New Delhi, India
*E-mail: dandyman2k3@yahoo.co.in

Drought is the major abiotic stress affecting growth and productivity of rice. Efficient use of water by genotype is one of the key mechanisms for minimizing fresh water requirement under irrigated ecosystem and yield stability under drought stress. Significant efforts have been made to unravel the physiological and molecular basis of transpiration during day time, while nocturnal transpiration has received limited attention. Global climate change is expected to increase night time temperature more than the day time temperature. Hence identification of donors and genomic regions associated with nocturnal transpiration will be critical for achieving more crop per drop. An experiment to study the diurnal and nocturnal transpiration and their contribution to total transpiration in rice genotypes was conducted in automated plant phenomics facility. Sixty rice genotypes were transplanted in pots with six replications each and grown under controlled environment conditions at the national phenomics facility, ICAR-IARI, New Delhi. One set of plants (three replications each) were imposed with moisture-deficit stress during reproductive stage, while the other set was well irrigated. Data on gravimetric change in soil moisture was recorded by using automated weighing and watering unit and plant stress responses were measured by using visual, IR and NIR imaging platforms. Results revealed considerable variations among the rice genotypes in nocturnal transpiration, and thus suggest the potential for using this trait for improving rice crop.

IDT4-019 | Determining transpiration efficiency of *bmr* sorghum genotypes for progressive drought tolerance

Romana KK[1], Kunapareddy A[1], Gupta R[1], Are AK[1]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: A.AshokKumar@cgiar.org

Food and energy security are fundamental to the economic development of nations and considering environmental issues, biomass-based energy is a promising option in India through lingo-cellulosic (2G) biofuel production. High biomass sorghum is a promising feedstock for 2G biofuels production. However, higher lignin content of the biomass and water-deficit stress are major issues in enhancing biomass sorghum based biofuels production. In sorghum, brown midrib (*bmr)* mutants with reduced lignin content were developed.The present glass house study summarizes a screening experiment of 14 *bmr* sorghum lines (Atlas, Atlas *bmr*-12, Early hegarisart, IS 18542, Kanas collier, N 592, N 593, N 594, N 595, N 596, N 597, N 598, Roxorange and R-16) for progressive drought tolerance. The results showed that among the various *bmr* lines tested, N 593 had the highest transpiration efficiency in water-stressed conditions, whereas N 592 had the highest in well-watered conditions. The lowest transpiration efficiency was observed in N 597 under water stressed treatment. However, for well watered treatments the lowest was observed in N 596. The genotypes having higher transpiration efficiency has more water holding capacity for longer time under water stressed conditions. This preliminary study helps to identify genotypes with more water-holding capacity to adapt well in drought conditions. The *bmr* genotypes used here showed reduced lignin content vis-à-vis white midrib sorghums. The identified lines with low-lignin, high biomass and higher water holding capacity can be used as feedstocks in 2G Biofuels production after appropriate testing in target environments.

IDT4-020 | Ion channels in rice: Development of a novel rapid screen for drought tolerance

Vinnakota R[1], Murugesan D[2], Sankaranarayanan K[3*]

[1]National Centre of Cell Sciences, Pune
[2]Regional Research Station, Tamil Nadu Agricultural University, Paiyyur
[3]AU-KBC Research Centre, MIT Campus of Anna University, Chromepet, Chennai 600044, INDIA.
*E-mail: skavitham@yahoo.com

Plants exposed to drought conditions adapt different physiological measures to counteract the stress imposed due to the water-deficit. While one such strategy would be an efficient water-uptake, the other is a stringent regulation of water-loss or transpiration from the leaves. Transpirational activities are regulated by the guard cells which line the stomatal aperture of the leaf. Changes in the turgidity of these guard cells orchestrate the opening and closure of these pores in the leaf through which water loss occurs and this is mediated by ion-channel proteins present in the plasma membrane of the guard cells.

In this study we report on an analysis of the difference in ion-channel expression and function in drought-tolerant and sensitive varieties of rice, using a combination of molecular biology and electrophysiology in conjunction with physiology experiments. Detailed studies reveal that ion-channel current measurements using electrophysiological tools could be potentially used as an indicator to distinguish between drought-resistant and drought-tolerant varieties of rice. Simulation of water-deficit conditions in the laboratory (both at whole plant and cellular levels) has revealed significant differences in the ion-channel currents in drought-tolerant rice breeds, thereby hinting at the development of a novel diagnostic tool for screening for drought-sensitivity (which is very laborious and time-consuming using conventional methods). Detailed biophysical characterization of the same has also been conducted. This technique along with water channel (aquaporin) function could not only serve as a rapid screening tool for drought-tolerance but also in the identification of appropriate parentage as donors for drought-tolerant traits.

IDT4-021 | Carbon allocation efficiency under drought: targeting the hexose/sucrose ratio based signaling mechanism

Sengupta D., Reddy A R*

University of Hyderabad, Hyderabad, 500046, Telangana, India,
*E-mail: attipalli.reddy@gmail.com

Improving allocation efficiency is the primary target for enhancing yield under drought. Hexose to sucrose ratio (H:S) acts as signal for regulating plant development and thus play a key role in determining allocation efficiency. Usually, higher H:S ratio favors cell division and expansion while low H:S favors differentiation and maturation. Spatial and temporal regulation of sugar transporters including SWEET efflux proteins, Suc-H+ symporters and hexose transporters, sucrose metabolizing enzymes *i.e.* sucrose synthase and invertases and cell cycle regulators such as cyclinD3 and cyclin dependent kinases constitute the overall mechanism of H:S signaling. However, the actual pathway of H:S signaling regulating the allocation efficiency and yield under drought is not yet known. Soybean yield is highly affected by drought stress, particularly during flowering and early pod development. Here, an integrated analysis of the regulatory role of H:S signaling on allocation efficiency of soybean under drought is undertaken. Interestingly, the H:S ratio of developing soybean pods increased under drought in the resistant soybean variety but declined in the sensitive one during R4 and R5 stage. Photosynthetic performance and transcript expression dynamics of key transporters, sugar metabolizing enzymes, cyclinD3 and cyclin dependent kinases were analyzed and correlated with the corresponding sugar levels under drought conditions. Present analysis provide a comprehensive picture of the H:S signaling under drought and also identifies the key molecular targets of the H:S signaling pathway.

IDT4-022 | High temperature influence on limited transpiration response at elevated vapor pressure deficitin maize

Shekoofa A[1*], Sinclair TR[2]

[1]Department of Plant Sciences, University of Tennessee Knoxville, Jackson, TN 38301, USA
[2]Department of Crop Science, North Carolina State University, Raleigh, NC 27695-7620, USA
*E-mail: ashekoof@utk.edu

Drought impacts nearly all crop production for at least a limited period of time across the US Corn Belt. Temperature and vapor pressure deficit (VPD) are two important environmental factors influencing stomatal conductance and transpiration under water deficit stress. A limited transpiration rate (TRlim) trait expressed under high VPD (> ~2kPa) has been shown to offer an approach to increase crop yield in water-limited areas. Previous studies at moderate temperatures (32°C and lower) identified maize (*Zea mays* L.) hybrids that express the TRlim trait. A critical question is whether the TRlim trait is also expressed by these hybrids under temperatures up to 38°C, which are relevant in environments where maize may be grown. Out of 12 maize hybrids, five failed to express the TRlim trait at 38°C, but seven hybrids had sustained expression of the trait at 38°C. The loss of expression of the TRlim response in the five hybrids was found to occur in the very narrow range of temperature increase from 36 to 38°C.The next question is how long it takes for stomatal conductance to be back at the same levels as before the high temperature (38°C) treatment? The result of a series of experiments on maize hybrids with expressing TRlim and not expressing the trait indicated that the recovery in the hybrids with expressingTRlimoccurredquickly (~ 6hrs). The genetic differences in water use among these maize hybrids could be useful in selecting hybrids that are especially well adapted for temperature conditions in a targeted production area.

IDT4-023 | Transpiration efficiency: further insights from species, sink strength, and soil comparisons

Vincent Vadez[1*], Jana Kholova[1], Sunita Choudhary[2], Mark Cooper[3], Charlie Messina[3], Anand Prandavada[2]

[1]International Crops Research Institute for the Semi–Arid Tropics (ICRISAT), Crop Physiology Laboratory, Patancheru 502324, Telangana, India.
[2]Pioneer Hibred, Hyderabad Research Station, Telangana, India
[3]DuPont Pioneer, Johnston, IOWA, USA
*E-mail v.vadez@cgiar.org

During ID-IV we reported that TE was closely related to the capacity to restrict transpiration under high vapor pressure deficit (VPD). Experiments were undertaken to evaluate other possible factors influencing TE. Experiments across seasons varying in VPD conditions and across water regimes showed that maize had a higher TE than sorghum and pearl millet. While C4 cereals should, theoretically, have similar TE, 100 years of breeding in maize could be responsible for these differences, possibly from increased rates of carbon fixation deriving from selective pressure underincreased planting densities. These results then open an opportunity to accelerate breeding in sorghum and pearl millet by specifically targeting the possible reasons for these differences (RUE, density "resistance"). Further experimentation was undertaken in which ears and panicles were severed from the plants and showed that TE was depressed in maize and sorghum, respectively, while it was not in pearl millet, which produced many new tillers and nodal tillers. This work then raised the question of source-sink relationship in setting carbon demand and then photosynthetic activity. Finally, TE assessed in C4 cereals, grown in four different soils and two different VPD seasons, showed large TE differences among soils during the high VPD season, with a degree of species-by-soil interaction. We interpret these differences to be a consequence of different hydraulic soil properties likely affecting the transpiration response under high VPD. Results will be discussed with regard to breeding targets in "less-bred" crops (pearl millet, sorghum) and with regards to better understanding GxExM interactions.

IDT4-024 | The role of leaf conductance and photosynthesis in genotypic differences in transpiration efficiency in sorghum

G. Geetika[1], E.J. van Oosterom[1*], K.S. Deifel[1], B. George-Jaeggli[2], G.L. Hammer[1]

[1]The University of Queensland, Brisbane, QLD 4072, Australia.
[2]The University of Queensland, Warwick, QLD 4370, Australia.
*E-mail: erik.van.oosterom@uq.edu.au

Sorghum is adapted to drought stress, and transpiration efficiency (TE) is an important trait that can increase productivity under water limitation. The objectives of this research were to determine if: (1) genotypic differences in TE could be explained as a consequence of differences in photosynthetic rate and/or in the response of transpiration rate to environmental conditions, (2) plant-level differences in transpiration rate reflect leaf-level differences in transpiration and therefore conductance, and (3) genotypic differences in TE occur in response to mild drought stress. Experiments were conducted in a lysimetry platform at Gatton, Australia, using diverse germplasm from the sorghum breeding program in Australia. Under well-watered conditions, high TE was generally associated with low transpiration rate (adjusted for plant size) and low photosynthetic capacity. However, among the lines with medium TE, there was variation in photosynthetic capacity for given levels of transpiration. Plant-level transpiration rates were highly correlated to rates of water loss at the stomatal level.

Mild drought stress had little effect on TE, but under high vapour pressure deficit, some genotypes tended to reduce their transpiration rates more in response to mild drought stress than others. Our results indicated different physiological pathways to achieve high TE. If combined with knowledge on the genetic control of responses, the insights obtained in this research could be used to assist breeding of drought-resilient sorghum germplasm.

IDT4-025 | Evaluation of plant growth, photosynthesis and intrinsic water-use efficiency of 25 Bambara groundnut landraces at Marapyane, South Africa

Yattara InamoudIbny F[1], Maseko ST[1], Dakora FD[1]*

[1]Tshwane University of Technology, Pretoria 0001, South Africa
*E-mail: dakoraFD@tut.ac.za

Bambara groundnut (*Vigna subterranea* L.Verdc) is an indigenous grain legume mainly cultivated by subsistence farmers in sub-Saharan Africa. It is primarily grown for its seeds, which contain significant quantities of protein, carbohydrate, and fat (Rowland, 1993). Although Bambara groundnut is known to exhibit drought tolerance (Berchie *et al*., 2012), there is limited information on the adaptation of available landraces when grown under rain-fed conditionsin South Africa. This experiment evaluated plant growth and the intrinsic water-use efficiency (WUEi) of 25 Bambara groundnut landraces grown under field conditions at Marapyane, South Africa. The landraces were laid out in a randomized complete block design with three replications. At flowering, five plants were randomly sampled from each plot, and separated into different plant parts. The shoots were oven dried (65ºC for 72 hours) and weighed to determine biomass. Gas exchange parameters such as photosynthesis (A), stomatal conductance (gs), were also measured using an infra-red gas analyser. The intrinsic water use efficiency was calculated as the ratio of A to gs. The data showed significant variations amongst the test landraces. Shoot biomass ranged from 7.65 to 31. 80 g. plant-1. The landraces NamaripeGurue, RuaceGurue, SSD 9 (red) combined a high shoot biomass and high water-use efficiency, while the landraces Medium brown, Light brown small, and OM1 were observed to have low shoot biomass but high WUEi. The results, therefore, suggest that the landraces which combined high biomass and high WUEi will be ideal in environments where water is limiting.

IDT4-026 | Effects of drought stress on light-dependent reactions and photosynthetic efficiency in tolerant and susceptible Barley (*Hordeum vulgare* L.) genotypes

Ali Akbar Ghotbi Ravandi[1], Mansour Shariati[2], ZahraSadat Shobbar[3], Paula Mulo[4], Maryam Shahbazi[3]*

[1]Faculty of Biological Sciences, Shahid Beheshti University, Tehran, Iran.
[2]Department of Biology, University of Isfahan, Isfahan, Iran.
[3]Agricultural Biotechnology Research Institute of Iran (ABRII), Education and Extension Organization (AREEO), 3135933151 Karaj, Iran.
[4]Molecular Plant Biology, Department of Biochemistry and Food Chemistry,University of Turku, FIN-20014 Turku, Finland.
*E-mail: mshahbazi@abrii.ac.ir

Drought stress is one of the most important abiotic factors which adversely affect growth, metabolism and yield of crops worldwide. The objective of this study was to determine the effects of drought stress on photosynthesis and examine the differential responses of photosynthetic apparatus in relatively tolerant (Yousof) and susceptible (Morocco) barley genotypes. Plants were subjected to different levels of soil water availability including control, mild and severe drought stress. In both genotypes, drought stress led to decrease in chlorophylls, β-carotene and stomatal conductance accompanied by decrease in CO2 assimilation rate. Significant increase in α-tochoperol content was only observed in Yousof cultivar under drought stress. Initial slope and plateau phase of CO2 response curve of drought-stressed plants as well as polyphasic chlorophyll a fluorescence transient curve (OJIP test) and fast fluorescence induction kinetics were influenced by drought stress. These parameters were more affected in Morocco by drought stress compare with Yousof. Drought stress also resulted in reduction of D1 protein content in both genotypes and accelerated photoinhibition process. Based on results, stomatal conductance is the main factor limiting photosynthesis in Yousof under mild drought stress. However, in Morocco, in addition to stomatal limitation, damage to photosystem II (PSII), reduced electron transport and carboxylation efficiencies were important parts of limitation in photosynthesis. Severe drought stress resulted in structural and biochemical impairment of light-dependent reactions as well as carboxylation process of photosynthesis in both genotypes. Alpha-tocopherol showed an important protective role against drought stress in Yousof cultivar as a relatively drought-tolerant cultivar.

Poster Theme V

Plant Productivity under Drought III:
Vegetative Growth

IDT5-001 | Phenotypic variation under moisture stress is regulated by variation in photosynthetic ability in Fingermillet (*Eleusine coracana*)

Afsanabanu Manik, Preethi NV, Nagasupreeta SR, Udayakumar M, Sheshayee MS*

University of Agricultural Sciences, GKVK Campus, Bangalore-560 065, India.
*E-mail: msheshshayee@hotmail.com

Fingermillet (*Eleusine coracana*) though a C4 species suffers under moisture stress conditions. Being predominantly grown as a rainfed crops yield loss due to stress is often significant and inevitable. Understanding the variability in stress adaptation is crucial for devising approaches for crop improvement. In the present investigation were studied variability in constitutive and acquired tolerant traits of selected genotypes of ragi. Stress was imposed during reproductive stage with moisture regimes of 100, 65 and 45% FC for the period of 25 days. Stress induced reduction in photosynthetic rate and stomatal conductance was significantly high in 45%FC than 65%FC. Relative water content of these genotypes varied significantly in all the three moisture regimes. Proline content was measured and it's varied from 100 to 650 μg/g FW in 45%FC compared to 10 to 80 μg/g FW in control. MDA as an end product of lipid peroxidation was quantified and there was a significant variability among the genotypes. Stress induced reduction yield was low for GPU28 a drought tolerant variety.

IDT5-002 | Screening for drought tolerance in lentil genotypes using thermal Imaging and multivariate data analysis

Biju S[1]*, Fuentes S[1], Gupta D[1]

[1]The University of Melbourne, Parkville, Victoria, 3010, Australia
*E-mail: sbiju@student.unimelb.edu.au

Lentil (*Lens culinaris*, Medik.) is an important legume crop, which often experiences water stress due to changing environmental conditions, especially at the flowering and grain filling phenological stages. Efficient screening tools based on relevant quantifiable traits would facilitate research on crop improvement for drought tolerance.The objective of this study was to evaluate the drought tolerance of 15 lentil genotypes, using thermal imaging, drought tolerance parameters and multivariate data analysis. The experiment was carried out in a growth chamber under controlled conditions. Potted plants were kept in a randomized complete block design with five replicates per genotype. Plants were subjected to three different drought treatments (100%, 50% and 0% field capacity) at the onset of reproductive period. The relative drought stress tolerance was determined based on a set of morpho-physiological parameters including plant height, root-shoot ratio (RS Ratio), relative water content (RWC), harvest index (HI), canopy temperature (Tc), canopy temperature depression (CTD) and crop water stress index (CWSI).The drought tolerance indices used were drought susceptibility index (DSI) and drought tolerance efficiency (DSI). Results showed that drought treatments significantly reduced the RWC, HI, CTD and DSI, whereas the values of Tc, CWSI, RS ratio and DTE significantly increased in all the genotypes. Cluster analysis from morpho-physiological parameters was able to separate the level of drought stress tolerance among the genotypes into three distinctive groups. The genotypes with higher values of RS ratio, RWC, HI, DTE and CTD and lower values of DSI, Tc and CWSI were identified as drought-tolerant genotypes. Based on this preliminary screening, Cumra, Indian head, ILL6002 and ILL5582 were identified as drought-tolerant genotypes, whereas CDCRichlea, ILL1796, PI468898 and Rose were considered as susceptible ones. These results provide a foundation for future research directed at identifying powerful drought assessment traits and understanding the biochemical and molecular mechanisms underlying lentil tolerance to drought.

IDT5-003 | Sorghum early vigor increases grain size, striga resistance and has linkages with some stay-green phenotype

Chadalavada K[1], Vadez V[1], Deshpande S[1], Kholová J[1]*

[1] International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, Telangana-502 324, India
*E-mail: j.kholova@cgiar.org

Promising agronomic crop traits could be more accessible to breeding if we understood their underlying plant processes and knew their genetics determinacy. Here, we attempt to progress understanding of the functional linkages between traits using PCA and quantitative trait loci (QTL) co-localization approach. A recombinant inbred lines (RIL; 181 progenies) population derived from a cross between senescent (N13) and stay-green(E36-1) parental lines was selected. This population was previously shown to segregate for stay-green expression and *Striga* resistance in the field. Here it was phenotyped for: (i) grain size variability under optimal field conditions; (ii) traits related to early-vigor (canopy size and growth rate) in a high-throughput phenotyping platform. Most traits had high heritability (>60%). Linkage map was constructed (271 molecular markers) and QTL analysis (Cartographer 2.5) performed using composite interval mapping function. Two major QTLs influencing canopy size were found on SBI04 and SBI05. The SBI05 QTL harboring canopy size co-localized with the grain size QTL and with the genetic region of stg-4 (stay green) QTL (responsible for leaf size distribution). This links the vigor traits to the variability in grain size and leaf development (i.e. stay-green mechanism) the latter possibly explaining the variability in grain size. Since grain size partially regulates grain nutrients profile, such linkage calls for further exploration in breeding. The SBI-04 QTL for canopy size co-localized with QTLs for *Striga* resistance, strengthening the hypothesis that plant vigor enhances *Striga* resistance. Vigor appears to explain several traits and could be rapidly screened at the LeasyScan facility.

IDT5-004 | Exploration of rice (*Oryza sativa.* L) land races for drought tolerance

Choudhury D[1], Samanta P[1], Kumari R[1], Dey N[1]*

[1]Department of Biotechnology, Visva-Bharati, Santiniketan (W.B), India
*E-mail: narottam.dey@visva-bharati.ac.in

Drought is one of the major constrains for rice production across almost all rice-growing regions. Rice lines differ greatly in their ability to tolerate drought and provide scope for combining drought tolerance in higher yield backgrounds. Genomics assistant breeding, particularly marker assisted selection and allele mining for drought tolerance genes, are two effective ways for utilization of promising lines through unlocking their genetic potentials. Keeping these as objectives, a small rice germplasm collection was developed, which included a good number of drought tolerant/ or avoiding upland rice lines. The studied lines were screened at physiological and biochemical level to decipher their ability for drought tolerance. In order to perform marker based genotyping, the genomic DNA was amplified with drought tolerance linked molecular markers. Genomic DNA was also genotyped with miRNA linked molecular markers for deciphering the presence of drought responsive miRNAs and respective targets. For allele mining of the associated genes/elements (*DREB, LEA, CALMOD),* the genomic DNA of studied lines were amplified and sequenced to find out the different allelic forms (in form of sequence diversity among different rice lines). The main outcome of this investigation were (i) conservation and phenotyping of the selected traditional rice lines (ii) preparation of a genetic database of the studied land races with their degree of drought tolerance and (iii) identification of suitable linked markers for marker assisted selection (MAS) in relation to drought tolerance (iv) genomics and bioinfomatics information of the selected genes in relation to drought tolerance.

IDT5-006 | Differential responses of maize (*Zea mays* L.) and pearl millet [*Pennisetum glaucum* (L.) R. Br] under augmenting drought stress

Odjegba J V[1,3], Alam A[1],, Sharma V[1], Iwuala EN[1,2]*

[1]Department of Bioscience and Biotechnology, Banasthali University, Rajasthan, India
[2]Department of Plant Science and Biotechnology, Federal University Oye Ekiti, Ekiti State, Nigeria.
[3]Department of Botany, University of Lagos, Akoka, Lagos State, Nigeria.
*E-mail: iwuala097@gmail.com

Drought stress is a major environmental stress that hinders plant growth and productivity. This study was conducted to identify maize landraces with drought tolerance, and compared with a drought-tolerant line of millet. Three genotypes, of *Zea mays* L.(DTSYN11 and LRN01) and *Pennisetum glaucum* L. (IP14787), respectively were screened to discover physiological indicators to drought tolerance. The genotypes were evaluated for their physiological responses during the vegetative growth stage to mild (4 days), moderate (8 days) and severe (12 days) of water stress treatments. Dry weight (DW), leaf water content (LWC) and water use efficiency (WUE) were measured, and photosynthesis, chlorophyll, carotenoid and protein contents were quantified during stress periods. The results showed that dry matter yield did not differ significantly among the two species with healthy watering, but DTSYN11 was superior to IP14787 and LRN01 under all levels of water deficit (4,8 and 12 days). All genotypes maintained RWC above 80% during well-watered condition. For LRN01 the recorded RWC was 10% less than the other variety. WUE was found to be the highest under healthy watering conditions in *Z. mays* and *P.glaucum* respectively. Apparently water use efficiency was the highest from the upper soil layers, especially under frequent irrigation. Among stressed plants, LRN01 extracted more water from the topsoil, while DTSYN11 and IP14787 had little water uptake from all layers of the soil profile. Under water stress, a decline was observed in the photosynthetic rate (ΔF/FM,) and electron transport rate (ETR sat) in LRN01, IP14787 and DTSYN11 genotypes respectively. Total chlorophyll, carotenoid and protein contents were significantly higher in DTSYN11 compared to the other two genotypes. The study has successfully identified drought tolerant genotypes of two different species, indicating these landraces are precious natural reservoirs to elucidate genetic mechanisms that will be helpful to attain drought tolerance.

IDT5-007 | Interdependence of plant photosynthesis with hydraulic efficiency in field grown mulberry (*Morus* spp.) genotypes under water deficit and recovery

Reddy KS, Reddy AR*

University of Hyderabad, Hyderabad-500046, India
*E-mail: attipalli.reddy@gmail.com

Mulberry (Morus spp.) is an economically important perennial crop in sericulture industry. Impact of drought stress on terrestrial plants is predicted to increase day by day due to rapid increase in air temperature and changes in precipitation patterns. Physiological and growth responses to drought stress may vary among genotypes within the species. Our study was aimed at screening of better performing mulberry genotypes based on their hydraulic dynamics and photosynthetic responses to drought stress and recovery. One year old mulberry genotypes were subjected to drought stress for 30 days followed by recovery. Plant hydraulic parameters, leaf gas exchange parameters and chlorophyll *a* fluorescence were measured in control, treated as well as rehydrated plants to assess their efficiency. 12 mulberry genotypes were characterized in to 3 functional groups including high, average and poor performing groups (HPG, APG and LPG respectively) based on their adaptive capabilities under drought stress. HPG genotypes maintained significantly higher leaf water status (ψL), stem hydraulic conductivity (Ks), sap flow rate (F) which resulted in enhanced photosynthetic efficiency compared to APG, LPG under prolonged drought regimes (30 days). Higher CO2 assimilation in HPG resulted in to continued growth facilitating higher total fresh biomass even under drought stress when compared other groups. Our data suggest that plant water transport efficiency plays a major role in photosynthetic efficiency which in turn results in better biomass yields during drought stress and recovery.

IDT5-008 | Multi-stage phenotyping of dynamic traits for increased efficiency of breeding experiments: A case study of plant height in chickpea

Kulwal P. L.[1*], Bohare T. V.[1], Mhase L. B.[3], Jadhav A. S.[1]

[1]State Level Biotechnology Centre, Mahatma Phule Agricultural University, Rahuri-413722, MS, India
[2]Pulses Improvement Unit, Mahatma Phule Agricultural University, Rahuri-413722, MS, India
*E-mail: pawankulwal@gmail.com

In plant breeding experiments, often the data on a trait is recorded at maturity. However, in nature, many developmental traits such as plant height are under the control of genes which are expressed at specific stages of development in response to existing environmental conditions. In the present study, a set of 49 chickpea genotypes from the central zone of India were evaluated under field conditions at different dates of sowing. Starting from the first week of November 2015, chickpea was sown at one month intervals till January 2016. Data on plant height was recorded at an interval of one month after germination. The maturity in the case of second and third sown trial almost coincided with third time observation. Interesting results were obtained regarding heritability (broad sense) of the trait which kept decreasing from the first month till maturity. For the November-sown trial, broad sense heritability decreased from 0.865 to 0.760, while for December-sown trial it decreased from 0.985 to 0.608. Similarly, for January-sown trial, it decreased from 0.864 to 0.473. The results show that for a dynamic trait like plant height, heritability is highest during the first month of growth compared to the end-stage phenotype. It also highlights that one can miss important QTL if only end-point phenotype is used for analysis. Another advantage is that one can identify the developmental stage at which heritability of the trait is the highest so that it can be used as the stage for measurement of the trait in subsequent analysis. This can also help in understanding the role of g × e interactions.

IDT5-009 | Screening chickpea for adaptation to water stress: associations between yield and crop growth rate

Lake L*[1], Sadras V O[1]

[1]South Australian Research and Development Institute, Waite Campus, Adelaide, 5064, South Australia, Australia
*E-mail: lachlan.lake@sa.gov.au

We seek to improvechickpea yield under drought by screening for crop growth rate under varying water stress. We measured crop growth rate using Normalised Difference Vegetative Index (NDVI) in 20 diverse chickpea lines, after calibration of NDVI against biomass. Crops were grown in eight environments differing for water stress and temperature; environments resulted from a combination of seasons, sowing dates and water supply. Yield ranged from 110 to 510 g m-2. For both sources of variation – environment and genotype - yield correlated with crop growth rate in the window 300oCd before flowering to 200oCd after flowering. In the range of crop growth rate from 0.07 to 0.91 g m-2oCd-1, the relationship was linear with zero intercept, as with other indeterminate grain legumes. Improved yield under water stress was associated with crop growth rate; genotype-driven associations between yield and crop growth rate were stronger under water stress rather than favourable conditions. Despite this general trend, lines were identified with high crop growth rate in both favourable and water stress conditions. We demonstrate that increased yield and reliability of chickpea in water stress conditions can be achieved by selection for crop growth rate in the window 300oCd before flowering to 200oCd after flowering.

IDT5-010 | Eco-physiological and genetic characterization of drought response index of rice (*Oryza sativa* L.) under upland conditions in temperate monsoon climate in Japan

Ramalingam P[1], Kamoshita A[1]*, Tong L[1], Nemoto K[1], Yusaku Uga[2]

[1] University of Toky, Tokyo, Japan
[2] National Agricultural Research Organization, Tsukuba, Japan
*E-mail: akamoshita@anesc.u-tokyo.ac.jp

In order to clarify eco-physiological meaning of drought response index, an synthetic indicator of drought resistance, we conducted 3 upland field experiments under both control and drought treatments (i.e., prolonged drought of 45 days), using 8 varieties with different adaptation to drought and with different phenology (Variety experiment as Exp.1), 5 near isogenic lines (NILs) of Koshihikari with different heading dates (NIL-phenology experiment as Exp.2), and 4 NILs of IR64 with different root growth angle and stele transversal area (NIL-root experiment as Exp.3), including both normal and staggered sowing for Exp.1 and Exp.2. We also conducted 5 upland field experiments under both control and drought treatments (i.e., prolonged drought of 45 to 60 days) in 2 years (QTL experiment as Exp. 4 to Exp.8) using 3 mapping populations from the 6 parents with contrasting adaptation to drought from Exp.1 to genetically characterize DRI. In Exp.1 Dular, Yumenohatamochi and IRAT109 were generally well adapted to upland control treatment; under the prolonged drought, Dular and earlier heading varieties attained higher yield with Dular having highest DRI under normal sowing, while Yumenohatamochi had highest DRI under staggered sowing in which the ranges of 50% flowering were reduced to within 9 days from 35 days of normal sowing. In Exp.2 yield under the prolonged drought in normal and staggered sowing was determined by the combination of yield potential and drought escape, with DRI not consistently determined by the difference in heading date. In Exp. 3, stele transversal area did not but proportion of deep root angle minimized flowering delay and contributed to higher DRI. Three and 2 QTLs for DRI were identified in Otomemochi/Yumenohatamochi and Kamenoo/Dular populations, respectively, three of which (RM6911-RM6379 in chromosome 2, RM6356-RM6999 and RM5637-RM6990 in chromosome 8) had epistasis with other intervals. More numbers of epistasis for DRI were identified; 6 for Otomemochi/Yumenohatamochi (Exp.4, Exp.6), 13 for Akihikari/IRAT109 (Exp.5, Exp.7), and 2 for Kamenoo/Dular (Exp. 8).

IDT5-011 | Sri Lankan rice is sensitive to photoperiod and temperature at early vegetative growth

Rathnathunga EUU[1], Senanayake SJGN[2] and Geekiyanage S[2]*

[1]Board of Study in Agriculture, Faculty of Graduate Studies, University of Ruhuna, 81000 -Matara, Sri Lanka
[2]Department of Agricultural Biology, Faculty of Agriculture, University of Ruhuna, Mapalana, 81100 Kamburupitiya, Sri Lanka.
*E-mail: sudarshanee@agbio.ruh.ac.lk,

Growth and development of rice are affected by environment. Photoperiod and temperature are among the main environmental factors that determine the ecological adaptation of rice through manipulating vegetative phase prior to flowering. The objective was to determine the effect of photoperiod and temperature on early vegetative growth of selected Sri Lankan cultivated and wild rice for future breeding programmes. Thirty six traditional rice accessions (TRA), improved rice (At 308 and Ld 368) and Sri Lankan wild rice (*Oryza nivara* and *Oryza rufipogon*) were grown under short day (SD), day neutral (DN) and long day (LD) conditions during late July, 2014 to mid-October, 2014 (Trial 01; average monthly temperature of 36. 875 ^{0}C); and late November, 2014 to mid-February, 2015 (Trial 02; average monthly temperature of 34.0 ^{0}C) in a non-temperature controlled photoperiod chamber. Days to reach the fifth leaf stage (DFL) of all accessions were affected by photoperiod or temperature or their interactions. DFL of TRA *Sulai* 4365 was only affected by photoperiod. DFL of 20 TRAs, Ld 368 and *Oryza nivara* were only affected by temperature. Plant height at DFL (PH) of 15 TRAs and *Oryza rufipogon* were not affected by photoperiod or temperature; PH of 11 TRAs, At 308 and *Oryza nivara* were affected by temperature. PH of TRA *Wanni heenati* 3401 and *Sudu wee* 3858 were only affected by photoperiod. The diverse response of Sri Lankan rice to temperature and photoperiod would be useful as a breeding resource for climate change adaptations.

IDT5-012 | Physiological and genetic insights towards understanding the canopy architecture in contrasting leaf size mutants of an upland size-Nagina 22 (N22)

Sowmya H.R[1,2], Sumanth Kumar K[1], Rajesh Kumar Singal[1], Niranjana P[2], Rajanna M.P, Sharma R P[4], Mohapatra T[5], Sarala N[6], Robin, S[7], M.S Sheshshayee[1*]

[1]University of Agricultural Sciences, GKVK, Bengaluru
[2]Kuvempu University, Shivgoga
[3]Zonal Agricultural Research Station, College of Agriculture. Mandya
[4]NRCPB, IARI, New Delhi
[5]Central Rice Research Institute, Cuttack
[6]Directorate of Rice Research Hyderabad
[7]Tamil Nadu Agricultural University, Coimbature
*E-mail: msshesh1@uasbangalore.edu.in

A set of contrasting leaf size mutants were identified from a stabilized population of EMS induced *Nagina-22* mutants. Phenotypically, these mutants differ for canopy architecture traits such as leaf number, leaf length and width, vein density and leaf angle. Owing to low leaf size and, hence, reduced canopy cover, the narrow leaf mutant (NL, N22_BADT_380_4) had reduced light interception compared to broad leaf mutant (BL, N22_BADT_437_1) and the wild type N22. The BL had high rate of shoot growth and low moisture retention capacity. However, the decreased leaf size of NL was compensated by increased leaf number, so that there was no difference in total leaf area (1540 and 1600 cm2.pl-1 respectively for NL and BL). Gas exchange analysis under two different water regimes revealed differences in photosynthetic and stomatal behaviour.The intrinsic WUE calculated by A/gs was high in narrow leaf mutant both under well watered (100% FC) and water limited (70% FC) condition. A MUTMAP population was developed by crossing NL with the wild type N22. The F2 population showed significant variability for the measured leaf traits. LL/LW ratio dramatically varied from 2.6 to 78.6 and the total leaf area ranged from 79 to 3544 cm2.pl-1. Anatomical features such as minor vein frequency per major veins was determined. The wild type had six while NL had four veins between the major veins. A significant diversity was also noticed among the MUTMAP population, which ranged between four and nine. However, the number of veins per unit distance ranged from 6 to 10.5. The population had significant correlation between seed weight and total leaf area, indicating the necessity of canopy architecture in determining crop yield.

IDT5-013 | QTL mapping for root architecture and transpiration efficiency in a maize introgression library

Giuliani Silvia[1], Salvi Silvio[1], Vadez Vincent[2], Busanello Carlos[1], Tuberosa Roberto[1]

[1]UDepartment of Agricultural Sciences – University of Bologna, Viale Fanin, 44, 40127 - Bologna – Italy
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
E-mail: mailto:roberto.tuberosa@unibo.it; roberto.tuberosa@unibo.it

High transpiration efficiency (TE) is one way to optimize water use. Although variation for root morpho-physiological traits can strongly affect the water status of a plant, the relationship between root traits and TE is not well understood. A maize introgression library (IL) derived from the cross between Gaspé Flint (an early line; donor parent) and B73 (an elite line; recurrent parent) were evaluated in order to identify QTLs for root system architecture (RSA), total biomass (TB), leaf area (LA), transpiration rate (TR), transpiration efficiency (TE), flowering time (FT), grain yield (GY) and yield components (YC). Two different experiments were carried out in order to study the genetic control of i) RSA, FT, GY and YC in response to drought in field conditions, at UNIBO, Italy and ii) TE, TR, TB and LA in controlled environment at different VPD, at ICRISAT, India. Differences in leaf area among the IL lines explained only 40% of the transpiration differences under high evaporative demand. QTLs were identified for all investigated traits. Overlaps between root and transpiration-related QTLs were detected on chromosomes 1 and 8. At these QTLs, the Gaspè Flint allele was associated with a TE decrease. A particularly interesting QTL for GY and YC, FT and TR was mapped on chromosome 3 (bin 3.3) where the Gaspè Flint allele was associated with an increase of both yield and transpiration rate and earliness.

IDT5-014 | Museum of whole-plant across crops

Shashidhar HE[1]*, Vinutha DN[1], Kavya HP[1,2], Bharathprasad CT[1], Manjunath V[1]

[1]University of Agricultural Sciences, GKVK, Bengaluru-560065, Karnataka, India
[2]Madurai kamaraj University, Palkalai Nagar, Maduari-625021, Tamil Nadu, India
*E-mail: heshashidhar@gmail.com

Whole plant breeding is important for drought resistance. Plants with a well-endowed root system which could contribute to faster growth before the onset of drought and high biomass are prerequisite for high grain yield and quality. Nineteen commonly cultivated food crops were evaluated for whole plant characteristics. Two varieties were chosen in each crop. Phenotyping was done at four growth stages.PVC (Poly Vinyl Chloride) tubes of different sizes were used. The experimental results indicated immense differences across crops, stages, and between varieties. Growth rate in terms of cm per day was greatly different. Roots may not have a direct correlation with grain yield but a well-endowed efficient root system bodes well before, during and after the onset of low-moisture stress. The link between deep, extensive, and efficient roots and higher grain yield and quality has to be established to justify the advantage of roots to a plant when challenged by drought. Whole plants, extracted as indicated above, are on display.

Poster Theme VI

Reproductive Development,
Yield, Yield Quality

IDT6-001 | Identification and characterization of flowering-delay rice lines under reproductive stage drought stress

Adeboye KA[1], Oyedeji OE[1], Stanley AE[2], Popoola BO[2], Oduwaye OA[1], Daniel IO[1], Semon M[2*]

[1]Federal University of Agriculture, Abeokuta, Nigeria
[2]Africa Rice Centre, Ibadan, Nigeria
*E-mail: m.semon@cgiar.org

Genome by Genome interaction is capable of producing new types of offspring with enhanced genomic content to outperform the parents under unfavourable conditions. Crosses were made between BRS PRIMAVERA (*O. sativa* japonica ecotype; drought susceptible) and WAB 638-1 (*O. sativa* indica ecotype; known for its plasticity). The progenies including reciprocals were screened for drought stress at F_3 to F_5. Several lines were identified that delayed flowering under drought stress, while a greater proportion of the population continued flowering under stress. In both flowering pattern groups, yield reduction under drought stress compared with well-watered condition is below 50%. The best yielding progenies were evaluated at F_6 in 2016 (January-May) to confirm Flowering-Delay rice lines under managed reproductive stage drought stress. The experiment was laid out in an alpha lattice design with two replications nested in six blocks for each of water-stressed and well-watered treatments. Flowering delay was calculated as the difference between days to 50% flowering under water stressed and well-watered treatments. Our results established the occurrence of flowering delay and no delay in rice plants under reproductive stage drought stress. Currently, 12 F_7 progenies selected across these groups together with the parents are being characterised for the above- and below-ground attributes under managed reproductive stage drought stress. This study aims at understanding mechanisms employed for drought adaptation and identify the most drought effective flowering pattern with grain yield and quality as indices.

IDT6-002 | Adaptability of pearl millet (*Pennisetum glaucum* (L.) R.Br) varieties in the semi- arid Kitui county of Kenya

Thomas E. Akuja[1]*, Benard M Mweu[1], Titus I. Kanui[1], Mary W. Mburu[1]

[1]School of Agriculture and Veterinary Sciences, South Eastern Kenya University, P.O. Box 170- 90200, Kitui, Kenya
*E-mail: akuja05@gmail.com

Selection of drought-adapted ecotypes having efficient use of water is the most important goal in breeding programs for drought stress environments. Cereal crops are mainly cultivated as rainfed crops, where grain yield is often limited by terminal drought stress. Therefore, identification of traits associated with water utilization of crops is important to increase crop productivity under terminal drought stress. The effects of water shortage (during panicle initiation, flowering and grain filling) on harvest index and plant height of pearl millet (*Pennisetum gluucum* (L.) R. Br.), were studied on farm during three seasons with close to average annual rainfall. In this study, six ecotypes of pearl millet [*Pennisetum glaucum* (L.) R. Br.] were evaluated under rainfed conditions to study their responses to drought and to identify the traits that are associated with drought adaptation. Data collection was done on the net plot i.e. three inner rows of each plot, on plant height and harvest index. General mean performance of the six pearl millet genotypes revealed significant differences ($p<0.05$) for days to emergence, days to anthesis, days to 50% flowering and days to 50% maturity. It also showed that millet varieties were superior in plant characters, such as days to emergence, days to anthesis, days to 50% flowering and days to 50% maturity. The early maturing group included Pvs-pm 1005 (66.1 days to 50% maturity) and Pvs-pm 1006(74.22 days), while the local landrace (Kimbeere) took the longest time (80.33 days) to mature over the three cropping seasons. The data recorded showed significant ($p<0.05$) differences in millet harvest index among the six pearl millet genotypes. Pvs-Pm 1006 recorded significantly ($p<0.05$) higher harvest index compared to the other five genotypes of pearl millet variety, followed by Pvs-Pm 1002 while it was Kimbeere which was the lowest. Based on the present study conducted with six diverse genotypes of pearl millet it can be concluded that during the present investigation, the hybrids showed better adaptability on yield components and harvest index to arid environment than the local farmer variety.

IDT6-003 | Influence of pollen germination and pollen tube length on pod setting and yield in groundnut (*Arachishypogaea*. L).

Mohammed Anwar Ali[1,2]*, Ananya Baidya[1], Anjankumar pal[1], Ashoka Rani Y[2], Rajendra Kumar B[2]

[1]Bidhan Chandra KrishiVisvavidyalaya, Mohanpur
[2]Acharya N. G. Ranga Agricultural University, Bapatla
*E-mail: anwar.mohammed225@gmail.com

Groundnut (*Arachis hypogaea* L.) is one of the world's most popular oilseed crops, cultivated in more than 100 countries of six continents. It is grown as oilseed, food and feed crop. The goal of the study was to identify the best suitable groundnut genotypes for pre-*kharif* or summer by studying the reproductive biology via four parameters -- pollen germination, pollen tube length, pod setting percentage and kernel yield -- of 19 groundnut genotypes. Results of experiments show that increase in pollen germination percentage upto 50% increases pollen tube length, pod setting percentage and kernel yield. Genotypes with pollen germination percentage above 60% and below 20% have reduced pod setting percentage and kernel yield. Genotype INS-1-2013-5 performed well with 50% pollen germination with 1864.337µm pollen tube length, 13% pod setting and 15.55 g kernel yield per plant. Whereas INS-1-2013-7 has a pollen germination percentage of 19% with pollen tube length 321.210 µm, but it has higher pod setting percentage of 13.08% and low kernel yield per plant.

IDT6-004 | Yield stability and response of common bean drought tolerance breeding lines to field disease in Uganda

Amongi W[1], Mukankusi C.M, Sebuliba S[1]*, Nakyanzi B[1] and Baguma G[2]

[1]International Center for Tropical Agriculture (CIAT), P. O. Box 6247, Kampala, Uganda
[2]Kachwekano Zonal Research and Development institute (KAZARDI), P. O. Box 421 Kabale, Uganda
*E-mail: c.mukankusi@cgiar.org

Drought is increasingly becoming a major production constraint for common bean covering >40% of bean production area in Africa. Development of high yielding drought-tolerant varieties is crucial for maintaining acceptable levels of productivity. In this study, 448 advanced breeding lines developed for drought tolerance by the CIAT bean breeding program were evaluated in two contrasting agro-ecologies; Kawanda in the lake Victoria crescent (1200masl) and Kachwekano (2200masl), in the southwestern highlands, in 2012, 2015 and 2016. Lines were organized into six nurseries namely; Drought Andean bean (DAB)-Set2, DAB-Set4, Drought-tolerant black, colored, small-red and mix-colored beans. Analysis of variance for AMMI model indicated significant differences ($P<0.05$) among lines for most variables and environments ($P<0.001$). Performance was better at Kachwekano with mean yields ranging from 928 kgha-1 to 2209 kgha-1, and 698 kgha-1 to 2008 kgha-1 at Kawanda. Angular leafspot, common blight and rust varied more among nurseries than locations with scores of 1-6. Basing on Finlay Wilkinson estimates, most lines had positive sensitivities for yield implying that they performed well in good environments and are sensitive to environmental changes. Of the 448 lines, 18.4% maintained >1500 Kgha-1, the minimum anticipated commercial yield of new varieties. The outstanding lines included DAB299 (3215-3438 kgha-1), DAB293 (2102-3075 kgha-1), DAB259 (2099-3043 kgha-1), DAD34 (2185-3944 kgha-1), SCN14 (2716-3536 kgha-1), SCR66 (2557-3150 kgha-1), SCN15 (2628-2634 kgha-1), SCN20 (2414-2568 kgha-1),NCB280 (2417-2882 kgha-1) and SER335 (2417-2802 kgha-1). Many superior lines were identified but only those with stable yields across environments are recommended for development of new varieties with drought tolerance.

IDT6-005 | Performance of some sorghum varieties as affected by heat stress under irrigation in Northern Nigeria

Angarawai, I.I[1]., Ajeigbe, H.A[1]., Umar, H G[1]. and Yeye, M[2].

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nigeria
[2]Institute for Agricultural Research, Ahmadu Bello University (IAR,ABU) Samaru Zaria, Nigeria
*E-mail: I.Angarawai@cgiar.org

Exposure of sorghum (*sorghum bicolor*) during flowering time for a period of 10-15 days to high temperature stress (>36-38°C) reduced pollen germination, failure of fertilization and flower abortion. A number of improved varieties of sorghum have recently been released for the Sudan and Sahel zones of Nigeria, with their dissemination limited by seed availability. In order to improve the supply of Breeder and Foundation seeds for production of certified, these varieties; SAMSORG 45 and SAMSORG 46 with two old but popular varieties SAMSORG 41 and SAMSORG 17 were grown under irrigation at Dadinkowa (10.18N, 11.27S) to assess their productivity during the dry season at two planting dates (October and January) for 2 seasons (2015 & 2016). Result showed that October planting which flowering and seed set coincided with the average maximum temperature of 27°C recorded in January produced good seed while December/ January planting which flowering and seed set coincided with average maximum temperature of 42°C recorded in April had poor or no seed set on panicles especially in 2016. Rise in the average maximum temperature (2016) in the month of March (35°C) and April 2016 (41°C) resulted to 90-100% no seed set on SAMSORG 17, SAMSORG 45 and SAMSORG 46 as it coincided with the flowering time thus producing sterile panicle. This suggest that planting date and temperature significantly affect seed production of sorghum in the dry season.

IDT6-006 | Influence of severe drought on oleic acid content and seed yield of high oleic Indian safflower varieties

Kammili A[1]*, Yadav P[1]

[1]ICAR-Indian Institute of Oilseeds Research, Hyderabad-500030, Telangana, India
*E-mail: k.anjani@icar.gov.in

High-oleic safflower (Carthamus tinctorius L.) oil is desired by industry because of its high oxidative stability for broader uses in food, fuel, and other sectors. Demand for oleic oils is increasing recently. Three high-oleic cultivars, ISF-1, ISF-2 and ISF-3, were developed for the first time in India at the ICAR-Indian Institute of Oilseeds Research, Hyderabad. The objective of this investigation was to test the influence of drought on oleic acid content of high oleic cultivars. During 2015-16, ISF-1, ISF-2 and ISF-3 and 13 non-oleic varieties were grown in RBD with three replications at 10 locations in India. Experiments were conducted under severe drought conditions at four locations and under irrigated (1or 2 irrigations) conditions at six locations. The mean rainfall received during safflower crop period (October-April) was 35 mm. ISF-1, ISF-2 and ISF-3 had high mean oleic acid content (75%-76%) as compared to non-oleic varieties (14%-17%) across locations. High oleic varieties had 3%-5% lower oleic content (72%-73%) under dry conditions than that (76-78%) recorded in irrigated conditions. High temperatures and severe moisture stress that prevailed at dry locations might have caused reduction in oleic acid levels. Oleic acid content of oleic varieties has not changed when grown in warmer-irrigated and cooler-irrigated locations. This suggests that the effect of temperature was mitigated when irrigation was provided. Drought has severely reduced seed yield in all varieties, however, ISF-1 and IFS-2 recorded 15% and 9% higher seed yield; and 23% and 27% higher oil yield than the best check variety, A1 over the locations.

IDT6-007 | The influence of drought on the expression of quality parameters in bread wheat

Veeresha, BA[1]*, Rudra Naik V[2], Suma S. Biradar[3], Desai, SA[4], Chetti, MB[5] Kalappanavar, IK[6], Deepak, DA[7] and Joshi, AK[8]

[1-3]AICRP on Wheat, MARS, UAS, Dharwad, Karnataka, India
[4]Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka, India
[5]Indian Council of Agriculture Research, New Delhi, India
[6]AICRP on Tobacco, ARS, Nippani, UAS, Dharwad, Karnataka, India
[7]Department of Genetics and Plant Breeding, UAS, Dharwad, Karnataka, India
[8]Global Wheat Programme, CIMMYT, India
*E-mail: ambavee@gmail.com

Wheat is an important cereal crop grown worldwide and has various end uses. Today, the most challenging task for wheat breeders is not only to increase grain yield but also to improve the grain quality for end products to meet the requirement of ever increasing population and consumer preference. Thus wheat quality becomes a major target in wheat breeding program for the world wheat trade. The environmental conditions like high temperature and water deficit can potentially affect wheat quality. The aim of this study was to assess the extent of effect of the drought stress on quality traits in different genetic backgrounds. A set of hundred bread wheat genotypes were evaluated under drought and irrigated conditions during *rabi* 2014-16. The pooled data was used to identify drought tolerant genotypes with better quality based on drought tolerance trait index (DTTI). Drought resulted in grain shriveling and increased grain hardness. The protein content and sedimentation value was substantially altered. This explains the wide variation in quality of wheat due to strong differences in terms of year conditions. Prolonged drought reduced grain yield, indirectly by reduced performance of sensitive traits *viz.,* thousand grain weight, number of productive tillers, relative water content and leaf waxiness. The genotypes *viz.,* HD 2967, HUW 689, BAXTER and QLD 68 with high protein content (%) and sedimentation value (ml) with average grain yield (kg/ha) were promising. Thus identified trait specific drought tolerant genotypes could be the source of donors for the improvement of quality traits under drought stress.

IDT6-008 | Genetic diversity and population structure among assorted group of genotypes pertinent to reproductive stage drought stress in rice (*Oryza sativa* L.)

A. Mahender, A. Anandan*, H. Shafina, S.K. Pradhan and O.N. Singh

Division of Crop Improvement, ICAR-National Rice Research Institute, Cuttack -753006, Odisha, India
*E-mail: anandanau@yahoo.com

Rice is an imperative foods crop for half of the world population and it needs enormous quantity of water throughout the life cycle as compared to other crops. Due to rise in temperature and global warming, sufficient quantity of water availability is one of the major challenges in present scenario for increasing the rice grain productivity. To overcome these situations, it is necessary to identify suitable rice genotypes for drought tolerance through phenotypic and genotypic approaches. Therefore, in the present experiment, 76 rice accessions were evaluated for their morphological and yield attributed traits under drought stress in reproductive stage during the dry season of 2012 and 2013 and the same set of genotypes were genotyped using 36 SSR markers covering twelve chromosomes. By phenotypic approaches, PC1 and PC2 of principal component analysis (PCA) for yield traits showed variability of 74.77% and 9.68% respectively in 2012 and 67.71% of PC1 and 16.22% of PC2 accounted of the total variance in the year of 2013. Molecular genetic diversity of these genotypes was studied and an average number of alleles were 2.66 per locus and estimated average polymorphism information content (PIC) was 0.67. Among the total 96 alleles, seven unique alleles, 18 rare alleles were found across 76 rice genotypes and an expected heterozygosity or gene diversity (He) ranged from 0.576 (RM237) to 0.01 (RM25368) with an average of 0.267 and Shannon's Information index ranged from 0.9611 (RM237) to 0.0396 (RM25368) with an average of 0.476. Further, STRUCTURE analysis of these genotypes were divided into two sub-populations (at K=2) with a membership percentage of 56.7% in Pop1 and 43.3% in Pop2 and their fixation index (FST) values of subpopulations were 0.496 and 0.021 for Pop1 and Pop2, respectively. AMOVA results revealed that 3.6% of the total variation was identified among the populations and 96.4% was within the population. The genetic similarity (GS) between 45 improved rice varieties and 31 land races of rice accessions varied from 0.0282 to 0.9679 and pair-wise genetic distance of genotypes showed two major clusters I and II at 0.30 and further divided into two sub-clusters at 0.24 respectively. Therefore, the phenotypic and genotypic evaluation results revealed significant diverse between the landraces and improved varieties.

IDT6-009 | Screening for drought tolerance among elite cowpea (*Vigna unguiculata* (L.) Walp) lines.

Attamah P[1]*, Akromah R[1], Kusi F[2], Nyadanu D[1], Huynh B[3], Close TJ[4], Roberts PA[3]

[1]Department of Crop & Soil Sciences Kwame Nkrumah University of Science & Technology, Kumasi, Ghana
[2]Council for Scientific and Industrial Research - Savannah Agricultural Research Institute (CSIR – SARI), Manga and Tamale, Ghana
[3]Department of Nematology
[4]Department of Botany & PlantSciences, University of California, Riverside, CA, USA
*E-mail: attamahpat@yahoo.com

A successful crop improvement program thrives on the availability of genetic variation. Thirty Savannah Agricultural Research Institute (SARI Ghana) favorite cowpea (*Vigna unguiculata* (L) Walp) genotypes were evaluated in two separate experiments for seedling stage and reproductive stage (terminal) drought tolerance. Seedling stage drought tolerance screening was done using the wooden box technique in a screenhouse while the terminal drought tolerance screening was conducted by growing the genotypes under drought stress and watered conditions on the field. Results showed that for seedling stage drought tolerance, low leaf wilting index, high survival rate (above 50%) and higher number of leaves per plant were useful criteria for identifying drought tolerant genotypes. Genotypes responded differently to terminal drought stress. High-yielding genotypes were greatly reduced than low-yielding genotypes, indicating the presence of genotypic variation. Yield under drought stress was correlated with number of pods per plant and pod length. A principal component biplot display of yield (stressed and non-stressed) and the quantitative indices of drought tolerance (mean productivity, geometric mean productivity, tolerance index, stress susceptibility index and stress tolerance index) grouped genotypes into four clusters based on yielding ability and drought tolerance. Asetenapa, SARC1-91-1, 374*APA, IT99K-573-1-1 and AV2 3224 were genotypes in cluster I that combined high yields with terminal drought tolerance. SARC1-91-1 and 374*APA combined both seedling and terminal drought tolerance. The presence of genetic variability among the genotypes used in this study provides opportunity for cowpea improvement for drought tolerance.

IDT6-010 | Evaluation of wheat (*Triticum aestivum* L.) genotypes for post anthesis drought tolerance

Bansal R*, Sharma S, Kumari J, Rana JC

National Bureau of Plant Genetic Resources, New Delhi 110012, India
*E-mail: Ruchi.Bansal@icar.gov.in

Wheat (*Triticum aestivum* L.) is an important staple food crop cultivated in a wide range of environment from tropical to temperate. Wheat productivity is critically limited by water scarcity at reproductive stages. Present study was conducted to evaluate wheat genotypes for post anthesis drought tolerance. A pot experiment was conducted in randomized complete block design with 24 wheat genotypes. Stress was imposed after two weeks of anthesis by maintaining 50% field capacity in stressed and 80% field capacity in control plants till maturity. Different physiological parameters including relative water content (RWC), chlorophyll content, chlorophyll fluorescence, membrane stability index (MSI), normalized difference vegetation index (NDVI), peduncle length, canopy temperature and proline content along with the yield per plant and 1000 seed weight were recorded in control and stressed plants. Results showed that RWC, MSI, NDVI, peduncle length, seed yield and test weight reduced, while, canopy temperature and proline content increased significantly during stress. Total chlorophyll and fluorescence did not follow any particular trend in the studied genotypes. Drought susceptibility index (DSI) for grain yield varied from 0.34 to 1.36. Linear correlation study showed that DSI was negatively correlated with RWC (0.49), NDVI (0.43) and 1000 seed weight (0.43). KP1855, KP 1858, KP1869 and KP1874 (DSI < 0.5) were drought tolerant among the studied genotypes. The study concluded that these traits can be useful as selection criterion for drought tolerance either separately or simultaneously. However, importance of trait in relation to stress severity and different developmental stages need to be considered.

IDT6-011 | Super early pigeonpea varities and hybrids: New intervener for maximized, time specific dry land production

Shruthi HB[1,2], Hingane AJ[1], ReddiSekhar M[2], Srivarsha J[1,3], Bhosle TM[1,3], Saxena RK[1], Varshney RK[1], Gaur PM[1], Wani SP[1], Sameer Kumar CV[1]

[1]International Crops Research Institute for Semi- Arid Tropics (ICRISAT), Hyderabad, India
[2]Acharya N. G. Ranga Agricultural University (ANGRAU), Guntur, India
[3]Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India
*E-mail: c.sameerkumar@cgiar.org

A neglected crop of yester-years, pigeonpea (*Cajanus cajan*[L.] Millspaugh) is a multi-purpose, versatile food legume, which has seen greater evolution in its plant architecture, duration and yield pattern as time passed. In rainfed ecologies across the globe, pigeonpea fits in as a remunerative option to the farmers. Frequent droughts in recent past have resulted in losses to crops such as cereals, millets and oil seeds, but pigeonpea in the same cropping niche provided at least minimum assurance to small and marginal farmers, owing to its drought tolerance and ability to withstand harsh environments. The enormous variability and plasticity of the crop provided an opportunity to breeders to develop super early maturity group with the life span of less than 100 days. The existing maturity duration -- early (less than 140 days) and medium (180 to 200 days) -- imposes restrictions on adaptation to drought. The super early genotypes provide the foundation for future pigeonpea breeding because of their earliness, photo insensitive nature, impressive per day productivity, adaptability across the varying range of altitudes, stress escape mechanism and niche to fit well in various agro-ecologist and cropping systems. Rapid generation turnover is a boon to breeders for faster introgression of traits of interest, to carry out studies on genetics of biotic and abiotic stress by developing mapping population within very short duration. In the above context, "super early varieties and hybrids, is a wonderful breeding material to secure future sustainable dry land pigeonpea production".

IDT6-012 | Fine mapping of QTL for grain yield under drought using rice lines adapted to target populations of environment

Bharathi A[1], Helan B. T[1], Reena S[1], Ashish R[1], Chandra Babu R[1*]

[1]Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, India
*E-mail: chandrarc2000@yahoo.com

Drought is one of the most serious challenges in rice production worldwide, especially in rainfed ecosystems. Developing high-yielding rice varieties combined with drought resistance will help to increase productivity in drought-prone areas. Conventional breeding for drought tolerance is slow due to difficulty in phenotyping of large progenies. Mapping quantitative trait loci for yield and its components under drought stress predominant in target populations of environment will help to overcome this limitation. A consistent QTL for yield under drought on chromosome 1 between RM8085 – RM3825 (1.6 Mb) was identified in this laboratory using a recombinant inbred (RI) lines of IR20 x *Nootripathu* and was used for fine-mapping in this study. A set of 67 SSR markers were selected within the QTL region and 12 markers polymorphic among the parents were used in genotyping of the 220 RI lines. The linkage map of chromosome 1 was reconstructed with these additional markers to a length of 251.6 cM and average marker interval of 11.4 cM. The grain yield QTL was fine-mapped to a smaller segment (42.8 kb). The same region was found to be linked to total biomass and plant height under drought in TPE.

IDT6-013 | Correlated response of various morpho-physiological and biochemical traits with yield under heat stress condition in chickpea (*Cicer arietinum* L.)

Bohare T. V.[1], Kulwal P. L.[2*], Mhase L. B.[3], Kale A. A.[4]

[1]Mahatma Phule Krishi Vidyapeeth, Rahuri- 413722 , Dist. Ahmednagar, Maharashtra (India)
[2]State Level Biotechnology Centre, M.P.K.V., Rahuri- 413722, Dist. Ahmednagar, Maharashtra (India)
[3]Pulses Improvement Project, M.P.K.V., Rahuri 413722, Dist. Ahmednagar, Maharashtra (India)
[4]State Level Biotechnology Centre, M.P.K.V., Rahuri-413722, Dist. Ahmednagar, Maharashtra (India)
[*]E-mail: pawankulwal@gmail.com

Chickpea is a temperate, cool season legume often experiences increasing high temperature stress with advancing stages of crop growth and results in significant yield reduction. Temperature of 35 ºC and above are said to be critical in differentiating heat-tolerant and heat-sensitive genotypes in chickpea under field conditions. In the present study, forty nine chickpea genotypes comprising released varieties and advance breeding lines from central zone were used and phenotyped in order to understand correlated response of morpho-physiological and biochemical traits with yield under variable natural environmental condition in respect to temperature. The genotypes were sown during three different late sown conditions *viz*., first week of November 2015, first week of December 2015 and first week of January 2016. Amongst the various morphological parameters, canopy temperature depression (CTD) and amongst the various biochemical parameters, activity of enzyme ascorbate peroxidase (APX) was found to be significantly correlated with yield in all the three different durations of sowing. On the basis of mean performance of yield/plot recently released variety Phule G 08108 was found to be less fluctuating genotype in response to heat stress than others and exhibited high total leaf chlorophyll, high CTD, low thermal stress index, high relative leaf water content and high APX content under all growing periods. The results reveal that high total leaf chlorophyll, high CTD, high RLWC with low TSI, and/ or enzymatic activities like APX can effectively be used to identify genotypes performing better under heat stress conditions.

IDT6-014 | An image-based automated pipeline for maize ear and silk detection in a high-throughput phenotyping platform

Brichet N[1], Cabrera-Bosquet L[1]*, Turc O[1], Welcker C[1], Tardieu F[1]

[1]UMR LEPSE, INRA, Montpellier SupAgro, 34060, Montpellier, France
*E-mail: llorenc.cabrera-bosquet@inra.fr

Water deficit strongly impacts silk growth and silk emergence in maize (*Zea mays* L.), which in turn determines the final number of ovaries developing grains (Turc *et al*. 2016, Oury *et al*. 2016). However, phenotyping silk growth and silk expansion is difficult at throughput needed for genetic analyses. We have developed an image-based automated pipeline for maize ear and silk detection in a high-throughput phenotyping platform. The first step consists of selecting the best whole plant side images containing maximum information for each plant and day as that containing the most leaves and whole stem, based on top view images. In the second step, the best side images are segmented and skeletonized, and potential ear positions are determined based on changes in stem widths. The x, y, z ear position identified in this way serves to pilot the movement of a mobile camera able to take a detailed picture taken at 30 cm from the ear, with the final aim of determining silk emergence and silk growth duration. These methods were tested at the PhenoArch plant phenotyping platform (www6.montpellier.inra.fr/lepse/M3P) in a panel of 300 maize hybrids. First results showed that in >80% of cases, ears were successfully detected before silking and duration of silk expansion significantly correlated with visual scores. The image pipeline presented here opens up the way for large-scale genetic analyses of control of reproductive growth to changes in environmental conditions in reproductive structures.

IDT6-015 | Yield stability under reproductive-stage drought stress in Swarna/Moroberekan advanced backcross introgression lines (BILs) of rice

Venkateshwarlu CH[1], Raman A[1,2], Ramayya PJ[1], Singh UM[1], Yadav S[2], Dixit S[1], Nagamallikadevi M[1], Nachimutthu VV[1], Naik SM[1], Jain A[1], Vipparla AK[1], Priyadarshi R[1], Alam S[1], Arvind Kumar[1,2]*

[1]International Rice Research Institute -South Asia Hub, ICRISAT, Hyderabad, India
[2]International Rice Research Institute, Metro Manila, Philippines
* E-mail: a.kumar@irri.org

Drought is one of the major abiotic stresses frequently affecting rice yield in many rainfed environments. Evaluation of breeding lines under both irrigated control and drought stress conditions would be useful in identifying lines that possess stable yield across the two conditions. In the present study, breeding lines were developed from a cross between Moroberekan, a drought-resistant tropical japonica variety with poor yield potential, and Swarna, a popular semi-dwarf indica variety that shows high yield potential. Advanced backcross introgression lines derived from the Swarna x Moroberekan cross and carrying *qDTY3.2* were then evaluated under both non-stress and reproductive-stage drought during the wet and dry seasons from 2012 to 2015 at the IRRI-South Asia Hub, ICRISAT, India. An initial population of 420 BC2F3 lines in 2012 was subsequently reduced to seven in the year 2015 by repeated selections. Drought stress was imposed at the onset of the reproductive phase and maintained until grain filling by withholding irrigation until water table depth reached 100 cm below ground level to cause severe leaf rolling in more than 50% lines including susceptible checks. The control trials were watered on a daily basis till crop maturity. Observations on days to flowering, plant height and grain yield were recorded. Promising lines yielding up to 1.5 to 2.0 t/ha under severe drought stress with yields of more than 5.0 t/ha under irrigated control and stable performance over the years were identified.

IDT6-016 | Characterization of low Ca2+ stress-induced embryo apoptosis response genes and their regulation of embryo development

Chen H[1,2,3], Zhang C[1,2,3], Cai TC[1,2,3], Deng Y[1,2,3], Zhou SB[2], Varshney RK[4], Zhuang WJ[1,2,3]*

[1]State Key Laboratory of Ecological Pest Control for Fujian and Taiwan crops, Fujian Agriculture and Forestry University, Fuzhou, 350002, Fujian, P.R. China
[2]Fujian Provincial Key Laboratory of Crop Molecular and Cell Biology, Fujian Agriculture and Forestry University, Fuzhou, 350002, Fujian, P.R. China
[3]College of Plant Protection, Fujian Agriculture and Forestry University, Fuzhou, 350002, Fujian, P.R. China
[4]International Crops Research Institute for the Semi-Arid Tropics, Center of Excellence in Genomics, Patancheru, Andhra Pradesh, India
*E-mail: weijianz@fafu.edu.cn

Ca2+ deficiency in soil induces early embryo abortion in peanut, producing empty pods, or ill-filled pods, especially under drought condition, which is a general problem. However, the underlying mechanism remains unclear. In this study, embryo abortion was characterized to be caused by apoptosis marked with cell wall degradation. Using a method of SSH cDNA libraries associated with library lift (SSHaLL), 62 differentially expressed genes were isolated from young peanut embryos, which were classified to be stress responses, catabolic process, carbohydrate and lipid metabolism, embryo morphogenesis, and regulation. The cell retardation with cell wall degradation was caused by up-regulated cell wall hydrolases and down-regulated cellular synthases genes. Two *CYP707A4* genes, encoding abscisic acid (ABA) 8′-hydroxylases, key enzymes for ABA catabolism, were up-regulated by 21-fold under Ca2+-deficient conditions, reducing the ABA level in early embryos. Over-expression of *AhCYP707A4* in *Nicotiana benthamiana* showed a phenotype of low ABA content with high numbers of aborted embryos, small pods and less seeds, which confirms that *CYP707A4* is a key player in regulation of Ca2+ deficiency-induced embryo abortion via ABA-mediated apoptosis. The results elucidated the mechanism of low Ca2+-induced embryo abortion. A set of varieties with different sizes of pods were evaluated for their tolerance to calcium stress, and we found that big pod varieties showed less tolerance to low calcium and more easy to produce ill-filled pods or empty pods. Drought will make worse of the phenomenon. Soil supplied with rich calcium will improve the pods filling and greatly reduce number of empty pods. We conclude big-pod varieties easier to produce empty pods are also associated with calcium level in the soil.

IDT6-017 | Variation in shoot biomass, δ13C and pod yield in an advanced breeding groundnut lines

Oteng-Frimpong R[1]*, Kassim B Y[2], Danful R[2], Dakora F D[3]

[1]Savana Agriculture Research Institute, Nyankpala, Ghana.
[2]Kwame Nkrumah University of Science and Technology, Kumasi, Ghana.
[3]Department of Chemistry, Tshwane University of Technology, Private Bag X680, Pretoria 0001, South Africa.
*E-mail: kotengfrimpong@gmail.com

The erratic rainfall pattern of the semi-arid Guinea savanna agro-ecology of Ghana and its devastating effect on smallholder farms has sparked an interest in developing varieties that are stable to stress imposed by drought. However, progress has been slow due to the complex nature of the drought tolerance trait. Yield has been used as an indicator for drought tolerance under water stress condition, but this is influenced by G×E. Hence there is a need to rely on traits that are easy to score and less prone to G×E effects. The study was carried out to (i) assess the performance of 21 advanced groundnut breeding lines in the semi-arid agro-ecozone of Ghana and (ii) determine the genetic variation in shoot δ13C among the groundnut genotypes. Twenty one genotypes of which two are known drought-tolerant lines were grown in six environments under rain-fed conditions, arranged in an RCBD with four replications. There was genetic variation among the genotypes for shoot δ13C, shoot biomass and pod yield. However, shoot biomass and pod yield were very susceptible to environmental effects, while shoot δ13C was minimally affected by the growth environment. Genotype ICGV 99247, which has been confirmed to be drought tolerant from previous field experiments, consistently recorded the highest shoot δ13C across environments. This confirms the superiority of the genotype as one with drought tolerance and also the method used. Since shoot δ13C values were less affected by environmental conditions as observed in this study, this traitmay be a suitable selection tool for drought tolerant groundnut genotypes.

IDT6-018 | Comprehensive assessment of drought tolerance related traits in temperate maize inbred lines

Z. A. Dar[1]*, J. A. Khan[2], A.A.Lone., M. S. Sheshsayee[2], Pratibha, M. D.[2], B.A. Alaie., P.A. Sofi and I. Abidi

[1] DARS, SKUAST-K
[2]University of Agricultural Sciences, Bangalore-560065, Karnataka, INDIA
*E-mail: zahoorpbg@gmail.com

Drought which is considered as a complex trait can be comprehensively accessed if plant physiology and phenotyping are prioritized. Temperate maize germplasm maintained at D(K)ARS, SKUAST-Kashmir consisting of twenty eight inbred lines and two checks were evaluated for various drought tolerance related traits which included root morphology, water use efficiency and epicuticular wax content (ECW). For root study special root structures, which mimic the real field conditions, were built and seeds were sown on appropriate spacing. Structures were dismantled after 40 days after sowing (DAS). Water use efficiency was assessed through use of isotopic surrogates (C13). Wax reagent was prepared using maize leaves and the samples were filtered using the filter paper and OD was read at 590 nm using spectrophotometer, a standard curve with a regression value (R^2) of 0.987 was developed. Promising lines identified were KDM-932A (82.00 cm) for root length, KDM-1095 for root volume (51.67ml), KDM-918A for root weight (5.31g/plant), which can be used as trait donor lines to transfer root traits. EWC ranged from 1.56 (KDM-921A) $\mu g/cm^2$ to 7.54 (KDM-954) $\mu g/cm^2$ with a mean of 4.25 $\mu g/cm^2$.The frequency distribution also indicated the spread of genotypes across the mean to suggest the existence of an appreciable genetic variability for these traits in maize genotypes and hence, having the differential capacity to withstand environmental stress. Varied drought tolerant strategies like root morphological changes and ECW deposition among different inbred lines, signify the requirement of next generation breeding strategies which undoubtedly needed a preliminary comprehensive assessment of drought tolerance.

IDT6-019 | Male sterility (Ms44) increases reproductive resilience under abiotic (drought and nitrogen) stress for maize hybrids

DeBruin J[1*], GhoC[2], Cooper M[3], Messina C[3], Collinson S[4], Albertsen M[3]

[1]Dupont Pioneer, Adair, 61411, Illinois, United States of America
[2]Dupont Pioneer, Viluco, Buin, Chile
[3]Dupont Pioneer, Johnston, 50131, Iowa, United States of America
[4]Dupont Pioneer, Woodland, 95695, California, United States of America
*E-mail: jason.debruin@pioneer.com

Drought during the flowering period in maize (*Zea mays L.*) slows ear growth, reduces kernels ear-1 (KPE) and grain yield. These changes may be the result of relative sink strength prioritizing the tassel over the ear. Male sterility could reduce competition between the tassel and ear and was first tested in a B73xMo17 hybrid with favorable yield and KPE results. Elite inbreds carrying Ms44 were developed and crossed to form a hybrid segregating 1:1 for sterility. Yield trials during two years in the USA (multiple stress environments) and one season in Chile (multiple drought stress and plant density treatments) compared segregating hybrids to fertile hybrids. Hybrids containing 50% sterile plants increased grain yield to 163 kg ha-1, 263 kg ha-1, and 94 kg ha-1 under drought, limited N, and moderate or limited stress, respectively. Yield improvement was associated with greater silk number (limited N) and maintenance of kernels (limited N and drought). A transgenic maintainer line(AG533) was developed that contains a seed marker, non-viable transgenic pollen and a fertility restoration function by silencing Ms44. The maintainer carries the Ms44 allele but maintains fertile (non-transgenic) pollen through the fertility restorer AG533. Seed produced from the inbred maintainer is non-transgenic and segregates 1:1 asfertile (red) and sterile (yellow). Sterile-female inbreds are crossed to fertile-male inbreds to produce hybrids that segregate 1:1 for fertility. The segregating hybridswould be available to growers and allows for deployment of the Ms44 technology to increase grain yield over a broad production area.

IDT6-020 | Studies on physiological and biochemical parameters in *hirsutum* cotton genotypes for drought tolerance

Deosarkar D.B.*, Dalvi D. G. and Kalyankar S. V.

Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani 431 402, Maharashtra, India
*E-mail : dbdeosarkar@gmail.com

Changing climate is influencing the onset withdrawal and distribution of monsoon rainfall. Cotton production is limited by biotic and abiotic stress factors, among them drought or water deficit is a complex phenomenon effecting the physiology of cotton plant in turn reduces crop growth and yield. An experiment was conducted during 2013-14 to 2014-15 using twenty Gossypium hirsutum genotypes grown in RBD design at cotton Research station Nanded to evaluated for genotypic variability on physiological and biochemical parameters under irrigated as well as in water deficit rainfed condition. The two years pooled data showed that among the 20 genotypes, the strain TSH-04-115 followed by RAH-806,BS-37,NH-615(LC) and BS-39 were recorded significantly highest seed cotton yield (kg/ha) associated with higher yield /plant (g), No. of bolls/plant and boll weight (g) in both protected and unprotected condition, whereas the genotypes ARBH-1352,GBHV-182,NDLH-1938 and SCS-1213 were recorded (9.0 to 15.5 %) least reduction in yield , chlorophyll stability index , drought susceptibility index (S) (< 1.0) , higher relative water content(%), Proline content(%) and yield stability index in rainfed condition. Similarly, these genotypes shows earliness in terms of 50% flowering, 50% boll brusting and indicating better water stress tolerance capacity under rainfed condition. These genotypes can be used as desirable genotypes for drought tolerance in breeding programme for development of new drought tolerance varieties and hybrids in cotton.

IDT6-021 | Transcriptomics of drought tolerant sorghum landraces

Devnarain N[1,2]*, Crampton BG[3,4], Olivier N[3], Becker JVW[5], O'Kennedy MM[1]

[1]Council for Scientific and Industrial Research (CSIR) Biosciences, Pretoria, South Africa
[2]Department of Genetics, University of Pretoria, Pretoria, South Africa
[3]Department of Plant and Soil Sciences, University of Pretoria, Pretoria, South Africa
[4]Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Pretoria, South Africa
[5]African Centre for Gene Technologies (ACGT), Pretoria, South Africa
*E-mail: natrisha.devnarain@gmail.com

Sorghum landraces are broadly adapted to the African climate and represent a reservoir of genetic biodiversity that may advance the understanding of molecular mechanisms governing drought tolerance. In this study, three drought-tolerant sorghum landraces (LR5, LR6 and LR35) were selected for transcriptomics from a previous investigation which evaluated their physiological responses to progressive water stress and moderate re-watering during the reproductive growth stage. Plants were subjected to mild (4 d) and severe (6 d) water stress treatments and a moderate re-watered treatment during which plants were harvested 5 h after re-watering on day seven. Subsequently, transcriptome profiling that represented a direct comparison between treatment and control was conducted. cDNA synthesized from leaf mRNA was dye-labelled and hybridized onto Agilent sorghum microarrays which comprised 35899 transcript probes. Data were analysed using GenePixPro 6.1, LIMMA and R-Statistics. The gene IDs and functional annotation information were sourced from online databases (BLAST, MOROKOSHI and SorghumCyc). A total of 1797 genes were differentially expressed in these landraces during progressive water stress and moderate re-watering. Quantitative RT-PCR was conducted on three genes belonging to a selected pathway of interest, which may play a significant role in ameliorating the effects of drought stress in sorghum. This study revealed an extensive gene expression profile underlying drought tolerance in three previously uncharacterized South African sorghum landraces. Differentially expressed genes identified in this study may be used as possible targets for marker-assisted breeding initiatives for sorghum, as well as other closely related crop species.

IDT6-022 | Yield and lint quality of Bt –cotton (*Gossypium hirsutum* L.) as influenced by seed polymer coating and foliar spray with micronutrients

Doddagoudar S. R[1*], Aralakkanavar Anup[1], Vasudevan S. N[1]., Shakuntala N. M[1]., Nidagundi J. M.[2]

[1]Department of Seed Science and Technology, College of Agriculture, University of Agricultural Sciences, Raichur-584104, Karnataka, India.
[2]Main Agricultural Research Station, Cotton Breeding Unit, UAS, Raichur
*E-mail: srdsst@gmail.com

Polymers encounter stress during seed germination in the field. They prolong the moisture supply under water stress conditions and increase the consumptive use efficiency. With this background, a field experiment was conducted during *kharif* 2014 at College of Agriculture, UAS, Raichur, with an objective to study the influence of seed polymer coating and foliar spray with micronutrients on yield and lint quality of *Bt* cotton hybrid. The experiment consisted of 17 different seed polymer coating and foliar spray treatments with micronutrients in laid out in randomized block design in three replications. The results revealed that seed polymer coating with ZnSO4 + FeSO4 + MgSO4 + MnSO4 each @ 4 g kg-1 of seed along with two foliar sprays (0.5 % + 0.5 % + 1 % + 0.5 %,respectively, in EDTA form except MgSO4) at an interval of ten days during flowering stage (65 AND 75 DAS) recorded significantly higher plant height (156.2 cm), chlorophyll content (45.20 SPAD values) at 90 DAS, number of bolls (41.57), boll weight (5.54 g), seed index (13.57 g) and seed cotton yield (29.03 q), compared to all other treatments and control (129.5 cm, 38.90 SPAD values, 36.83, 4.35 g, 11.37 g AND 24.77 q, respectively). The lint quality parameters did not show any significant difference due to seed polymer coating and foliar spray with micronutrients in *Bt* cotton hybrid.

IDT6-023 | Morpho-anatomical and productive traits in wheat genotypes contrasting for peduncle water-soluble carbohydrates content

Dodig D[1]*, Šešlija A[2], Kandić V[1], Vucelić-Radović B[2], Rančić D[2]

[1]Maize Research Institute Zemun Polje, 11185 Zemun-Belgrade, Serbia
[2]University of Belgrade, 11080 Zemun-Belgrade, Serbia
*E-mail: dejanza@yahoo.com

Water-soluble carbohydrates (WSC) assimilated during vegetative and early reproductive growth in wheat is temporarily stored in stem internodes, and can later be remobilized and transported to developing grain. In this study the WSC content and the WSC specific content (WSSC) were determined in the uppermost internode (peduncle) of the main stem at 10 days after anthesis (10 DAA) across 44 wheat genotypes in two-year field trials. The defoliation was done at 10 DAA by cutting off all leaf blades and these plants (DP) were grown along with the intact control plants (CP). Genotypes contrasting for WSSC were compared for productive and other traits in DP and/or CP plants. Estimated contributions of peduncle assimilate reserves to grain weight/spike in high-WSSC genotypes had significantly higher contribution ($P < 0.001$) in CP than low-WSSC genotypes (19.1 vs. 8.6%, respectively). The similar one-fold higher contribution ($P < 0.001$) to grain weight/spike from peduncle in high-WSSC genotypes than in low-WSC genotypes was estimated for DP plants (28.4 vs. 14.8%, respectively). Among 16 morphological, anatomical and developmental traits, the area of pith intercellular of peduncle, chlorophyll content in flag leaf and the flag leaf area appeared to be most important for WSC accumulation in peduncle, while biomass per main stem, area of parenchyma and again chlorophyll content in flag leaf had the greatest effect on WSSC. High WSSC genotypes tended to have higher grain weight per spike than low WSSC genotypes both in DP and CP plants.

IDT6-024 | Cultivars for flowering date and yield stability

Flohr B.M.[1]*, Hunt J.R.[2], Kirkegaard J.A.[1], Evans J.R.[3]

[1]CSIRO Agriculture, PO Box 1600, Canberra, ACT, 2600, Australia
[2]La Trobe University, AgriBio Centre for AgriBiosciences, Bundoora, VIC 3086
[3]The Australian National University, Research School of Biology, Canberra, ACT 0200,
*E-mail: bonnie.flohr@csiro.au

In drought-prone environments such as the Australian wheat belt, the time at which wheat flowers is a critical determinant of yield. Timing of flowering in a given environment is a function of establishment date, genotype (cultivar) and prevailing seasonal temperatures. Since the introduction of photoperiod insensitive semi-dwarf cultivars during the 1970s, breeding programs in Australia have focussed on cultivars in which development is fast and driven only by accumulation of thermal time.Establishment dates for fast developing cultivars which allow them to flower during the optimal flowering period for yield coincides with the most severe period of recent rainfall decline in southern Australia. A field experiment based in Temora, New South Wales, with four times of establishment investigated how flowering time stability has changed in local breeding programs since 1901, using a set of historic cultivars and a set of elite cultivars with varying development rates. Results from 2015 and 2016 show that over time genotypes have become less stable (due to reducing vernalisation and photoperiod sensitivities), removing the genetic x management advantages of a longer development phase delivered by early sowing and slow development. Results also show that when flowering time coincides, there has been no genetic yield gain in cultivars adapted to southern NSW since the 1970's. The highest yields were achieved by cultivars that flower within the optimal flowering period when sown over a wide sowing window i.e. have high flowering time stability. We explore the opportunities that exist to slow down development and stabilise flowering time in modern genotypes in order to offset the negative effects on wheat yield of recent autumn rainfall decline in south eastern Australia.

IDT6-025 | High throughput phenotyping (HTP) of root architecture to enhance the drought tolerance in maize (*Zea mays* L.)

Varsha Gayatonde[1]*, J. P. Shahi[1], K. Srivastava[1], Prudhvi Raj Vennela[1], A. Mahato[1]

[1]Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, U.P, India, 221005
*E-mail: varshapanchu@gmail.com

Maize is an important cereal after rice and wheat, grown mainly under rainfed conditions and is a the second most drought-susceptible cereal next to rice. Shallow root system in maize is a key reason behind drought proneness, as the roots are crucial for water acquisition and can be targeted to enhance plant productivity under various growth conditions. Root phenotyping is pivotal to reduce the genotype-phenotype gap, which are the major determinants of drought tolerance. It is primarily correlated with root angle, stem diameter, and root branching. Major traits are large diameter of primary roots, many seminal roots with shallow growth angle, small diameter, many lateral and long root hairs, abundant branching of crown roots, and more cortical aerenchyma. Gel or soil filled chambers, soil pouches, paper roles, soil digging and Wax layer mimicking hard soil pan are the basic materials to estimate the penetrating ability of different genotypes. Popular HTP techniques are: 1) Imaging: which includes, shovelomics, mini-rhizotrons to study fine roots, tube installation followed by imaging techniques to measure root depths, hand held capacitance meter to take direct measurements of uprooted plants, X-ray microphotography, Magnetic Resonance Imaging (MRI), ground-penetrating radar (GPR), automatic root image analyser (ARIA), gel based imaging, X-ray captured tomography (CT), high field microscopy followed by imaging. 2) Sensors and laser scanners. 3) Hydroponics and aeroponics - the rare methods to quantify the exact requirement of water. HTP helps in identifying the effects of temperature, genotype, water uptake and nutrient availability for root growth with high spatial and temporal precision. Some automated software to analyse these traits are WinRhizTRON, RootView, RooTracker, and MR-RIPL.

IDT6-026 | Inheritance and combining ability studies on drought tolerance and grain yield among early maturing inbred lines of maize (*Zea mays* L.)

Issa. Z.M.M.[1]*, Nyadanu. D[2], Richard. A[3]

[1]Natural Resources Management Department, National Institute of Agriculture Research of Niger
[2]Crop and Soil Sciences Department, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana
[3]Crop and Soil Sciences Department, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana
*E-mail: issazakarym@yahoo.fr

Utilization of stress tolerance maize is key to sustainable production and food security. Limited knowledge on genetics of drought tolerance hampers development of drought tolerant varieties. The objective of this study was to study inheritance and combining ability of drought tolerance and grain yield among early inbred lines of maize (*Zea mays* L.). Five tropical inbred lines were mated in full diallel in major season 2015. The resultant 20 hybrids, 5 parents and 2 checks were evaluated under drought stress and well watered conditions in a screen house in 2016. Data was collected on days to 50% tasseling (DT 50%), days to 50% silking (DS 50%), anthesis-silking interval (ASI), leaf rolling, leaf senescence, plant aspect (PASP), plant height (PHT), ear height (EHT), ears per plant (EPP), ear weight, hundred grain weight (100 GW) and grain yield per plant (GYPP). Drought condition was induced 40 days after planting but watering was continued once per week till maturity. Results from combined ANOVA showed there was high and significant ($p<0.01$) level of genetic variability among parental lines and hybrids used in all the traits studied except DT 50%, leaf senescence, PHT, EHT, EPP and 100 GW. There were significant variation in the combining ability of the inbreds under both conditions. Both additive and non-additive gene actions were important as well as GCA/SCA ratio variance. Therefore the predominance of GCA over SCA mean square for seven traits indicates that additive genetic action was more important than non-additive genetic action for inheritance of these traits. Lines TZEI-23 (3.91) and TZEI-25 (1.40) had the highest and highly significant ($p<0.01$) positive GCA effects for GYPP under drought condition. Hybrids TZEI-25 x TZEI-13 showed the highest positive and highly significant ($p<0.01$) SCA effects for GYPP (7.00) followed by its reciprocal TZEI-13 x TZEI-25 (5.66) under water stress. High narrow sense heritability were observed in only DT 50% (0.69), DS 50% (0.20) and leaf senescence (0.61) under drought condition. Eighteen and nineteen hybrids had positive HPH under water stress and well watered conditions, respectively for GYPP.

The parents TZEI-23 and TZEI-25 were identified as the best general combiners respectively under drought and well watered conditions. The highest HPH were observed in many traits for TZEI-13 x TZEI-25 and TZEI-124 x TZEI-13. It is recommended these hybrids for further evaluated in different environments for release to farmers to increase yield.

IDT6-027 | Drought priming induces thermo-tolerance to post-anthesis high-temperature in offspring of winter wheat

Zhang X[1], Wang X[1], and Jiang D[1 *]

[1]Key Laboratory of Crop Physiology and Ecology in Southern China, Ministry of Agriculture/Hi-Tech Key Laboratory of Information Agriculture of Jiangsu Province, Nanjing Agricultural University, P. R. China
*E-mail: jiangd@njau.edu.cn

High temperature stress is a worldwide environmental constraint on crop production. Exposure of plants to a stress event could induce tolerance in them and even in their offspring to subsequent stresses. This study was to test the hypothesis that drought priming of parent plants could trigger a cross tolerance to high-temperature stress in their offspring. Winter wheat plants were used and were firstly subjected to a drought stress during grain filling, and their offspring were exposed to a post-anthesis high-temperature stress. Grain yield, photosynthesis, anti-oxidation, and proteomic profile in wheat flag leaves of the offspring were determined. The results showed a less yield loss in the next generation of the wheat plants that had received drought priming, which could be ascribed to the improved photosynthesis because of the up-regulated expression of proteins involved in the light reaction and in the Calvin cycle, and to the enhanced anti-oxidation capacity as exemplified by the decreased contents of MDA and H_2O_2 because of the improved activities of SOD and POD. In addition, the proteomic analysis suggested that the enhanced thermo-tolerance could also be attributed to the more robust signal perception and transduction, better maintenance of protein structures, up-regulation of sucrose synthesis and accumulation of heat shock proteins.

IDT6-028 | Identification of genomic regions associated with the yield and related traits in pigeonpea (*Cajanus cajan* L. Millsp.)

Kaoneka SR[1,2], Saxena RK[1], Singh VK[1], Sameerkumar CV[1], Shimelis HA[2], Varshney RK[1,3]*

[1]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India
[2]University of KwaZulu-Natal, Pietermaritzburg, South Africa
[3]School of Plant Biology and Institute of Agriculture, The University of Western Australia, Crawley, WA, Australia
*E-mail: r.k.varshney@cgiar.org

Pigeonpea [*Cajanus cajan* (L) Millsp.] is an important multi-use shrub legume of the tropics, sub-tropics and warmer regions of the world, growing between 30°N and 35°S latitude. The goal of this study was to identify genomic regions associated with yield and related traits in three newly developed F2 mapping populations of pigeonpea; AL 201 × ICPL 20325, ICP 5529 × ICP 7035 and ICP 8863 × ICPL 87119. Genotyping by Sequencing (GBS) platform was used for genetic analysis and linkage analysis was performed using JoinMap version 4. Quantitative Trait Linkage (QTL) analysis of eight yield and yield-related traits were performed using single marker analysis (SMA) employing composite interval (CIM) using stepwise regression linear model. A total of 42 QTLs were detected, with 5 in AL 201 × ICPL 20325, 7 in ICP 5529 × ICP 7035 and 30 in ICP 8863 × ICPL 87119. Individual QTLs ranged from 1-4 per trait and the phenotypic value explained (PVE%) ranged between 10.35 -16.27% in AL 201× ICPL 20325,10.44 -17.9 in ICP 5529 × ICP7035 and 10.71-89.12% in ICP 8863 × ICPL 87119. The detected QTLs were co-localized within the same genomic regions, indicating the presence of pleiotropic effect or close genetic linkage. For further fine mapping and use in marker assisted transfer, validation for the accuracy and consistency of the identified QTLs in several, independent and diverse mapping populations transfer is crucial.

IDT6-029 | Less water better rice g(r)ains

Kavya HP[1,2], Ganesh D[1], Bharathprasad CT[2], Vinutha DN[2], Shashidhar HE[2]*

[1]Madurai Kamaraj University, Madurai - 625021, Tamil Nadu, India
[2]University of Agricultural Sciences, GKVK, Bengaluru - 560065, Karnataka, India
*E-mail: heshashidhar@gmail.com

Rice (*Oryza sativa* L.) grains lose valuable nutrients on polishing. Across crops, deficit irrigation, a mechanism of artificially inducing drought, is known to have a positive impact on quality and taste of produce. Naturally occurring drought may have positive impacts on grain nutritive value. The present study with 12 genotypes grown under aerobic and wetland conditions at GKVK in RCBD during *Kharif* 2015 and summer 2016 gave strong indications of biofortified rice with high yield. Phenotyping studies involved grain yield, zinc and iron content in brown rice and at varied levels of polishing. High zinc content in brown rice (Azucena; 40.2 ppm in *kharif*, and AM-1; 33.17 ppm in summer) and varied level of polishing (AM-72; 31.53 to 34.93 ppm in *kharif* and AM-65; 26.80 to 27.80 ppm in summer) was observed in aerobic condition in both seasons as compared to wetland. Meanwhile, percent loss in Fe content was more due to polishing of rice.High GCV, PCV coupled with high heritability at broadsense and GAM % was observed in Grain weight, number of tillers, number of productive tillers in all the genotypes in both seasons and contrasting water regimes. In addition, high GCV, PCV and heritability was noticed for Fe content in brown rice, and Fe and Zn content in varied level of polishing for 60 and 120 seconds in both seasons under contrasting water regimes.

IDT6-030 | Autophagy is critical to cope up with drought tolerance in rice (*O. sativa* L.)

Khan MS[1]*, Hemalatha S[1]

[1]B. S. Abdur Rahman University, Chennai-600048 (TN), INDIA
*E-mail: shahnawazkhandrr@gmail.com

Drought is a major constraint for rice production under rainfed conditions. Genomic analysis of drought resistant traits and yield under drought will help to develop resistant cultivar through gene silencing or transgenic approaches. Autophagy (self-eating) is an intracellular degradation process of recycling degraded or damaged proteins and organelles. It plays an important role during plant development, nutrient starvation, stress and senescence. All organisms (yeast to plants) contain multiple autophagy-associated genes (ATG). For the current study, drought stress was analyzed at morphological, biochemical, cellular and molecular level in the rice (*O. sativa*) seedlings. The real-time PCR analysis of genes encoding CAT, SOD, POX, WRKY53, MAPK1 and Bax-Inhibitor1 involved in programmed cell death and defense showed the differential expression of genes during drought stress in rice. The expression of autophagy genes ATG1, ATG3, ATG6, ATG7, ATG8, ATG9, ATG10, and ATG13 were analyzed in rice seedlings grown under drought stress. The identification of constitutive or differential expression of autophagy genes under drought stress will open up new avenues to identify the role of autophagy under stress conditions. This will also be helpful in developing drought resistant autophagy mutants and transgenics in rice.

IDT6-031 | Does bran drain the grain?

Khan, J. A[1]., Holla, S. K. M[1]., Shashidhar, H. E.[1*]

[1]University of Agricultural Sciences, Bangalore-560065, Karnataka, INDIA
*E-mail: heshashidhar@gmail.com

Science of drought needs to move forward from "*more crop per drop*" to "*more nutrition per irrigation*". This well-known concept can be applied to an array of crops, especially aerobic rice. Enormous efforts made to enrich micronutrients in aerobic rice highlighted the main issue: 'loss of micronutrients during polishing'. Hence, 'pushing the micronutrients from aleurone layer into endosperm' appeared as a potential solution. To verify this hypothesis, an experiment was conducted to elucidate the 'bottlenecks' which affect zinc accumulation in rice grain and consequently selecting the super elite line(s) from a set of elite aerobic rice accessions. Nine elite genotypes were analysed for zinc concentration using XRF. Results revealed that there was a significant loss of zinc after polishing, but AM65 (33.90 mg/kg) manifested the highest zinc even after polishing, making it super elite aerobic rice. It was found that there was no effect of levels of deep polishing on micronutrient concentration, indicating that aleurone layer is rich in zinc. As it can be predicted, bran of these genotypes was over-loaded with zinc. However, there was little variation in bran zinc (40-45 mg/kg), indicating that there is a cap for accumulation of micronutrients in aleurone layer and it is not a bottleneck. This suggests that instead of trying to push the micronutrients from aleurone layer to endosperm, it is practical to pump more micronutrients into aleurone layer which will be further transported into endosperm. Thus aerobic rice will not only be drought resistant but also be nutri- rich.

IDT6-032 | Constitutive stress response confers tolerance to osmotic stress and is linked to successful asexual reproduction in a crucifer

Olga Kirioukhova[1*], Jubin N. Shah[1], Pallavi Pawar[1], Muhammad Tayyab[1], Juan L. Mateo[2], Amal J. Johnston[1,2]*

[1]Laboratory of Germline Genetics & Evo-Devo
[2]Centre for Organismal Studies, University of Heidelberg, Heidelberg, Germany
*E-mail: olga.kirioukhova@cos.uni-heidelberg.de, amal.johnston@greentechlab.net

In parallel to dissection of drought tolerance in plants, solving the mystery of apomixis – clonal asexual reproduction through seeds – could improve breeding success by clonally propagating desired "elite" stress-tolerant crop varieties. The *Boechera* genus consists of sexual as well asexual species closely related to economically relevant crops of the Brassicaceae family, providing natural genetic resources instrumental for dissection of genetic regulation underlying apomixis. We hypothesized that apomicts, which evolved in environmentally challenging conditions, would exhibit genome-wide transcriptional reprogramming compared to the sexuals, and that a shift in gene expression might occur early in vegetative development. Apomict-specific transcriptome-wide changes in seedlings and floral stages were in agreement with our hypothesis. We found over-representation of stress-related gene groups, including upregulated NAC transcription factors that were previously shown to be modulated upon abiotic stress or confer higher tolerance in other plant systems. In line with constitutive stress-related gene expression, *Boechera* asexuals exhibited enhanced tolerance to osmotic and salt stress at the seedling stage *in vitro* as well as to drought later in ontogenesis. The transcriptional shift was concomitant with acute deregulation of key meiotic and hormone-related genes in the apomictic seedlings, indicating an early global predisposition to meiotic circumvention. Gene expression analysis suggests that meiotic, stress-related and hormonal reprogramming is conserved across independently evolved *Boechera* apomicts and might form an evolutionary basis for stress tolerance and apomixis. Our findings suggest that better adapted apomicts might undergo less oxidative stress compared to the sexuals, hence less DNA damage to be repaired during meiosis.

IDT6-033 | Screening groundnut genotypes using TIR (Temperature Induction Response) technique for thermotolerance

Rekha Rani. K[1], Latha. P[2], Sujatha. K[2], Vasanthi R.P[2], Janila. P[3], Usha. R[1]*

[1]Sri Padmavati Mahila Visvavidyalayam (Women's University), Tirupati, Andhra Pradesh – 517502
[2]Institute of Frontier Technology, Regional Agricultural Research Station, ANGRAU, Tirupati, Andhra Pradesh–517502
[3]ICRISAT, Patancheru, Hyderabad, Telangana – 502324
*E-mail: ushatirupathi@gmai.com

Heat is one of the major abiotic stresses that adversely affect crop production worldwide at different stages of development. Groundnut is a major crop cultivated in tropical and sub-tropical regions where high temperature stress is a serious constraint for its production. In the present study, temperature induction response (TIR) was conducted for screening the tolerant genotypes, where the seedlings were exposed to sublethal temperature from 34ºC-54ºC for 4 hours 30 minutes followed by lethal temperature at 58ºC for 3 hours. From the 100 diverse genotypes screened, 24 showed tolerance to high temperature with mean percent seedling survival of 92%, 30 showed moderate tolerance and 46 were identified as temperature susceptible compared with checks (100% survival). Results suggested that TIR is used to identify stable thermotolerant genotypes and could be explored as donor source useful in breeding programmes. Further work will be focused on the physiological and molecular basis of thermotolerance in selected tolerant and susceptible genotypes for the identification of heat stress tolerant genes which could be useful for engineering plants with improved heat tolerance.

IDT6-034 | Genetic gain in heterosis of maize reciprocal composites

Kolawole AO[1,2,3], Menkir A[1*], Blay E[2], Ofori K[2]

[1]International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
[2]West Africa Centre for Crop Improvement (WACCI), University of Ghana, Legon
[3]Ladoke Akintola University of Technology, Ogbomoso, Nigeria
*E-mail: a.menkir@cgiar.org

Two improved tropical maize composites representing complementary heterotic pools have been subjected to four cycles of reciprocal recurrent selection (RRS). The objectives of this study were to evaluate the effect of selection on genetic gain in heterosis for grain yield and other agronomic traits. The C_0 to C_4 populations of the two composites and their five varietal crosses along with a commercial check were evaluated at four locations in Nigeria for two years. Mean grain yield of the C_4 x C_4 was 6 % greater than that of a late-maturing commercial hybrid check. Grain yield of varietal crosses increased by 3% per cycle and was accompanied by desirable changes in anthesis-silking interval, ear aspect, plant aspect and resistance to foliar diseases. These improvements in varietal crosses may result from the fixation of different favourable alleles at each locus in each composite through RRS. Mid-parent heterosis in grain yield increased from 4% at C_0 x C_0 to 25% at C_4 x C_4. The positive average heterotic effects on grain yield may arise from the presence of non-additive genetic effects. The results of our study highlight the potential that exists to exploit the advanced selection cycle of the two composites as useful sources of diverse and stable inbred lines with improved combining ability and as potential parent to develop improved varietal crosses to increase farmers' access to improved seeds in specific production zones.

IDT6-035 | Enhancement of pigeonpea productivity through adoption of drought mitigating strategies

M. V. Nagesh Kumar[1], M. Venkata Ramana[1], V. Ramya[1], D. Vishnu Vardhan Reddy[1], A. Srinivas[1], C. V. Sameer Kumar[2] and G. V. Ranga Rao[2]

[1] Professor Jayashankar Telangana State Agricultural University, Hyderabad, Telangana, India
[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: psoilseeds@gmail.com

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) is an important drought tolerant legume crop in Indian rainfed agriculture. Though India accounts for nearly 90% of the world's pigeonpea acreage (3.73 million ha) and production (3.07 million t), the productivity is lower at 707 kg/ha than the world average. The Morocco India Food Legumes Initiative in collaboration with the ICRISAT is aimed at improving the livelihood of small farmers to strengthen food and nutritional security through adoption of improved technologies. This paper is focused on developing and disseminating strategies to improve pigeonpea productivity in dryland regions which are characterized by erratic rainfall, frequent and prolonged dry spells and soil nutrient depletion. During 2013-16, demonstrations were conducted in 1200 farmers' fields in Mahabubnagar district, Telangana, India, with an objective of enhancing the productivity of pigeonpea using three drought mitigating strategies: (i) adoption of short-duration cultivar PRG 176, a high-yielding and early-maturing pedigree selection of ICPL 88034 x ICPL 88039 with a duration of 130-135 days; (ii) foliar application of soluble fertilizer to maintain vegetative growth and ultimately improve pod filling; (iii) life saving irrigation at the rate of 20 mm with water harvested from farm ponds during mid season drought and prolonged dry spells. Adoption of PRG 176 resulted in an average yield of 1400 kg/ha compared to LRG 41 (1120 kg/ha). The yield improvement of 25% can largely be attributed to the good branching habit (8-13 primary branches) and high flower to pod conversion ratio of PRG 176 under dryland conditions. Foliar application of multi-K during flowering and pod formation stages enhanced the yield to 1360 kg/ha compared to the yield of 1100 kg/ha obtained in fields without foliar spray. Life saving irrigation in PRG 176 during mid season dry spell which persisted for 17-21 days improved the yields by 20 % compared to the yield of 1200 kg/ha obtained in rainfed crop. In conclusion, the study demonstrated that the productivity of pigeonpea in dryland regions can be enhanced to an average 1560 kg/ha through an integrated drought mitigating approach by exploiting the short-duration and high-yielding potential of PRG 176, providing life saving irrigation during critical growth stages and foliar application of nutrients at flowering and pod formation stages.

IDT6-036 | Phenotyping of plants for drought and salt tolerance using infra-red thermography

Kwon TR[1]*, Kim KH[1], Siddiqui ZS[2]

[1] The National Academy of Agricultural Sciences, Jeonju 54874, Republic of Korea
[2] University of Karachi, Karachi 75270, Pakistan
* E-mail: trkwon@Korea.kr

Drought or salt stress induces several common physiological responses in plants such as water relation and photosynthetic capacitiy. It is because both stresses lead to cellular dehydration in the plants, particularly, during the early phase of stress imposition. Drought and salinity decrease CO2 availability for photosynthesis via stomatal limitation, as well as elevate leaf temperature due to partially closed stomata. In this scenario, stomatal regulation and plant water status are important aspects in abiotic stress environment. These physiological responses have a function to stabilize the temperature inside plant/leaf. Therefore, phenotyping through an infrared thermography (heat sensitive sensor) could be a useful tool in the selection of a tolerant genotypes. Infrared thermography is a part of the electromagnetic spectrum which emits a certain amount of radiation as a function of the temperature. In general, plants which have less water would have higher temperature and display more infrared radiation. In abiotic stresses such as drought and salinity, the plant water status is affected and varied from the sensitive to tolerant level. Infrared images of plants are often linked with some of the physiological attributes to the tolerance. This paper covers the limits, advantages, linkages, comparison and other prospective of using thermal imagaes in modern phenotyping techniques.

IDT6-037 | Molecular mapping of flowering time genes in chickpea (*Cicer arietinum* L.)

Mallikarjuna BP[1,2], Samineni S[1], Thudi M[1], Sajja SB[1], Khan AW[1], Patil A[2], Viswanatha KP[2], Varshney RK[1], Gaur PM[1,3]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad 502 324, India
[2]University of Agricultural Sciences, Raichur 584102, Karnataka, India
[3]The UWA Institute of Agriculture, University of Western Australia, M082, Perth WA 6009, Australia.
*E-mail: p.gaur@cgiar.org

Flowering time is an important trait of chickpea that influences crop adaptation to a given climate. Earliness in both flowering time and maturity are important traits for increasing and stabilizing chickpea productivity in short season environments by avoiding end of season drought. A study was conducted to identify genes/quantitative trait loci (QTLs) controlling flowering time in chickpea using four F2 populations (ICCV 96029 × CDC Frontier, ICC 5810 × CDC Frontier, BGD 132 × CDC Frontier and ICC 16641 × CDC Frontier). Genetic studies revealed monogenic control of flowering time in the crosses ICCV 96029 × CDC Frontier, BGD 132 × CDC Frontier and ICC 16641 × CDC Frontier, while in the cross ICC 5810 × CDC Frontier, it was under digenic control with complementary gene action. The genetic linkage maps developed from four crosses consisted of 75, 75, 68 and 67 markers spanning 248.8 cM, 331.4 cM, 311.1 cM, and 385.1 cM, respectively. A consensus map spanning 363.8 cM with 109 loci was developed by integrating four genetic maps. QTL mapping detected major genomic regions controlling early flowering genes *efl-1* (*Qefl1*-2) on CaLG04, *efl-2* (*Qefl2*-1, *Qefl2*-2, *Qefl2*-3, *Qefl2*-4) on CaLG01, 03, 04 and 08, *efl-3* (*Qefl3*-3) on CaLG08 and *efl-4* (*Qefl4*-1) on CaLG06. Analysis of QTL regions on CaLG04 and CaLG08 provided several important candidate genes involved in regulation of flowering time and homeotic functions. The identified genomic regions with linked molecular markers can be deployed for introgressing early flowering trait into elite chickpea cultivars through marker-assisted breeding (MAB).

IDT6-038 | Screening mungbean lines for salinity tolerance using Salinity Induction Response (SIR) technique

Manasa R[1], Reddy R[1], Bindumadhava H[2], Nair RM[2], Prasad TG[1] and Shanker AG[1]*

[1]University of Agricultural Sciences, GKVK, Bengaluru, 560065, Karnataka, India
[2]World Vegetable Center, South Asia, ICRISAT campus, Greater Hyderabad, Telangana, 502324, India
*E-mail: ambara8@hotmail.com

Mungbean [*Vigna radiata* (L.) Wilczek] is one of the important fast maturing warm season legumes of the world. However, static productivity in last decades largely accounts for its susceptibility to various biotic and abiotic stresses at different growth stages. Among them, salinity severely limits growth and yield worldwide. Tolerance to salinity involves complex responses at cellular, molecular, physiological and whole-plant levels. Largely, intrinsic response of crop varieties/genotypes differ to adjust several physiological and biochemical processes for salt stress. Considering these, the present study was aimed at screening mungbean lines for salinity tolerance using Salinity Induction Response (SIR) technique. Forty mungbean lines procured from WorldVeg, South Asia, were screened at seedling stage for salinity response. Germination and seedling recovery response during the stress and post recovery were accounted as selection criteria. The identified nine tolerant and nine susceptible lines were further evaluated and validated for field level salinity tolerance (whole plant level with 150 and 300 mM NaCl stress). The results indicate that there is a substantial reduction in growth and yield performances of both tolerant and susceptible lines, however a few lines could maintain relatively better biomass and pod yield, which was on par with non-stressed (non-saline) plants. Based on seedling and whole plant level tolerance, a few tolerant (EC 693358, EC 693366, ML 1299, EC 693371) and susceptible lines (NM 94) were identified for further investigation, which showed consistency in their salinity response.

IDT6-039 | Screening of cotton (*Gossypium hirsutum* L.) germplasm for drought stress under field condition

Meshram J. H.[1]*, Sheeba Annie J[2] , Mohan Punit

[1]ICAR-Central Institute for Cotton Research (CICR), Nagpur, 440010 (M.S), India
[2] ICAR- RS Central Institute for Cotton Research (CICR), Coimbatore, Tamil Nadu, India
*E -mail: j.h.meshram@gmail.com

Cotton (*Gossypium hirsutum* L.) cultivation in India (>60 %) is under rainfed condition. Drought stress is one of the major abiotic stresses that adversely affect cotton production. In the present study, 104 germplasm accessions of cotton were screened for their performance in drought-tolerant traits. A field experiment was conducted under rain-fed condition at ICAR-CICR, Nagpur, during 2015-16. The study was aimed at characterizing the physiological mechanism by which high temperature and water deficit impair productivity under field conditions (temperature at day 43oC and night 25oC) under dry and irrigated conditions. The physiological changes induced due to water stress were quantified by withholding irrigation for continuous 25 days to 45 days old cotton plants. From the screening experiment, 17 contrasting germplasms were identified for drought tolerant traits; viz, IC-325280 (better performing), IC-357406 (moderate) and (IC-357045 (poor) lines based on RWC (%), Mid-day leaf water potential, epicuticular wax content and low Δ13C (‰) value of the plants. The identified lines could serve as donor parent in cotton breeding program aimed to develop suitable cultivar to cope in present and projected warmer climates.

IDT6-040 | Silk elongation rate response to water deficit mediated by ARGOS influence on ethylene sensitivity in maize (*Zea mays.*)

Messina CD[1]*, Shi J.[1], Clark R.[1], Lafitte R.[3], Gho C.[2], Habben J.[1], Cooper M.[1]

[1]DuPont Pioneer Johnston, IA 50131, USA
[2]DuPont Pioneer, Semillas Pioneer Chile Ltda, Santa Filomena 1609 – Buin, Chile
[3]DuPont PioneerWoodland-US-Research, CA 95695, USA
*E-mail: charlie.messina@pioneer.com

Water deficit is ubiquitous in maize cropping systems around the world. Ethylene insensitivity in maize was implicated in kernel set and yield improvement under drought (Habben et al., 2014; Guo et al., 2014; Shi et al., 2015,2016). ARGOS genes modulate ethylene signal transduction, reducing the plant sensitivity to ethylene upon over-expression. It was shown that ARGOS1 can reduce anthesis-silking interval (ASI), and ARGOS8 reduced maize root elongation response to ethylene at early stages of development. Because of the separation of male and pistillate flowers in maize, their differential sensitivity to water deficit, and the high sensitivity of silk elongation to reduced water potential (Westgate and Boyer, 1985), effects of ARGOS genes on silk elongation response to water deficit would be coherent with documented effects on organ expansion, ASI and the improved yields under drought. Experiments in controlled environments were conducted to test this hypothesis. Silk and ear lengths, and water use were monitored continuously using transducers and load cells; and water deficits estimated by the fraction transpirable soil water. ARGOS plants maintained silk elongation rate at higher water deficit relative to controls under controlled environments and exposed silk faster than controls. These results taken together contribute to understand the mechanism underpinning ARGOS effect on maize yield improvement in drought environments.

IDT6-041 | Overexpression of transcription factor SbAP37 improves grain yield in rice undersalt and drought stress and modulates the proteome as revealed by Q-TOF analysis

Maheshwari Parveda[1], Kiran. B[2] and P. B. Kavi Kishor[1] *

[1]Department of Genetics, Osmania University, Hyderabad, Telangana-500 007, India.
[2]Bayer's Bioscience Pvt. Ltd., Inorbit mall road, Hitech city, Hyderabad, Telangana-500 081, India.
*E-mail: maheshwariraop@gmail.com

Transcription factors with an APETELA2 (AP2) domain have been implicated in various cellular processes involved in plant development and stress responses. *AP37*,a transcription factor has been cloned from *Sorghum bicolor* and the gene *SbAP37* was inserted under the control of stress inducible *ABA2* promoter into pCAMBIA1301 vector using GUS as reporter gene and hygromycin as a selectable marker. The vector was immobilized into *Agrobacterium tumefaciens* strain LBA4404. The transformed *Agrobacterium* containing gene and promoter were used for genetic transformation of rice. For *in planta* transformation, plantlets were raised from *Agrobacterium* infected seedlings. The putative transgenics of T_o generation were confirmed by PCR amplification for *SbAP*37 gene, *hptII* marker (hygromycin) and *ABA2* promoter. While gene insertion and gene copy number were ascertained by Southern blot analysis, expression of *SbAP37* gene at the transcriptional level was checked by real-time PCR analysis. Transgenic plants *ABA2:SbAP37* (second generation) showed significantly enhanced salt and drought tolerance at the reproductive stage (a stage that is highly sensitive to stress) over untransformed control plants in greenhouse conditions with higher grain yield. Transgenics exposed to 150 mM NaCl stress modulated a whole gamut of proteins as revealed by Q-TOF analysis. A total 331 proteins have been found modulated which are functionally annotated. Out of them transgenic plant showed 11 downregulated proteins, 26 upregulated proteins, 101 common proteins, 193 new proteins when compared with untransformed control plant.

IDT6-042 | Drought tolerance studies in *Gossypium hirsutum* cotton genotypes

Patil B C*, Mummigatti U.V., Ashvathama V.H

College of Agriculture, Vijayapura, University of Agricultural Sciences, Dharwad, Karnataka, India
*E-mail: patilbc10195@uasd.in

Twenty cotton genotypes (varieties) collected from across the three cotton growing zones (north, central and south) in India were evaluated for their drought tolerance. These genotypes were selected from breeding trials of the All India Coordinated Cotton Improvement Project (AICCIP). These genotypes were grown in irrigated and rainfed situations during south west monsoons - and - at the Agricultural Research Station, University of Agricultural Sciences, Dharwad (Karnataka, India; Latitude ., Longitude . and elevation) having medium deep black soil.

The drought susceptibility index (DSI) was worked out using Fisher and Maurer (1973), and it ranged from 0.44 to 2.31 in the present genotypes. The genotype BS-279 recorded the highest cotton yield of 2109 kg/ha, followed by BS-79 (2091 kg/ha), RHC-0717 (2083 Kg/ha) and HAG-805 (1833 kg/ha) under irrigated condition. In rainfed condition also, the genotypes BS-79 (1831kg/ha) had recorded highest yield, followed by HAG-805 (1719 kg/ha) and BS-279 (1689). The percent reduction in yield in rainfed condition as compared to irrigated condition was comparatively less in BS-79 (14.92 %) and HAG-805 (8.34 %) which recorded less drought susceptibility indices of 0.90 and 0.44 respectively. Whereas, the genotypes H-1454 (14.98%), H-1462 /12 (27.64 %) and RHC-0717 (32.03 %) recorded low yield and high drought susceptibility indices of 1.07, 1.83 and 2.31 respectively indicating their susceptibility to drought. These results are supported by morpho-physiological parameters.

IDT6-043 | Effect of drought stress on growth, yield and assimilates partitioning in rice (*Oryza sativa*) genotypes at reproductive phase

Pervin MS[1, 2]*, Pramanik HR[2], Biswas JK[1]

[1]Bangladesh Rice Research Institute (BRRI), Gazipur-1701, Bangladesh
[2]Bangladesh Agricultural University (BAU), Mymensingh-2202, Bangladesh
*E-mail: pervinsalma@yahoo.com

Drought is one of the major constraints for crop production in the north-western region of Bangladesh owing to insufficient rainfall and causes a substantial yield loss in T. Aman rice. With a view to developing drought-tolerant variety, 259 rice genotypes were screened, out of which six genotypes [IR74371-70-1-1, BR7873-5(Nils)-51-HR6, Batraj, BR11, Muktahar and Bunadhan] were evaluated under drought stress for 5, 10 and 15 days at reproductive (PI, booting and flowering) phase. Irrespective of genotypes and growth stage, drought stress significantly reduced relative water content (RWC), leaf area, dry matter accumulation, panicle exertion and spikelet number; and increased sterility percentage. The relative yield loss (RYL) was less than 50% in IR74371-70-1-1 and Batraj even at 10 days drought stress, while the other genotypes had about 50% RYL even at five days of drought stress. Assimilate translocation percentage and apparent contribution percentage were increased in water-stressed plants in both tolerant and susceptible genotypes, except in Muktahar and Bunadhan. The genotypes IR74371-70-1-1 and Batraj had significantly high RWC, low spikelet sterility, high grain yield, high proline and soluble sugars accumulation, enhanced water use efficiency, maximum quantum yield and high photosynthesis rate, and high activities of GST and GlyI enzymes compared to the other genotypes for imposing drought and those traits enabled them for the better physiological functions and adaptation under drought. Therefore, the genotype IR74371-70-1-1 appears to be suitable for cultivation in drought-prone areas and Batraj can be used as potential donor for development of drought tolerant variety through breeding practices.

IDT6-044 | Alternate wetting and drying enhances photosynthesis in rice

Phukon M[1]*, Shaw S[1], Douglas A[1], Norton G[1], Price A[1]

[1]University of Aberdeen, Aberdeen, United Kingdom
*E-mail: r01mp13@abdn.ac.uk

Rice is one of the most important global foods. Due to increasing scarcity of freshwater resources and escalating demand of food around the world, it's necessary to produce more food with less water. Alternate wetting and drying (AWD) is an irrigation method which saves water and also maintains yield. During an AWD cycle, soils are flooded to 5 cm above soil surface on the first day and then allowed to dry naturally. When the water level reaches 13 cm below the soil surface, the soils are re-flooded and the AWD cycles are repeated. For continuous flooding (CF), soils are kept continuously flooded to 5 cm above soil surface.

Four rice genotypes (BRRIdhan28, BJ1, TEPABORO508 and Pachodi427) were grown in a large box experiment in greenhouse. During the 5th AWD cycle, when water level was 9cm below the soil surface, the leaf transcriptomes were analysed to characterise the expression profile of rice in response to AWD and CF. Differential gene expression analysis showed increased expression of cytochrome P450 gene due to treatment effect. A total of 1,750 up-regulated genes including photosynthesis and water stress responsive genes and 900 down-regulated genes including nitrogen transport responsive genes were found with evidence (5% FDR) of genotype by treatment interaction.

This study provides a preliminary analysis of the molecular mechanisms underlying adaptation of rice to AWD. With detailed investigation at gene level, this research outcome can be utilized through various breeding and biotechnology tools for development of new rice varieties with adaptation to AWD.

IDT6-045 | Drought tolerance of sunflower genotypes with contrasting root traits

Lakshmi Prayaga[1]*, Lakshmamma P[1], Sarada C[1], Alivelu K[1]

[1]ICAR-Indian Institute of Oilseeds Research, Hyderabad - 500030, Telangana, India
*E-mail: lakshmi.prayaga@icar.gov.in

Sunflower is grown in India in all seasons. But in the *kharif* season, it is subjected to intermittent stress and in *rabi* to end-season stress. Though many traits have been reported to be contributing to drought tolerance, root traits are of particular importance as they mine water from soil and aid in avoiding drought. Contrasting genotypes with high and poor root growth were selected, based on a composite index computed considering root and shoot traits simultaneously. High root genotypes recorded per plant mean root length, root volume and root dry weight of 120 cm, 129 cc, 20.5 g as against 65 cm, 35 cc and 5.3 g in poor root types. Fifteen high root and three poor root genotypes were evaluated in field during summer season for two years (2013 and 2014) by growing them in a strip plot with three replications. Stress was imposed at the most sensitive stage *i.e.* flowering, by withholding irrigation. The results indicated that drought affected leaf area and dry matter production significantly. However, the number of days to flowering and leaf number were the least affected. The per plant seed weight in poor root types was only 50% of that of high root types, both in control and stress though percent reduction due to stress was similar in both types. Based on drought susceptibility index and seed weight per plant in stress, genotypes SCG 49, SCG 64 and GP9-515-7-3-1 were identified as drought tolerant.

IDT6-046 | Traits that confer post-flowering drought tolerance in short duration pigeonpea

Purushothaman R[1], Krishnamurthy L[1], Hingane AJ[1], Sameer Kumar CV[1]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana, India
*E-mail: C.Sameerkumar@cgiar.org

Pigeonpea (*Cajanus cajan*) is one of the most important legume crop, ranking fifth in importance among edible legumes globally. It is adversely affected by intermittent and terminal droughts. As grain yield under drought is heavily influenced by genotype × environment interactions, a trait-based selection had been considered more beneficial in drought tolerance breeding. The objective of this study is to identify putative traits that confer yield advantages under post-flowering drought stress. Fifteen super early and early genotypes including breeding and germplasm lines, as a subset of greater number of test genotypes were field evaluated for pre and post-harvest physiological and agronomical traits. Significant variation was observed, among the genotypes, for the traits normalized difference vegetation index (NDVI) and SPAD chlorophyll meter reading, measured at different days after sowing at the reproductive phase, shoot biomass productivity, and yield components. Genotype × drought treatment interactions were found to be meager, especially in super early lines. Grain yield under drought was closely associated with NDVI measured at podfilling stage (r=0.86***), shoot biomass at maturity, harvest index (HI) and yield components. Though the genotypic variation in SPAD chlorophyll reading was large, its correlation with grain yield under drought was not significant. NDVI, a high throughput measure, was found to be significantly correlated with the other putative traits such as shoot biomass (r=0.91***), HI, pod number m-2 and seed number m-2 and therefore, can be used as a proxy in identifying better drought tolerant lines in crop improvement for early and super early pigeonpea.

IDT6-047 | Overexpression of plasma membrane Na+/H+ antiporter gene NHX7: strategy for imparts salinity tolerance in rice

Pushpa, B.N,[1]* Sushma, M[1], Shashibhushan, N.B[1], Sashidhar, V. R[1], Shankar, A.G[1].

[1]University of Agricultural Sciences, GKVK, Bengaluru-560065, Karnataka, India.
*E-mail: pushpalatha0001@gmail.com

Soil salinity is a major abiotic stress for plants in agriculture. Sodium ions in saline soils are toxic to plants because of their adverse effects on K+ nutrition, cytosolic enzyme activities, photosynthesis, and metabolism. To maintain growth and productivity, plants must adapt to stress conditions and exercise specific tolerant mechanisms. In the present study, an attempt was made to identify salt tolerance putative T1 transgenic plants harbouring *NHX7,* a plasma membrane Na+/H+ antiporter, which is involved in pumping of Na+ from the root cells, and plays an important role in preventing the accumulation of Na+ in cytosol to toxic levels. This *NHX7* cDNA clone was obtained from Rice Genome Research Center (RGRC), Japan. It was transformed into rice (var-Vikas) genome by *Agrobacterium* mediated *in planta* technique which showed success of transformability. About 30 T0 transgenic plants were obtained with about 11,251 seeds from them. Screening the putative transgenic rice for salt tolerance was done at primary screening at seedling level with 350 mM NaCl and secondary screening was done by visual observation by measuring the root and shoot length in survived plants. Results showed that putative T1 transformants performed better compared to wild type at high salt level. Tolerant plants were selected for PCR analysis. The results showed that out of 5,518 plants were PCR positives. These results clearly demonstrate that transgenic rice plants over-expressing *NHX7*, plasma membrane Na+/H+ antiporter have better salt tolerance.

IDT6-048 | Influence of epigenetic regulations on cotton

Rakhmanov BK[1]*, Buriev ZT[1], Shermatov ShE[1], Saha S[2], Wubben JM[2], Jenkins JN[2], Abdurakhmonov IY[1]

[1]The Center of Genomics and Bioinformatics of the Academy of Sciences of the Republic of Uzbekistan, Tashkent, Uzbekistan
[2]Genetics and Sustainable Agriculture Research, United States Department of Agriculture –Agricultural Research Service, Starkville, Mississippi, United States of America
*E-mail: bakhtiyor.rakhmanov@gmail.com

Epigenome-wide association studies (EWASs) in plants to identify epigenetic variations have become a hot field of plant genomics because of its importance in providing a novel understanding on regulation of complex agronomic traits such as tolerance, adaptation, yield and quality. To date DNA methylation, histone modification and RNA interference have been the mostly studied epigenetic phenomena. However, so far, only few epigenetic studies have been performed in cotton. In this study, we explored the epigenetic signatures of the promoter region of *Gossypium MIC*-3 (Meloidogyne Induced-Cotton-3) gene that has root-knot nematode (RKN) resistance-associated properties. Our goal is to study and distinguish the impact of epigenetic regulations on the gene expression of RKN resistant (M-315) and RKN susceptible (M-8) cotton cultivars. To this end, we performed a bisulfite-sequencing of genomic DNAs isolated from the root and leaf tissues of these cotton genotypes. The targeted promoter region was hypermethylated sites of the *MIC-3* promoter with 307 base-pair in length. Sample DNAs were treated with sodium bisulfite through application of sodium bisulfite conversion method to measure methylation levels between leaf and root organs of cotton. Results revealed that methylation levels were 60% higher in leaves than root parts of both genotypes. Our preliminary results suggested that a root-specific expression of *MIC*-3 gene is epegenetically regulated with a metylation mechanism, which fueled a new understanding on the genetic functionality of *MIC-3* genes during RKN pathogenesis. Comparisons of methylation profiles between resistant and susceptible genotypes will be discussed.

IDT6-049 | Isolation and characterization of a drought inducible transcription factor, erd15 from mulberry

Saeed B[1], Khurana P[1]*

[1]South Campus, University of Delhi, New Delhi 110021, India
*E-mail: bushra.saeed1@gmail.com

Early responsive to dehydration (ERD) genes were isolated on the basis of their capacity to be rapidly induced by dehydration. ERD15 has emerged as a novel stress-induced transcription factor which might be involved in mediating diverse responses in plants. The expression of ERD15 was found to be induced not only by drought stress, but also by ABA, salinity and temperature extremes. In order to understand its putative functions, we isolated and characterized *MiERD15* and its upstream regulatory region (URR). The URR of ERD15 drives high-level expression under normal conditions, which is further enhanced by ABA application and water deficit treatments (drought and salinity). This data correlates with our expression data, which suggests that the expression of MiERD15 is induced under those conditions. Over-expression of ERD15 rendered transgenics drought sensitive as showed by reduced growth and increased water loss. We also analyzed transcription activation potential of ERD15 and it was found to drive high level reporter gene expression in yeast, suggesting that it can act as a functional transcription factor. Our results indicate that the region between 70 to 100 amino acids is critical in conferring transcription activation activity. Moreover, ERD15 was found to be localized to nucleus as well as cytoplasm which further indicates its role as a stress inducible transcription factor.The present study, thus, identifies ERD15 as astress responsive gene and furthers our understanding of its function especially under abiotic stress conditions.

IDT6-050 | Development of high-yielding, medium-duration groundnut tolerant to early leaf spots in Mali

Sako D.[1]*, Traoré M.[1], Diallo F.[1], Doumbia F.[1],Tapo A.[1]

[1]Groundnut Programme, Institutd' Économie Rurale, Samé, Kayes, Mali
*E-mail: dramanesako@yahoo.fr

Early Leaf Spots (ELS) is one of the major fungal foliar diseases in Mali, negatively affecting agronomic performance of groundnut. Yield reduction can exceed 30%. It is important to develop new varieties that combine yield potential and tolerance to diseases. This study aims to develop highly-yielding, medium-duration groundnut tolerant to ELS. A crossing bloc was established with three ELS tolerant varieties (ICGV 01276, ICGV 99029 and ICG 7878) obtained from ICRISAT Bamako, as female parents; and three farmers-preferred varieties (Fleur 11, JL 24 and ICIAR 19BT) from IER to generate a number of F1's using North Carolina mating design II. Backcrossing has been performed on confirmed hybrids using farmers-preferred varieties as recurrent parents at Same' Research Station, 281 masl, 9°23''W and 15°02"N in the Sahelian zone of Kayes area, annual rainfall 600 to 800 mm per year. Besides, 81 lines tolerant to ELS from ICRISAT have been evaluated in preliminary trials using lattice 9x9 in three replications. From the preliminary trials, 33 best performing lines and three local checks were selected for use in advanced trials using 6x6 lattice in three replications. Ten promising lines showing tolerance to ELS have been identified and will go for registration. Furthermore, nine backcross populations are available for background selection and best performing lines will be identified for multi-location trial. Five varieties (ICGV 86015, ICGV 86024, J11, ICGV 99029 and ICGV 86124) have been released and are being used by farmers already.

IDT6-051 | Development and identification of high productive doubled haploid rice lines

Debina Sanasam*[1], Rohit, K[2], Udayakumar, M[1], Kavita, K[1], Mohan Raju, B[1]

[1]University of Agricultural Sciences, GKVK, Bengaluru- 560065, Karnataka, India
[2]Tamil Nadu Agricultural University, Coimbatore- 641003, Tamil Nadu, India
*E-mail: debina01@gmail.com

Doubled haploid technology serves as one of the promising ways of producing pure and completely homozygous lines and inbreds from heterozygous parents, whilst shortening the breeding cycle. However, many factors regulate the successful production of anther-derived haploids and subsequent diploidization and it, therefore, warrants the development of high throughput haploid generation protocol. Towards developing doubled haploid rice lines, F1 anthers of a leading rice hybrid, KRH4, collected at uninucleate stage, were cultured on a standardized N6 basal media. A good callusing was obtained, which was later cultured in a standardized regeneration media. The regenerated plantlets were hardened, and through markers and flow cytometry analysis, true haploids and spontaneously formed doubled haploids (DH) were identified. While the spontaneously formed DH lines were planted in the pots, the haploids were treated with colchicine before transferring them to pots where they were grown to maturity and the seeds collected. These DH seeds from different lines were characterized in the field and it was found that some of the DH lines were indeed productive compared to leading rice varieties. This is evident from the fact that the tiller and productive tiller number, number of seeds per panicle, and seed weight were significantly high in some DH lines compared to leading varieties. Therefore, it can be inferred that DH technology can help in developing high productive lines, besides developing pure lines/ inbred lines which can be used in breeding programmes.

IDT6-052 | Interaction effect of heat and drought stress at reproductive phase in rice

Rajendran Sathishraj[1*], S.V. Krishna Jagadish[2], Raveendran Muthurajan[1]

[1]Centre for Plant Molecular Biology and Biotechnology, TNAU, Coimbatore - 641 003
[2]Department of Agronomy, Kansas State University, USA
*E-mail: r.sathishrajbiotech@gmail.com

Drought and high temperature stresses occur as companion stresses and their cumulative effect on rice yield is very high. To understand the interaction effect of heat and drought at reproductive stage in rice, a field trial was conducted with 276 diverse rice germplasm lines during wet season 2012 (WS2012) and dry season 2014 (DS2014). During DS2014, all the 276 rice genotypes were subjected to two treatments *viz.,* i) normal irrigation and ii) withholding the irrigation before heading to impose alternate wetting and drying (irrigation given when the tensiometer reading reaches -35 to -45 centibars). Yield and yield components were measured in all the trials. Multiple regression analysis showed that day temperature had negative influence on yield and night temperature had positive influence on yield invariable of the treatments, but the magnitude differs between the treatments. During WS2012, with one degree increase in day temperature, yield was reduced by 5.5%. During DS2014, H with one degree increase in day temperature, yield was reduced by 5.6%. But in DS2014 H+D, with one degree increase in temperature, yield was reduced by 8.7%. During WS 2012, with one degree increase in temperature, sterility increased to 0.6%. The interaction of heat and drought stress at reproductive phase had enhanced negative effect on rice yield, than high temperature alone. Breeding double (drought and high temperature) tolerant rice genotypes is one of the most effective strategies to sustain rice productivity under changing climatic scenario.

IDT6-053 | ABA induced seed dormancy and climate resilience in proso millet

*Anil S.[1], Vasudevan S. N[2]., Kissan B. [2] and Hanumanthappa D. [2]

[1]TNAU,Coimbatore, Tamil Nadu, 641003
[2]UAS Raichur, Karnataka, 584104
* E-mail: sebastiananil.151@gmail.com

Millets possess advantages such as early maturing, drought tolerance, require minimal purchased inputs and mostly free from biotic and abiotic stresses which makes them 'climate smart crops'. Proso millet (*Panicum miliaceum* L.) is mainly grown in temperate and subtropical regions of Asia and USA. Dormancy of proso millet is generally attributed to its coat colour and ABA content. A laboratory experiment was conducted at Department of Seed Science and Technology, UAS Raichur to estimate ABA content in proso millet using Phytodetek ABA Test Kit. Six genotypes were studied in the present investigation. All the six genotypes recorded germination less than 75 per cent and hence considered as dormant. The highest germination percentage was recorded in DHP-2721 (28.67 %) followed by DHP-2782 (24.00 %). The lowest germination percentage of 13.33 per cent was recorded in DHP-2650. Highest ABA concentration was found in DHP-2650 (3.365 pmol/g f. w.) and lowest ABA concentration of 3.283 pmol/g f. w. was recorded in DHP-2721. Germination system may serve as a seed survival strategy under unfavourable conditions. So, genotypes with highest ABA content can be recommended for unfavourable conditions. ABA content can be used as a tool to screen the genotypes for adverse conditions like water scarce conditions. Thus it was concluded that ABA in millet seeds makes them 'climate smart crops' and during the climate change regime, it is only millets that can ensure India's food and nutrition needs in future.

IDT6-054 | Impact of drought stress on floral biology of two species of *Dianthus* (caryophyllaceae)

Sushma Sharma

Botany Department of C.C.S. University, Meerut, India
*E-mail: sushma_sharma130@yahoo.co.in, sushma_sharma130@yahoo.co.in

The plant of *Dianthus* (*D. barbatus* & *D. latifolius*) belonging to family Caryophyllaceae. Drought stress is one of the most prevalent adverse factors for floral organs development, reproductive biology, plant growth and development. Drought is a condition lack of water, it governed by temperature and photon. More than 40 plants including of *Dianthus*, as thrive in climates that see both rain and drought. The Pollination and photosynthesis are senstive to drought stress due to disruption of Photosystem II, stomata close and decrease in electron transport system. During drought period D. barbatus and D. latifolious showed delayed flowering, but time of anthesis and blooming of flower was not effected. The size of the buds also affected by drought stress in both speceis, it was recorded in D. barbatus, (2.5cm) & D. latifolious (2.4 cm). During drought condition size of the bud decreased 2.2 cm in D. barbatus and less than 2.0 cm in of D. latifolious. In both species of *Dianthus* the number of stamens per anther remain the same, but lenght of the filaments and size of stamens slightly decreased due to drought stress. The colour of the anther was change in D. latifolious due to drought it become purple. The pollen fertility & size of the pollen decreased during drought stress. The stigmatic condition did not effected during drough stress it remain same as normal condition but length of the style, ovary and stigma was decreased in both species of *Dianthus*.

IDT6-055 | Yield maintenance under drought: expansive growth and hydraulics also matter in reproductive organs

Turc O[1]*, Oury V[1], Gibon Y [2], Prodhomme D [2], Tardieu F[1]

[1] INRA LEPSE, Montpellier, F-34000, France;
[2] INRA Biologie du Fruit et Pathologie, Villenave d'Ornon, F-33882, France;
*E-mail: olivier.turc@supagro.inra.fr

Yield maintenance under drought in maize (*Zea mays*) is associated with flowering synchrony which requires the rapid extension of styles and stigma (silks) to be accessible for pollen. We have shown that the control of grain set under moderate water deficits similar to those in the field result from a developmental process linked to the timing of silk growth, in opposition to the common view that abortion is linked to the sugar metabolism in ovaries. A switch to abortion occurs 2-3 days after first silk emergence in water-stressed plants, when silk growth stops simultaneously for all ovary cohorts, and explains abortion rates in different treatments, genotypes and positions on the ear. Analyses of transcripts and metabolites indicate that the first molecular events occur in silks rather than in ovaries, and involve genes affecting expansive growth rather than sugar metabolism. Sugar availability is preserved in ovaries until the switch to abortion, and the disruption of carbon metabolism only occurs afterwards. Hence, changes in metabolite contents, transcript amounts and enzyme activities involved in ovary sugar metabolism would be a consequence rather than a cause of the beginning of ovary abortion. Patterns of silk growth responses to environment share common features with those of leaf growth, with both kinetic and genetic evidences. These findings have large consequences for breeding drought tolerant maize and for modelling grain yields under drought. Oury et al (2016) *Plant Physiology*171: 986-996 and 171: 997-1008
Turc et al (2016) *New Phytologist* 212: 377–388

IDT6-056 | An aromatic twist in the quest of biofortification

Vanishri B R[1], Holla S K M[1], Sowjanya M S[1], Avinash M[1], Kakade S[1], Shashidhar H E[1]*

[1]Depatment of Plant Biotechnology, UAS, GKVK, Bangalore 560065, Karnataka, India
*E-mail: heshashidhar@uasbangalore.edu.in

Aerobic rice has been an effective strategy to combat drought. However, this technology was not focusing on quality parameters such as micronutrients. Zinc deficiency causes hidden hunger and is the usual target for biofortification. Aroma in rice plays a significant role in enhancing the market value and consumer's preference. Zinc and aroma are highly valued grain quality traits. In the quest of enhancing micronutrients, getting a biofortified, aromatic, aerobic rice variety would be an added advantage. Considering all these factors, a study was conducted to dissect the relationship between micronutrients and aroma under aerobic condition using 14 aerobic rice genotypes. All these elite accessions were screened for zinc content and aroma along with yield parameters. Genotypes exhibited significant variation for all traits studied. Sensory evaluation of aroma showed that nine genotypes were scented and five were non-scented. Azucena, an aromatic variety, had highest zinc content before and after polishing. Among all the tested genotypes *Chittimutyalu* was strongly scented and showed very less loss of Zn after polishing. The top four genotypes for brown rice zinc concentration, which are above the international target, were aromatic lines. AM65, a rice accession in the pipeline as a micronutrient-rich aerobic accession, was highly aromatic. Molecular marker analysis was done by using markers designed specific to gene *LPAAT*. All seven designed markers were monomorphic. Sequencing of the amplicons indicated nucleotide variations in six markers which were associated to aroma and zinc. Our results indicate that there is positive relationship between low moisture, Zn content and grain aroma.

IDT6-057 | Genetic variability for fodder quality traits in sorghum under different water regimes

Kanuganahalli V[1], Kodukula P[2], Devulapall R[2], Deshpande S[1]*, Vadez V[1], Blümmel M [2],

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]International Livestock Research Institute, Hyderabad, India
*E-mail: s.deshpande@cgiar.org

Sorghum is grown as a dual purpose crop yielding food (grain) and fodder (stover) in marginal environments of Asia and Sub-Saharan Africa. Application of genomics and trait discovery tools in breeding program can expedite genetic improvement of fodder quality. Earlier reports suggested that a difference of one percentage unit in stover digestibility increases livestock output of 6 to 8%. To characterize fodder quality traits in sorghum and to identify genomic regions related to t[hose traits, a set of mapping population parents (24) were evaluated under two water regimes (control and stress) over 3 years at ICRISAT-Patancheru. *In vitro* organic matter digestibility (IVOMD%) – a key stover quality trait, test weight (TW-g), stalk yield (SY-Kg/ha) and grain yield (GY-Kg/ha) recorded significant variation across genotype, treatment, year and interaction effects. Across season analyses revealed a range of 45.8% to 50.4% for IVOMD, variation from 1.9g to 4.1g for TW. The SY and GY recorded a mean value of 4552 Kg/ha and 3152 Kg/ha, across years. While heritability estimates across seasons were on higher side for TW (0.85), SY (0.77) and IVOMD (0.70), it was lower for GY (0.39). A positive correlation of 0.63 and 0.79 was observed for SY – IVOMD and plant height (PH) - SY, respectively. This further implied that an opportunity exists for simultaneous improvement in both yield and fodder quality. We identified a parental set of ICSV1 and ICSV700 having consistently contrasting values across all seasons for IVMOD for further genetic mapping of the fodder quality traits in sorghum.

IDT6-058 | Identification of QTL and eQTL for drought stress tolerance and leaf senescence in juvenile barley

Wehner G[1,2], Balko C[1], Humbeck K[2,3], Zyprian E[4], Ordon F[1,2]*

[1]Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Resistance Research and Stress Tolerance, Quedlinburg/ Groß Lüsewitz, Germany
[2]Interdisciplinary Center for Crop Plant Research (IZN), Halle (Saale), Germany
[3]Martin-Luther-University Halle-Wittenberg, Institute of Biology, Halle (Saale), Germany
[4]Julius Kühn-Institut (JKI), Federal Research Centre for Cultivated Plants, Institute for Grapevine Breeding Geilweilerhof, Siebeldingen, Germany
*E-mail: frank.ordon@julius-kuehn.de

Premature leaf senescence induced by drought stress is a main factor for yield losses in barley (*Hordeum vulgare* L.). Research in drought stress tolerance has become more important, as climate change will increase the number of drought periods. Hence, tolerance to drought stress has become an important goal in barley breeding. The aim of this study was to identify genomic regions involved in drought tolerance and leaf senescence in early developmental stages of barley. For this purpose phenotyping, genotyping and expression analyses were conducted on 156 genotypes, and based on these data genome wide association studies (GWAS) were performed. After a four weeks stress period (BBCH 33), six physiological parameters for drought stress and leaf senescence were determined in the control and stress variant in greenhouse pot experiments. Leaf colour and biomass yield, the main traits for leaf senescence and drought stress, were significantly correlated (r=0.36) under drought stress conditions and significant phenotypic variation was observed. Analysis of variance revealed significant genotype and treatment effects. Based on these phenotypic data and 3,212 polymorphic SNPs with a minor allele frequency >5 % derived from the Illumina 9k iSelect SNP Chip, 47 quantitative trait loci (QTL) were detected under stress conditions. Major QTL for drought stress and leaf senescence were located on chromosome 2H and 5H. Expression analyses of a set of 14 genes involved in drought stress and early leaf senescence on these 156 genotypes resulted in the identification of 13 eQTL, of which one is located in the same region of chromosome 5H as the QTL for biomass yield and leaf colour under drought stress. Respective markers may be used in future barley breeding programmes for improving tolerance to drought stress and leaf senescence.

IDT6-059 | Identification of maize mutants with enhanced drought tolerance and increased grain yield

Zhang X[1], Ding WH[2], Tang Y[2], Lu XD [3], Feng HZ[2], Zhang CY[1], Zhao J[1]*

[1]Faculty of Maize Functional Genomics, Biotechnology Research Institute, National Key Facility for Crop Gene Resources and Genetic Improvement, Chinese Academy of Agricultural Sciences, Beijing 100081, China
[2]Experimental Station, Xinjiang Academy of Agricultural Sciences, Urumqi 830012, China
[3]School of Life Sciences, Qilu Normal University, Zhangqiu 250200, China
*E-mail: zhaojun01@caas.cn

Maize (*Zea mays* L.) is an important cereal crop with the largest contribution to the global cereal production. Water deficit or drought stress is one of the major factors constraining or destabilizing maize grain production. Drought occurring at flowering and early seed development causes substantial maize grain yield loss due to the potential lack of synchrony between silk emergence and pollen shed. In order to discover causative genes or alleles conferring drought tolerance and thus yield improvement, we made an effort to screen Ethyl Methane Sulphonate (EMS) induced maize mutant population for drought tolerance mutant (s) through withdrawal of irrigation at flowering in field trials. Mutants displaying shorter anthesis-silking interval (ASI) (ASI < 2) and alleviated leaf senescence were isolated and used for evaluation of cross hybrids for grain yield under normal irrigation and drought stress conditions. We identified desirable mutants which exhibited improved performance and an average of 20% increase in grain yield than the wild type when subjected to drought stress at flowering stage. The drought-tolerant mutants also showed better performance for physiological parameters including photosynthesis, relative water content, cell membrane stability, and chlorophyll concentration upon drought stress in pot experiments. The mutants identified and characterized here will allow for further identification of the causal mutations by NGS-assisted MutMap approach by crossing the drought-tolerant mutant with its wild type followed by selfing of F1 individuals to generate F2 progeny that segregate for contrasting morphological traits related to ASI and leaf senescence.

Poster Theme VII

Breeding for Water-Limited Environments

IDT7-001 | Testcross performance and screening for drought tolerance in a bi-parental maize cross improved through marker assisted recurrent selection

Abdulmaliki RO[1, 2] Menkir, A[1]*, Hearne S[3], Ado SG[2], Olarewaju JD[2], Aba DA[2], Crossa J[3], Gedil M[1].

[1]International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.
[2]Institute for Agricultural Research (IAR), Ahmadu Bello University, Zaria, Nigeria.
[3]International Maize and Wheat Improvement Center (CIMMYT), Mexico DF, Mexico.
*E-mail: a.menkir@cgiar.org

The performance of bi-parental tropical maize test crosses derived from four cycles of marker-assisted recurrent selection (MARS) program was evaluated to select the best testcrosses for drought tolerance and investigate the efficacy of different drought indices. The bi-parental crosses are drought tolerant and *Striga*-resistant maize inbred lines. A total of 200 testcrosses were evaluated under drought-stressed (DS) and well-watered conditions (WW) at Ikenne, Nigeria, for two years and screened for the advanced cycle (C_3) using the IITA base index. Drought tolerant indices such as drought tolerant index (DTI), geometric mean performance (GMP) and yield stability index (YSI) were used to assess the level of tolerance. The results of the analysis showed that the advanced cycle produced 40%-90% mean grain yield above the hybrid checks. Pairwise comparisons showed that grain yield and plant height was significantly ($P<0.01$) different between cycles. The index revealed that most of the testcrosses are tolerant to drought. However, entries 189, 195, 177, 152, 173 were found to be the most promising drought-tolerant testcrosses. DTI, GMP, MP and YI were positively correlated to yield under DS and were able to separate testcrosses under 'A' group from other groups. These indices were very suitable for the identification of drought tolerance in maize. This is highly desirable for the identification of the promising testcrosses with drought tolerance for inbred line developments.

IDT7-002 | Breeding tef [*Eragrostis tef* (Zucc.) trotter] for drought tolerance in Northern Ethiopia

Abraha MT[1, 2]*, Hussein S[1], Laing M[1], Assefa K[3]

[1]University of KwaZulu-Natal, African Centre for Crop Improvement, Private Bag X01, Scottsville 3209, Pietermaritzburg, South Africa
[2]Tigray Agricultural Research Institute, Axum Agricultural Research Centre, P.O. Box 230, Axum, Ethiopia c
[3]Ethiopian Institute of Agricultural Research, Debre-Zeit Agricultural Research Centre, National Tef Research Project, P.O. Box 32, Debre-Zeit, Ethiopia
*E-mail: mizantesfay90@gmail.com

Moisture stress is among of the main production problems of tef production. A research project was conducted with the objective of developing drought-tolerant tef varieties with wide adaptation and better performance in moisture-stressed areas. At first, participatory rural appraisal was conducted on 240 sampled farmers and the results indicated that high grain yield, increased panicle length, straw yield, white seed colour and early maturity were the most important farmer-preferred traits. Moisture stress (60.4%), weeds (61.2%), shoot fly (58.2%), lodging (53.3%) and seed shattering (60.8%) were rated as severe tef production constraints in the study areas. This study prioritized production constraints and farmers'-preferred traits useful in the breeding of tef to enhance its productivity under drought-prone environments in northern Ethiopia. Next, 144 tef genotypes were evaluated using four experiments representing optimum moisture and moisture-stressed environment in 2014 main and off-season. The results indicated that genotypes DZ-Cr-387, DZ-01-787, DZ-01-3186, 9432, 9403, 9415, 205917, 205896, 215678, 213237, Jano, Kaye-Agachew, Purpurea, Kaye-Murri and Dschanger as promising parents with superior grain yields, reduced lodging, tall plant height and long panicles in a non-stressed environment. Conversely, the genotypes DZ-Cr-385, DZ-Cr-37, HO-Cr-136, DZ-01-2053, Dabbi, 207832, Zagure and Shawa-Gemerra were identified as superior parents for their early maturity and good yield performances under moisture stress. From the morphological diversity study, 60 tef genotypes were selected and subjected to DNA level diversity analysis using 10 selected diagnostic and polymorphic simple sequence repeat (SSR) DNA markers and this enabled identifying agronomically complementary tef genotypes which are valuable genetic resources for further breeding. Using the selected parents, 17 F2 generations were produced and evaluated along with their eight parents under moisture-stressed and non-stressed conditions in northern Ethiopia during 2015 and 2016. Under both test conditions, the genotypes DZ-Cr-387 and 9415 were the best general combiners for increased grain yield and yield components, except for days-to-maturity. Conversely, genotype 222076 was the best general combiner for reduced maturity period only. The selected parents are novel genetic materials for tef breeding programs. to improve grain yield and yield components with reduced days-to-maturity for drought tolerance breeding. The families ofDZ-Cr-387 x 207832 and DZ-Cr-387 x 222076 were high grain yielders with early maturity under both test conditions. There were marked genotypic and phenotypic variation among the crosses at the F2 generation for plant height, panicle length, peduncle length, number of productive tillers per plant, main shoot panicle seed weight, biomass yield and grain yield under both test conditions, this for successful selection and genetic advancement.

IDT7-003 | Improved productivity of *Corchorus olitorius* L. varieties under moisture stress through nutrient management

Adediran O.A.[1*], Oladiran J.A.[1], Simeon O.F.[1], Yusuf I.M.

[1]Federal University of Technology, Minna, Nigeria
*E-mail: o.adediran@futminna.edu.ng

Water deficit is the most important factor limiting crop yield. Two glass house experiments were conducted in 2015 and repeated in 2016 to determine the effects of soil moisture stress on four varieties of *Corchorus olitorius* L. and the use of nutrient management to improve the productivity of moisture-stressed *Corchorus olitorius*. The treatments consisted of four varieties of *Corchorus olitorius, viz*: '*Oniyaya*', '*Amugbadu*', *Local* and *FUTCo1* and four watering intervals (daily, 2, 4 and 6 days). The result revealed that the growth and yield parameters reduced as the watering interval increased. However, there was no significant difference between most of the values obtained in daily and two-days-watered plants in all the varieties. Though the performance of '*Oniyaya*' variety followed this same trend, the variety recorded the highest growth, yield and quality values at four and six days watering interval, suggesting that it is more tolerant to moisture stress. '*Oniyaya*' variety had the highest values of crude protein and ash, which increased with increase in moisture stress. In the second experiment, the moisture stress tolerant variety ('*Oniyaya*') was treated with different nutrient sources (organic, inorganic and organo-mineral) and subjected to moisture stress to see how nutrient management could further reduce the effect of moisture stress in the plant. Results revealed that application of inorganic and organo-mineral fertilizer significantly improved the performance of the crop under stress, compared to the control plants and those treated with organic fertilizer.

IDT7-004 | Identification of large-effect QTL for drought tolerance in rice in West African conditions

Adegbehingbe FT[1], Fofana M[2], Adetimirin VO[1], Venuprasad R[2]

[1]University of Ibadan, Ibadan, Nigeria
[2]AfricaRice Centre, Ibadan Station, PMB 5320
*E-mail: R.Venuprasad@cgiar.org

In Asia, there has been considerable success in breeding for drought tolerance in rice (*Oryza sativa*). Improved drought-tolerant Asian rice varieties developed through MAS when introduced in West Africa performed poorly. QTLs for drought tolerance identified in Asia did not show the same phenotypic effect in Africa. This could be attributed to QTL x environment interaction. This necessitates the need to explore local drought-tolerant donors in well-adapted genetic backgrounds to identify QTLs for drought tolerance. Such large-effect drought QTL could be used to increase breeding efficiency through marker-assisted selection in West Africa. In West Africa, IRAT109 has been identified as a highly drought-tolerant line whereas WITA4 as high yielding but drought susceptible genotype. Recombinant Inbred Lines (RIL) was developed with IRAT109 as donor parent while WITA4 as recurrent parent. 400 BC1F3 RIL of IRAT109 and WITA4 were evaluated under reproductive stage drought and under control conditions to identify QTLs associated with grain yield under severe drought. The population was genotyped by SNP markers. Data analysis is ongoing and results will be presented at the meeting.

IDT7-005 | Breeding for water-limited environment: Performance of extra early tropical maize (*Zea mays* L.) genotypes under artificial drought stress using secondary traits

Adejumobi, II[1]*, Akromah, R[1], Nyadanu, D[1], Ige, AD[1]

[1]Kwame Nkrumah University of Science and Technology, Kumasi, Ghana.
*E-mail: adejumobiidris@yahoo.com

Increasing drought is an important abiotic stress causing severe maize yield loss in Sub-Saharan Africa. Breeding progress for drought tolerance in maize has been slow because drought tolerance is a complex trait that is controlled by polygenes. Breeders improving maize for drought tolerance have, therefore, been using secondary traits to enhance the selection of the best genotypes under drought stress. The objectives of this study were to identify genotypes that combine drought tolerance with high yield in some groups of extra early inbred lines and their F1 hybrids; and to validate the use of secondary traits in improving selection efficiency. Twenty-seven genotypes consisting of 20 F1 hybrids from complete diallele crosses, five parental inbred lines, and two local hybrids were evaluated under artificial drought and well-watered conditions in a plant house. The genotypes were evaluated using the completely randomized design with four replications. The artificial drought was imposed at 35 DAP. The performance of the genotypes varied significantly in both environments for yield and other agronomic traits. The line TZEEI-76 was the best inbred line that combined high yield with drought tolerance. The best hybrids that possess drought tolerance were TZEEI-21×TZEEI-38, TZEEI-29×TZEEI-76, TZEEI-38×TZEEI-21, TZEEI-38×TZEEI-76, and TZEEI-76×TZEEI-6. Negative significant correlation was observed for yield and anthesis-silking interval, and leaf senescence, while positive significant correlation was observed for leaf chlorophyll content, root length, and root weight. The results showed that anthesis-silking interval, leaf senescence, and leaf chlorophyll content could be relied upon in the selection of high-yielding genotypes under drought stress.

IDT7-006 | Drought tolerance traits: indices of resistance to pre-harvest aflatoxin contamination in groundnut (*Arachis hypogaea* L.)

Ahmed HO[1]*, Echekwu CA[1], Oyekunle M[1], Hassan LB[1], Usman A[1], Lawan ZM[2], Usman M[1], Adulmalik RO[1], Aliyu RS[1]

[1]Ahmadu Bello University, Zaria, Kaduna state, Nigeria
[2] Bayero University Kano, Kano state, Nigeria
*E-mail: hauwaahmed21@gmail.com.

Attainment of potential yield in groundnut is severely constrained by environmental stresses. Drought is the most important abiotic stress in the semi-arid tropics. About 90% of the crop is grown in the sub region which is characterized by low and erratic rainfall. The development of drought-tolerant varieties is an important strategy to meet global food demands with limited water resources. This article presents the importance of breeding for drought tolerance for improving aflatoxin resistance. Terminal drought increases susceptibility of groundnut to fungal invasion and subsequent infection of groundnut seeds by *Aspergillus flavus* which results in the contamination of the seed with aflatoxins. Aflatoxin contamination of agricultural commodities poses considerable risk to human and livestock health, and has significant economic implications for the agricultural industry worldwide. Progress in aflatoxin resistance breeding has been limited due to low levels of resistance to different components of resistance, existence of genotype x environment interaction (GEI), and lack of reliable screening protocols. Simultaneous screening for aflatoxin contamination and drought tolerance has been proposed since drought stress strongly influences seed infection by *A. flavus.* Recent studies have shown a negative association between drought tolerance and aflatoxin production in groundnut. However, improvement of drought tolerance in the crop based on yield is hindered by high GEI. Drought tolerant traits with low influence of GEI are, therefore, promising as indirect selection indices for improving resistance to pre-harvest aflatoxin contamination (PAC). An indirect measure of PAC resistance in groundnut will accelerate progress in breeding programs.

IDT7-007 | GGE biplot to analyse the response of recombinant inbred lines (RILs) of peanut to water stress

Ajay BC[1*], Chuni Lal[2], A. L. Rathnakumar[1], B. M. Chikani[1] and H. K. Gor[1]

[1]ICAR-Directorate of Groundnut Research, P.B.No.5, Ivnagar road, Junagadh - 362001, Gujarat, India
[2]ICAR-Indian Institute of Wheat and Barley Research, Karnal – 132001, Haryana, India
*E-mail: ajaygpb@yahoo.co.in

The study was undertaken with the objective to examine the nature and to quantify the magnitude of genotype x environment interaction effects on pod yield of peanut and to determine the best genotype (s) for water deficit conditions. The experiment was conducted for two years (2010 and 2012) under two treatments involving (1) mid-season stress (*i.e* pod formation) and (2) regularly irrigated conditions using 186 Recombinant inbred lines (RILs) along with their parents (TAG 24 and TMV2NLM). Experiment was laid out in split plot design with treatment in main plot and RILs in subplots. ANOVA was performed with year/treatment effects as fixed and genotype as random. ANOVA for pod yield was significantly affected by treatment x year (46.55%), genotype (15.14%), Genotype x year (11.84%), Genotype x treatment x year (3.2%) and Genotype x treatment (1.1%). The result depicted differential performance of RILs at different test environments and hence the presence of interaction effects. The genotype main effect plus genotype x environment interaction (GGE) biplots were applied to analyze and visualize pattern of the interaction component. The first two principal components (PC1 and PC2) of the GGE explained 82.39% with PC1=66.42% and PC2=15.97% of the GGE sum of squares using environment standardized model. RILs, 7, combined both high mean yield and high stability performance across the environments and could be characterized as ideal genotypes.

IDT7-008 | Simulating the effects of plant traits for increasing grain sorghumin water-limited environments: a case study of West Africa Sudano-Sahelian region

Akinseye, FM[1, 2*], Ajeigbe, HA[1], Birhanu, BZ[3], Angarawai, I[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria
[2]Department of Meteorology and Climate Science, Federal University of Technology, Nigeria
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), WCA Region, Bamako, Mali
*E-mail: F.Akinseye@cgiar.org

The need to improve the performance of dryland crops in semi-arid environments cannot be over emphasized, because growth and development of such crops are often limited by moisture and other abiotic factors. Sorghum production in commercial situations requires maximising grain yield on limited available water resources, which requires maximizing the ratio of yield to evapotranspiration. In this study, a system analysis was undertaken to identify those plant traits that might be altered to improve sorghum yield in a moisture-limited environment. APSIM model was used to simulate sorghum (*Sorghum bicolor L. moench*) for 30-year period at two locations (Kano, Nigeria and Bamako, Mali), characterized by high inter-annual rainfall variability and evapotranspiration in the Sudano-Sahelian region of West Africa. Since sorghum is known to be better adapted to drier environments, a number of individual plant traits were adjusted in the calibrated APSIM sorghum-module for the two selected varieties. In the tested environments, it was found that decreasing leaf size and increasing seed growth both resulted in decreased yield while the ratio of grain yield to evapotranspiration was decreased. Combining sorghum plant traits in the model resulted in increased yield and the ratio of grain yield to evapotranspiration when the average for all the years simulated. In addition, the simulated grain yield show decline up to 25% in Bamako, Mali and 35% in Kano, Nigeria for both varieties. These results indicate future adaptations strategy to climate variability and change for sorghums variety is required while maintaining improving soil quality in a continuing process.

IDT7-009 | Genotype x environment interactions and identification of trait donors for reproductive stage drought stress in maize (*Zea mays* L.)

Alam MA[1], Zaidi PH[1]*, Seetharam K[1], Vinayan MT[1]

[1]International Maize & Wheat Improvement Centre (CIMMYT), Hyderabad, Telengana-502324, India
*E-mail: phzaidi@cgiar.org

Drought is a major abiotic stress that affects maize (*Zea mays* L.) growth and reproduction, and eventually results in significant yield reduction. Developing hybrids that can perform better under drought stress, without yield penalties under optimal condition, is a challenge to researchers, especially in areas where intensities of drought stress and other agro-climatic conditions vary significantly in different growing environments. Understanding the genotype environment interaction (G x E) effects under drought stress is needed to develop drought-tolerant genotypes with improved-stable performance across environments. Selection for yield under stress along with key secondary traits such as anthesis silking interval (ASI,) might help in identifying genotypes with good repeatability across locations. The present study was conducted involving a panel of CIMMYT-Asia lowland tropical lines test-crossed with a common tester and evaluated in three different locations under managed drought stress. Significant GxE term indicated that the tested hybrids had large differences in performance across the environment under drought stress. Based on superiority index (pi), 59 hybrids were identified as the best performers across the environments. Among the identified hybrids, 24 were in narrow range ASI group (<7 days), where grain yield (GY) varied between 1.91 to 2.98 t/ha, with an average of 2.22 t/ha. The remaining 35 hybrids had ASI >7 days and grain yield ranged between 1.8 to 2.63 t/ha, with 2.06 t/ha mean. Selection of genotypes for drought environment based on stable performance, while considering narrow ASI, will ensure adequate pollination and potential improvement in yield. The lines with consistent cross-performance in term of low ASI and reasonably good yields under stress are being identified for use as traits donor for drought stress breeding programs.

IDT7-010 | Determination of agronomic traits and drought susceptibility index (DSI) of drip irrigated maize landraces

Albayrak O[1*], Akinci C[1], Kizilgeci F[2], Basdemir F[1], Yildirim M[1]

[1]Dicle University, Faculty of Agriculture, Diyarbakir, 21280, TURKEY
[2]Sırnak University, Faculty of Agriculture, Sirnak, 73300, TURKEY
*E-mail: onderalb@hotmail.com

The purpose of this study was to determine agronomic traits and drought susceptibility index of maize landraces. For this aim, 25 Turkish maize landraces were used to define agronomic traits and drought susceptibility index under different irrigation treatment at Dicle University research station in Turkey. Full irrigation treatment was managed for high productivity at 1.50 Epan (I-150), whereas deficit irrigation treatment at 0.50 Epan (I-50) represented extreme drought conditions. Plants in both water treatments were irrigated equally from sowing to five-leaf stage, and then water stress applied until physiological maturity by using drip irrigation systems. Leaf width, SPAD value, plant height, first ear height, stem diameter, plant weight, fresh husked ear weight, and grain yield were investigated in this study. The range among landrace genotypes under drought stress conditions changed between 7,980 and 21,220 for fresh husked ear weight, between 80 and 275 cm for plant height, between 225 and 9864 kg ha^{-1} for grain yield, and between 0.57 and 1.26 for DSI. There were wide variations for agronomic traits of genotypes to create starting populations for future selection as parents of hybrid breeding. Drought-tolerant genotypes based on drought susceptibility index can be examined in future breeding programs.

IDT7-011 | Drought response of field cultivated potatoes: the interaction between canopy growth and yield

Aliche E.B.[1], Theeuwen T.[1], Oortwijn M.[1], Bachem C.W.B.[1], Visser R.G.F.[1],van der LindenC.G.[1]*

[1]Plant Breeding, Wageningen University and Research, Wageningen6708 PB, The Netherlands
*E-mail: gerard.vanderlinden@wur.nl

Potato is the third most important food crop, but it suffers major yield losses because of drought. We studied a set of 104 commercial cultivars representing the genetic diversity in the European potato market. The cultivars were grown in different field locations in three years (2013 – 2015), with the aim to understand how different field drought regimes affect canopy growth in potato, and how these effects translate into tuber yield. Field environmental characteristics were monitored, and canopy growth captured during the growing season. Canopy growth parameters were extracted by an iterative method using the beta sigmoid growth model. At harvest, we measured yield traits. A GGE bi-plot and Finlay Wilkinson's regression were used to investigate G x E interaction, and marker-trait associations were identified using a 14K SNP array. We observed that the timing of the drought stress in the growing season differentially affected canopy growth and tuber yield. Under drought stress, fast attainment of exponential growth and maximum canopy cover had negative effects on tuber formation and tuber bulking. Growth rate, maximum canopy cover, and area under the canopy curve (photosynthetic capacity over the growth season) were more important for tuber bulking than they were for tuber formation under drought.We identified cultivars with high yields in different environments as material for improvement of drought tolerance in cultivated potato. We also found SNP markers associated with canopy growth parameters and yield under drought, which can be further exploited inmarker assisted breeding for drought tolerance in potato.

IDT7-012 | Salicylic acid exogenous application boosts biochemical, physiological and chlorophyll a fluorescence transient of *Vicia faba* L. under irrigation with salt water

Fatima Anaya[1]*, Rachid Fghire[1], Said Wahbi[1], Kenza Loutfi[1]

[1]Laboratoire de Biotechnologie et Physiologie Végétales, Faculté des Sciences Semlalia, BP2390, Marrakech, Morocco
*E-mail: anaya.fatima@gmail.com

Irrigation with salt water can act as an alternate water resource and, thus, plays an important role in saving fresh water resources as well as promoting agriculture. The current study evaluated the effect of salinity constraint on faba bean (*Vicia faba* L. cv. Lobab and Sbai), originating from Morocco. The biochemical and physiological responses to two salt stresses levels (0 and 120mM NaCl) in *V. faba* L., and the effect of exogenous salicylic acid (0.5mM SA) with and without salt stress, were investigated. The biochemical and physiological characteristics of *V. faba* L. were measured, including Ψ, gs and membrane permeability and antioxidant activity. The effects of salt stress with and without salicylic acid on PS II in faba bean leaves were also studied. 'Chlorophyll a' fluorescence parameters such as Fv/Fm and performance index were measured in response to salt stress with/without SA. The results showed that the physiological and biochemical parameters were affected by salt concentration, and there were varying responses between varieties. Thus, irrigation with saline water significantly reduced all plant biochemical and physiological parameters in comparison to the respective controls. Indeed, salinity affected Ψ, gs and perturbed the membrane permeability. However, salt stress caused an activation of oxidative enzymes (PPO, POD and SOD). The increase in the antioxidant activities was significantly ($p<0.05$) correlated with salt stress. These results suggest that antioxidant enzymes play an important role in reducing oxidative stress in *V. faba* exposed to salt stress. Alleviation of growth arrest was observed with exogenous applications of salicylic acid (SA) under salt stress conditions. Our results indicate that in *V. faba* leaf, 'chlorophyll a' fluorescence parameters can be used as sensitive methods for measuring the salt stress damage to the photosynthetic apparatus, and to identify the action sites of salt stress. Overall, the positive effect of SA towards resistance to the salinity of *V.faba* L. will provide some practical basis for *V. faba* L cultivation.

IDT7-013 | NH 635: A new high yielding variety of American cotton suitable for rainfed ecosystem of Maharashtra

Baig K. S.[1*], Waskar D. P.[2], Deosarkar D. B.[2] and Gaikwad A. R.[1]

[1] Cotton Research Station, Nanded, Maharashtra, India
[2] Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India
*E-mail : khizerbaig1@rediffmail.com

Under changing climatic conditions, severe drought prone situations were witnessed since last couple of years resulted drastic reduction in average yields. NH 635, a new cotton variety of *G hirsutum* developed and released by Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India is having high yield, superior fiber qualities and tolerance to drought, sucking pests and diseases. On an average of 25 state multi-location varietal trails conducted in Maharashtra during 2012-13 to 2014-15, the variety NH 635 recorded 12.54, 18.10, 32.07 and 16.41 per cent increased seed cotton yield over checks *viz.*, NH 615, PKV Rajat, AKH 828 and Phule 688, respectively. On an average of 26 trials conducted under AICRP on Cotton, it had recorded 17.44 and 16.36 per cent increased seed cotton yield over zonal check, LRA 5166 and local check NH 615, respectively. Similarly in adoptive trials conducted over farmers' field, it had recorded 20.63 per cent increased seed cotton yield over check, NH 615. The variety NH 635 also recorded superior fiber length (29.25 mm), strength (19.67 g/tex) and fine micronaire (4.15). The variety NH 635 is found tolerant for pests (jassids, white fly) and diseases (*Alternaria* leaf spot, bacterial blight). In addition, it had also recorded suitable for cultivation under high density planting system.

IDT7-014 | Characterization of Ethiopian sorghum [*Sorghum bicolor* (L) Moench] germplasm collection for drought adaptation traits associated with roots

Temesgen M[1], Kassahun B[1]*, Tebeje A[1], Borrell A.K[2], Jordan,D.R[2], MaceE[2]

[1]College of Agriculture and Veterinary Medicine, Jimma University, P.O. Box 307, Jimma, Ethiopia
[2]Queensland Alliance for Agriculture and Food Innovation (QAAFI), Hermitage Research Facility, University of Queensland, Warwick, Qld 4370, Australia
*E-mail: kassahunb@gmail.com

Drought is the most important abiotic stress affecting sorghum production in Ethiopia, leading to huge crop failures. Recently, Mace *et al.*(2012) identified significant QTL for root angle that co-locate with QTL for stay-green. This makes root angle a potentially valuable trait in developing drought-tolerant sorghum varieties. The objective of this study was to systematically characterize the Ethiopian sorghum germplasm collection for drought adaptation traits associated with roots.

The germplasm used for this study includes sorghum land races collected from sorghum-growing regions of Ethiopia and varieties/lines from the Ethiopian and Australian sorghum breeding programs.The experiment was conducted in a glasshouse using purpose-built root chambers (50 cm high, 45 cm wide and 3 mm thick), using row and column design, replicated four times. Plants were harvested when six leaves were fully expanded and the first flush of nodal roots was visible. The root system that was visible through the clear perspex was photographed on both sides of each chamber, using digital cameras. The images were used to measure the root angle of each of the first pair of nodal roots at two cms distance from the base of the stem, using software. Significant genetic variation for nodal root angle was observed among the genotypes screened. Nodal root angle ranged from 12.8º to 34.0º for 187 genotypes tested so far, with S35 having the narrowest (12.8º), followed by Teshale (13.0whereas Abamelko with the widest (34.0º) followed by ETSL101708 (33.3o) root angles.

IDT7-015 | Breeding investigations for improving drought tolerance in maize (*Zea mays* L.)

Praveenkumar B[1]*, Sridevi O[2], Salimath P M[3], P. H. Kuchanur[3]

[1]Agricultural Research Station, Kalaburagi, Karnataka, India
[2]University of Agricultural Sciences, Dharwad, Karnataka, India
[3]University of Agricultural Sciences, Raichur, Karnataka, India
*E-mail: praveenbarurkar@gmail.com

Maize (*Zea mays* L.) is the leading cereal crop with the highest genetic yield potential and wide adaptability under varied agro-climatic conditions. The goal of this study was to isolate inbred lines and develop high-yielding single-cross hybrids tolerant to drought by assessing the combining ability and heterosis with respect to yield and drought tolerance traits. 80-S3 inbred lines developed from two top cross, four three-way cross, one composite×composite cross hybrids, were evaluated under both situations. Thirty inbred lines selected based on yield and ASI from S3 progenies were crossed with five testers, and the resulting 150 hybrids were evaluated along with parents and checks. The combining ability analysis revealed that SCA variance was higher than GCA indicating predominance of non-additive gene action in controlling majority of the traits under non-stress situation and under stress situation all traits. Out of 30 inbred lines, (Rajkumar×CML446line37) and (NK6240×CI4line24) under non-stress, and (Rajkumar×CML446line18) under stress situation were found to be good general combiners. The hybrids (Rajkumar×CML446line18)×HS7, Rajkumar×CML446line46) ×HS4, (Allrounder×HS17line34)×HS7, (NK6240×HS17line14) HS7 and (Allrounder×HS17 line45) ×HS10 were found superior for grain yield over best checks NK-6240 and Rajkumar under stress situation. The hybrid (Allrounder×HS17line34)×HS7 was found promising with stable grain yield over the best checks under both situations. The single cross hybrids *viz.,* HS-15×HS-17, KDMI-15×NEI-9202B and CI-4×HS-4 were identified as stable under stress, non-stress and rainfed conditions, respectively. These single cross hybrids were also equally high-yielding under optimal environment, indicating their suitability for both optimum and stress situation.

IDT7-016 | Canopy temperature and flag leaf greenness association with yield traits under heat stress in spring bread wheat

Barutçular C[1]*, ElSabagh A[2], Youldas MK[1], Yıldırım M[3], Toptas I[1]

[1]Department of Field Crops, Faculty of Agriculture, University of Çukurova, Adana, Turkey
[2]Department of Agronomy, Faculty of Agriculture, University of Kafrelsheikh, Egypt
[3]Department of Field Crops, Faculty of Agriculture, University of Dicle, Diyarbakır, Turkey
*E-mail: cebar@cu.edu.tr

This study was conducted to evaluate the adaptability of wheat genotypes under hot environment by measuring of canopy temperature and flag leaf greenness (SPAD value). Canopy temperature and flag leaf greenness of wheat genotypes were determined at different sowing dates, with corresponding changes in yield and yield traits. Fifty eight wheat genotypes were grown on two sowing dates, i.e. normal sowing date (01 October, 2015) and late sowing date (01 March, 2016), at the agricultural research area of Cukurova University in Adana, Turkey. The experiment was arranged in a split plot design with three replications. Sowing times -- normal sowing time and late sowing --were allocated in the main plots; and sub plots were allocated the widely adapted spring bread wheat genotypes comprising current genotypes from Australia (8), Egypt (9), ICARDA (2), Japan (3), USA (1), Pakistan (5) and Turkey (30), which were tested. The results indicated that the cultivation environment (normal, hotter) remarkably influenced wheat yield, as reflected in the overall reduction in yield traits, and finally decreased yield for major genotypes at late sowing (hot environment), compared to the same measures taken in the control environment. According to the correlations of genotypes in cool environment (optimum planting date), cooler canopy indicates more grain yield; cooler canopy at the grain establishment (ZGS:71) helps to increase grains per square metre, and grain weight was negatively influenced by increase in grain number. Further, grain number is more sensitive to high canopy temperature at the grain establishment (ZGS:71). Regarding the hot environment (delayed planting date) it was found that grain yield is more affected by the grain number than grain weight, and further, grain weight negatively influenced by the grain number. Under the hot environment, there was no relationship between SPAD and canopy temperature, while the canopy temperature was strongly correlated with grain yield under conditions of the study. On the other hand, the stay-green trait in wheat at the drought stage (ZGS:84) indicates more grain number and grain yield. Based on the results, the stay green trait and canopy temperature can be used as selection criteria to identify heat stress-tolerant genotypes in wheat under Mediterranean conditions.

IDT7-017 | Physiological characterization of trait introgressed lines of rice (*Oryza sativa* L.) under drought

Pooja Bharti[1], Prathibha MD[1], Smitharani JA[1], Udayakumar M[1], Rajanna MP[2], Sheshshayee MS[1*]

[1]University of Agricultural Sciences, GKVK, Benguluru, 560065, Karnataka, India
[2]Zonal Agricultural Research Station, College of Agriculture, Mandya, Karnataka, India
*E-mail: msheshshayee@hotmail.com

Water uptake and water use efficiency together have great relevance in improving plant productivity. Therefore, introgression of these traits on to a single genetic background is more appropriate to achieve reduced water requirement for a given yield potential.

To verify the relevance of trait introgression, progeny (DCBC$_3$F$_5$) from an elaborate Double Cross Back Cross program were utilized. AC-39020 was selected as root trait donor parent and IET-16348 was selected as WUE donor parent and the respective traits were introgressed into IR-64 by Marker Assisted Backcross Breeding (MABCB) strategy. Trait Introgressed Lines (TILs) with improved root traits and WUE were identified. These TILs were grown under three different water regimes (100% FC, 65% FC and 45% FC). Several physiological parameters such as root traits, gas exchange, water relations and yield were recorded. TILs were able to sustain sufficiently positive turgor even under stress conditions. Hence, yield reduction was not noticed under stress condition in these TILs compared to IR-64. The TILs recorded significant increase of yield while saving more than 50% of irrigation water. Therefore, combining root related traits and WUE is beneficial for sustaining rice productivity under semi-irrigated aerobic condition.

IDT7-018 | *In vitro* polyploidization a novel approach for producing polyploids and screening for drought tolerance in acid lime (*Citrus aurantifolia Swingle*)

Bora L[1] *, Vijayakumar R. M[1], Meenakshi Ganesan N[2], Ganga M[1]

[1.]Horticultural College & Research Institute, Tamil Nadu Agricultural University Coimbatore, 641003, India
[2]Centre for Plant Breeding and Genetics, Agriculture College and Research Institute, Tamil Nadu Agricultural University Coimbatore, 641003, India
* E-mail: lokeshbora36099@gmail.com

Polyploidy is a frequent occurrence in the plant kingdom and is a major force of plant evolution. The induction of polyploidy ameliorates the adverse effects of drought in many plants. Drought stress is the most common cause of leaf curl in citrus group. Production constraints of lime are a group of abiotic factors. Breeding or developing a superior variety for water-limited environments can be an alternative option. In this study, polyploid plants were obtained by *in vitro* methods, using colchicine treatment in MS media. The effects of drought stress on citrus were studied by investigating the following parameters in leaves: relative water content (RWC), proline content, malondialdehyde (MDA) content, and somatic conductance. Under drought stress, polyploids had higher RWC and chlorophyll fluorescence parameters and lower levels of MDA and proline compared to diploids, and can be useful for developing improved genotypes to mitigate abiotic stress. Studies pertaining to combined physiological and molecular data can help in deciphering the actual mechanism for enhanced drought tolerance by polyploidization. Further studies are needed for better understanding of the differential regulation of genes in autotetraploid genotypes compared with diploids.

IDT7-019 | The influence of water stress on yield, some physiological characteristics and Leonurine contents of some ecotypes of *Leonurus cardiaca* in Iran

Borna F[1*], Nazeri V [1], Shokrpour M[1], Ghaziani F[1]

[1]Campus of Agriculture and Natural resources, University of Tehran, Karaj, Iran
*E-mail: fatemehborna@gmail.com

Drought stress has become the major limitation factor on plant yield at global scale. Plant response to water deficit dependent on the length and severity of water lost and also on the species or genotype. The amount of rainfall in many parts of Iran does not provide the water requirements for plant growth and thus facing to water stress especially in summer seasons is inevitable. To obtain satisfactory yields, the irrigation is necessary to compensate water deficit. Motherwort (*Leonurus cardiaca*), a medicinal plant of the Lamiaceae family, has a great diversity and wide distribution in Iran. It is important due to having Leonurine with blood dilution and muscles relaxation effects. In order to evaluate the response of the Motherwort ecotypes in drought environments, an experiment was carried out in split plot design based on RCBD, with three replications. Three irrigation levels were considered as main plots, including %, one third and two third of FC and four ecotypes as sub plots including Kerman, Taleghan, Sarab and Khansar. The results showed that, water stress affected the yield significantly. Water stress had significantly increasing effect on the phenolic and flavonoid contents and antioxidant activity of Motherwort ecotypes. The highest and the lowest total phenol content were observed in Taleghan and Sarab ecotypes, respectively. Interaction effects of water deficit levels and ecotypes on proline, proteins, hydrogen peroxide were not significant while on activity of catalase, superoxide dismutase, guaiacol peroxidase were significant. The amount and percentage of Leonurine were increased by water deficit. The highest value of Leonurine was observed in Taleghan and the lowest in Sarab in all three levels of irrigation. There were significant positive correlations between water deficit levels and the amount of total phenol, flavonoids, antioxidant, proline, catalase, guaiacol peroxidase, hydrogen peroxide and the amount and percentage of Leonurine. Based on physiological and biochemical results, the ecotype of Taleghan was the most tolerant and Sarab was the most susceptible ecotype to water deficit among the studied ecotypes.

IDT7-020 | Relationships between morpho-physiological root traits and the performance of spring wheat genotypes under water-stress in Mediterranean environments

Brunel-Saldias N[1,2*], Madrid J[3], Guerra F[4], del Pozo A[1,2]

[1]Centro de Mejoramiento y Fenómica Vegetal, Facultad de Ciencias Agrarias, Universidad de Talca, Chile,
[2]PIEI Adaptación de la Agricultura al Cambio Climático (A2C2), Universidad de Talca, Chile.
[3]Laboratorio de Genómica Funcional, Instituto de Ciencias Biológicas, Universidad de Talca, Chile.
[4]Laboratorio de Genética y Biotecnología Forestal, Instituto de Ciencias Biológicas, Universidad de Talca, Chile.
*E-mail: nidiabrunel@gmail.com

The role of morphological and physiological roots traits in the productivity of wheat under water-stress conditions is widely recognized. Despite the association of several genotypic variations in root traits with drought tolerance, there are still few results that strengthen root phenotyping as a tool to improve crop yield in areas with severe drought, such as the drought in Mediterranean climates. The main objective of this work was to identify roots traits that can be related to the degree of drought tolerance of spring bread wheat (*Triticum aestivum*) in central to south zone of Chile. Roots length and biomass distribution of five genotypes (three tolerant and two susceptible to water stress) were evaluated under field and controlled conditions, with and without water stress. In addition, an analysis of the expression of aquaporin´s genes was evaluated using real-time PCR. The results indicated genotypic differences in root architecture in depth and in gene expression under water stress conditions. Thus drought would regulate, temporarily and spatially, the root system and the expression of aquaporin genes PIP1 and PIP2.

IDT7-021 | Evaluation of drought tolerance QTL effect in adapted genetic background

Caguiat JD[1*], WaingFP[1], Tabanao DA[1], Enriquez JOS[1], Caguiat XGI[1], MillasRA[1], Santiago JIIC[1], Palanog AD[2]

[1]Philippine Rice Research Institute, Central Experiment Station, Maligaya, Muñoz, Nueva Ecija 3119, Philippines
[2]Philippine Rice Research Institute, Murcia, Negros Occidental 6129, Philippines
[*]E-mail: jmdomingo83@yahoo.com, jm.domingo@philrice.gov.ph

Development of drought tolerant rice varieties is one of the most effective ways to combat drought which causes 50% of rice production losses globally. This study aimed to introgress the QTL for drought to improve the drought tolerance of NSIC Rc160 and NSIC Rc222; and to evaluate the generated lines through genotypic and phenotypic selection. BC4F4 populations of PR47201 in NSIC Rc222 (qDTY12.1) background and PR47202 in NSIC Rc160 (qDTY2.2 and qDTY4.1) background were developed through marker-assisted backcrossing. These populations were screened for grain yield under lowland drought reproductive stress and non-stress conditions. During 2015 dry season, grain yield ranges from 39 to 6006 kg/ha with an average grain yield of 1103 kg/ha. PR47201 and PR47202 with introgressed drought tolerance out-yielded all the parent lines (without drought QTL) and tolerant checks Vandana NIL and IR64 NIL. In 2016 dry season, average grain yield of selected PR47201 population under drought stress was 928 kg/ha with yield ranging from 111 kg/ha (PR47201-A102A-29-51-1) to 3,057 kg/ha (PR47201-A102A-29-14-1), while PR47202 population had an average yield of 862 kg/ha with yield ranging from 247 kg/ha (PR47202-A103-25-5-1) to 2,159 kg/ha (PR47202-A103A-18-236-1). The check varieties NSIC Rc160, NSIC Rc222 and Vandana NIL yielded 1140, 1197 and 506 kg/ha, respectively. Improvement of drought tolerance will increase yield of these varieties under drought condition. This study utilized the importance of combining genotype and phenotype data in order to accelerate the development of high-yielding drought-tolerant varieties.

IDT7-022 | Discovering adaptive responses of alfalfa (*Medicago sativa* L.) to drought stress

M. Rokebul Anower[1], Christy M. Motes[1], and Maria J. Monteros[1]*

[1]The Samuel Roberts Noble Foundation, Ardmore, OK 73401. USA.
E-mail: mjmonteros@noble.org

Alfalfa (*Medicago sativa* L.) is an important forage legume species worldwide due to its high biomass yield, relative feed value, persistence, and capacity for symbiotic nitrogen fixation. Drought is a significant factor affecting the productivity of global agricultural products for feed, food and fiber. The objective of this research was to identify genetic variation for biomass productivity under drought stress in alfalfa and evaluate physiological, transcriptomic and metabolomics approaches used to cope with limited water availability. A total of 233 diverse alfalfa germplasm accessions were evaluated in the field for agronomic performance and capacity to persist in water deficient environments. Overall performance, yield, persistence, relative water content, forage quality and other morphological traits were used to select promising accessions from the field. Of those, the top 20 performing accessions were further evaluated in the greenhouse under water-sufficient and water-limited conditions at the physiological and molecular level. Soil moisture sensors were used to monitor drought conditions in real time and assess the rates of water use by each plant. Drought physiology parameters evaluated include leaf water potential, osmotic potential, stomatal conductance, relative water content, chlorophyll content, as well as root growth and biomass yield. Drought tolerant accessions maintained a higher osmotic potential and synthesized numerous osmoprotectants in roots and shoots compared to the drought sensitive accessions as adaptive mechanisms to the water deficit conditions. Sequence-based genotyping and transcriptomics (RNA-Seq) provided further insights on the genetic differences and variation in gene expression of drought-tolerant vs. drought-sensitive accessions. The multi-omics approach utilized to explore a diversity of adaptive responses to drought stress in alfalfa will provide valuable insights to develop alfalfa cultivars in the future that are productive under limited water availability.

IDT7-023 | Analysis of leaf yield components in fluted pumpkin (*Telfairia occidentalis* Hook F.) using path coefficient and GGE Biplot in derived savannah agro-ecology

Chukwudi UP*, Agbo CU, Ene CO, Uba CU, Enyi JI

University of Nigeria Nsukka, Enugu State, Nigeria,
*E-mail: uchechukwu.chukwudi@unn.edu.ng

Twelve maize genotypes were collected from the International Institute for Tropical Agriculture (IITA), along with seven landraces to identify contribution of different traits to yield improvement in the seasons. The experiments were carried out in two different seasons (early and late season) in a randomized complete block design with three replications. The results showed that 'TZE - Y -POR STR QPM CO' and 'TZE- Y - POP DT STR QPM' had significantly ($p < 0.05$) shorter number of days to tasselling and silking. One of the landraces, *Ugwuachara*, gave significantly higher grain yield in both seasons. Early-season planting had a higher grain yield when compared to late season, with 27.81% increase in grain yield of 3.02 tons/ha over late season. The number of ears per plant and shelling percentage were not influenced by seasonal effects. Grain yield had positive correlation with plant height, ear height, ear length, number of ears per plant, shelling percentage and ear weight in both seasons. Furthermore, ear weight had the highest correlation coefficient with grain yield in both seasons. Ear weight, followed by days to tasselling, showed the highest direct positive effect on grain yield in early season, while ear weight followed by shelling percentage exerted the highest direct positive effect on grain yield at late season. The genotypes, *'Ugwuachara'* and ''TZE- Y - POP DT STR QPM'' could be selected for late season planting because of their higher significant grain yields. Selection of genotypes with higher ear weight increased grain yield in both seasons.

IDT7-024 | Genetics of important traits for moisture stress tolerance in derived test cross hybrids of Maize (*Zea mays*. L)

Deshpande, S. K[1]*, Mani, B. R[2]

[1]Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad-580 005, India.
[2]University of Agricultural Sciences, Dharwad-580 005, India.
*E-mail: sanjeevgpb@gmail.com

Maize is an important cereal crop of India, with high yield potential. The crop yield needs to be enhanced under varying climatic regimes to meet the requirements of human food, agro based industries and different farm sectors. A study was planned to determine an appropriate breeding approach to enhance moisture stress tolerance and, in turn, increase yield *per se* using test cross hybrids and their parents. Previous studies had confirmed significant correlation of ASI, RWC-1(30 days after stress), RWC-II (60 days after stress), SPAD-I (30 days after stress), SPAD-II (60 days after stress), drought tolerant indices *viz*., DSI, TOL (yield difference between irrigated and stressed field), MP and GMP, with grain yield under moisture stress. The present study confirmed higher dominance variance (σ^2 D) than additive variance (σ^2 A) at F=0, for all the ten important traits for drought studied. Dominant variance depicted role of non-additive genes in controlling inheritance of traits. To exploit the effects of non-additive genes in the form of moisture stress tolerance, we suggest heterosis breeding as a better choice. Estimates of weighted pooled *gca* inferred inbreds PDM6518, PDM6528, PDM6554 and HKI163 as best general combiners. These inbreds may be pooled to derive superior inbreds for moisture stress tolerant traits, may be intercrossed to study heterosis in the form of stress tolerance and high yield per se, and also can be used in development of synthetics and composite populations. In present study, the best specific cross combinations for the improvement of ASI, RWC-II, SPAD-II, TOL and grain yield are PDM6528xLM13, MLB34xLM17, PDM6541xLM17, PDM4191xLM13 and PDM4211x LM17 respectively.

IDT7-025 | Advances in groundnut breeding for drought prone West and Central Africa

Desmae H[1]*, Ntare B[1], Motagi BN[2], Falalou H[3], Upadhyaya H[4], Oteng-Frimpong R[5], Sako D[6], Echekwu C[7], Miningou A[8], Monyo E, Varshney RK[9]

[1]International Crops Research Institute for the Semi-Arid Tropics, Bamako, Mali;
[2]International Crops Research Institute for the Semi-Arid Tropics, Kano, Nigeria;
[3]International Crops Research Institute for the Semi-Arid Tropics, Niamey, Niger;
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India;
[5]Savannah Agricultural Research Institute (SARI), Tamale, Ghana;
[6]Institut d'Economie Rurale (IER), Kayes, Mali ;
[7]Institute of Agricultural Research (IAR), Zaria, Nigeria;
[8]Institut de l'Environnement et de Recherches Agricoles (INERA), Kamboinsé, Burkina Faso ;
[9]International Crops Research Institute for the Semi-Arid Tropics, Nairobi, Kenya
*E-mail: h.desmae@cgiar.org

The West and Central Africa region accounts for more than 70% of the groundnut production in Africa. The crop is challenged by various biotic and abiotic production constraints with drought being the main abiotic constraint. ICRISAT has been working with national breeding programs to develop improved groundnut varieties. The approach used included identifying sources of resistance, developing populations, evaluating in target environments and releasing improved farmer preferred varieties for production. The Tropical Legumes project initiated in 2007 has been instrumental in strengthening the breeding program in the region. Nine drought resistant/tolerant accessions were identified from evaluation of the mini core collections, and these accessions have been utilized as parents in crossing programs. Since 2007, ICRISAT distributed more than 1000 advanced breeding lines to national programs. Farmer participatory variety selection was found very useful for fast track release and adoption of improved varieties. Twenty two varieties have been released/registered across the region as a result of project efforts (4 in Ghana, 5 in Mali, 4 in Niger, 3 in Nigeria and 6 in Senegal). These varieties are high yielding (yield advantage of >20%) with resistance or tolerance to drought and major diseases. Currently, efforts are underway to improve the efficiency of breeding programs and to enhance genetic gain. These include designing product pipelines based on traits of breeding interest; reducing generation advancement process of breeding populations by growing 2 to 3 generations per year; integrating modern genomic tools; digitizing data collection, analysis, management and sharing by using BMS; and enhancing the skills of breeders and technicians.

IDT7-026 | Pyramiding of mega effect multiple QTLs and development of 'climate-resilient rice'

D.Dhivyapriya[1]*, A.Kalamani[2], S.Ramchander[1], M.Raveendran[3] , S.Robin[4]

[1]Department of Rice, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India
[2]Professor & Head (Rtd), Department of Forage Crops, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India
[3]Professor, Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India
[4]Dean (SPGS), Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India
*E-mail: dhivyaraj.89@gmail.com

Changing climate scenario accelerated the frequent occurrence of abiotic stresses where drought and salinity remain the devastating stresses affecting rice production and productivity. Developing climate-resilient crop varieties are of foremost importance to combat the effect of abiotic stress in order to ensure food security. The present investigation focused on the development of resilient Improved White Ponni (IWP) pyramided with mega effect drought and salinity QTLs from Apo and FL478 respectively. Inter-mated (pseudo-backcrossing F_1) progenies were identified and forwarded to F_2 generation. Forty five superior lines were selected based on the grain parameter and genotyped using foreground SSR markers. F_3 lines were grown under Rain out shelter (ROS) where terminal drought was imposed. The F_3 lines *viz.,* F_3-IWP-900, F_3-IWP-853, F_3-IWP-157, F_3-IWP-848, F_3-IWP-172, F_3-IWP-839 and F_3-IWP-859, recorded higher spikelet fertility, higher grain yield and harvest index than the parents and check which indicated the pronounced effect of introgressed QTLs (*DTY 2.2*, *DTY 3.1* and *DTY 6.1*) on grain yield under drought. Under salinity stress (100 mMNaCl) the F_3 lines harboring *SalT* QTL were found to possess lesser sodium/potassium ratio than the non-*SalT* lines. Graphical genotyping revealed that the pyramided F_3 line was found to be higher (>80%) recurrent parent genome recovery with medium slender kernel with intermediate gelatinization temperature. The overall study revealed that, the genotypes *viz.* F_3-IWP-747- 301, F_3-IWP-747- 304, F_3-IWP-747-338, F_3-IWP-747-339 and F_3-IWP-900-1096 were found to possess all positive grain quality traits of Improved White Ponni and, in addition, they exhibited enhanced level of tolerance against drought and salinity stresses.

IDT7-027 | Pyramiding genes to develop multiple stress-tolerant rice lines

Dixit S[1],Singh UM[1], Nachimutthu VV[1], Ramaya PJ[1], Nagamallikadevi M[1] , Priyadarshi R[1], Yadav S[2], Alam S[1], Kumar VA[1], Naik SM[1], Jain A[1], Venkateshwarlu CH [1], Kumar A*[1],[2]

[1] International Rice Research Institute-South Asia Hub, Building # 303, ICRISAT, Patancheru 502324, Telangana State, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
*E-mail: a.kumar@irri.org

Rice (*Oryza sativa* L.) is one of the most important food crops that nurture nearly half of the world's population. Rice crops are prone to various types of stresses, both biotic and abiotic. Biotic stresses such as gall midge, brown plant hopper, bacterial blight and blast, and abiotic stresses such as droughts and floods are serious constraints that reduce rice yield. Swarna is a very popular high-yielding mega variety of rice grown in different parts of India; nevertheless, its susceptibility to pests, diseases and abiotic stresses deflate its performance and yield. These days, gene/QTL pyramiding is gaining considerable importance as it would improve the efficiency of plant breeding, leading to the development of genetic stocks with broad-spectrum resistance capabilities for different stresses and enhancing the performance of high-yielding varieties under frequent weather extremes. Pyramiding of major QTLs and genes for BLB (*xa5,xa13,Xa21*), blast (*Pi9*),gall midge (*Gm4 & Gm8*), brown plant hopper (*Bph3 & Bph17*), drought (qDTY1.1, qDTY3.1) and submergence (*Sub1*) in the background of Swarna was undertaken to combine resistance/tolerance against different stresses. A systematic complex crossing program using donors for different genes/QTLs followed by genotyping using peak and flanking markers allowed development of F3 lines possessing the targeted genes for different stresses in different combinations.

IDT7-028 | Fine tuning phenology genes to safeguard wheat (*Triticum aestivum* l.) yield in water limited environments

Nazim Ud Dowla M A N[1*], Edwards Ian [1,2], O'Hara Graham[a], Ma Wujun [1,3]

[1]School of Veterinary and Life Science, Murdoch University, Perth, Western Australia
[2]Edstar Genetics Pty. Ltd., Murdoch University, Perth, Western Australia
[3]Australia China Centre for Wheat Improvement
*E-mail: m.dowla@murdoch.edu.au

In Western Australia, moisture stress seriously limits wheat yield, as it mostly coincides with stem elongation, flowering and grain filling stages of wheat. Adjusting flowering time and the duration of developmental phases with environmental cues are often advocated to avoid stress during sensitive developmental stages. Thus, crop phenology is a critical component of yield physiology and is controlled by vernalization (*Vrn*), photoperiod (*Ppd*), and autonomous earliness *per se* (*Eps*) genes. The interaction of both the vernalization and photoperiod genes in the flowering pathway determines the development and maturity of wheat.

The aim of this study was to find out the optimal allelic combination of *Vrn* and *Ppd* genes that would provide better adaptation for water-limited environments and optimize wheat yield. In a series of experiments with a double haploid (DH) population and set of advanced lines, we observed more than one month variation in physiological maturity. Lines with all the recessive alleles of *Vrn1* were the latest in heading, while those with all the dominant alleles were not the earliest. But inclusion of the insensitive allele of *Ppd1* with any combination of Vrn1 *genes* advanced the heading time by at least one week to three weeks. This differences in heading also impacted the spike length, seed per spike, tiller number per plant, thousands kernel weight and seed roundness. More interestingly, variation in total and periodic water consumption was observed among the tested lines, as developmental stages were modified due to this allelic variation. These results suggest that breeding varieties with suitable phenology genes could safeguard wheat yield in water limited environments.

IDT7-029 | Landrace based top-cross pearl millet hybrid development for the Sahel Zone in Burkina Faso

Drabo Inoussa

West Africa Centre for Crop Improvement (WACCI), University of Ghana, Accra, Ghana
E-mail: idrabo@wacci.edu.gh

Pearl Millet (*Pennisetum Glaucum* (L.) Br.) is an important staple food and forage crop for people and livestock living in the semi-arid tropical regions of West Africa and India. It is extremely important in West Africa where it is either the first or the second ranked cereal crop. In Burkina Faso, it is the second most grown cereal crop after sorghum. The production area is subject to drought at every growing stage. Only landraces and few improved OPVs are currently available to farmers. The yield is very low and the production is not able to feed farmers for more than five to six months. Hybrid option is the rapid way of breeding high-yielding pearl millet cultivars and top-cross hybrids are likely to be a high-yielding stable in Sahel environment. Eighteen landraces growing in the Sahel zone of Burkina Faso were crossed with two male sterile A-lines developed from improved OPVs to produce 36 top-cross hybrids.

These hybrids were evaluated along with pollinators and standard checks in an alpha lattice design at Dori in the north Sahel (≤ 500 mm annual rainfall) and at Gampela and Saria in the North Sudan Zone of Burkina Faso. At least 10 hybrids showed positive 'high parent heterosis', among which four were superior to the best OPV and hybrid check. The cross MS_SOSAT/PE03012 is the highest yielding and the most stable in the Sahel zone, and is a promising hybrid for the Sahel areas in Burkina Faso.

IDT7-030 | Genome-Wide Association analysis for yield and yield-related traits in bread wheat (*Triticum aestivum* L.) under contrasting moisture regimes

Fellahi Z[1]*, Dreisigacker S[2], Sehgal D[2], Hannachi A[1], Yahyaoui A[2], Bouzerzour H[3], Burguenõ J[2]

[1]Faculty of Life and Natural Sciences, Agronomy Department, VRBN Lab, Ferhat Abbas University Setif-1, Algeria.
[2]International Maize and Wheat Improvement Center (CIMMYT), km. 45 Carretera Mexico-Veracruz El Batan, Texcoco, Estado de Mexico, CP 56130.
[3]Faculty of Life and Natural Sciences, Ecology and Plant Biology Department, VRBN Lab, Ferhat Abbas University Setif-1, Algeria.
*E-mail: zinou.agro@gmail.com

To meet future production demands, multi-disciplinary breeding approaches are needed to achieve genetic gains. Genome-wide association mapping (GWAM) can be a powerful tool for the identification of genes associated with important agronomic traits in wheat. A set of 600 F_4 bread wheat lines representing 20 bi-parental populations generated from crosses between nine parents in a line x tester mating design was established. The genetic material was tested in a field trial in 2014/15 cropping season in Setif (36°12'N, 05°24'E, 981 m asl), Algeria, under rain-fed and irrigated environments. The objective was to identify marker-trait associations (MTAs) for 14 physiological, morphological and relevant agronomical traits for improving wheat to drought stress using GWAM approach. The 600 lines were genotyped using the Illumina 15K Infinium SNP array. A linear mixed model in ASReml package was used to obtain the genotypes' best linear unbiased predictors (BLUPs) for each trait recorded, which were subsequently used in GWAM along with 8551 filtered and mapped SNPs. Population structure analysis revealed four sub-populations. For GWAM results, a significant threshold of $p < 0.001$ was used to declare MATs. Markers with more than 10 cM apart were considered as unlinked. This resulted in the identification of several significant MTAs detected in one or more environments for 14 measured phenotypic traits in rain-fed and irrigated environments, plus combined data across environments. Chlorophyll content revealed most MTAs, with 61 SNPs on chromosomes 1B, 1D, 2A, 2B, 3A, 3B, 3D, 4D, 5A, 5B, 5D, 6B, 7A and 7B. The lowest number of 14 MTAs was detected for spike weight on chromosomes 1A, 2A, 3B, 5B, 6A, 6B and 7B. No relevant SNPs were revealed for flowering time under rain-fed environment. Grain yield MTAs were found on chromosomes 1A, 2A, 4A, 6A in two out of three environments, including both rain-fed and irrigated, and a combined analysis. Other MTAs were detected on chromosomes 3D, 4B, 5B and 7B under rain-fed conditions and three MTAs on chromosome 3B showed the strongest association with yield under irrigated conditions. Multi-trait QTLs were obtained on many chromosome regions of which chromosomes 1A, 2A, 3B, 3D, 4B, 5B, 6A and 7B are most significant having QTLs of grain yield co-located with flag leaf area, plant height, number of spikes, spike weight, thousand kernel weight, number of grain, biological yield, straw yield and harvest index. However, only those on 1A, 2A and 6A were stable across two over three environments. Future breeding strategies can be devised to initiate marker-assisted breeding, following proper validation of those QTL, to accumulate the favorable alleles associated with yield-related traits to increase grain yield in water-limited environment.

IDT7-031 | Studies on drought tolerance in maize (*Zea mays* L.) inbred lines using morphological and molecular approaches

Asima gazal[1*], F.A. Nehvi[2], A.A.Lone[3], A.B. Shikari[4], Z.A. Dar[3] and M.A. Bhat[1]

[1]Division of Genetics and Plant Breeding, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir, 190025.
[2]Saffron Research Station, konibal, Pampore, SKUAST-K, 192121
[3]Dryland (*Karewa)* Agricultural Research Station, Budgam, SKUAST-K, 191111
[4]Division of plant biotechnology, Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir, 190025
*E-mail: asimagazal@gmail.com

Lack of potential hybrids showing genes for moisture stress is responsible for low maize productivity in Kashmir. Present study was an attempt in this direction to identify elite maize lines showing resilience to moisture stress for 24 traits under study related to maturity, morphological, physiological, yield, quality and root traits. Study was carried over two years at DARS, Budgam a constituent research station of SKUAST-K. Evaluation confirmed a wide range of variability revealing significant response of main effects (lines, irrigations and years and their respective digenic & trigenic interactions) as indicated by the magnitude of *per se* performance, PCV & GCV implying considerable scope for maize improvement through phenotypic selection. Application of water made plants photosynthetically more efficient thus, contributing to more grain yield. Selection index & genetic divergence constructed for maturity, morphological, physiological, yield, quality, seedling and root traits exhibited elite nature of fifteen lines (KDM-361A, CM-129, KDM-372, KDM-331, KDM-1051, KDM-402, KDM-463, KDM-717, KDM-912A, KDM-932A, KDM-343A, KDM-961, KDM-918A, KDM-1156 and KDM-1236) occupying first fifteen ranks for the traits under study. However, molecular characterization using 40 SSR loci identified diverse nature of only six lines (KDM-372, KDM-343A, KDM-331, KDM-961, KDM-1051 and KDM-1156). Commercial exploitation of six diverse maize lines as parents for developing single cross hybrids in all possible combinations will help in boosting maize productivity of the state as 70 % of maize is rainfed. However, SSR loci viz., umc-1766, umc-1478 and phi-061 recorded PIC > 8 and alleles per locus > 9 and therefore discriminated lines more efficiently.

IDT7-032 | Wild lentils as genetic resources to drought proof cultivated lentil

Gorim, L.Y.[1*], Vandenberg, A.[1]

[1.]University of Saskatchewan, Saskatoon SK S7N 5A8 SK Canada
*E-mail: linda.gorim@usask.ca

Increasingly unpredictable and variable annual rainfall patterns have far reaching implications for pulse crop production. In the case of lentils, potential effects include not only disease incidence, but also seedling and whole plant survival given that water is a key factor in plant photosynthesis. Wild relatives of cultivated lentil currently grow mainly in drought-prone areas, making them good candidates for identification and evaluation of drought-tolerant traits and ultimately, genes that can be transferred to their cultivated relative. We evaluated a set of eight lentil genotypes representing parents of interspecific crosses, under two water deficit conditions (40% and 25% field capacity) compared to fully watered conditions. The genotypes evaluated included one cultivated (*Lens culinaris*'Eston') and seven wild parents (*L. orientalis* IG 72643, *L. orientalis* PI 572376, *L. tomentosus* IG 72805, *L. odemensis* IG 72623, *L. lamottei* IG 110813, *L. ervoides* LO1-827A and *L. ervoides* IG 72815). All genotypes were grown on field soil from the A, B and C horizons. Soil was used to fill split tubes that were segmented into three sections. Above ground parameters and root characteristics were analyzed. We observed that the genotypes tested employed diverse mechanisms to evade or tolerate water deficit conditions. In some cases within the same genotype, more than one strategy was employed to survive water stress. Secondly, how closely the genotypes were related did not affect what mechanisms were employed to avoid drought stress. Additional experiments are underway to evaluate crosses between some of the wild parents and cultivated cultivars as an assessment of potential for introgression of drought tolerance.

IDT7-033 | Potential of *in vitro* screening for drought tolerance in crops

Hassan LB[1*], Oyekunle M[1], Ahmed HO[1], Abdulmalik RO[1], Aliyu RS [1], Usman M[1]

[1]Ahmadu Bello University, Zaria, Kaduna State, Nigeria
*E-mail: lbhassan@abu.edu.ng

Water stress is one of the main abiotic stresses that hinder crop growth and productivity. Studies have shown that screening for abiotic stress tolerance *in situ* was based on necrosis scores and reduction in shoot biomass when exposed to stress, compared to unstressed controls. However, such a measure of screening for tolerance has been reported to be laborious, destructive and time-consuming; and results are subjected to environmental variation. The use of *in vitro* screening method is a potential and cost effective technique for screening large set of germplasm within a short period of time, with more accuracy. Efforts had been made to screen tomato germplasm under *in vitro* condition, using polyethylene glycol (PEG) of different concentrations. A mutant hybrid tomato and its derivatives were reported to have outstanding capacity of continuous root growth under *in vitro* stress conditions, indicating their ability to survive under severe water stress. Also, effects of drought stress on germination of wheat genotypes were studied using PEG at three different concentrations. The PEG induced a drop in the shoot length, root biomass and coleoptiles length, which was reported to be more in some genotypes than the others. In addition, the effectiveness of physiological, biochemical and /or molecular markers in screening for abiotic stress had been reported. Thus, in *vitro* screening technique can be used as an efficient tool for screening large number of germplasm within a short time.

IDT7-034 | Identification and evaluation of chickpea genotypes for tolerance to heat stress under normal and heat stress environments for rice fallow condition in West Bengal.

Hotti AH[1,2], Sadhukhan R[2]

[1] University of Milan, Italy
[2] Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India.
*E-mail: avihotti@gmail.com

The study was conducted using 20 early maturing *desi* chickpea (*Cicer arietinum* L.) genotypes with two local check varieties, which were sown on 18 November 2014 as normal, 10 December as late, and 1 January 2015 as very late under rice-fallow conditions in West Bengal. It aimed to check their tolerance to terminal heat stress. Analysis of variance was performed separately for all planting regimes, and was found to have significant variation for plant phenology, growth, and grain yield per plant, including pod number per plant, filled pod number per plant, hundred seed weight and harvest index. The highest genotypic and phenotypic coefficient of variation was exhibited by plant biomass and grain yield per plant for all seasons, whereas high heritability and high genetic advance was observed for all traits under normal and late sown conditions. Grain yield per plant was positively and significantly correlated with total and filled pod number per plant, plant biomass, hundred seed weight and harvest index in normal and late sown condition. The average grain yield loss in the genotypes varied from 50% to 60% of potential yield under late and very late planting regimes. Increase in temperature beyond the optimum temperature range during the reproductive period of the crop is one of the major reasons for yield loss among the genotypes. On comparing the mean values of the selected traits, three heat-tolerant genotypes were identified such as ICCV 10, BG 256 and RAJAS.

IDT7-035 | Screening of some functional markers in *Helianthus argophyllus*, *Helianthus annuus* and their derived population for adaptabilty under abiotic stress conditions

Muhammad Mubashar Hussain[1], Maria Kausar[1], Saeed Rauf[1], Jakub Paderweski[2], Maria Khan[1]

[1]Department of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Pakistan, 40100
[2]Department of Experimental Design and Bioinformatics, Warsaw University of Life Sciences, Poland, Nowursynowska 159, 02-776 Warsaw
*E-mail: mubashar_uca@yahoo.com

Abiotic stresses including drought are major crop production constraints. However, specific functional phenotypic markers induce resistance against these stresses. Therefore, a study was initiated to study the variability, inheritance and selection of epicuticular waxes (EW) and leaf hairiness (LH) along with low cell membrane injuries (CMI) within F2 populations derived by crossing *H. annuus* × *H. argophyllus* lines. The studied parent populations (species) showed contrasting values of the traits. The F1 hybrids had mean values of the three studied parameters in the range of parent lines, but some of F2 individuals extend beyond this range (parents and F1s). The two-step selections maintained high variability especially of LH for set of F2 individuals (*H. annuus* CMS-20 × *H. argophyllus* 1806). Simultaneous selection of F2 individuals with high values of LH or EW with low CMI was possible. The high value of LH and EW was not an index of the low CMI value. The selected plants were further studied for narrow leaf, high fertility and silver canopy color. Selected material will be promoted as the candidate inbred lines. The study could help to increase the abiotic stress tolerance and functional diversity within sunflower.

IDT7-036 | Combining ability of cowpea [*Vigna unguiculata* (L.) Walp] lines for grain yield and drought tolerance under managed moisture condition.

Ibitoye DO[1,2,3]*, Boukar O[2], Tongoona P[3], Offei SK[3], Blay ET[3], Fatokun CA[2]

[1]National Horticultural Research Institute, P.M.B 5432, Ibadan, Oyo State, Nigeria
[2]International Institute of Tropical Agriculture (IITA), P.M.B 5320, Ibadan, Oyo State, Nigeria
[3]West Africa Centre for Crop Improvement, University of Ghana, P.M.B. 30, Legon-Ghana
*E-mail: bunmiajisafe@yahoo.com

Drought is a major constraint limiting the productivity of cowpea grain and fodder in the dry regions of Sub-Saharan Africa (SSA) where it is mostly grown under rain-fed conditions. The goal of this study was to identify lines with good general combining ability for high yield under drought stress conditions, which can be used as donor parents in crosses to generate segregating populations from where selection could be carried out for the development of high-yielding drought-tolerant varieties. Combining ability for grain yield and related drought-tolerant traits in adapted lines and germplasm accessions of cowpea was estimated under drought stress and non-stress conditions at the International Institute of Tropical Agriculture (IITA), Ibadan (07o 29.221′ N, 003o54.204′ E) and Minjibir-Kano (12o08.416′ N, 008o40.185′ E), Nigeria. One hundred hybrids generated using North Carolina Design II mating scheme were evaluated in a 10x10 α-lattice with three replications under different irrigation regimes. Hybrids differed significantly for all measured traits. General combining ability (GCA) and specific combining ability (SCA) were significant ($P < 0.01$) for many of the agronomic traits and delayed leaf senescence (DLSC). Additive gene effects were more important than non-additive genetic effects in controlling grain yield and DLSC under drought stress (GCA > 60%). TVu79, TVu6707 and TVu9693 had positive and significant GCA female effect, and TVu9797 had significant positive GCA male effect on grain yield under drought stress.

IDT7-037 | Evaluating for drought stress tolerance of some soybean promising mutant lines

Yuliasti[1]*, Indriatama WM[1] and Taufik A[2]

[1]Center for Isotope and Radiation Application (CIRA-BATAN), Indonesia
[2]Indonesian Legume and Tuber Crops Research Institute (ILETRI), Ministry of Agriculture, Indonesia
*E-mail: yuliasti@batan.go.id

Drought-tolerant soybean variety has an important role in maintaining yield stability. The aim of the research was to evaluate the tolerance of promising mutant lines of soybean to drought stress. The experiment was conducted in the greenhouse of Indonesian Legume and Tuber Crops Research Institute (ILETRI) in Malang, East Java, from November 2014 to March 2015. Ten promising soybean mutant lines, Panderman (the wild type variety), and Dering 1 (the check drought tolerant variety) were evaluated at two levels of soil water availability (100% and 40% availability of water). The combination of treatments was arranged in randomized complete block design with four replications. The results showed that drought stress treatment (40% of water availability) during growth period reduced yield and its components, and also delayed flowering and maturity time. There were five lines (G10K, G6K, G8K, G3K and G9K) that indicated higher tolerance to drought stress than the check variety. The potential yield, seed size and water use efficiency of those five lines were better than that of Panderman and Dering 1 varieties. The physiological maturity time of four lines (G10K, G8K, G3K and G9K) were longer than Panderman variety, but it were shorter than Dering 1 variety. Those lines could be proposed as potential candidates for drought stress tolerance.

IDT7-038 | Evapotranspiration rates influence biogenic silica concentration in the shoots of *Pennisetum pedicellatum* Trin. at intraspecific level in semi-arid environment, West Africa

Issaharou-Matchi I.[1,2,]*, Barboni D.[3], Meunier J.-D.[3], Saadou M.[4], Dussouillez P.[3], Contoux C.[3], Saley K[4]., Zirihi-Guede N.[1]

[1]Université Felix Houphouët Boigny, BP 165 Abidjan 31, Côte d'Ivoire
[2] Université de Diffa, BP 78 Diffa, Niger
[3]Aix-Marseille Université, CNRS, IRD, CEREGE UMR7330, Technopole Arbois-Méditerranée, BP80, 13345 Aix en Provence, Cedex 4, France
[4]Université Dan Dicko Dankoulodo Maradi, BP 465 Maradi, Niger
*E-mail: issakissaharou@gmail.com

Biogenic silica (BSi) contents in a widespread drought-adapted grass (*Pennisetum pedicellatum* Trin.) and associated surface soil samples from 12 sites along a climatic gradient of precipitation and drought-stress in South Niger were determined. Plant traits of these 12 specimens of *Pennisetum pedicellatum* were also analysed. We used the 1%Na2CO3 (nc) digestion method, and the acid plus heavy-liquid extraction method (bz) to quantify phytolith/amorphous silica (ASi). We used a microscope to analyze phytolith morphotypes. Our findings show that specimens from drier Sahelian sites contained more ASi in their shoot than the Sudanian one, meaning that ASi in plant specimens increases from South to North (with decreasing AET/PET and precipitation). ASi in plants shows higher correlation with length of dry season ($r=0.83$, $p<0.001$), precipitation of the wettest month (Pwet, $r=-0.84$, $p<0.001$), and AET/PET ($r=-0.73$, $p<0.01$). However, ASi in soil shows a contrasting trend, decreasing from South to North, which would be attributed to higher plant productivity at humid sites. With regard to plant traits, plant height increases with increasing precipitation ($r=0.61$, $p<0.05$) while leaf area increases when ASi in soils increases ($r=0.81$, $p<0.01$). The highest abundance of silicified bulliform motor cells was observed in *P. pedicellatum* growing under the driest climate. Thus, the highest negative correlation was observed between the abundance of silicified bulliform cells and AET/PET ($r=-0.93$, $p<0.001$). We conclude that drought and evapotranspiration rates increase Si concentration in the shoots of the C4 grass *P. pedicellatum,* influence its functional traits, and favour silicification of the bulliform (motor) cells.

IDT7-039 | Combining ability analysis for yield and its contributing traits in rice (*Oryza sativa* L.) under water limited condition

Jain A[1, 2]*, Balaravi P[3], Kamalnath Reddy KR[2, 4], Priyadarshi R[1, 2], Payasi D[2,5], Shenoy,V[2,6]

[1] International Rice Research Institute (IRRI), ICRISAT campus, Patancheru, Hyderabad, India
[2] Barwale Foundation, Himayatnagar, Hyderabad, India
[3] Osmania University, Hyderabad, India
[4] Indian Institute of Rice Research, Hyderabad, India
[5] JNKV, Regional Agricultural Research Station, Sagar, India
[6] Kaveri Seeds, Hyderabad, India
*E-mail: a.jain@irri.org

Rice yield in rainfed lowland areas is often affected by drought. The yield in these areas can be enhanced by developing rice varieties or hybrids adaptable to water stress condition. The present investigation was carried out to study the gene action and combining ability analysis for yield and its contributing traits in rice under contrasting moisture regimes. The evaluations were based on a line x tester set consisting of 64 F_1s and their 20 parents along with two checks in randomized block design with 2 replications. The 64 F_1s were generated by crossing four cytoplasmic male sterile (CMS) lines and 16 advanced breeding lines. The analysis of variance for treatments, parents and crosses revealed significant differences for most of the studied traits, signifying the existence of variability in the treatments, parents and crosses under both irrigated as well as water stress conditions. The significance of mean squares due to lines x testers for most of the traits under reproductive stress depicted the role of non-additive variance and the possibility of obtaining good heterotic response under moisture stress condition. It was concluded that parental genotypes IR 79156A, IR 68897A, IR 77298-5-6-18 and IR 78908-193-B-3-B and crosses IR 58025A x IR 83376-B-B-91-3, IR 68897A x IR 79956-B-60-2-3 and IR 79156A x IR 77298-5-6-18 can be used in breeding programs to exploit hybrid vigor and to obtain transgressive segregants for developing varieties / hybrids suitable for both irrigated and water stress conditions.

IDT7-040 | Molecular breeding for drought tolerance in pearl millet [*Pennisetum glaucum* (L.) R. Br.], using microsatellite markers

Jangra S*[1], Rani A[1], Yadav RC[1], Yadav NR[1], DevVar[1]t[1]

CCS Haryana Agricultural University, Hisar 125004, Haryana, India
*E-mail: sumit.jangra712@gmail.com

Pearl millet is a monocot species belonging to family *Poaceae*. Terminal drought stress is the most common environmental constraint, reducing its mean yield and hence making stress tolerance an essential attribute of pearl millet improvement. Marker assisted breeding is an efficient tool for attaining these objectives. Linkage group 2 and 5 are reported to have major QTLs associated with drought tolerance. The pearl millet hybrid HHB226 was used for improvement against terminal drought stress, where QTLs identified for drought tolerance were transferred from PRLT2/863B (donor parents) to HBL11 (recipient parent), one of the parent in HHB 226. Molecular analysis was carried out between donor and recurrent parent using SSR markers for drought tolerance where four SSR markers were found polymorphic out of 11 markers. The F_1 plants were raised and backcrossed with recurrent parent till BC_4F_1 generation, which was then selfed to produce BC_4F_2 generation. The plants were screened in each generation using polymorphic SSR markers. In BC_3F_1 generation a total of 90 plants were analyzed for the presence of drought tolerance QTLs and 21 plants were found positive for both the crosses. The selected plants were used for background selection of plants with maximum recurrent parent genome recovery. Background selection is in progress for BC_4F_2 generation. Phenotypic data were also observed in each generation and it was found that under post flowering drought stress such QTLs introgression had a significant positive effect for grain yield improvement.

IDT7-041 | Evaluation of selected lines of *Withania somnifera* for their root quality and yield performance

Ahmed N[1], Singh P[1], Jhang T[1]*

[1]CSIR-Central Institute for Medicinal and Aromatic Plants, Lucknow-226015, Uttar Pradesh, India
*E-mail: t.jhang@cimap.res.in

Ashwagandha (*Withania somnifera*) is a drought-hardy crop which requires dry climate for better development. Winter low temperatures are known to improve the root quality and yield and hence it is a potential choice to be opted as an intercrop with food crops for water-limited environments. FDA has approved it as "GRAS" (generally regarded as safe food plant) and it fetches a premium market price in the pharmaceutical industry, being the major rich plant source of withanolide and withanamides. The dried roots, rich in withanolide, are the primary economic part and the chief constituents of herbal drugs and various nutraceuticals. Brittle, robust and lengthy roots have high market value because of their high starch and fiber ratio which accounts for their ease in making a powder and which are quoted to be characteristic root textural features of commercial *Ashwagandha.* Information on root textural quality parameters is not available. So, the present investigation was carried out to know the pattern of starch and crude fiber accumulation. The comparative yield performance of selected breeding lines with the all *Withania* varieties released in India has been presented here. The yield components under consideration are leaf length, leaf breadth, number of primary branches, number of secondary branches, plant height, root length, root diameter, root weight, plant biomass. Under morpho-textural quality parameters, root fracture, primary root branches, secondary root branches root colour and root starch and fiber estimation will be presented.

IDT7-042 | Development of hybrid parents and hybrids in pearl millet (*Pennisetum glaucum* L.) for the arid north-western India (A1 Zone)

Jukanti AK[1]*, Manga VK[1]

[1]ICAR-Central Arid Zone Research Institute, Jodhpur-342003, Rajasthan, India
*E-mail: aravindjukanti@gmail.com

Pearl millet is an important cereal of arid/semi-arid regions with inherent adaptability to water-limited conditions and high temperature. Pearl millet's resilience and high nutritional value make it a significant contributor to food and nutritional security in these regions. The A1 zone of pearl millet production is highly prone to drought and high temperatures. Open pollinated varieties such as CZP 9802 (drought tolerant) and short-duration hybrids such as HHB 67 (improved) are mostly cultivated by the farmers. No substantial increase in grain yield is observed in extremely arid regions due to lack of adaptability of improved cultivars. Adaptability of parents to harsh conditions of arid regions is essential for successful cultivation of hybrids. ICAR-CAZRI, Jodhpur, has developed a successful restorer parent development program (developed >100), using mostly locally adapted material. CZI 2010/11, CZI 2007/9 and CZI 9621 are potentially well adapted restorers to local conditions. Further, to overcome the limited adaptability of male sterile lines (MS), we at ICAR-CAZRI, in collaboration with ICRISAT, have been successful in developing MS lines (CZMS 1A to CZMS 27A), including both A1 and A4 cytoplasm types from drought/high temperature tolerant material. CZMS 19A, CZMS 20A and CZMS 21A are some promising A4 type MS lines. CZH 233, a hybrid whose pollen parent (CZI 2010/11) is potentially heat tolerant, was found to perform well under local conditions and this hybrid has been promoted to AHPT-2nd year testing. Development of adapted parents and hybrids will add to the existing genetic diversity for extremely arid regions.

IDT7-043 | Evaluation of chickpea genotypes in state multilocation varietal trial in rainfed condition.

Patil, D.K[1], Waskar, D.P[1]., Sarode, S.B[1*], Kalpande, H.V[1].

[1.]Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani
*E-mail: shri_sarode@yahoo.com

Chickpea is one of the important *Rabi* pulse crop of Maharashtra. More than 90 % area of chickpea in Maharashtra is under rainfed condition. To test the chickpea genotypes in rainfed condition, three Agricultural Universities of Maharashtra viz. Vasantao Naik Marathwada Krishi Vidyapeeth, Parbhani, Dr.Panjabrao Deshmukh Krishi Vidyapeeth, Akola and Mahatma Phule Krishi Vidyapeeth, Rahuri conducted coordinated trials in 9 locations in 2015-16. Seventeen chickpea genotypes including checks were evaluated at 9 locations in Maharashtra to judge the yield performance under rainfed condition. On the basis of mean performance of 7 locations, the results revealed that the genotype Phule G 08108 (1337 kg/ha) was numerically superior over checks JAKI 9218 (1329 kg/ha) followed by SAKI 9516 (1318 kg/ha).

IDT7-044 | Genetic variability in post rainy *Sorghum* (*Sorghum biocolor (L.)* Monech) genotypes for drought tolerant parameters

Kalpande, H.V[1]*, More A.W[1]., Waskar D.P.[2], Aundhekar R. L.[1] and Avinash K.[3]

[1]Sorghum Research Station
[2]Directorate of Research
[3]Department of Agril. Botany Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani Maharashtra India
*E-mail: hvkalpande@rediffmail.com

Forty germplasm lines of *rabi* sorghum (*Sorghum biocolor (L.)* Monech) were evaluated to assess genetic variability, heritability and genetic advance for grain yield and drought associated traits at Sorghum Research Station, V.N.M.K.V., Parbhani during *rabi* 2015. The results revealed highly significant differences among all the treatments for all the characters under study indicating presence of sufficient amount of variability. Significantly high GCV and PCV values were noted for traits panicle dry weight (22.64 & 24.72), total dry weight (21.82 & 22.17) and grain yield per plant (20.37 & 21.97). Whereas the traits third leaf area, flag leaf area, relative water content, transpiration index, stomatal count, harvest index and biological yield per plant recorded moderate GCV and PCV. High heritability accompanied with genetic advance was observed for traits third leaf area (99.20 & 93.59), flag leaf area (99.50 & 46.36) and total dry weight (96.84 & 46.63) suggesting additive gene control in the inheritance of these characters and scope for selection of these characters is effective. While traits days to 50 per cent flowering, panicle dry weight, chlorophyll content, transpiration index, stomatal count, harvest index and grain yield per plant recorded high heritability and low genetic advance suggesting variability for these traits is governed by non- additive gene action. Genotypes SLV 168, RSV 1345, RSV 1516, RSV1772, SLV181, SLV 182, BJR 4951, BJR 40813 and SLV 193 exhibiting high and desirable values for most of the drought parameters can be selected and subsequently may be used in future breeding programme.

IDT7-045 | Genetic dissection of stem water-soluble carbohydrates and agronomic traits in wheat under different water regimes

Khan Nadia[1],[2], Xiaoping Chang[1],Ruilian Jing[1]

[1]National Key Facility for Crop Gene Resources and Genetic Improvement / Institute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, China
[2] Department of Genetics, University of Karachi, 75270, Pakistan
*E-mail: nadiakhan@uok.edu.pk; jingruilian@caas.cn

Drought is a major environmental stress that threatens wheat (*Triticum aestivum* L.) productivity worldwide. Although drought impedes wheat performance at all growth stages, it is more critical during the flowering and grain-filling phases and results in substantial yield losses. In this context, stem water-soluble carbohydrates (SWSC) were dissected at flowering and grain filling stages under drought stress (DS) and well-watered (WW) conditions, using a population comprising 116 wheat accessions in this research. The main goal was to dissect the genetic basis of water-soluble carbohydrates and the agronomic traits using association mapping approach, and identify linked molecular markers for marker-assisted selection. Four favorable alleles for plant height and grain yield were identified in two water environments. *Xbarc78-4A163* and *Xbarc78-4A155* were variant alleles for plant height, which were identified in DS and WW conditions respectively. *Xwmc25-2D151* and *Xgwm165-4B191* were positively linked with grain yield in WW. Although *Xwmc420-4A121* and *Xwmc112-2D215* were alleles for stem water-soluble carbohydrates at flowering (SWSCF) and stem water-soluble carbohydrates at grain filling (SWSCG) in DS, the frequency was <5% and so they were considered as rare alleles for this trait. These SSR markers which explained significant levels of phenotypic variability for chosen traits could be used for selection of genotypes in wheat breeding programs through marker-assisted selection.

IDT7-046 | Identification of selection indices for drought tolerant common bean (*Phaseolus vulgaris*) genotypes in the southern highlands of Tanzania

Mazaengo KD[1], Kilango M[2], Tryphone GM[3]

[1]Ministry of Agriculture Training Institute, P.O. Box 2292, Mbeya, Tanzania
[2]Agriculture Research Institute, Uyole, P.O. Box 400, Mbeya, Tanzania
[3]Sokoine University of Agriculture, P.O. Box 3000, Morogoro, Tanzania
*E-mail: michaelkilango@yahoo.com

The effects of drought on common bean are dependent on intensity, type and duration of stress. This study was conducted in 2015 to evaluate and select common bean genotypes for drought tolerance in southern Tanzania. Yields under water stress and non-water stress treatments were used to calculate yield indices which were then used to predict tolerant genotypes. Selection indices used were yield index (YI), stress tolerance index (STI), stress susceptibility percent index (SSPI); and mean productivity (MP), harmonic mean (HM), geometric mean productivity (GMP) and percent reduction (PR). The most tolerant genotypes selected by YI were BFS60, KG104-72 and SER16; b y STI were SER16, BFS60 and KG104-72; MP and GM: SER16, BFS60 and KG104-72; HM: BFS60, SER16 and KG104-72. In contrast SSI and PR selected 41-EX-VAM, RCB266 and PASI as most susceptible, while SSPI selected RCB266, 41-EX-VAM and SER83, all in respective descending order. Overall, SER16, BFS60 and KG104-72 were the most tolerant, based on mean yield indices and cluster and principal component analyses. Yields under non stress condition (Yp) were significant ($P < 0.001$) and positively correlated with STI, SSPI, MP, HM, and GM while yields under stressed condition (Ys) were highly significant ($P<0.001$) and positively correlated with YI, STI, STI, GM, HM and GM, but non-significant and negatively correlated with SSSI and PR. SER16, BFS60 and KG104-72 are recommended for cultivation in a drought prone environments or use as parents in drought tolerance breeding programs.

IDT7-047 | Studies on rice genotypes suitable for direct seeded condition (DSR)

Basavaraj.S.Kovi[1]., J. R. Diwan[1*]., K. Mahantashivayogayya[2]., M.S. Ramesha[3]., R. Lokesha[1],. T.C. Suma[1].

[1]University of Agricultural Sciences, Raichur.
[2]ARS, Gangavathi
[3]IRRI-South Asia Hub, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: diwan@rediffmail.com

Rice (*Oryza sativa* L.) is one of the most important food crops in the world. Increasing water scarcity, rising labor costs and low-input use have driven attention towards direct-seeded rice (DSR) cultivation over the past few years. The development of early-maturing varieties, improved nutrient management techniques and efficient chemical weed control methods have encouraged many farmers in the Philippines, Malaysia, Thailand and India to switch from transplanting to the DSR method of rice cultivation. Farmers at the tail-end of the Tungabhadra Project (TBP) area do not get sufficient water at right time, resulting in delayed transplanting, and forcing the farmers to go for the DSR method of rice cultivation. The development of rice varieties for direct-seeded conditions can be accelerated by selecting suitable traits. The field experiment was conducted at ARS Gangavathi, UAS, Raichur during *Kharif* 2016, to investigate genetic variability for yield and yield components, early seedling vigour, field emergence, grain quality (physical and chemical), and molecular characterization, using already reported trait specific SSR markers for early seedling vigour and quality traits. The RCBD design with two replications was conducted to investigate 32 medium slender rice genotypes which are in the background of BPT-5204 provided by IRRI, India -ICRISAT. The data revealed that, the line 16KDSBPT-28 exhibited the highest field emergence (28 seedlings/m2) followed by 16KDSBPT-22 (27.5) and IET-19251 (26) and the lowest exhibited by IET-22066 (6.5 seedlings/m2), 16KDSBPT-31/BPT-5204 (11) and IR14K-10214 (12.5). Finally, the lines which outperform the local checks will be identified and used for further crop improvement or commercial cultivation.

IDT7-048 | Development and characterization of sequence based markers in highly draught tolerant legume Horsegram [*Macrotylomauniflorum* (Lam.) Verdc.] for various genomic applications

KumarR[1]*., Singh G[2]., Chahota R.K[3]., Sharma T.R.[3]

[1]DAV University
[2]CSIR_IHBT, Palampur, Himachal Pradesh
[3]CSKHPKV, Palampur, Himachal Pradesh
*E-mail: rahulihbt@gmail.com

Horsegram [*Macrotylomauni florum* (Lam.) Verdc.] commonly known as *kulthi*, *kulth*, *gahet* and Madras gram, is an important drought-tolerant legume crop used as food as well as fodder in India and across the globe. Due to many desirable traits such as tolerance to drought, salinity and heavy metal stresses, horsegram is considered a potential future crop species. Despite being a multi-utility crop, genomic resources in this crop have not been exploited for genetic improvement programs. We used available transcriptome data to design 7352SSR markers. A polymorphism study of 60 newly developed genic SSRs, carried out on 48 diverse lines of horse gram, revealed good diversity measures such as expected heterozygosity (He), observed heterozygosity (Ho), and polymorphism information content (PIC) level (0.51, 0.60, and 0.43) respectively. Results of Analysis of Molecular Variance (AMOVA) revealed high degree of genetic variation within the population.

Dendrogram based on Jaccard's similarity coefficient and UPGMA method, Principal Component Analysis (PCA), revealed two groups existing in the population, and this was further reconfirmed by Bayesian genetic STRUCTURE. These newly developed sequence-based markers will enrich the existing repertoire of genomic resources in horsegram and be immensely useful in various genomic applications and breeding programs in this crop.

IDT7-049 | ***Alternaria*** **leaf blight of groundnut influenced by moisture deficit stress**

Narendra Kumar[1]*, Chuni Lal[2], Rathnakumar AL[1], Jadon KS[3], Ajay BC[1], Chikani BM[1]

[1]ICAR-Directorate of Groundnut Research, P.B.No.5, Ivnagar road, Junagadh – 362 001, Gujarat, India
[2]ICAR-Indian Institute of Wheat and Barley Research, Karnal -132001, Haryana, India
[3]ICAR-Central Arid Zone Research Institute, Jodhpur - 342 003, (Rajasthan), India
*E-mail: narendrapb09@gmail.com

Groundnut (*Arachis hypogaea* L.) is an important oilseed, food and fodder crop and valued as a rich source of oil (48%–50%) and protein (25–28%). It has been reported that drought stress affects the physiology of the plant resulting increased susceptibility of plants towards diseases. Hence, this study was carried out to investigate the effect of drought stress on disease incidence of *Alternaria* leaf blight (ALB) on groundnut genotypes. ALB has been reported to cause 13%-22% reduction in pod yield and 24%-63% haulm yield in groundnut. Sixteen advanced breeding lines and varieties of Spanish groundnut were field screened in post-rainy season of 2015 (February to May) at ICAR-Directorate of Groundnut Research, Junagadh, Gujarat, India. The crop was grown by adopting recommended package of practices. Each genotype was sown in non-stress (regularly irrigated) and stress condition of mid-season drought. Moisture deficit stress condition was imposed by withholding irrigation after 51-77 days of field emergence of the crop. Disease severity was assessed using a 1-to 9 scale. The data revealed that incidence of ALB under moisture deficit stress condition increased from 5.3% (PBS-15044) to 28.6% (PBS-15020, PBS-15025) and other genotypes exhibiting higher incidence of ALB were PBS-15054 (27.3%); PBS-11085 (14.3%) and TG-26 and TG-37A (11.1%) as compared to irrigated condition, while three genotypes *viz*., PBS-15047 (-5.9%), PBS-11088 (-5.6%) and Dh-86 (-5.0%) showed less incidence as compared to moisture deficit stress condition. Therefore, it was concluded that moisture deficit stress condition may predispose the genotypes to *Alternaria* leaf blight susceptibility in groundnut.

IDT7-050 | **Breeding sugarcane for water-limited environments: integration of phenomics to improve clone selection**

Lakshmanan P[1]*, Basnayake B[2], NatarajanS[2], Jackson P[3]

[1]Sugar Research Australia, Brisbane, Australia
[2]Sugar Research Australia, Burdekin, Australia
[3]CSIRO Agriculture, Townsville, Australia
*E-mail: plakshmanan@sugarresearch.com.au

Water limitation is the single largest production constraint for sugarcane worldwide. Nearly 70% of sugarcane is grown under rain-fed conditions globally, with substantial impact on yield. For instance, an estimated annual loss of A$260 million due to lost cane production caused by water deficit has been reported in Australia. Despite the large economic loss, there is no breeding effort to increase sugarcane water productivity due to lack of necessary practically useful screening tools. Our work with a large genetically diverse germplasm grown under different commercial production regions over multiple years (27 crop cycles) with varying water supply has shown that canopy conductance (*gc*), and a related easy-to-measure trait canopy temperature (CT), when integrated with canopy development, have a strong genetic correlation with crop yield, irrespective of the growing condition. In order to exploit this result for variety development in the Australian sugarcane breeding program, canopy parameters were measured by different phenotyping methods (aerial screening using UAV, continuous real-time absolute CT measurements using ArduCrop infra-red radiometers, hand-held infrared thermometers) for their accuracy, practicality and trait heritability. Both UAV- and ArduCrop-based CT measurements of 3-6-month-old crop showed high heritability (0.89) and genetic correlation with final yield (12-month-old crop). Results of field experiments suggest that aerial measurements of CT and other canopy attributes taken at the right condition will be an effective, rapid screening method for selecting superior, water-efficient and high-yielding clones. The translational aspects of these results to breeding application/methodology, currently being validated, will be presented.

IDT7-051 | Drought response of field cultivated potatoes: the interaction between canopy growth and yield

Aliche E.B.[1], Theeuwen T.[1], Oortwijn M.[1], Bachem C.W.B.[1], Visser R.G.F.[1], van der Linden C.G.[1]*

[1]Plant Breeding, Wageningen University and Research, Wageningen 6708 PB, The Netherlands
*E-mail: gerard.vanderlinden@wur.nl

Potato is the third most important food crop, but it suffers major yield losses because of drought. We studied a set of 104 commercial cultivars representing the genetic diversity in the European potato market. The cultivars were grown in different field locations in three years (2013 – 2015), with the aim to understand how different field drought regimes affect canopy growth in potato, and how these effects translate to tuber yield. Field environmental characteristics were monitored, and canopy growth captured during the growing season. Canopy growth parameters were extracted by an iterative method using the beta sigmoid growth model. At harvest, we measured yield traits. A GGE biplot and Finlay Wilkinson's regression were used to investigate GxE interaction, an marker-trait associations were identified using a 14K SNP array. We observed that the timing of the drought stress in the growing season differentially affected canopy growth and tuber yield. Under drought stress, fast attainment of exponential growth and maximum canopy cover had negative effects on tuber formation and tuber bulking. Growth rate, maximum canopy cover, and area under the canopy curve (photosynthetic capacity over the growth season) were more important for tuber bulking than they were for tuber formation under drought. We identified cultivars with high yields in different environments as material for improvement of drought tolerance in cultivated potato. We also found SNP markers associated with canopy growth parameters and yield under drought that can be further exploited in marker assisted breeding for drought tolerance in potato.

http://ceg.icrisat.org/idv/program/
Proposed section/ conference topic: Breeding for water-limited environments
Alternative section: Plant productivity under drought – Vegetative growth

IDT7-052 | Physio-biochemical evaluation of F_2 population of chickpea (*Cicer arietinum* L.) for drought tolerance

Lokhande PK[1*], Naik RM[1], Mhase LB[1], Harer PN[1]

[1]Mahatma Phule Agriculture University, Rahuri-413 722, Ahmednagar, Maharashtra, India
*E-mail: pklokhande@gmail.com

Two each of deep and shallow root system chichpea (*Cicer arietinum* L.) parents were used in direct and reciprocal crosses. The four parents and 10 F_2 crosses were evaluated at 50% flowering stage for physio-biochemical traits under control and drought stress. The cross of ICC 4958xVijay, both with prolific and deep root system, recorded higher increase of 78.77% in root length. The crosses involving either of ICC 4958 or Vijay as male or female parents showed substantial root trait improvement, both under control and stress. The crosses of PG 5xVishal and VishalxPG 5, both with shallow root system, showed less increase in root length and other root traits. The F_2 plants of crosses ICC 4958xVijay, VijayxICC 4958, VishalxVijay and PG 5xVijay recorded less increase in lipid peroxidation rate and higher level of proline, SOD, CAT and APX activity under drought stress condition over the unstressed control. The estimates of heritability and genetic advance as percent mean was high, indicating that additive gene action is playing a predominant role in the inheritance of long root length under control and stressed conditions. The antioxidative metabolism and deep root system can be considered as a critical trait while evaluating breeding population of chickpea for drought tolerance.

IDT7-053 | Comparative and evolutionary analysis of drought-responsive transcription factor families in maize

Mallikarjuna Mallana Gowdra[1], Shikha Mittal[1], Pooja Banduni[1], AR Rao[2], Nepolean Thirunavukkarasu[1]*

[1] Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India
[2] Centre for Agricultural Bioinformatics, ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India
*E-mail: tnepolean@gmail.com

Drought is one of the major factors limiting maize production worldwide. However, maize possesses a variety of physiological and molecular responses at cellular and morphological levels. Transcriptional regulation of gene expression provides a molecular mechanism by which plants modulate the developmental processes and respond to water stress. The regulation is mediated by various transcription factors through recognizing specific DNA motifs in regulatory elements of genes. A comparative analysis of all the drought-responsive transcription factors gives an insight into drought tolerance mechanism in maize, which could be effectively utilized in breeding drought-tolerant maize cultivars. In the present investigation, thousands of genes falling under 15 drought-responsive TF-families of maize were structurally and functionally characterized. The major drought related functions of the selected genes were ABA signaling, ROS scavenging, photosynthesis and stomatal development. The evolutionary studies identified several duplication events, including tandem duplications, block duplications and paralogs in the genome. Among several *cis*-regulatory elements identified in TF families, a few were found to be common across all the drought-responsive TFs. These elements are the key determinants in the temporal and spatial expression of TFs in maize. Intron analysis of the genes revealed that the 72% of genes were intron-rich. Expression analysis showed maximum differentially-expressed TFs in roots and leaves. Additionally, TFs interaction analysis identified several intra and inter interactions in imparting drought tolerance in maize. The information generated from the study will be useful for customizing TFs for enhanced drought tolerance through marker assisted selection and genome-editing approaches.

IDT7-054 | Utilizing genomic resources for understanding the stay-green QTLs interactions in Sorghum

Manasa KG[1], Deshpande SP[1]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
* E-mail: s.deshpande@cgiar.org

Sorghum [*Sorghum bicolor* (L.) Moench] is a fifth most important cereal crop in the world providing food, fodder/forage and bio-fuel. The postrainy sorghum crop in India is grown on residual moisture and inadvertently faces terminal drought. “Stay-green" (delayed senescence) is a post-flowering drought tolerance response, which help plants to maintain photosynthetically active leaf area and continue to fill their grains normally under stress.

Sorghum crop is referred to express functional type of stay-green and the trait has been mapped to six major QTLs viz., Stg1, Stg2, Stg3A, Stg3B, StgC and Stg4. However, the gap in understanding the key mechanism has not been deciphered clearly. In this scenario to understand the actual mechanism of the stay-green pathway the information from different crops on candidate genes responsible for stay-green phenotype were considered *viz.,* STAY-GREEN (SGR) along with one or two homologous (SGR1or NYE1/SGRL); Pheophytin Pheophorbide Hydrolase (PPH); Pheophorbide a Oxygenase (PAO); Red Chlorophyll Catabolite Reductase (RCCR); Non-Yellow Coloring (NYC) and it’s homologous NYC1-Like (NOL); 7-Hydroxymethyl Chlorophyll a Reductase (HCAR) from *Zea mays, Arabidopsis thaliana* and *Orzya sativa*. Apart from these, senescence associated genes SAG2, SAG102 and SAG39 were also considered from *Arabidopsis thaliana* and *Orzya sativa* respectively. The sequence and functional/annotation information for these genes retrieved for sequence similarity search and it has revealed 45 to 88 % of similarity in sorghum. The mapping of these candidate gene sequences within the defined QTL regions contributing for Stay-green has given an insight to utilize the re-sequencing data for improved drought tolerance in sorghum.

IDT7-055 | A multi-dimensional approach from seed-to-seed to understand and improve heat stress tolerance in rice

Mangrauthia SK[1]*, Vishnu Prasanth V[1], Sailaja B[1],[2], Sarla N[1], Voleti SR[1], Subrahmanyam D[1], Babu VR[1]

[1]Indian Institute of Rice Research, Hyderabad-500030,Telangana, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad-502324, Telangana, India
*E-mail: skmdrr@gmail.com

In changing climatic conditions, stress caused by high temperature poses a serious threat to rice cultivation. Physiological, biochemical, and molecular analysis of rice cultivars revealed that *Nagina22* (N22) shows lesser reduction in chlorophyll content, net photosynthetic rate, spikelet fertility and grain yield, but increased membrane thermal stability, antioxidant enzymes activity and transpiration rate (*E*) at high temperature. *DREB*, *RAB*, *LEA*, and genes associated with hormones signalling were induced during germination, while *OsFd* (an iron sulphur cluster binding protein) and *CWIP* (cell wall integrity protein) emerged as high priority candidate genes in seedling and reproductive stages. Their function is being analysed by transgene expression and CRISPR/Cas genome editing approaches. Field screening in polyhouse, late sowing and temperature gradient chamber for 20 morpho-physiological traits indicated the importance of both yield and spikelet fertility, and photosynthesis traits. N22 showed the least Heat Susceptibility Index (HSI) for yield/plant, spikelet fertility, flag leaf SPAD and stomatal conductance, while *Vandana* showed the highest HSI for spikelet fertility and flag leaf temperature. QTLs for HSI of spikelet fertility were identified on chromosome 1 and HSI of yield per plant on chromosomes 1, 2, 3, 4, 7 and 8; and PV of 6% to 57% using 174 F2-3 *Vandana* x N22 mapping population. Simultaneously, RNAseq was performed to identify the genome wide miRNAs and transcriptome of N22 and Vandana from shoot and root after short and long duration of heat stress treatments; and recovery phase for an eQTL-guided function-related co-expression analysis to identify the putative regulators and gene regulatory networks.

IDT7-056 | Selection of superior parents to derive single cross hybrids of maize for water limited and well watered conditions through development of new heterotic pools

Mani, B. R[1]*, Deshpande, S. K[2].

[1.] University of Agricultural Sciences, Dharwad-580 005, India.
[2.] University of Agricultural Sciences, Dharwad-580 005, India.
*E-mail: mbreddys8102014@gmail.com

Maize is a major cereal crop of India and the world. It is used as food, fodder, poultry feed and agro industrial raw material. Growth stages, *viz.,* flowering and grain filling, are critical periods and moisture stress during these stages reduces grain yield to the extent of 70%-90%. Therefore, development of stable Single Cross Hybrids (SCH) in maize for limited water environment is essential. We studied new heterotic pools and identified superior parents among these pools. Thirty one potential inbreds were selected, based on ASI, RWC, SPAD, yield reduction under stress and drought tolerant index. These top 31 lines were test crossed with two testers (LM13 and LM17) to derive 62 test cross hybrids. Combining ability studies were conducted during *summer*-2016 under water limited (WL) and well watered (WW) conditions, and the data was analyzed using *Windostat v8.1* software. Heterotic grouping was done according to *Heterotic Group's Specific and General Combining Ability* (HSGCA) method. HSGCA is the difference between mean grain yield of crosses and testers. The signs of HSGCA of lines and grain yield SCA of testers were compared to make heterotic groups. Out of 31 inbreds, 17 from WL and16 from WW were assigned to heterotic group-A as that of tester-1 (+sign). Similarly, 14 from WL and 15 from WW were assigned to group-B as that of tester-2 (-sign). Inbreds with the highest positive HSGCA from group-A and the least negative HSGCA from group-B were identified as superior parents to derive SCH for water limited and well watered conditions.

IDT7-057 | Physiological and molecular insights into the high salinity tolerance of *Pongamia pinnata* (l.) pierre, a potential biofuel tree species

Sureshbabu M[1], Reddy A. R.[1]*

[1]University of Hyderabad, Hyderabad-500046, Telangana State, India
*E-mail: arrsl@uohyd.ernet.in

Soil salinity is gradually becoming a threat to the global economy by affecting agricultural productivity worldwide. In the present study, we analyzed the salinity tolerance of *Pongamia pinnata,* a promising biofuel tree species with an insight into the underlying physiological and molecular responses. Despite a reduction in net photosynthetic rate, *P. pinnata* efficiently maintained its leaf water potentials even at 500 mM NaCl for 15 days and displayed no stress symptoms. CoroNa-Green AM analysis revealed effective Na+ sequestration in the roots. Elemental analysis showed K+/Na+ to be significantly up-regulated in leaves of salt-treated *P. pinnata*. At the molecular level, salt stress significantly induced the expression levels of salt overly sensitive1 (SOS1), SOS2, SOS3, high affinity K+ transporter (HKT1), ABA biosynthetic and receptor genes (NCED and PYL4), guaiacol peroxidase (POD), exclusively in the roots. Tonoplast localized Na+/H+ exchanger (NHX1) was significantly enhanced in the salt-stressed leaves. Our results clearly demonstrate that leaves and roots of *Pongamia* exhibit differential responses under salt stress, although roots are more efficient in sequestering the Na+ ions. The present study certainly provides crucial inputs for understanding salt tolerance in a tree species which can be further utilized for developing salt tolerance in higher plants.

IDT7-058 | Response of common bean genotypes (*Phaseolus vulgaris* L.) to drought in relation to growth and yield characteristics in the southern highlands of Tanzania

Mazaengo KD[1], Kilango MA[2], Tryphone GM[3]

[1]Ministry of Agriculture Training Institute, P.O. Box 2292, Mbeya, Tanzania.
[2]Agriculture Research Institute, Uyole, P.O Box 400, Mbeya, Tanzania
[3]Sokoine University of Agriculture, P.O Box 3000, Morogoro, Tanzania
*E-mail: mkarantin@yahoo.co.uk

Drought is the second most important yield-limiting factor in common bean after diseases, causing up to 60% yield losses worldwide . Despite these challenges, more than 75% of rural households in Tanzania depend on common bean for food and income. The objective of this study was to evaluate the growth and yield of common bean genotypes under induced water stress in the field and screen house. The results under field and screen house conditions were consistent with significant differences ($p<0.05$) across water treatments and genotypes. Genotypes SER16, BFS60, KG104-72 and CZ109-22 were selected for higher grain yields (kg ha). Further, BFS60 had the highest number of leaves, shoot dry weight, number of pods, pod and seed weight per plant, while KG104-72 had the highest root length, and earliest 50% flowering and 85% maturity. These genotypes can be considered as drought tolerant and recommended for production or use as parents in drought tolerance breeding program.

IDT7-059 | Evaluation of rice near isogenic lines for drought tolerance under aerobic condition

Nagamallikadevi M[1], Raman A[1], VenkateswarluCH[1], Naik SM[1], Yadav. S[1], Singh UM[1], Janaki Ramayya P[1], Dixit S[1], Abhilash Kumar[1], Nachimuthu VV[1], Jain A[1], Priyadarshi R[1], Alam.S[1], Kumar.A[1],[2]*

[1]International Rice Research Institute South Asia Hub, ICRISAT, Hyderabad, India.
[2] International Rice Research Institute, Metro Manila, Philippines.
*E-mail: a.kumar@irri.org

Rice widely grown under irrigated condition consumes more than 50% of fresh water. Aerobic rice which combines the drought tolerance property of upland rice and the yield potential of lowland rice uses only 50%-70% of the water required for rice production. NILs in the background of *Vandana* and *Anjali* possessing drought-tolerant QTL *qDTY12.1* were evaluated across five years at four sites in India from 2011 to 2015 during wet seasons. The test sites were chosen to represent the target region in South Asia. The trials were conducted under both non-stress and reproductive-stage drought conditions. Measurements on days to 50% flowering, plant height and grain yield (t/ha) were recorded. After harvest, the trials were classified as moderate or severely stressed if the mean yield reduction as compared to the non-stress was between 65%–85%. The best performers under non-stress, moderate and severe stress as compared to the checks *Vandana* and *Wayrarem* were IR 84984-83-15-862-B, IR 90019:17-159-B, IR 84984-83-15-110-B and IR 84984-83-15-481-B. Among the NILs in the background of *Anjali* evaluated at one site during wet season (WS) 2014 to WS2015, were IR 99742:2-11-17-1-9, IR 99742:2-2-224-1-2 and IR 99742:2-2-74-1-5 performed considerably well across all three seasons as compared to the checks *Anjali* and *Vandana*.

IDT7-060 | Comparison of genomic selection models for drought tolerance in sub-tropical maize

Mittal S[1], Arora K[1], Rao AR [2], Mallikarjuna MG[1], Mohapatra T[3], Gupta HS[4], Nepolean T[1]*

[1] Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India
[2]Center for Agricultural Bioinformatics, ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India
[3]Indian Council of Agriculture Research, New Delhi, India
[4]Borlaug Institute for South Asia, New Delhi, India
*E-mail: tnepolean@gmail

Genomic selection (GS) is becoming an important selection tool in crop breeding in which genome-wide markers are used for prediction of breeding values. In this study, we examined the breeding values of 240 maize subtropical lines phenotyped for drought at different environments using 29,619 cured SNPs. We tested the Pearson correlation coefficient of parametric (Ridge regression, LASSO, Elastic Net, Bayes A and Bayes B), semi-parametric (Reproducing Kernel Hilbert Space) and non-parametric (Random Forest) GS models for seven agronomic traits (ASI, GY, KR, KRN, EG, EL and HKW). Bayes B model outperformed other GS models with the highest value of 0.97. Further Bayes B model was used to select 1053 SNPs on the basis of high marker effects across all the datasets for validation of genes and QTLs. Out of these 1053 SNPs, 77 SNPs were found to be mapped on 10 drought-responsive transcription factors (AP2-ERF, MYB, NAC, WRKY, NF-YA, NF-YB, GRAS, bZIP, BHLH and CAMTA) in the vicinity of 150 kb of each SNP. These transcription factors were associated with different physiological and molecular functions– stomatal closure, root development, hormonal signaling and photosynthesis. The result of our experiment is important for the selection of superior genotypes and candidate genes for breeding drought tolerant maize hybrids.

IDT7-061 | Physiological and genetic diversity among cowpea (*Vigna unguiculata* L. Walp) landraces from Northern Ghana, determined by δ15N, gas exchange, RAPD and SSR markers

Haruna M.[1, 2*], Jaiswal S.K.[1], Dakora F.D.[1], Boukar O.[3], Katokun C.[3]

[1]Tshwane University of Technology, South Africa
[2] Council for Scientific and Industrial Research (CSIR)-Savanna Agricultural Research Institute Tamale Ghana
[3] International Institute for Tropical Agriculture (IITA), Ibadan, Oyo State, Nigeria
*E-mail: haruna_mohammed67@yahoo.com

Cultivated cowpea (*Vigna unguiculata* L. Walp) is a source of major cheap protein in most Ghanaian diets which is predominantly starchy cereals, roots and tubers. Despite its importance, yields on farmers' fields are low partly due to poor soil fertility especially nitrogen (N) and phosphorus (P) deficiency and insufficient moisture during crop growth periods. Thereforethe study sought to evaluate 49 cowpea landraces at the physiological and genomic levels in-order to identify genotypes with higher N2 fixation, higher water-use efficiency (WUE) and genetically diverse for breeding purposes. The 15N natural abundance technique and Δ13C were used to assess N2-fixation and WUE of the test genotypes. Polymerase Chain Reaction (PCR) was conducted for analysis of RAPD and SSR markers. The results showed that, based on %Ndfa, 69% of the test genotypes were high N2-fixers. Among the eight RAPD primer combinations that were used, six primers distinguished the genotypes into three clusters with 0.00 to 0.5 Jaccard's similarity coefficient. 29 of 33 SSR primer combinations yielded polymorphic bands. A total of 59 alleles with an average of 2.03 alleles per locus were detected. Eleven most polymorphic SSR primers successfully distinguished all 49 cowpea varieties. Primers SSR25 and CLIM30 formed the highest number of alleles, 5 in total. The dendrogram generated from SSR data grouped the test accessions into 21 clusters with 0.72 to 0.96 Jaccard's similarity coefficient. The cluster, ormondow", showed highly significant genetic diversity among all accessions. The polymorphic information content (PIC) ranged from 0.04 to 0.48 (mean = 0.15).

IDT7-062 | Potential of *Erianthus procerus* introgressed sugarcane clones under water deficit stress

Mohanraj K[1]*, Oshin PJ[2], Suganya A[1], Appunu C[1]

[1,]ICAR-Sugarcane breeding Institute, Coimbatore, India
[2]Providence Women's College, Calicut, India
*E-mail: K.Mohanraj@icar.gov.in

A novel intergeneric hybrid GU04(28)EO-2 (IC0612056;INGR15032) was developed between *Erianthus procerus,* a wild relative of sugarcane 'IND 90-776', and *Saccharum officinarum* 'PIO 96-435' at the ICAR-Sugarcane Breeding Institute, Coimbatore, and registered with NBPGR, New Delhi, as a genetic stock. The hybrid was backcrossed with sugarcane to improve agronomic traits and 25 BC1 progenies were obtained from the cross GU04(28)EO-2 x Co 06027. In the present study, seven BC1 hybrids and their parents were selected for cytological analysis and evaluated under water deficit condition during 2015-16. The somatic chromosome number of the BC1 hybrids ranged from 88 to 94. The introgression of *Erianthus procerus* in BC1 hybrids was also confirmed using 5SrDNA markers. Evaluation under water deficit condition showed that there were highly significant differences among the treatments as well as genotypes for shoot and root traits. Four clones *viz*., GU 12-28, GU 04(28) EO-2, GU 12-31 and GU 12-34, recorded significantly higher root dry weight; and clones GU 12-28 and GU 12-31 had larger root system under water deficit condition.The clone GU 12-28 recorded the highest dry biomass (shoot and root) under both well-watered and water deficit condition. The BC1 hybrid GU 12-31 recorded the highest Drought Tolerant Efficiency (DTE) of 77.67% and lowest Drought Susceptibility Index (DSI) of 0.354. The clones GU 12-28, GU 12-31, GU 12-34 had high DTE and low DSI, and were identified as drought tolerant. They could serve as potential donors for breeding sugarcane under water limited conditions.

IDT7-063 | Combining ability and heterosis in *rabi* Sorghum (*Sorghum biocolor (L.)* Monech) hybrids for yield and drought Parameters

More A. W[1]., Kalpande. H.V[1]., Deosarkar D.B.[2], Aundhekar R.L.[1], Dhutmal R. R[1] and Nirde A. V[3].

[1.] Sorghum Research Station
[2.] Department of Agril. Botany
[3.] Department of Agril. Botany, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani Maharashtra India
E-mail: ambikamore@rediffmail.com

Present investigation was carried out to identify elite parental lines and heterotic hybrids of *rabi* sorghum (*Sorghum bicolor* (L.) Moench) for grain yield, fodder yield and drought parameters. The experiment was confined to fifteen hybrids, developed through line x tester method, by utilizing three widely adapted females lines (M-35-1, Phule Anuradha, Parbhani Moti) and five testers (10538,4189,10515,10704,10593). The results revealed, presence of significant differences due to parents, crosses, parents vs crosses and line x tester for almost all the traits. The ratio of б2 gca: б2sca variance for general and specific combining ability was less than unity for all the characters indicating preponderance of non additive gene action. Parents; Phule Anuradha, 10593 and 10515 showed significant gca effects in desirable direction for grain, fodder yield and drought related traits. Significant sca effects and heterosis along with high per se mean were observed in crosses Phule Anuradha X 10515 (7.85 and 75.76%) and Parbhani Moti X 10704 (6.66 and 32.81%) for grain yield/plant and in Phule Anuradha x 10538 (20.06 and 45.41%) for fodder yield/plant. Two crosses, M-35-1 X 10593 and Phule Anuradha X 10515, exhibited significantly high SCA effects, heterobeltiosis and mean performance for grain yield, fodder yield, days to 50% flowering, leaf area, chlorophyll content and harvest index. These hybrids may be advanced to further generations to select best segregates and the parents Phule Anuradha, M-35-1 10515 and 10593 has scope to breed high yielding genotypes with early maturity duration adaptable to dry land farming.

IDT7-064 | Advances of groundnut breeding and seed systems in Tanzania

Mponda O.[1*], MonyoE.[2], OkoriP. [3], Akpo E.[2]

[1]Naliendele Agricultural Research Institute, Mtwara, P.O. Box 509, Tanzania
[2]International Crops Research Institute for the Semi-Arid Tropics,Nairobi, P.O. Box 39063, Kenya
[3]International Crops Research Institute for the Semi-Arid Tropics, Lilongwe,P.O. Box 1096, Malawi
*E-mail: kalanjekanduru@gmail.com

Groundnut (*Arachis hypogeal* L.) is an important oilseed crop, mainly grown by smallholder farmers on 839,631 ha in four agro-ecological zones (Lake, central, western and southern) of Tanzania. The average yield is 965kg/ha with a national production of 810,000 tons. The major production constraints are foliar diseases (rosette, early leaf spot, late leaf spot, and rust), drought, aflatoxin contamination, and low soil fertility. This paper explores the advances made in a breeding program to solve these challenges. The genotype by environment interaction with linkage to good agronomic practices, using effective selection molecular tools, was used and significant achievements were recorded. Eight improved varieties were released with support from ICRISAT-led programs. The newly-released varieties command high-yielding ability (1800-2500 kg/ha), and tolerance to rosette disease and drought, and are highly preferred by farmers and market. The improved varieties increased yields and productivity at the farm level and groundnut production from 400,000-810000 tons over the last 10 years.

Effective seed delivery to smallholder farmers did not automatically follow. The Tropical Legumes Project, through NARI, designed rural seed fairs which are used to create awareness, increase accessibility, and create working contacts among community seed producers. Other seed delivery models tested and used include: farmer research groups, demonstrations, field days, community seed production, radio and TV events, political figures' engagement and multi-stakeholder engagements. These models have raised awareness, increased demand of improved seed, and enhanced smallholder seed supply at affordable price with a significant number of beneficiaries reached (1,600,000 farmers).

IDT7-065 | Identification of climate resilient pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes

Muniswamy S[1]*, Ramesh[1], Mahalinga D.M[1]

[1]All India Coordinated Research Project on Pigeonpea, ARS Kalaburagi, Karnataka, India.
*E-mail: muniswamygpb@gmail.com

Pigeonpea [*Cajanus cajan* (L.)] is the important grain legume crop under rainfed Agriculture. The goal of this study was to identify climate resilient pigeonpea genotypes. During *kharif*-2011 evaluated 443 genotypes under both irrigated and rainfed condition and recorded various quantitative traits. Based on the *per se* performance under stress conditions 50 genotypes were promoted for evaluation during *kharif*-2012 and evaluated for various quantitative traits. During *kharif*-2013, based on their *per se* performance 40 genotypes were evaluated and were divided in to two groups based on the maturity *viz.,* <170 days and > 170 days maturity group. Each group consist of 21 and 19 genotypes respectively both were sown under irrigated and rainfed condition and evaluated for various quantitative traits. The same two maturity groups consisting of total 40 genotypes were evaluated during *kharif*-2014 and *kharif*-2015 to study stability in their performance. Out of 40 genotypes 18 genotypes were identified as well performing and stable lines. These 18 genotypes seeds will be multiplied during *kharif*-2016 and they will be evaluated for irrigated and rainfed condition. The best performing lines are Bennur local, JKM-189, JKM-7, RVK-275, WRP-1, AKT-9913 *etc.* which we can call as climate resilient genotypes. Two years field screening for *Fusarium* wilt and SMD yielded resistant genotypes for these diseases. However only one (JSA 59) out of these genotypes showed multiple disease resistance reaction for both *Fusarium* wilt and SMD Hence, this genotype can be used directly as a variety or choice of parent for hybridization programme.

IDT7-066 | Phenotypic and genetic dissection of water stress adaptationsin pearl millet (*Pennisetum glaucum*)

Murugesan Tharanya[1, 2], Jana Kholova[1], Kaliamoorthy Sivasakthi[1, 2], Vincent Vadez[1]*, Deepmala Seghal[3], Charles Tom Hash[4], Basker Raj[1], Rekha Baddam[1], Thiyagarajan Thirunalasundari[2], Rattan Yadav[3]

[1]International Crops Research Institute for the Semi–Arid Tropics (ICRISAT), Crop Physiology Laboratory, Patancheru 502324, Telangana, India.
[2]Bharathidasan University, Tiruchirappalli 620 024, Tamilnadu, India.
[3]Institute of Biological, Environmental and Rural Sciences (IBERS), Aberystwyth University, AberystwythSY23 3EB, UK.
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), ICRISAT Sahelian Center, Pearl Millet Breeding, BP 1204, Niamey, Niger.
* E-mail: v.vadez@cgiar.org

Pearl millet is an important staple food for farming communities across semi-arid tropical systems of South Asia and Sub-Saharan Africa where production suffers uncertain precipitation. This work is undertaken under the premise that maximizing grain yield under water-limited conditions depends on both maximizing water use and ensuring water availability for the grain filling period. Here we discuss the phenotyping methods targeting the variability in plant water use strategies which determine the crop production success in water-limited environments. A fine-mapping population of pearl millet, segregating within the previously identified drought tolerance quantitative trait locus (QTL) on chromosome 2 (LG02), was tested across different experimental environments (pot culture, high-throughput phenotyping platform (LeasyScan), Lysimeter, and Field). Recombinants were then analyzed for traits at different levels of plant organization, ranging from water-use traits (transpiration rate, leaf area, plant organ dry weights, etc.) to crop production and agronomic traits (grain yield, tiller number, harvest index, etc.) The linkages between traits across the experimental systems were analyzed, using principal component analysis (PCA) and QTL co-localization approach. The functional relevance of the phenotyping systems was traced by PCA analysis. Furthermore, we found four regions within the LG02-QTL underlying substantial co-mapping of water-use related and agronomic traits. These regions were identified across the experimental systems and justified linkages between water-use traits were phenotyped at lower level of plant organization to the agronomic traits assessed in the field. Therefore, the phenotyping systems at ICRISAT are validated and well set to accelerate crop breeding for drought adaptations.

IDT7-067 | Variability studies for quantitative traits in upland rice (*Oryza sativa* L.)

Muthuramu S, Muthuramu S[1]*, Sakthivel S[1].

[1]Agricultural Research Station, Tamil Nadu Agricultural University, Paramakudi – 623 707, India.
*E-mail: smuthuramu@gmail.com

Rice (*Oryza sativa* L.) is one of the main food crops, and one-third of the world population and two-thirds of the Indian population use rice as the staple food. Yield is a complex character, which is highly influenced by the environment and, hence, direct selection for yield alone limits the selection efficiency and ultimately results in limited success in yield improvement. Genetic variability studies are important in selection of parents for hybridization because crop improvement depends upon the magnitude of genetic variability in the base population. The present experiment comprised 22 advanced rice cultures that were collected from various research institutes from India. It was conducted during *rabi* 2015-16 in ARS, Paramakudi under upland rice ecosystem. The analysis of variance revealed that all the treatments are significant for various characters under study *i.e.* days to 50% flowering, plant height, number of productive tillers per plant, number of panicles per square metre plot area, panicle length, number of filled grains per panicle, grain yield per plot, straw yield per plot and harvest index. Higher PCV values were recorded for the number of productive tillers per plant, number of filled grains per panicle, grain yield per plot and harvest index; and higher GCV was recorded for the number of filled grains per panicle. Days to 50% flowering, plant height, number of panicles per square metre plot area, panicle length and number of filled grains per panicle showed high broad sense heritability and moderate for grain yield per plot, straw yield per plot and harvest index. High heritability coupled with high genetic advance was recorded for plant height and number of filled grains per panicle, indicating the major role of additive gene action in the inheritance of these characters. Thus, these characters may serve as an effective selection parameter during breeding program in the upland rice ecosystem.

IDT7-068 | Discovery of Quantitative trait loci (QTL) underlying drought tolerance in a F5 RIL Andean intragene cross population (BRB191/SEQ1027) of common bean (*Phaseolus Vulgaris* L.)

Nabateregga M[1]*, Mukankusi C[2], Edema R[1] and Nkalubo S[3]

[1]Makerere University, Kampala, Uganda
[2]International Centre for Tropical Agriculture (CIAT) / Pan African Bean Research Alliance (PABRA), Kampala, Uganda
[3]National Crops Resources Research Institute, Namulonge, Legumes program, Kampala, Uganda.
*E-mail: mnabateregga@gmail.com

Drought is a major constraint of common bean (*Phaseolus vulgaris* L.) production in Uganda where irrigation for the crop is very uncommon. Genetic improvement of the crop has been a challenge as drought integrates effects of several complex mechanisms. Indirect selection based on genetic markers linked to QTL associated with these mechanisms is considered a more feasible solution. This study aimed to identify phenotypic traits and consequentially QTL underlying drought tolerance in 128 F5 common bean RILs derived from an Andean intragene cross between drought tolerant SEQ1027 and BRB191 (source of the bc3 gene). A total of 20 adaptive traits comprising of phenological, physiological, photosynthate accumulation and remobilization traits were evaluated under stress and non-stress environments in both field and greenhouse experiments. Partitioning indices remained relatively stable under drought and G x E effects while maintaining significant positive correlations with yield under field conditions ($P<0.001$). A genetic map spanning 204.7 cM with 60 SNPs on 11 linkage groups was constructed. QTL analysis revealed 29 QTL comprising of 8 consistent QTL associated with seed weight and partitioning traits. Co-localization of QTL associated with days to flowering, biomass partitioning and accumulation traits with seed yield QTL *SY2.1BS* (that explained 68% of phenotypic variation) suggested pleiotropic effects between these genetic factors on linkage group 2. Furthermore, QTL associated with phenology, number of pods per plant and seed weight traits mapped near previously reported QTL. Our current findings will facilitate introgression of major partitioning genes into breeding cultivars especially in Andean bean breeding programs.

IDT7-069 | Mutation in Zeaxanthin Epoxidase excess energy dissipation and improved drought tolerance improved drought tolerance in Rice-Study using mutants.

Nagasupreeta S R[1], Sowmya H R[1], Preethi N V[1], AfsanabanuManik, Rajesh Kumar Singal[1], Sumanth KumarK[1], MP. Rajanna[2], R.P. Sharma[3], T Mohapatra[4], N Sarala[5], S Robin[6], AK. Singh[7]

[1]University of Agricultural Sciences, GKVK, UAS Bengaluru-560065, Karnataka, India
[2]Zonal Agricultural Research Station, College of Agriculture, Mandya
[3]National Research Centre on Plant Biotechnology, New Delhi, India
[4]National Rice Research Institute, Cuttack-753006, India
[5]Indian Rice Research Institute, Hyderabad, India
[6]Department of Rice, Tamil Nadu Agricultural University, Coimbatore, India
[7]National Bureau of Plant Genetic Resources, New Delhi, India
*E-mail: mssheshshayee@hotmail.com

It has been estimated that one-third of worlds potentially viable lands suffer from an inadequate supply of water and crop yields are periodically reduced by drought. Most of the world's major rice growing areas is threatened by moisture stress and hence saving water is the major challenge. Unconventional techniques such as creations of EMS mutants improve the efficiency and time required to create genetic variability. A large mutant population was created and variability in drought adaptive traits was assessed. Screening for root traits led to the discovery of mutants differing in root traits. A high root mutant (392-9-1) was able to maintain significantly higher water relations and photosynthetic rate even at stress conditions. Stress response of the 392-9-1 was almost similar to control to increasing CO2 and light. Whereas the low root mutant (491-3-2) was saturated at 750ppm and 1000µmol for CO2 and light respectively in stress condition. The excess electron transport rate (ETR*) was lower in 392-9-1 compared to 491-3-2. Qualitative NBT staining indicated a higher level of superoxide production in low root mutant. It was evident from leaf temperature that high root mutant was able to maintain cooler canopies with better transpiration and biomass even at stress conditions. This study has paved way for deeper analysis of the photosynthetic characters using these mutants.

IDT7-070 | Performance of elite potato clones for drought tolerance in Uganda

Namugga, P., Kesiime,V., Imelda Kashaija, I.N and Barekye, A.

National Agricultural Research Organisation (NARO), Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) P.O. Box 421
Kabale Uganda
*E-mail: namuggak@gmail.com

Potato (*Solanum tuberosum* L.) is a major food and cash crop worldwide. Currently, potato production is affected by fluctuations in timing and amount of precipitation. This study identified potato clones potentially resilient to drought. A set of 12 potato clones was evaluated both on-station (three sites) and on-farm (three sites) for two seasons, using a completely randomized block design with two replications. Farmer participatory approach was employed to determine acceptability of the clones. High significant differences were observed among clones ($p<0.001$) from all the on-station trials. Clone 395111.13 gave the highest mean yields for all the on-station sites of 22 t ha^{-1}, 10 t ha^{-1} and 7 t ha^{-1}for Kalegyere, Mbarara and Mubuku, respectively. From the on-farm sites, Mwongyera gave the highest yield of 31 t ha^{-1}. Clones showed significant differences in the number of flowered plants, number of flowers, number of leaves, number of stems, leaflets length and width plus leaf area. Significant interactions were observed for plant height, number of stems and number of leaves. Maximum plant height was recorded for clone 393382.44 (59.3 cm). Clone 395111.13 added more leaves (4), 393382.44 had more flowered plants (26), 396034.103 more flowers (21), while 395029.250 had a bigger leaf area (11.8). Strong positive correlations were observed between leaflet length and; petiole length (0.82), number of leaflets (0.86), and leaflet width (0.79). Plant height, leaflet length and width, number of leaves and added leaves explained 94% of the observed variation.

IDT7-071 | Evaluation of combining ability and heterotic responses in maize (*Zea mays* L.) for drought tolerance

N.Kumari Vinodhana[1]*, K.N.Ganesan[1]

Tamil Nadu Agricultural University, Tamil Nadu, INDIA
*E-mail: soundhini@yahoo.co.in

Improving drought tolerance in maize has become one of the top priorities in maize breeding programs. A study was conducted at the Maize Research Station, TNAU, Vagarai, during 2014-15 to identify potential parents, superior cross combinations and formulate breeding strategies for yield improvement in maize under both irrigated and induced moisture stress conditions. The material for the study comprised six lines VIM 57 (L1), VIM 61 (L2), UMI 1200 (L3), VIM 244 (L4), VIM 15 (L5), VIM 108 (L6), and four testers VIM 236 (T1), VIM 93 (T2), VIM 418 (T3), VIM 153 (T4). These parents were crossed in a Line x Tester mating design to synthesize 24 hybrids which were evaluated under contrasting soil moisture regimes. The selection indices of drought included anthesis silking interval (ASI), relative water content (RWC), leaf rolling, root dry weight, root volume and drought recovery rate, apart from biometrical traits. Results of the study revealed significant differences among the hybrids for all measured traits. The relatively smaller proportion of GCA to SCA ratio indicated the predominance of non-additive genetic effects for all the traits under study. Under induced moisture stress conditions, the parents L5 (plant height, ASI, RWC), L3 (cob weight and grain yield), L4, L1 (cob length) and T4 (days to flowering, number of kernels per row, leaf rolling and RWC) had desirable *per se* and *gca* effects. On the basis of *per se*, *sca* and standard heterosis, under induced moisture stress, L5 x T4, L1xT2, L4xT4, L6xT3, L3xT2 and L3xT4 crosses were found to be desirable for yield/plant and most yield components under drought. The hybrids L3 x T4 (UMI 1200 x VIM 153) and L5xT1 (VIM 15 x VIM 236) recorded positively significant values for grain yield and are considered the best hybrids for both the conditions. The study revealed that the identified hybrids showed desirable heterotic levels for yield and drought parameters that are desirable in areas with marginal rainfalls and could be utilized in maize breeding programs.

IDT7-072 | Variation among white clover interspecific hybrid families for traits associated with improved drought resistance

Nichols SN[1]*, Hofmann RW[2], Williams WM[3,4]

[1]AgResearch, Hamilton 3214, New Zealand
[2]Lincoln University, Lincoln 7647, New Zealand
[3]AgResearch, Palmerston North 4442, New Zealand
[4]Massey University, Palmerston North 4442, New Zealand
*E-mail: shirley.nichols@agresearch.co.nz

Interspecific hybridisation with *Trifolium uniflorum* has potential to improve the poor drought resistance of *Trifolium repens* (white clover), a major species in temperate pastoral agriculture. A field experiment in a rain shelter facility was conducted to determine the impact of hybridisation on responses to drought stress. First generation backcross (BC1) and second generation backcross (BC2) hybrid families and white clover parental cultivars were studied. After four months of treatment (no watering vs weekly irrigation), the shoot dry weight of three BC1 families was unaffected by drought, and all seven BC1 families were significantly less drought-affected than their respective cultivar parents. Senescence of all BC1 families was unchanged by drought stress, but increased in three out of the five white clover cultivars. Three BC1 families also had significantly lower senescence than their parents under drought conditions.There was variation among hybrid families and white clover cultivars in the accumulation, and response to drought, of phenolic compounds associated with drought responses in white clover. Quercetin and hydroxycinnamic acid accumulation increased under drought in some lines but not others, whereas kaempferol levels increased in one line only. There were few differences among the plant lines for quercetin accumulation under drought, but we observed more variation for kaempferol and hydroxycinnamic acid. These results indicate that while some traits and responses are relatively consistent across hybrid families, others are more variable.This suggests potential for further improving the drought resistance of white clover above the average improvements already seen at the BC1 generation level, by selection of hybrid families based on targeted traits.

IDT7-073 | Phenotypic variability of drought-avoidance shoot and root phenes and their relationships with yield under drought and low P conditions in cowpea

Belko N[1]*, Boukar O[1], Fatokun C[2], Togola A[1], Chamarthi S[1], Moukoumbi Y[1], AbbertonM[2]

[1] International Institute of Tropical Agriculture, IITA Kano Station, Nigeria
[2] International Institute of Tropical Agriculture, IITA-HQ Ibadan, Nigeria
*E-mail: N.Belko@cgiar.org

Cowpea (*Vigna unguiculata* (L.) Walp.) is the most important grain legume crop cultivated by resource-limited farmers in marginal lands of Sub-Saharan Africa's dry savannahs. Although the crop is well adapted to this region, it could benefit from genetic improvement aimed at enhancing its tolerance to drought and low soil fertility. Cowpea minicore collection and breeding lines were phenotyped under both screenhouse and field conditions to (i) assess genotypic differences in water-saving shoot traits and root system architecture and (ii) evaluate the contributions of these traits to crop yield and adaptation to drought and low phosphorus. The parameters considered included whole plant transpiration rates, canopy temperature, chlorophyll content, adventitious and basal root numbers and growth angle. Correlation analysis revealed significant positive relationships between the plant shoot and root traits and the crop yield under stress conditions. Overall, Dan'Ila, IT86D-1010, IT98K-205-8, IT97-499-35, IT99K-573-2-1, TVu-9486, TVu-14788, TVu-15391,TVu-11986, and TVu-14676 with conservative soil water-use attributes and steep root systemsas well as IT98K-1111-1, IT07K-318-33, IT99K-494-6, TVu-9797, TVu-11982 and TVu-15055 with shallow root systems are potential for adaptation to drought and low P, respectively. These results reveal the possibility for improving the productivity of cowpea in water deficit and poor soil environments by exploiting its genetic potentials.

IDT7-074 | Molecular mapping of seed protein content in pigeonpea – a drought tolerant crop of the semi-arid tropics

Obala J[1],[2], Saxena RK[1], Singh VK[1], Kale SM[1], Garg V[1], Kumar V[1], Sameerkumar CV[1],Tongoona P[2], Sibiya J[2], Saxena KB[1],Varshney RK[1]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]School of Agricultural, Earth and Environmental Sciences,University of KwaZulu-Natal, Pietermaritzburg, South Africa
*E-mail: r.k.varshney@cgiar.org

Pigeonpea is a uniquely drought and heat tolerant crop that provides a major source of dietary protein to nearly a billion people in the tropical and semi-arid tropics of the world. Despite its importance as a source of dietary protein the genetic control of its seed protein content (SPC) is poorly understood. The present study used high density linkage maps to identify quantitative trait loci (QTL) associated with SPC and its relationship with 100-seed weight (HSW), seed yield (SY), days to first flower (DTFF) and growth habit (GH). Five F2 mapping populations segregating for SPS including ICP 11605 × ICP 14209, ICP 8863 × ICP 11605, HPL 24 × ICP 11605, ICP 5529 × ICP 11605 and ICP 8863 × ICPL 87119 were genotyped using genotyping-by-sequencing and phenotyped for the traits. The average inter-marker distance on the population-specific maps varied from 1.6cM to 3.5cM.On the basis of the population-specific and consensus linkage maps, 48main effect QTLs (M-QTLs)with phenotypic variance explained (PVE) ranging from 0.7 to 23.5% were detected across five populations, of which 15 M-QTLs were major (PVE≥10). Twenty seven of the M-QTLs could be collapsed into six consensus QTL regions. In addition, 34 epistatic QTLs (E-QTLs) with PVE ranging from 6.3% to 69.8% were detected across populations. Co-localization of M-QTLs and E-QTLs affecting SPC and the agronomic traits explained the genetic basis of the significant ($P < 0.05$) correlations of SPC with HSW ($r2 = 0.22$ to 0.30), SY ($r2 = -0.18$ to -0.28), DTFF ($r2 = -0.17$ to -0.31) and GH ($r2 = 0.18$ to 0.34). The quantitative nature of genetic control of SPC and its relationship with agronomic traits suggest that marker-assisted recurrent selection or genomic selection would be effective for the simultaneous improvement of SPC and other important traits.

IDT7-075 | Qtl mapping for drought resistant in cowpea

Bolarinwa KA[1], Ogunkanmi LA[2], Ogundipe OT[3] and Amusa OD[2]

[1]Department of Education Science, Distance Learning Institute, University of Lagos, Lagos
[2]Department of Cell Biology and Genetics, Faculty of Science, University of Lagos, Lagos 3Department of Botany, Faculty of Science, University of Lagos, Lagos
E-mail: adebayoogunkanmi@yahoo.com

Wide crosses were made between drought tolerant (IT98K-205-8) parent and the susceptible parent (NG/SA/01/09/004) with a view to raising mapping population for Linkage and QTL mapping in cowpea. The drought tolerant seeds were white while the susceptible parents were all brown seeds. Parental lines were screened to ascertain their tolerance level using the method of Singh with little modifications. The drought tolerant parent (IT98K-205-8) was confirmed to have retained its drought tolerant level. Sixteen crosses out of 227 attempts were successful only when IT98K-205-8 was used as the female plant. The F2 plants were raised from the sixteen successful F1 seeds using single seed decent method. It was observed that some seeds from F1 generation were not viable and did not germinate. The F2 plants were selfed and raised to F3 for mapping population. Phenotyping was carried out on the mapping population and the two parental lines using ten characters traits. Seventy five SSR markers were developed and screened for polymorphism. Forty polymorphic markers were identified and used for bulk segregant analysis for marker development and linkage analysis.

IDT7-076 | Breeding tropical legume crops for resilient cropping systems in Sub-Saharan Africa

Chris O. Ojiewo[1]*, Asnake Fikre[2], Haile Desmae[3], Babu N. Motagi[4], Ousmane Boukar[5], Clare Mukankusi-Mugisha[6], Emmanuel Monyo[7], Varshney K. Rajeev[8]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Addis Ababa, Ethiopia
[2]Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria
[5]International Institute of Tropical Agriculture (IITA), Kano Station, Kano, Nigeria
[6]International Center for Tropical Agriculture (CIAT), Kampala, Uganda
[7]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya
[8]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: c.ojiewo@cgiar.org

Legume crops are important components of sustainable agricultural production, household income and dietary systems. However, legume production in the tropics is challenged by a number of biotic (diseases and pests) and abiotic (heat, and drought) stresses. With support from bilateral projects such as Tropical Legumes (TL1, TL2 and TL3), CGIAR centers together with national research partners devoted resources and time to address these challenges. Genetic resources such as reference sets, pre-breeding, magic and intraspecific mapping populations, as well as genomic resources such as comprehensive genetic maps, whole genome sequences, QTLs and trait-specific markers have been developed for tropical legume crops such as chickpea, groundnut, common bean, pigeonpea, soybean and cowpea. Besides, integrated breeding approaches including high throughput genotyping and phenotyping platforms, marker-assisted selection (MAS) in pedigree breeding schemes, marker-assisted backcrossing (MABC) and marker-assisted recurrent selection (MARS) have contributed to accelerated development of breeding lines and varieties. Improved varieties have been released and disseminated together with integrated crop management practices. Innovative seed and associated technology dissemination systems including public-private sector partnerships, community seed production initiatives, quality declared seed, mini seed packs, contractual seed production, and revolving seed fund, among others, were used to popularize these varieties. This has resulted in enhanced adoption and subsequent improvement in productivity. More efforts are needed to enhance genetic gain by reducing time required for cultivar development through application of genomic and phenomic tools, enhancing selection intensity through automation, mechanization and digitization, and increasing the crossing scale and number of cycles per year.

IDT7-077 | Field screening finger millet germplasm for drought tolerance

Ojulong HF[1]*, Sheunda P[1], Mgonja F[2], Kibuka J[1], Otwani D[1], E. Manyasa[1]

[1]International Crops Research Institute for Semi-Arid Tropics (ICRISAT) Box 39063-00623, Nairobi, Kenya.
[2]Selian Agricultural research Institute, PO Box 6024, Arusha, Tanzania
*E-mail: H.Ojulong@CGIAR.ORG

Drought stress is the most important abiotic constraint limiting finger millet production. Limited research on tolerance to drought in finger millet has been done in Africa. As a result, the only varieties adapted to high-rainfall regions have been developed and promoted. Twenty-four potential drought-tolerant varieties selected from regional trials, and a short-duration commercial check (U15), were screened for drought in three locations in Kenya (KALRO-Kiboko, KALRO-Kampiya Mawe (KYM)) and Tanzania (DRD-Miwaleni). Genotype was significant for all the traits, location for all except yield, and GxL interaction for all except plant height. Sixteen of the varieties outperformed the commercial check (1.10 tha-1), with the best yielders being IE2187 (2.02 tha-1), IEFV0009 (1.50 tha-1), IE501 (1.1.48tha-1), IE593 (1.45 tha-1) and IE2030 (1.43 tha-1). All varieties except one had shorter DAP than the commercial variety. GGE biplot for yield showed Kiboko and Miwaleni locations to be effective in discriminating genotypes. Genotypes IE501, IE593, were specifically adapted to the Kiboko environment while IE546, KNE 741 and IE5791 were more adapted to the Miwaleni environment. Genotypes IE3104, IE5736, IE5733, IE6475 and IEFV0009 were stable across locations. Principal component analysis revealed the first four PC accounted for 85.72% of the variation with plant height, agronomic score, biomass, number of lodged plants, and number of productive tillers contributing the most. Five of the varieties -- IE2187, IEFV0009, IE501, IE593 and IE2030 -- have been advanced to PVS in Kenya and Tanzania, while KNE 741 is at NPT in Kenya.

IDT7-078 | Current status of groundnut improvement in Uganda

Okello D. K.[1]*, Ugen M. A.[1], Odong T. L. [2], Monyo E.[3], Akpo E. [3], Okori P. [4], Deom C. M.[5]

[1]Department of Groundnut Improvement, National Semi-Arid Resources Research Institute,
[2]Department of Crop Production, School of Agricultural Sciences, Makerere University,
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Lilongwe, Malawi
[5]Department of Pathology, University of Georgia, Athens, USA.
*E-mail:kod143@gmail.com

In Uganda, groundnut (*Arachis hypogaea* L) is the second most important legume after beans. Groundnuts is cultivated on nearly 260,000 ha, representing 24.6% of the total arable land. On-farm pod yields are low, averaging 800 kg/ha of dry pods, compared to on-station potential yields of 3,000kg/ha. Sales from current production could potentially generate $344 million to the producers who are largely small-scale farmers. The yield gaps are attributed to a combination of biotic, abiotic, cultural and political factors. Since the 1920s, research efforts have released 24 varieties, the most recent commercial varieties being the Serenut 1-14 series. These varieties have overcome some of the mentioned production constraints. However, varied growing agroecologies, land tenure systems, diverse market preferences, and emerging stresses call for continuous research. Current research agenda includes breeding for high oleic, leafminer resistance, confectionery, aflatoxin tolerance, drought tolerance, early to medium maturing varieties, high yielding, and rosette disease resistant varieties. We have initiated Marker Assisted Selection for high oleic breeding and adopted BMS for Digitalization of data capture, management, analyses and storage. Recently developed regeneration protocol will aid in introgressing additional traits across taxa. The bimodal rainfall pattern and active hybridization programme increases our breeding cycles. To date, the groundnut breeding program has an active breeding pipeline frequently releasing varieties and lines which have already been shared with National Programs across Africa, Haiti and the USA with many additional National Programs making requests. We have strong partnerships in Research and Development among the African Countries, USAID, ICRISAT, and BMGF.

IDT7-079 | Increasing cowpea (*Vigna unguiculata* (L.) Walp) production and productivity in drought prone agro-ecologies of Nigeria

Olufajo O.O.[1]*, Umar M.L.[1], Boukar O.[2], Fatokun C.[2], Ishiyaku M.F.[1]

[1]Institute for Agricultural Research, Ahmadu Bello University, Zaria, Nigeria
[2]International Institute of Tropical Agriculture, Ibadan, Nigeria
*E-mail: sojiolufajo@yahoo.com

Cowpea, (*Vigna unguiculata* (L.) Walp), is the most commonly grown and consumed grain legume in the dry savanna regions of West and Central Africa where more than 60% of the global cowpea is produced. The average grain yield of cowpea is about 495 kg ha^{-1} compared with the potential yield of 2500 kg ha^{-1}. This is due to biotic and abiotic stress and the unpredictable rainfall pattern. There is a projection of an accelerated annual demand of 2.7% and shortage supply of 2.5% for cowpea from 2007 to 2030. In order to bridge this gap, several breeding lines were evaluated on farmers' field in the major cowpea-growing areas of Nigeria for terminal drought tolerance, using planting dates. After series of drought phenotyping and farmers' participatory selection, five promising drought-tolerant lines: IT97K-499-35, IT99K-573-1-1 IT99K-573-2-1, IT07K-292-10 and IT07K-318-33, were selected by farmers over a period of eight years. These lines were further subjected to multi-location and on-farm testing, following which they were all registered and released in Nigeria as drought tolerant and *Striga/Alectra* resistant varieties. These varieties have potential grain yield of up to 2.6 t ha^{-1}. Also, lines derived through marker-assisted recurrent selection (MARS) are being phenotyped for drought, *Striga* and low P tolerance. It is expected that cowpea production will further increase and marginal areas will be put into production. Greater emphasis is also being placed on making available the high-yielding and stress-tolerant improved cowpea varieties to farmers in order to enhance food security, productivity and income.

IDT7-080 | Performance and yield stability of groundnut (*Arachis hypogaea* L.) in the guinea savanna zone of Ghana

Oteng-Frimpong R[1]*, Denwar N. N.[1], Issah A. R.[1], Wohor Z. O.[1]

[1]Council for Scientific and Industrial Research (CSIR) -Savanna Agricultural Research Institute, Tamale Ghana.
*E-mail: kotengfrimpong@gmail.com

Groundnut remains the most important grain legume in Ghana, with the Guinea savanna zone accounting for over 70% of groundnut produced. In this region, the high-protein fodder and kernel serves as a major source of income for the over 90% farming households engaged in its cultivation. Yield on farmers' fields remains low due to biotic and abiotic stress and the use of low potential genotypes. This study aimed at identifying high-yielding genotypes with stable yield across the Guinea savanna zone of Ghana. Seventeen advanced breeding lines plus four release varieties were tested at three locations in two consecutive years, using randomized complete blocks with four replicates. The soils are sandy loam, slightly acidic and generally low in nutrients. There results showed variable performance of the genotypes across locations, with mean pod yield ranging from 0.58 to 2.1 t ha-1. There was a significant GxE and the genetic variation was highest at Damongo. Analysis of GxE following the AMMI2 model showed that the first two principal components were highly significant ($p<0.05$) and explained 90% of total variation. Genotype ICGV-IS 08837 had the highest yield. From the AEC-GGE biplot, genotypes NKATIESARI and ICG (FDRS) 4 successfully combined high pod yield with stability. Two mega environments were also identified for groundnut selection and superior lines (ICGV-IS 08837, ICG (FDRS) 4 and ICG 6222) have been earmarked for release. These lines showed over 50% yield advantage over Chinese, the most commercially important cultivar in the target region.

IDT7-081 | Towards the improvement of tolerance to early-season-drought in wheat – assessment of candidate traits

Jairo A. Palta[1,2,3] *, Robert J. French[4]

[1]CSIRO Agriculture, Private Bag No. 5, Wembley WA 6913, Australia
[2]School of Plant Biology, The University of Western Australia, LB 5005 Perth, WA 6001, Australia
[3]The UWA Institute of Agriculture, The University of Western Australia, LB 5005 Perth, WA 6001, Australia
[4]DAFWA Dryland Research Institute, PO Box 432, Merredin, WA, Australia
*E-mail: Jairo.palta@uwa.edu.au

Early winter rainfall in Western Australia has been decreasing since 1900, exposing wheat crops sown at the onset of first autumn rains to increased risk of early season drought (Fletcher et al 2014). In WA, 82% of wheat growers are sowing their whole cropping land dry, which increases the risk of early season drought (Fletcher et al 2014). Wheat crops sown into dry soil will germinate on the first rainfall, potentially leaving crops vulnerable to 20-32 days of drought after emergence. While seedlings subject to early drought often survive, their growth and development are significantly slow, reducing anthesis biomass, duration of grain filling and grain yield. In severe cases, yield can be halved (Armstrong et al. 1996). The aim of this study was to assess candidate traits related to the variation in yield in dependence of drought after seedling emergence. The traits evaluated were high leaf area under early-season drought and, upon recovery, tiller survival and time to anthesis. Field studies were conducted during the 2015 and 2016 seasons using the MEF facilities at Merredin, WA. The early season water deficit was very mild, but it accelerated time to flowering and physiological maturity. The varieties Magenta and Bonnie Rock were sensitive to the mild early-season drought, but Wyalkatchem and Estoc were not affected. Leaf area and above-ground biomass did not recover by anthesis, but grain yield was not affected in Magenta and Bonnie Rock because their flowering and maturity was earlier allowing them to escape terminal drought.

IDT7-082 | Performance of good root and drought tolerant castor (*Ricinus communis* L.) germplasm in *kharif* under rainfed conditions

Lakshmamma P[1]*, Lakshmi Prayaga[1], Alivelu K[1]

ICAR- Indian Institute of Oilseeds Research, Hyderabad, Telengana, India -500030
*E mail: lakshmiparvathaneni@rediffmail.com

Six germplasm accessions with good root growth in terms of root volume, dry weight and known drought tolerance (low DSI) along with checks (48-1, DCH-519) were grown under rainfed conditions for two years during *kharif*, 2014-16, with three replications in RBD. A total rainfall of 337 mm in 2014-15 and 299 mm in 2015-16 was received during the crop growth duration (126-128 days). Mean seed yield from the study showed that primary seed yield was higher in RG 1494, and RG 2797. In RG 2797 secondaries were produced only during 2015-16. Secondary seed yield was higher in RG 1437 followed by RG 298, RG 1494. Germplasm lines RG 298 and RG 1826 produced tertiary spikes during both years. RG 111, RG 1437 and RG 1494 also recorded tertiary seed yield during 2015-16. Total seed yield was significantly higher in RG 1494 (101g/pl.) followed by RG 1826 (96g/pl.) and RG 298 (91 g/pl.) which showed better performance of these genotypes in rainfed conditions though, other genotypes also showed drought tolerance under field conditions during previous years of experimentation by withholding irrigation from 30-90 DAS. RG 1494 recorded high TDM at harvest and also high seed yield, showed low HI of 25.6% due to low stem reserve mobilization. RG 298, RG 1826 recorded high HI of 36.1% and 42.6% respectively. Hence, RG 1494, RG 298 and RG 1826 with good root growth and high seed yield under rainfed conditions, and with drought tolerance could be used in breeding programs.

IDT7-083 | Characterization of drought adapted grain sorghum varieties and favorable root phenotypes in BTx623 X IS3620C recombinant isogenic line population.

Person T[1], Jahn CE[1]*

[1]Colorado State University, Fort Collins, 80523, Colorado, USA
*E-mail: Courtney.Jahn@colostate.e

With increased demands on freshwater, the development of crop varieties with improved performance under reduced water conditions is important for food and fuel security. One approach to improving water use efficiency is to capitalize on the inherent drought tolerance ability in crops. Sorghum (*Sorghum bicolor*) is an internationally important food and fuel crop with large genetic variation in agronomically important traits such as resistance to drought. While many traits contribute to drought adaptability, plant survivability and yield production under water-limited conditions is not fully understood. Here, we utilize a phenotypically diverse set of 252 F8 to F10 recombinant inbred lines (RILs) derived from an elite hybrid, BTx623, and a guinea line, IS3620C, to identify associations between morpho-physiological traits and drought response. We determined panicle weight, growth rate, height, total shoot dry weight, tiller number, stem diameter, and harvest index; traits that contribute to yield, growth, and total biomass accumulation. The lines exhibited significant variation in response to water deficit for the four of the seven traits listed (respectively). Furthermore, shoot dry weight was highly correlated to plant height and panicle weight for both treatments, while a positive correlation was significant among tiller number, shoot dry weight, plant height and panicle weight only under water deficit. A subset of this RIL population will be used to assess root biomass to determine whether particular root traits are favorable under drought and which genes are responsible for those traits.

IDT7-084 | Identification of stable grain yield QTLs under reproductive-stage drought stress in rice (*Oryza sativa* L.)

P. Mamatha[1*], Shailesh Yadav[1,2], Rahul Priyadarshi[1], S. Vanisri[3], Arvind Kumar[1,2], CH.V. Durga Rani[3], T. Ramesh[3,] Uma M. Singh[1], C. Venkat[1], J. Ramaya[1], S. Dixit[1], V. Vishnu[1], S. Alam[1], N.Mallikadevi[1], V. Abhilash Kumar[1], Abhinav Jain[1], S. Naik[1]

[1]International Rice Research Institute, South Asia Hub, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad- 502324, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
[3]Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad- 500030, India
*E-mail: pettemmamatha23@gmail.com

Drought stress is the largest constraint in rice production in rainfed systems, affecting 23 million hectares of upland and rainfed lowland rice in Asia. Water scarcity in this region is becoming alarming because of recent shifts in rainfall patterns. The development of drought-tolerant rice varieties to reduce climate-related risks, increase productivity and alleviate poverty among rainfed farmers has always been a tough challenge for plant breeders. Identification of stable QTLs for grain yield under drought will help rice breeders develop better drought-tolerant rice varieties. Recently some stable QTLs in rice have been reported for grain yield under drought, with effect against multiple genetic backgrounds as well as under diverse ecosystems. Keeping in view the above hypothesis, RILs (F5:6) derived from the cross MTU 1010/IR 91648-B-117-B-1-1 were phenotyped under stress and non-stress environments. Parental polymorphic survey with SSR markers covering 12 chromosomes was done for using them in QTL identification. The identified QTLs will be validated in alternate populations with different genetic background in IR 64/IR91648-B-117-B-1-1 population.

IDT7-085 | Molecular approaches to improve performance of barley under water limited environments

Pokharel B.B.[1]*

[1]Agriculture and Forestry University, Rampur, Chitawan, Nepal.
*E-mail: bhanu.pokharel@gmail.com

Due to continuous depletion of the water table, drought has become one of the major environmental constraints for farmers and agricultural scientists. Drought tolerance is a complex phenomenon and progress in breeding has been limited as drought becomes more complicated with different abiotic stresses such as higher temperature and solar radiation, genetic factors, low trait heritability, and the size and complexity of the genomes. In the past, farmers and researchers fully utilized traditional breeding approaches such as selection with morphological traits to tackle droughts. However, numerous field and lab experiments and their results revealed that it is almost impossible to develop fully drought-tolerant crops with the traditional breeding approach. Nowadays, with advances in the molecular arena and development of SNP markers, it is possible to detect differences up to sequence level. Molecular approaches are becoming essential to get accurate results, reduce research duration, and minimize research expenses. Holistic strategies combining traditional and molecular breeding, and physical and physiological approaches should be applied for more reliable and effective results. To include all these approaches is beyond the scope of this review paper, so only the advanced molecular and physiological approaches are included. In this complex scenario, while developing drought tolerance in barley, a research program should study a series of problems in a multi-disciplinary manner, considering interaction between multiple stresses, integrating the physiological anatomy of drought-tolerance traits and the modern genetic and genomics tools such as quantitative trait loci, association mapping, microarrays, and genomics/proteomics.

IDT7-086 | Identification of rice genotypes under different water-limiting practices

Ramesha MS[1], Pranesh KJ[1]*, Durgaraju CH[1], Venkateshwarlu CH[1]

[1] International Rice Research Institute, ICRISAT, Hyderabad, India
*E-mail: k.pranesh@irri.org

Water deficit is one of the environmental factors that greatly reduce rice grain yield. With this perspective, an investigation was carried out to evaluate rice genotypes with broad genetic diversity under different water-limiting practices such as dry directed seeded rice (DSR), zero tillage (ZT), and alternate wetting and drying (AWD). A set of 32 new genotypes developed at IRRI, South Asia Hub, ICRISAT, Hyderabad, were evaluated in different water-limiting environments along with the normal transplanted puddled rice (TPR) situation. The experiment was laid out using alpha lattice design with two replications and included two checks *viz.*, *Sahbhagihan* and MTU1010. The average performance of the genotypes was 6227 kg/ha, 6145 kg/ha, 5411 kg/ha and 4065 kg/ha in TPR, ZT, AWD and DSR respectively. The genotypes showed differences in grain yield and were influenced differently by the water limitation. The range for grain yield in TPR situation varies from 7675 kg/ha to 4267 kg/ha. Similarly in zero tillage, grain yield varied from 7905 to 4944 kg/ha, whereas the grain yield in alternate wetting and drying varied from 7292 kg/ha to 4100kg/ha. The maximum grain yield was 5542 kg/ha and minimum was 3208 kg/ha in dry direct seeded rice situation. We identified the best genotypes over the check in all situations; 15 genotypes in DSR, 10 in ZT, 18 in AWD and three in TPR situation. Our study showed the magnitude of yield penalties associated with different rice-growing practices to which they are not adapted.

IDT7-087 | Comparative assessment of drought adaptation in rice and wheat

Preethi NV[1,2]., Sheshshayee MS[1*], Xinyou Y[2], Nataraja NK[1], Udayakumar M[1] and Struik PC[2*]

[1]Department of Crop Physiology, University of Agricultural Sciences, GKVK campus, Bengaluru- 560065, India
[2]Centre for Crop Systems Analysis, Wageningen University & Research, Wageningen, The Netherlands.
*E-mail: msheshshayee@hotmail.com and paul.struik@wur.nl

Rice (*Oryza sativa*) and wheat (*Triticum aestivum*), the most important staple cereals, require very different amounts of water for a given yield potential. Understanding the physiological mechanisms of stress adaptation in wheat would pave way for devising strategies to improve rice grain yield under semi-irrigated aerobic conditions. An investigation was carried out to study two cultivars of rice with contrasting drought stress response *viz*., IR64 (susceptible) and Apo (tolerant), in comparison with one wheat genotype (Weebil) which is known to be drought tolerant. Plants were subjected to two moisture stress regimes (100% and 60% field capacity (FC)) during the GSI stage.Variability in water conservation, water mining and osmotic potential were assessed. Wheat had better water mining capacity, with better root traits, and was able to maintain better water relations even at 60% FC than rice genotypes. Wheat showed photosynthetic rates of 30 and 26 µmol m-2s-1 in 100% and 60% FC respectively, which was significantly higher than that of Apo (26 and 18 µmol m-2s-1) and of IR64 (22 and 14 µmol m-2s-1) and wheat maintained higher growth rates than rice genotypes. Between rice genotypes, stress induced reduction in root traits was less for Apo which also maintained better water relations compared to IR64. There was less reduction in leaf expansion rate in Apo which was comparable to that of wheat. Water uptake and carbon assimilation capacity are the relevant traits that need to be improved in rice so as to render it suitable for water saving agriculture.

IDT7-088 | Identification of QTLs for reproductive stage drought and high-temperature stress in rice (*Oryza sativa* L.)

Priyadarshi R[1], Mamatha P[1], Yadav S[1, 2], Singh UM[1], Venkateshwarlu CH, Ramaya J[1], Dixit. S[1], Vishnu V[1], Alam S[1], Mallikadevi N[1], Vipparla AK[1], Jain A[1], Naik S[1], Arvind Kumar[1, 2*]

[1]International Rice Research Institute, South Asia Hub, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad- 502324, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
*E-mail: a.kumar@irri.org

Drought stress is the most serious threat to both rainfed lowland and upland rice production, and causes significant yield losses. Increased temperature during reproductive stage, especially in dry season, is another serious concern reducing rice yield. Most of the times, drought and high temperature stresses occur together. Climate change prediction indicates an increase in frequency and severity of both the stresses. Mitigation of these challenges through development of tolerant rice varieties will be the key to improving rice production and ensuring food security. Breeding for abiotic stress tolerance has always been a tough challenge for plant breeders due to complexity of the trait, poor understanding of the inheritance mechanisms of tolerance and lack of efficient techniques for screening breeding materials. Identification of novel Quantitative Trait Loci (QTLs) will provide opportunities to enhance rice yield through pyramiding consistent QTLs for reproductive-stage drought and high temperature. Keeping in view the above hypothesis, an advanced backcross-mapping population derived from MTU 1010/IR 91648-B-117-B-1-1 was phenotyped for reproductive-stage drought and high temperature, and genotyped following simple sequence repeat (SSR) markers spread over the 12 rice chromosomes to identify QTLs governing tolerance to reproductive-stage drought and high temperature. The introgression of these yield QTLs in backgrounds of high-yielding rice varieties will help develop better rice varieties for rainfed ecosystems and allow farmers to obtain high and stable yields under the changing climate scenario.

IDT7-089 | Evaluation of partial stay-green QTL introgression lines of Indian post-rainy sorghum lines

R Madhusudhana[1]*, HS Talwar[1], Jai Kishan[1], Shiwesh Kumar[1], VA Tonapi[1]

[1]ICAR-Indian Institute of Millets Research (ICAR-IIMR), Rajendranagar, Hyderabad, India
*E-mail: madhu@millets.res.in

'Stay-green' in grain sorghum is an important trait for imparting drought tolerance under terminal moisture stress. Several quantitative trait loci (QTL) associated with stay-green are documented in sorghum, of which Stg3a and Stg3b on SBI-02 were consistently identified across genetic backgrounds. A study was initiated to transfer these two key QTL into post-rainy adapted genotypes, CRS4 and RSLG262, using marker-assisted breeding. Targeting Stg3a (57-62 Mb) and Stg3b QTL (69-71 Mb) region, 48 new microsatellite or simple sequence repeat (SSR) markers were developed to carry out marker-assisted breeding. Foreground selection was followed in BC_1F_1 and progeny were advanced to BC_1F_3s. Initial evaluations of partial introgrression lines (BC_1F_3 generations) of CRS4 and RSLG262 carrying Stg3a and Stg3b from donor parent B35, in both well-watered and post-flowering stress environments was carried out during post-rainy 2015-16 at ICAR-IIMR, Hyderabad. Some of the introgression lines had higher green leaf area retention at maturity, grain yield and stover yield under both stress and no-stress conditions. The introgression lines also showed significantly better drought tolerance in terms of their low drought susceptibility index compared to respective recurrent parents. Under stress, 56-150% higher green leaf area retention was observed in introgressed lines of CRS4 and RSLG262. For green leaf area retention, few of the RSLG262-derived lines were better than stay-green donor B35. Among the introgression lines of CRS4 and RSLG262, 16-20% superiority for grain yield, and 26-71% superiority for stover yield was recorded. Thus, the study provided practical confirmation that the marker-assisted backcross transfer of stay-green QTL, Stg3a and Stg3b from B35, into post-rainy adapted lines, CRS4 and RSLG262, has the potential to enhance the post-flowering drought tolerance in senescent sorghum genotypes.

IDT7-090 | Exploiting finger millet as a source for isolating novel genes controlling abiotic stress tolerance

Rahman H.[1], Raveendran M[1]*

[1]Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India-641003
*E-mail: raveendrantnau@gmail.com

Finger millet (*Eleusine coracana* (L.) Gaertn) is a hardy cereal crop known for its superior level of tolerance against drought, salinity and foliar diseases, and also for its nutritional values. Comparative physiological and biochemical studies in a set of contrasting rice and finger millet genotypes under salinity stress condition revealed superiority of finger millet over rice in overcoming dehydration/osmotic stress due to salinity. Finger millet genotypes exhibited relatively higher level of osmotic tolerance, enhanced level of accumulation of soluble sugars, and lesser reduction in gas exchange parameters under salinity stress. Salinity responsive RNA-Sequencing in leaves of contrasting finger millet genotypes CO 12 and Trichy 1 resulted in the identification of several novel genes and transcription factors associated with dehydration tolerance in finger millet. A novel salinity responsive NAC transcription factor (*EcNAC67*) was isolated from a finger millet genotype Trichy 1 and characterized through genetic transformation. Transgenic rice (ASD16) plants engineered with *EcNac67* showed enhanced tolerance against drought and salinity stresses. During vegetative stage drought stress, transgenic plants showed much delayed leaf-rolling symptom and were able to maintain 20% (approx.) higher relative water content in the leaves when compared to non-transgenic ASD16 plants. Reduction in grain yield/plant and drought induced spikelet sterility was found to be lesser in the transgenic lines as compared to NT-ASD16. Results indicated that finger millet can be exploited as a novel source for investigating the mechanism of dehydration tolerance in plants.

IDT7-091 | Characterization of lentil germplasm and identification of potential morphological marker(s) linked to drought tolerance

Akter Shahid [1], Rahman A.K.M.M [2], Hasan Ahmad Khairul[3], Hossain Md. Amir[1] , Sarker Ashutosh [4]

[1]Department of Genetics & Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh
[2]Pulses Research Centre, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh
[3]Department of Agronomy, Bangladesh Agricultural University, Mymensingh, Bangladesh
[4]International Centre for Agricultural Research in the Dry Areas (ICARDA),India
*E-mail: kbdbabu@gmail.com, amirgpb@bau.edu.bd

A total of 30 lentil genotypes were evaluated for drought tolerance, of which 12 were local varieties collected from BARI and BINA, and the remaining 18 were exotic lines introduced from ICARDA. Stress condition reduced yield for all the genotypes compared to normal conditions. ILL-5099, ILL-5105 and BLX-20085-75 showed tolerance against drought, where yield loss is minimum (9%, 13.20% and 19.95%, respectively); whereas ILL-2508, ILL-2509, showed moderate tolerance in drought condition and yield losses were 22.21% and 25.09%, respectively. The genotype ILL-4707 (70%) was most sensitive to drought, followed by BINA Masur-6 (65.83%), ILL-5135 (62.58%) and BARI Masur-4 (58.26%). Phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV) in all of studies traits. Moderate to high heritability (range from 50%-93%) was found for all traits. High heritability along with high genetic advance was found for number of pods per plant (62.72), number of seeds per pod, (49. 92), pod length (45.55) and plant height (40.05). A significant positive correlation was found for most of the studied characters. For validation, the hydroponic culture technique was used to screen drought tolerance genotypes at seedling stage and drought stress was imposed by taking out the 15 day-old seedlings from the nutrient solution (Peter's professional) and exposing them to air for five hours on every alternate day for four days. Among the genotypes studied, only three genotypes, ILL-5099, ILL-5127 and ILL-5105, showed maximum seedling survivability and minimum reduction in the growth parameters, with a drought score of 0.0–1.0 indicating tolerance to drought stress.

IDT7-092 | Identification of superior alleles of known rice genes for high yield-potential under drought

Rai P[1], Sen P[1], Sen S[1], Goswami J[1], Shatish V[1], Ganguly S[1], Roy A[1], Saha S[1], Bhattacharyya S[1]*

[1]Bidhan Chadra Krishi Viswavidyalaya, Mohanpur, PIN 741252, West Bengal, India.
*E-mail: somnathbhat@yahoo.com

Several land races of rice are well adopted for hundreds of years in drought-prone areas of Bengal. Drought tolerance ability, particularly at the reproductive stage, of these genotypes is assessed under rain-out shelter for consecutive two years. Relative expression of known genes involved in increasing yield under water deficit conditions, such as OsNAC10 (NAC domain containing gene), OsAP37 (Apetallous), DROI (deep root 1), and NAL1 (Narrow keaf1), was compared in a set of contrasting genotypes. Comparing the yield performance under drought and relative expression of the known genes, superior alleles are identified. Sequencing of the target allele is made in probable donor and recipient parents to identify SNPs. Crossing between tolerant genotypes with the high-yielding varieties are already made to generate the mapping population. Identified SNPs will be validated in the mapping population, which are under the process of development (F2).

IDT7-093 | Breeding for drought resilience in rice: root growth and yield under drought in managed stress and target populations of environments

Rajurkar A B[1], Raveendran M[1], R. Chandra Babu[1]*

[1]Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India 641003.
*E-mail: chandrarc2000@yahoo.com

Drought is a major constraint to rice (*Oryza sativa* L.) production and yield stability, especially in rainfed ecosystems. Developing resilient rice varieties is important for food security of majority of the population in Asia, Sub Saharan Africa and South America. Roots are considered to contribute in drought resistance in rice. Genetic improvement of root system through conventional breeding is not possible due to difficulty in phenotyping root traits. Marker assisted breeding (MAB) will hasten development of genotypes with improved root system. Consistent QTLs for root traits have been mapped leading to MAB for improved root traits in rice. However, a positive impact of improved root traits on grain yield under drought is yet to be demonstrated, especially in target populations of environment (TPE). Precise phenotyping of root system is critical for understanding the biological value of roots in drought resilience. Thus rice lines introgressed with root QTLs were evaluated in the field for root system and plant production under managed stress and drought in TPE, as well as under stress using PVC pipes. Rice lines showed considerable variation in root growth and yield under stress in these different systems of evaluation. The agronomic value of the root QTLs in terms of yield under drought, especially in TPE will be discussed.

IDT7-094 | Molecular mapping of quantitative trait loci for drought tolerance and yield traits in lentil

Rana M[1,2]*, Verma P[3], Hussian W[4], Kaldate RC[2], Divya Shikha[2], Kaachra A[5], Chahota RC[2], Bhatia S[3], Sharma TR[2]

[1] ICAR- Indian Grassland and Fodder Research Institute, Jhansi, Uttar Pradesh-284003, India
[2] CSK Himachal Pradesh Agricultural University, Palampur, Himachal Pradesh-176062, India
[3] National Institute of Plant Genome Research, Aruna Asaf Ali Marg-110067, New Delhi
[4]University of Nebraska, Lincoln, USA- 68583-0915
[5]CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh-176062, India
*E-mail: rana.maneet@gmail.com

Lentil (*Lens culinaris* Medik subsp. *culinaris*) is a cool season food legume crop cultivated globally. Among various stresses, drought is one the major production constraints causing up to 70% yield losses in lentil. In order to dissect the complex nature of drought tolerance and to use genomics tools for enhancing yield of lentil under drought stress conditions, an intraspecific RIL mapping population (L830 x *Precoz*) segregating for these traits was used. A total of 1229 SSR markers were screened for parental polymorphism and 293 were found to be polymorphic. Of these, 291 were mapped on seven LGs at LOD 4.0 spanning 1199.0 cM, with an average marker density of 4.8 cM. ANOVA revealed significant differences for all the 27 measured traits between the drought tolerant 'L830' and the susceptible cultivar '*Precoz*'. Significant effect of drought stress was observed for all the traits measured, except phenological traits and seed size. Phenotypic data from the RILs were used to identify QTLs for drought tolerance and yield traits by CIM. A total of 75 QTLs (LOD $\geq$ 2.5) were detected across the three environments (control, drought stress and cylinder culture) across all the LGs. Among these, 13 were stable, 12 were consistent and 27 were drought specific. PVE by QTLs ranged from 5.4% to 45.9%. In conclusion, it is envisaged that the present linkage map would provide genomics tools to breeders for further genetic enhancement of this crop species as this is the first report on genetic control of drought tolerance coupled with yield traits in lentil.

IDT7-095 | Studies on drought tolerance using some morpho-physiological parameters in wheat (*Triticum aestivum* L.)

Raina K[1], Rana V [1]*, Dhiman R[2], Chaudhary K[2], Rana U[2], Shubhanshu A[1], Sharma R[1]

[1] Rice & Wheat Research Centre, Malan (176 047), Himachal Pradesh, India
[2] CSK Himachal Pradesh Agricultural University, Palampur (176 062), Himachal Pradesh, India
*E-mail: vijayrana_2005@rediffmail.com

Twenty five wheat genotypes varying in their adaptability to different agro-ecological conditions and yield potential were evaluated in randomized block design with three replications under non stress (E_1) and moisture-stress (E_2) environments. The aim was to characterize variation in their response to moisture-stress using some morpho-physiological characters and drought resistance indices, and to find out association between morpho-physiological characters for identifying simple selection criteria for drought tolerance. Analysis of variance indicated that mean squares due to genotypes were statistically significant for all the characters except grain weight per spike under E_1 and grain weight per spike and effective tillers per plant under E_2. High to moderately high PCV, GCV and genetic advance were observed for grain growth rate II and grain growth rate III under both the environments. Correlation studies indicated significant positive correlations of grain yield with all the grain yield attributes, biological yield, harvest index, flag leaf area and relative water content under both the environments. Besides, grain yield had significant negative correlations with excised leaf water loss and drought susceptibility index ('S'), and significant positive correlations with stem reserve mobilization, grain growth rate (I,II, III), peduncle length, plant height, seedling height and drought response index (DRI) only under stress conditions. Biological yield and harvest index had high positive direct effects on grain yield both under E_1 and E_2 environments. Significant negative correlation of 'S' with DRI indicated that DRI can be used as a simple reliable criterion for assessing drought tolerance.

IDT7-096 | Optimizing high throughput phenotyping for productive use of water in mungbean and chickpea (*Cicer arietinum* L.)

Rane J[1]*, Bindumadhava H,[2], Nagel K[3], Kumar M[1], Raina S[3], Govindasamy V[5], Hanjagi P[1], Giri R[1], Nair R[2], Basu, PS[5], Singh NP[1]

[1] ICAR-National Institute of Abioric Stress Management (NIASM), Baramati, India
[2] World Vegetable Centres, Hyderabad, India
[3] LemnaTec Gmbh, Achen , Germany
[4]ICAR-CITH, Srinagar, India,
[5] ICAR-Indian Agricultural Research Institute, New Delhi, India
[6] ICAR-Indian Institute of Pulse Research, New Delhi, India
*E-mail: jagrane@hotmail.com

Mungbean (*Vigna radiata* L.) and chickpea (*Cicer arietinum* L.) are the key legumes cultivated in arid and semi-arid regions of the world. Enhanced productivity of these crops is critical for meeting protein requirements of a vast population in general, and particularly of those who depend on vegetarian diet. Since these crops are largely grown in soil moisture deficit environments, productive use of water (PUW) by these plants is crucial for high and stable yield. The goal of this study was to optimize image-based high throughput methods for screening germplasm, particularly for PUW. We employed image-based screening tools such as thermal imaging system, near infrared imaging, chlorophyll fluorescence imaging and visible-range imaging to capture responses of plants to imposed water stress treatment in both controlled conditions and in field. Methods developed could differentiate the genotypes varying in their capacity to use soil moisture productively. Methods for assessing PUW were based on the assumption that the genotypes that can produce more biomass with less water relative to locally adapted check can serve as better source of drought tolerance. Parameters derived from the image captured by different imaging systems could sufficiently explain the genetic variability in PUW, suggesting that these parameters can serve as potential surrogate traits for screening mungbean and chickpea genotypes for their suitability to drought-prone areas. Images in the visible range could explain genetic variation in leaf senescence pattern while those from NIR imaging system could explain variation in water content of leaf tissues. Chlorophyll fluorescence imaging could explain variation in Photosystem-II efficiency of pods. While the developed methods will be useful for assessing genetic diversity in plant responses to drought stress, their high throughput features can facilitate efforts to establish association between traits and genes with greater precision relative to conventional methods.

IDT7-097 | Breeding for drought resilience in rice: mapping QTLs for yield under drought in TPE using local landraces, development and testing of QTL lines for drought physiology, root growth and transcriptome

Ranganathan Chandrababu[1]*, Ashish Rajurkar, B[1]., Raveendran, M[1], Amelia Henry[2]

[1]Tamil Nadu Agricultural University, Coimbatore, India-641003
[2]International Rice Research Institute, Philippines
*E-mail: chandrarc2000@yahoo.com

Drought is a serious limitation to rainfed rice production. Discovery and deployment of QTLs for drought resistance can accelerate breeding of resilient rice cultivars. We have mapped consistent large effect meta-QTLs for grain yield under drought in target populations of environment (TPE) using local landraces viz., *Norungan* and *Nootripathu*. These QTLs are fine-mapped and deployed in genomics-assisted breeding for drought resistance improvement of mega rice varieties. Genome-wide association mapping of diverse lines identified consistent and additional genomic regions for yield and root growth under drought in TPE. QTLs for deep and thick roots as well as yield under drought from CT9993, an upland drought-tolerant *japonica* ecotype with deep and thick roots were introgressed into IR20, a lowland drought sensitive indica with shallow and thin roots through MAB and rice lines consistently yielding high under drought were identified through repeated evaluation under field conditions in TPE. The rice lines were phenotyped for root growth under water stress using PVC cylinders under a controlled environment condition. Effect of the QTL on root transcriptome under water stress was also studied. These rice lines were further characterized for drought physiology by phenotyping under drought stress during reproductive growth stage in upland field conditions in IRRI, Philippines, during the 2016 dry season and physiological indices such as canopy temperature, NDVI, biomass, yield and root growth were determined. Results on mapping meta-QTLs for yield under drought using landraces, development and testing of root QTL lines for drought physiology, root growth and transcriptome under stress will be presented.

IDT7-098 | Phenotyping dryland sorghum (*Sorghum bicolor* (L.) Moench) for drought tolerance across semiarid tropical climates- an overview of research progress

Rao SS[1]*, Tonapi VA[1], Nirmal SV [2], Asvathama VH[3], Prabhakar[5],[8], Kalpande HV[4], Talwar HS[1] , Ghorade RB[6], Prasad PVV[7], Mishra JS[9]

[1]ICAR-Indian Institute of Millets Research, Rajendranagar PO, Hyderabad 500030 (TS), India
[2]Sorghum Improvement Project, Mahatma Phule Agric. University, Rahuri, India
[3]AICRP Sorghum, University of Agric. Sciences, Bijapur, India
[4]AICRP Sorghum, Marathwada Agric. University, Parbhani, India
[5]Centre on Rabi Sorghum (IIMR), Solapur, India
[6]AICRP Sorghum, Dr Punjabrao Deshmukh Agric. University, Akola, India
[7]Agronomy Dep., Kansas State University, Manhattan, Kansas, 66506, USA
[8] ICAR-PC Unit, AICRP on Small Millets, Bengaluru, India
[9] ICAR-Research Complex for Eastern Region, Patna, Bihar, India
*E-mail: ssrao@millets.res.in

Sorghum (*Sorghum bicolor* (L.) Moench) is a major dryland crop grown for food, feed, and bioenergy around the world. The objectives of this research were to characterize and identify putative drought traits determining grain and stover productivity, besides isolating potential germplasm for mid-and terminal drought. Research done over the past 25 years is presented. Inbred PVK809 produced 19.0% more biomass. Specific leaf area (SLA) has shown significant negative correlations ($p<0.01$) with specific leaf nitrogen (SLN) and specific leaf weight (SLW). During 30-day mid-season drought, cv.Indore12, CSH16, 27B, and PVK809 did not show leaf wilting (RWC: 71- 88%). Post-rainy sorghum hybrids recorded 16.0% more photosynthesis rate (Pn) than inbreds, while transpiration efficiency (TE) was greater (19.0%) in inbreds. Landrace RSLG 262 recorded 4.0% and 20.7 % higher Pn than checks M35-1 and Sel.3, res., while it also produced 11.0 and 36.0% higher grain yields in medium and 17.0 and 35.0% in shallow soil in 20 multi-environment tests. RSLG262 was released as *Phule Maulee* for shallow to medium soils and possessed desirable drought tolerant traits. Δ13C ranged from 4.351 to 6.05%. Cv. E36-1, CRS4 recorded lower Δ13C (4.86 & 4.92%). Landraces recorded 19-12% more root length than staygreen. Thirty landrace sorghums identified and utilized in breeding include IS2312, IS4757, IS2835, Lakadi, Sel.3, IS3962, IS4576, BRJ119, CR4, CR6, etc. Putative traits proposed for improving drought tolerance include early maturity (7-d earlier to M35-1), staygreen, greater Pn and TE rates, higher SPAD, and SLN. The implication of these results is discussed for enhancing sorghum drought tolerance.

IDT7-099 | Agronomic and physiological performance of TeqingxLemont introgression rice (*Oryza sativa* L.) lines under limited irrigation system

Rohila JS[1]*, Edwards JE[1], Zhao, H[1], McClung AM[1]

[1]Dale Bumpers National Rice Research Center, Stuttgart, AR 72160 USA
*E-mail: jai.rohila@ars.usda.gov

Rice is a staple food for almost half of the world. Most rice in the world, including USA, is produced under a flooded paddy system that makes rice one of the most irrigated grain crops on earth. With many water resources being depleted due to high irrigation demands, it has become essential to develop rice varieties and management systems that can produce high yields and grain quality with less water. Production of rice under alternate-wetting-and-drying (AWD) system is one such choice. Research was initiated using a set of 117 introgression lines (TILs) derived from the varieties Teqing and Lemont to identify genomic and trait (agronomic and physiological) relationships that are important for rice production using AWD. The TILs were previously genotyped using 178 Simple Sequence Repeat (SSR) markers resulting in one marker every 0.5cM, on average. Following a two-year field trial evaluating the TILs under flood and AWD management, 14 high-yielding TILs were selected for a greenhouse study using flood and AWD. Statistical analyses of growth and yield components indicated significant differences for several agronomic traits among individual TILs. Interestingly, when compared between the flooded and AWD systems, several TILs had increased photosynthesis, tiller number, and biomass, but none had greater yield than Lemont. This suggests the complexity of physiological responses to water stress and the need for further recombination of selected TILs to produce high yield under AWD.

IDT7-100 | Genetic molecular dissection of drought tolerance in winter wheat (*Triticum aestivum* L.) using QTL mapping

Ahmed Sallam[1], Vikas Belamkar[2], Wassem Hussain[2], P. Stephen Baenziger[2]

[1] Department of Genetics, Faculty of Agriculture, Assiut University, 71526-Assiut, Egypt
[2] Department of Agronomy & Horticulture, University of Nebraska-Lincoln, USA.
*E-mail: amsallam@aun.edu.eg

The genetic architecture of drought tolerance is complex and needs to be understood. To address this challenge, a population of 145 recombinant inbred lines (F9) derived from crossing between Harry (drought tolerant) and Wesley (drought susceptible) was used to study the genetic variation in drought tolerance, identify the best tolerant genotypes for drought tolerance, and identify genomic regions associated with drought tolerance in wheat. At seedling stage, all genotypes were sown in three replications with a randomized complete block design under controlled conditions. Seven traits were scored and grouped into two divisions; tolerance traits (days to wilting, wilting score, and stay green) and surviving traits days to regrowth, regrowth, drought survival rate, and recovery after drought). Three selection indices were calculated: i) tolerance index, ii) survival index, and iii) drought tolerance index (DTI). In addition, the same set of lines was evaluated in two well-watered and two dry locations for 2014/2015 and 2015/2016 seasons. A high genetic variation was found between all genotypes for all traits scored in this study. No or weak significant correlations were found between tolerance and surviving traits. The heritability estimates ranged from 0.53 (SG) to 0.88 (DTR). DTI showed high significant phenotypic and genotypic correlation with all traits scored in this study. The QTL analysis revealed 14 QTL associated with drought tolerance. Two QTLs showed a pleotropic effect. We concluded that the tolerance and surviving traits are controlled by different genes. Only one genotype showed a combination of high drought tolerance and yield under drought.

IDT7-101 | Development of rice (*Oryza sativa* L.) varieties and hybrids for aerobic conditions

Thippeswamy Sanka[1]*, Chandramohan Y[2], Srinivas B[1], Padmaja D[3]

[1] Rice Research Scheme, Regional Agricultural Research Station (RARS), PJTSAU, Polasa - 505 529, Jagtial, Telangana, India
[2] AICRP on Rice, Agricultural Research Institute, PJTSAU, Rajendranagar, Hyderabad, India
[3] AICRP on sesamum, Regional Agricultural Research Station (RARS), PJTSAU, Polasa - 505 529, Jagtial, Telangana, India
*E-mail: thippeswamys@gmail.com

Rice (*Oryza sativa* L.) is the staple food for half of the world's population and plays an important role in ensuring food security. Aerobic rice is a projected sustainable rice production methodology, requires 60% less water and emitting 80%-85% less methane gas into the atmosphere. The goal of this study was to identify rice varieties and hybrids for aerobic rice cultivation. A total of 24 varieties along with four checks were evaluated under aerobic conditions during *kharif* 2013. Genetic analysis showed significant variability for days to flowering, plant height, number of grains per panicle and grain yield, but not for effective bearing tillers, panicle length and test weight. Influence of environment on expression of all seven characters was evident by higher values of PCV than GCV. High heritability estimates were observed for days to flowering (0.96), test weight (0.93) and plant height (0.81); whereas low heritability coupled with low genetic advance as percent of mean (0.62; 16.1) was exhibited by number of effective bearing tillers. Results revealed significant positive association of plant height (0.33) and panicle length (0.25) with grain yield, indicating grain yield and these traits have the same physiological basis for expression. Path coefficient analysis also emphasized the importance of plant height and panicle length as they showed the highest positive direct effect (0.321. 0.156) on grain yield. Three varieties and one check (JGL21005 (7.6 t/ha), JGL21133 (7.5 t/ha), JGL20171 (7.3 t/ha), MTU1010 (7.01t/ha) yielded more than 7.0 t/ha among the test entries. Among these, JGL20171 showed consistence performance in the last two years. Further, newly developed rice hybrids and promising rice varieties are being evaluated during *kharif*, 2016. These aerobic rice varieties and hybrids will help to address water scarcity and environmental safety in the scenario of global warming.

IDT7-102 | Genomic regions associated with drought tolerance in maize in Asian tropics

Seetharam K[1],*, Zaidi PH[1], Vinayan MT[1], Hindu V[1], R.B. Dubey[2]

[1] International Maize and Wheat Improvement Centre, Hyderabad, Telangana, India.
[2] Maharana Pratap University of Agriculture and technology, Udaipur, Rajasthan, India.
*E-mail: k.seetharam@cgiar.org

In Asian Tropics, drought is the major factor responsible for year-to-year fluctuation in maize production, as about 80% of maize is grown in rainfed conditions. While drought adversely affects all stages of maize crop growth and development, reproductive stage is the most sensitive to drought stress. to The present study was formulated to identify superior alleles through genome-wide association studies (GWAS), and use in forward breeding through marker-assisted introgression of desirable genomic regions in elite genetic background. An association mapping panel was constituted by involving about 400 Asia-adapted maize inbred lines and the panel was test-crossed with CIMMYT tester line (CML-474) and evaluated under managed drought stress at Hyderabad, Banswara and Udaipur locations in India. Performance of test-crosses across-locations showed significant genotype x environment term under drought stress. A total of 955, 690 SNPs were generated through GBS v2.7 using Illumina Hi-seq 2000/2500 at Institute for Genomic Diversity, Cornell University, Ithaca, NY, USA. Based on criteria of call rate (CR) >0.7 and with minor allele frequency (MAF) > 0.03, we obtained 331, 390 SNPs from the total SNPs for association analysis using GLM and MLM model. 177 SNPs in Hyderabad, 84 SNPs in Udaipur and 31 SNPs in Banswara were found to be significantly (6.64x10-4 to 1.68x10-11) associated with grain yield under drought and the phenotypic variance explained by these SNPs ranged from 4.6 to 16.4%. S1_192491083, S2_215915475, S3_180598606 and S10_124525334 were found common between Hyderabad and Udaipur, whereas SNPs: S10_2657853 and S10_2657869 were found common between Udaipur and Banswara locations. Among the total significant SNPs associated 84 SNPs in Hyderabad, 22 in Udaipur and 17 in Banswara location were in the gene models. The SNPs identified for yield, related to drought tolerance mechanism, might help in selecting trait-specific donor lines or lines with favorable allele.

IDT7-103 | Improving drought resilience of a mega rice variety by pyramiding QTLs for root traits and yield under drought

Reena S[1], Suresh R[2], Ashish R[1], Bharathi A[1], Helan B. T[1], Babu R[1]*

[1]Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, India
[2]Tamil Nadu Rice Research Institute, Tamil Nadu Agricultural University, Aduthurai, India
*E-mail: chandrarc2000@yahoo.com

Drought stress is the most serious constraint in rice production in Tamil Nadu, the most water- starved state in India. Developing resilient rice varieties is critical for food and livelihood security for millions of farm families dependent on rice cultivation. Deep root growth is considered to positively impact rice production under drought. QTLs for deep and thick roots have been mapped, and QTL for yield under drought is also located in this genomic region. Marker-assisted pyramiding of the QTLs from a *japonica* cultivar, CT9993, into a popular mega rice variety, ADT43, has been taken up. CT9993 was crossed with ADT43 and true F1s were identified using polymorphic markers. These true F1 were backcrossed with ADT43 and the BC1F1s were genotyped to identify the desired QTL region using foreground markers. The selected BC1F1s were further backcrossed with the recurrent parent and the foreground selection was done in the resulting BC2F1s. Further backcrossing and foreground selection of lines with desired QTLs is being done. The lines with the candidate QTLs will be tested for drought resistance under rainfed condition in TPE. Progress made in this study will be discussed.

IDT7-104 | Identification of drought tolerance traits for addressing yield protection in western Canadian conditions

Paula Ashe[1], Hamid Shaterian[1], Leonid Akhov[1], Manoj Kulkarni[1], Gurudatt Sudarshan[1],[2], Yong He[3],[4], Ron Knox[3], Hong Wang[3], Richard Cuthbert[3], Ron DePauw[3], Asheesh Singh[3], [5], Gopalan Selvaraj[1]*

[1]National Research Council of Canada, 110 Gymnasium Place, Saskatoon SK S7N 0W9;
[2]Semi-Arid Prairie Agricultural Research Centre (SPARC), Agriculture and Agri-Food Canada (AAFC), Swift Current, SK, Canada, S9H 3X2
[2]Bayer CropScience, Morrisville NC;
[4]Chinese Academy of Agricultural Sciences, Beijing, China;
[5]Iowa State University, Ames, IA, USA.
*E-mail: gopalan.selvaraj@nrc-cnrc.gc.ca

Western Canadian conditions for growing wheat present challenges relating to water stress. These challenges, while uncertain, generally affect development during anthesis and grain filling and therefore have a significant negative impact on wheat yield. The development of wheat cultivars with better water stress tolerance is important for sustainable wheat productivity. Water stress is complicated, affecting physiological processes, growth and development. Understanding drought adaptation traits under controlled as well as targeted field environments will help to build durable drought tolerant cultivars for western Canadian conditions. Comparative analysis of the durum wheat cultivars Pelissier (drought tolerant) and Strongfield (drought sensitive) under growth chamber (using tubes) and under field conditions suggested a number of contrasting traits relating to drought tolerance as well as agronomy. Pelissier demonstrated better drought adaptation as compared to Strongfield, supported by a conducive root development that was evident in un-stressed and water stress conditions. Using a mapping population developed from these two contrasting wheat cultivars, we are addressing the physiology, genetics and expression aspects of selected traits. A genetic linkage map was developed and QTLs for photosynthesis, height, lodging and spike length were identified. Further efforts are being made to characterize the genomic regions associated with larger root biomass.

IDT7-105 | Pyramiding of drought tolerance QTLs and P-deficiency tolerance genes in rice.

Sen P[1], Sen S[1], Rai P[1], Vangaru S[1], Ganguly S[1], Ganguly J[1], Roy A[1], Saha S[1], Sarkar S[1], Bhattacharyya P[1], Bhattacharyya S[1]*

[1]Bidhan Chadra Krishi Viswavidyalaya, Mohanpur, PIN 741252, West Bengal, India.
*E-mail: somnathbhat@yahoo.com

The main objective of this work is to develop rice genotypes which will produce higher grain yield than those of existing cultivars in ambient situations, and also show minimum yield loss during water scarcity. As most drought-prone areas are deficient in phosphate, attempts are made to pyramid P-deficiency tolerant genes with two QTLs for reproductive drought tolerance. N22 and *Vandana* are used as the source of drought tolerance QTLs and a few advance lines of a cross between *Gobindabhog* and *Satabdi* are used for the source of three superior alleles of P-deficiency tolerance genes and grain quality parameters. Allele-specific markers were selected and validated in a RIL population. Segregating population between drought-tolerant and P-deficiency tolerant lines were raised and screened by allele-specific markers. Based on genotyping, four segregating plants carrying desirable alleles for all loci were selected. Progenies of selected plants were harvested and evaluated under rainout shelter as well as on P deficiency soil. Lines with heterozygote alleles were again genotypes for further selection. GS3 based markers were also employed for selection of long grain homozygous lines at the early generation. Their yield-attributing parameters along with some physiological parameters such as stomatal conductance, and net photosynthesis rate leaf area were compared for further follow-up.

IDT7-106 | Breeding for water-limited environments

Shah AA[1], Mir RR[1,2]

[1] Sher-e-kashmir University of Agricultural Sciences and Technology (SKUAST-J), Jammu , India
*E-mail: ashu.ashraf@gmail.com

Humanity is heading towards the major challenge of having to increase food production by about 50% by 2050 to cater to an additional three billion inhabitants, in a context of shrinking arable land, land degradation, nutrient deficiencies, increased water scarcity, and uncertainty due to the predicted climatic changes. Water limitation and drought are one of the most serious production constraints for world agriculture, and are projected to worsen due to climate change. Inter-disciplinary scientists have been trying to understand and dissect the mechanisms of plant tolerance to water/drought stress, using a variety of approaches. However, success has been limited. Breeding methods for water-limited environments are the same as for yield and other economic characters. Considerable research progress has been achieved on this front through QTL or gene discovery through linkage and association mapping, QTL cloning, candidate gene identification, transcriptomic and functional genomics. Molecular breeding approaches such as marker-assisted backcrossing, marker-assisted recurrent selection and genome-wide selection have been suggested to be integrated in crop improvement strategies to develop drought-tolerant cultivars that will enhance food security in the context of a changing and more variable climate. Increasingly huge data sets are being derived from genome-wide studies at the transcriptomic, proteomic, and metabolomic levels, but how to efficiently explore these data sets to extract the essential functional pathways or networks for genetic improvement of water limitation/drought resistance remains a significant challenge.

IDT7-107 | Selection for improved maize (*Zea mays* L.) variety performance under drought stress conditions in South Africa

Shandu SF[1], Mashingaidze K[1], Derera J[2]

[1]ARC-Grain Crops Institute, Potchefstroom, South Africa
[2]University of KwaZulu-Natal, Pietermaritzburg, South Africa
*E-mail: ShanduS@arc.agric.za

South Africa is among the largest maize (*Zea mays* L.) producing countries in the world. However, due to frequent occurrence of drought, maize production is currently limited. To mitigate the effect, developing drought-tolerant maize varieties is fundamental to improved productivity and food security. The aim of the study was to develop stable, drought-tolerant varieties. Three hundred and eighty maize hybrids developed from conventional breeding approaches were evaluated for drought tolerance in four environments in South Africa during 2015/16 summer season. Performance was measured based on grain yield. Phenotyping for drought tolerance was achieved by growing maize hybrids under managed drought, random drought stress in drought-prone areas, as well as under optimum moisture conditions. The yields ranged from 3.26-10.29 t ha-1 under optimum, 1.48- 6.68 t ha-1 under managed drought, and 2.16- 9.1 t ha-1 under random drought. The 10 best performing genotypes were selected and evaluated for genotype x environment interaction using genotype main effects and genotype x environment interaction (GGE) analyses. The GGE biplots were constructed using GEA-R package. Two genotypes were high-yielding but were unstable; this suggested that these varieties may have specific adaptation to some regions. Three genotypes were most stable and were among the highest yielding under drought environments. The identified stable, drought-tolerant hybrids should be eventually advanced for release and deployment to South African farmers. These observations suggested that there would be an increase in maize production under drought stress.

IDT7-108 | Development of HP-RILs in rice (*Oryza sativa* L.) through MAS suitable for aerobic cultivation

Shashidhara. N[1]*, Hanamareddy Biradar[1], Shailaja Hittalmani[1]

[1]Marker Assisted Selection Laboratory, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bangalore-560065,
*E-mail: shashidhara.gpb@gmail.com

Total grain protein (TGP) content is the most important parameter in rice quality production. TGP is a complex trait controlled by several genes and it is also tightly linked with grain yield. Therefore, segregating generations is a good breeding material to understand the genetics of inheritance pattern of several traits as well as to break the tight linkage if it is required. Recombinant inbred lines (RILs), being the derivatives of two genetically diverse parents, serve as good source of genetic diversity as well as permanent mapping population to study the complex quantitative trait controlling protein content in rice. The wide range of TGP content in selected 100 F2 lines was recorded with a range of 5.25% to 22.83%, with an average of 12.01% and moderate PCV (19.57%) and GCV (15.63%) with high heritability of 63.79%, coupled with high GAPM of 25.72%. However, in F6 generation, it ranges from 8.44% to 12.55% with an average of 10.39%, and the lowest of PCV (6.57%) and GCV (6.24%) with high heritability (49.13%) coupled with moderate GAPM of 10.83%. Similar decreasing trend was also observed for micronutrients (iron, zinc, copper and manganese), grain quality parameters (grain length, grain breadth, grain L:B ratio, kernel length, kernel breadth and kernel L:B ratio); as well as for yield and yield attributing parameters in successive generations of RIL (F2 to F6) development.

IDT7-109 | Population structure and genome-wide marker-trait association of key agronomic traits in wheat under drought-stressed and non-stressed conditions

Mwadzingeni L.[1], Shimelis H.[1]*, Tsilo T.J.[2]

[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa
[2]Agricultural Research Council-Small Grain Institute (ARC-SGI), Bethlehem, South Africa
*E-mail: Shimelish@ukzn.ac.za

Genome-wide association study (GWAS) facilitates understanding of the genetic bases and dissection of complex genes controlling economic traits such as drought tolerance.The objective of this study was to determine the population structure and genome-wide marker-trait association of key agronomic traits of wheat for drought-tolerance breeding. A population of 93 diverse bread wheat genotypes was genotyped using the Diversity Arrays Technology sequencing (DArTseq) protocol. Also, the following agronomic traits assessed under drought-stressed and non-stressed conditions were considered for the study: the number of days-to-heading (DTH), number of days-to-maturity (DTM), plant height (PHT), spike length (SPL), number of kernels per spike (KPS), thousand kernel weight (TKW) and grain yield (GYLD). Population structure analysis and genome-wide association mapping were undertaken based on 16,383 silicoDArTs loci with < 10% missing data. The population evaluated was grouped into nine distinct genetic structures. Inter-chromosomal linkage disequilibrium showed the existence of linkage decay as physical distance increased. A total of 62 significant ($P< 0.001$) marker-trait associations (MTAs) were detected explaining more than 20% of the phenotypic variation observed under both drought-stressed and non-stressed conditions. Significant ($P< 0.001$) MTA event(s) were observed for DTH, PHT, SPL, SPS, and KPS; under both stressed and non-stressed conditions; while additional significant ($P< 0.05$) associations were observed for TKW, DTM and GYLD under non-stressed condition. These MTAs were identified on chromosomes that have previously been associated with the respective traits.The markers identified in this study are useful genomic resources to initiate marker-assisted selection and trait introgression of wheat for drought tolerance breeding and for fine mapping and cloning of the underlying genes and QTL. Further studies are required to validate the significant markers identified in the present study.

IDT7-110 | Genetic analysis of yield and other important traits in wheat under moisture stress conditions

Singh, Jang Bahadur[1]*, Chauhan Anil[1], Patidar Indar[1], Ambati Divya[1], Prakasha TL[1], Prasad SV Sai[1]

ICAR – Indian Agriculture Research Institute-Regional Station, Indore (MP) INDIA
*E-mail: jangbsingh@gmail.com

Bread wheat (*Triticum aestivum* L. em Thell) is agronomically and nutritionally the most important cereal essential for food security. Hostile environmental conditions such as drought, high saline levels, extreme temperatures, soils poor in nutrients, and others pose serious problems, especially in the most disadvantaged areas in the world, as well as in India. Keeping in view the reducing water availability due to erratic rains, breeding for water use efficient genotypes will not only help in spreading wheat cultivation to traditional drought areas but also optimize wheat yield in traditional cultivation conditions in central India under restricted irrigation conditions. Therefore, breeding for water use efficiency in wheat cultivars requires understanding of the physiological responses of wheat crop to water stress, which may help in identifying traits to be used as selection criteria. These identified traits will give direction to water use efficiency breeding programs in wheat. The present investigation was undertaken to study different aspects of wheat genotypes under limited water conditions, understand the responses of wheat genotypes to moisture stress, and find out the genetic behavior of important traits and yield-contributing traits. Bread wheat genotypes (57) were evaluated in moisture stress conditions (one irrigation was given after sowing *i.e.* come up irrigation and the second irrigation was supplied after 35 days of sowing) at the experimental farm of the Indian Agriculture Research Institute-Regional Station, Indore during the *rabi* 2014-15.

Varietal differences are highly significant for all 15 characters studied, except for the starch trait which was found to be non-significant. Genotypic co-efficient of the variation for most of the characters *i.e.* days to flowering, days to anthesis, days to maturity, hectoliter weight, plant height, spike length and grain yield were almost equal to the phenotypic co-efficient of variation. This suggests that the major portion of the phenotypic coefficient of variation of these characters is due to genetic causes. Results of heritability and genetic advance as percent of the mean showed that grain yield, days to flowering, days to anthesis, spike length and protein content had high heritability coupled with high genetic advance as percent of mean, suggesting that genotypic variation for these characters may be possibly due to high additive genetic variance. Character association analysis revealed that biological yield, harvest index, number of grains per spike, and starch should be given utmost consideration during breeding for moisture stress condition in order to minimize losses in grain yields. Selection for shorter height and delayed maturity could also be effective for the above purpose. It was concluded that selection of genotypes for better performance under moisture stress conditions should be based on characters having direct effects on grain yield, such as harvest index, biological yield and grains per spike. Selection could also be done for characters such as 1000 grain weight and grains per spike *via* their indirect effects. Characters such as effective tillers and phenological traits such as grains per spike, 1000 grain weight and biological yield have scope for selection for better yield under moisture stress conditions.

IDT7-111 | Elasticity of drought tolerance among Indian peanut cultivars during rainy season

Singh A.L[1]*., Zala P.V[1]., Kalariya K.A[1]., Chakraborty K[1]., Patel C.B[1]., V Chaudhari[1]

ICAR-Directorate of Groundnut Research, PB 5, Junagadh-362 001, India
*E-mail: alsingh16@gmail.com

Peanut is grown mostly under rain fed conditions in India. By now, India has about 200 cultivars of peanuts, but hardly 40 are under cultivation and most of these have not been tested for drought. Ninety six peanut cultivars were evaluated for their elasticity for drought tolerance under various conditions in two experiments, each conducted for two consecutive years during *Kharif* season, and the promising ones were identified. First, 60 cultivars were grown under protective irrigation (P) and rain-fed (RF) conditions and compared for physiological and yield attributes. In the second experiment, 36 cultivars were grown under P, RF as well as mid-season drought (MSD, 40-70 DAS), and late season drought (LSD, 70-90 DAS). The RF crops faced sufficient drought and hence three to four irrigations were provided in the P crop. The study reveals several interesting results. LSD was the most detrimental. Though varietal differences were noticed, drought delayed flowering and maturity, causing reduction in flowers, pods and yield, but the SCMR increased. The cultivars with early flowering, high SCMR, high yield, high HI, and early maturity escaped LSD and were highly suitable for RF conditions. Among various botanical groups, Spanish bunch was more suitable with desirable traits compared to Virginia bunch and runner, and Valencia. The cultivars Kadiri 7, GG 20, GG 16, HNG 123, RG 510, RG 578, ICGS 5, JGN 23, AK 265, AK 159 were more suited to RFH however under MSD, Pratap 1, GJG 9, JL 501 RG 425, RG 510, RG 578 and HNG 123 were promising.

IDT7-112 | Wheat pre breeding for drought prone environments

Sukhwinder Singh[1]*, Prashant Vikram[1], Carolina Paola Sansaloni[1], Kevin Pixley[1]

[1]International Maize and Wheat Improvement Center, México
* E-mail: suk.singh@cgiar.org

Landraces, wild relatives and other traditional cultivars represent an important reservoir for improvement of wheat varieties targeting rain-fed ecosystems of the world. However, considering the challenges in handling GeneBank resources for practical purposes, a systematic and strategic approach is required. CIMMYT's Seeds of discovery project has initiated efforts towards large-scale characterization of wheat GeneBank (WGB) accessions. Till date 40% of the CIMMYT's WGB has been genotyping-by-sequencing. Phenotypically, approximately 100K WGB accessions have been characterized for one or the other traits. These efforts were followed by systematic and strategic mobilization of WGB to the breeding pipelines. So far, over 1000 exotics have been mobilized to the breeding pipelines after a thorough evaluation of the segregating pre-breeding populations under drought stress. In the first year evaluation trial, better performing pre-breeding lines have been identified under drought stress. In addition, minor haplotypes were found on chromosome 4A using GWAS analysis of the pre-breeding population (1000 lines) which were contributed by exotics. Pre-breeding germplasm is shared with partners in South Asia, Africa and Americas for thorough evaluation, thereby, ensuring strategic support to drought breeding through deploying GeneBank resources. Better performing lines have also been identified based on multi-location evaluation. The ongoing CIMMYT's wheat pre-breeding efforts need to be scaled up for leveraging resource and deliver significant impact at the farmer fields.

IDT7-113 | Phenotypic diversity of trait specific mapping populations to determine QTL allelic effect in rice (*Oryza sativa* L.)

Smitharani JA[1], Sunitha NC[1], Pooja Bharti[1], Raveendran M[2], Robin S[2], Sheshshayee MS[1]*.

[1]University of Agricultural Sciences, GKVK, Bengaluru-560065, Karnataka, India
[2]Tamil Nadu Agricultural University, Chennai, India
*E-mail: msheshshayee@hotmail.com

Drought is an insidious hazard of nature and water saving practices for the cultivation should be the mission. This led to a spurt in research attempting to discover QTLs for relevant drought adaptive traits. However deployment of these QTLs in accelerating rice improvement has been appallingly low. Therefore, these markers need to be validated before using in marker-assisted breeding. This can be achieved by two strategies. One is to hybridize the QTL donor with a recipient line and evaluate the co segregation of markers and traits. The other strategy is to perform QTL mapping using biparental mapping populations. These strategies are being examined at our center. Here we report the identification of an appropriate set of biparental mapping population for QTL validation.

Parental lines used for developing trait-specific mapping populations were screened for drought adaptive traits such as roots and WUE. We selected two mapping populations where IR 64 was used as one of the parents. In one population, IR 64 represented the low root trait parent, and in the other it was a high root parent. The two recombinant inbred populations provided an excellent option to examine the effect of QTL marker allele from the parent to trait expression. We have found that the population shows more variability of low type where IR 64 was the low-root type; and shows less variability of high type where IR 64 is high-root type. This suggests the recessive nature of IR 64 and that IR 64 is an excellent recurrent parent in breeding programs.

IDT7-114 | Grain yield stability, heritability and genotype by environment interaction among double haploid maize hybrids under drought stress and optimum conditions

Julius Pyton Sserumaga[1]*, Barnabas Kiula[2], Alois Kullaya[3], Ismail Ngolinda[2],Justine Ringo[2], Sylvester O. Oikeh[4], Stephen Mugo[5], Godfrey Asea[1], Michael Otim[1], Yoseph Beyene[5], Grace Abalo[1]

[1]Cereals program, National Agricultural Research Organization; National Crops Resources Research Institute, Namulonge, P. O. Box 7084 Kampala, Uganda
[2]Ilonga Agricultural Research Institute, P.O. Box 66 Kilosa, Morogoro, Tanzania
[3]Mikocheni Agricultural Research Institute (MARI), P.O. Box 6226, Dar-Es-Salaam, Tanzania
[4]African Agricultural Technology Foundation (AATF), P.O. Box 30709-00100, Nairobi, Kenya
[5]International Maize and Wheat Improvement Center (CIMMYT), ICRAF House, UN Avenue, Gigiri, Village Market, P.O Box 1041, Nairobi 00621, Kenya
*E-mail: j.serumaga@gmail.com

Drought is the most significant environmental stress in agriculture thus enhancing productivity under drought is a major goal of plant breeding. A review of breeding progress emphasizes selection for high yield in stress-free conditions to a certain extent, indirectly improved yield in many water-limiting conditions. Thirty one Double haploid hybrids and 5 checks were evaluated in a lattice design across 13 environments in east Africa to select the most suitable hybrids for release and cultivation. The objective of this study was to identify superior and stable varieties (ii) assess genotype × environment interactions (GEI) for grain yield (GY) and other agronomic traits and (iii) define the different maize production mega-environments. Data were recorded on major agronomic traits. GGE biplot analysis was used to assess stability of varieties within various environments and across environments. In the combined analysis of variance across optimal and drought locations, mean squares for genotypes and GE were significant for most measured traits. The best hybrids CKDHH1097 and CKDHH1090 showed GY advantage over commercial varieties Under Optimal and Drought conditions respectively. Across environments genotypic variance was less than genotype x environment variance for GY. The genetic correlations among locations were high (0.990), suggesting little GEI between most environments used. Cluster analysis of genotypes across locations revealed three major groups. The DH testcross hybrids produced higher grain yield and possessed acceptable agronomic traits compared to the commercial hybrids developed earlier. Use of best DH testcross hybrids, well targeted to the production environments, could boost maize production among farmers.

IDT7-115 | Selective fertilization for inducing water stress tolerance in coconut (*Cocos nucifera* L)

Roy Stephen[1]* , Manju R.V[1]., Aisha Renju[1], Viji M.M[1], Jayaprakash Naik[1]

Kerala Agricultural University, Thiruvananthapuram, Kerala 695522, INDIA
*E-mail: roy.stephen@kau.in

Coconut is the most important plantation crop of the state of Kerala, having a major role in cultural and socio-economic development of the people. Coconut is frequently exposed to soil and atmospheric drought since 90% of the crop is grown as rainfed. Development of water stress tolerant coconut hybrids is essential since the impact of water stress sustains for two to three years in coconut. At this juncture, *in vitro* pollen selection followed by selective fertilization is an efficient and time-saving approach in this direction. Water stress was imposed during pollen germination, and the pollen grains that tolerated water stress and germinated in the stress medium were utilized for fertilization. The resultant hybrid seeds were collected at maturity and sown in containers. One-year-old seedlings were exposed to three levels of moisture stress for three months and were evaluated for water stress tolerance and water use efficiency. The selectively fertilized coconut hybrids were water stress tolerant, based on specific physiological and molecular traits. The water use efficiency estimated using gravimetric method and using carbon isotope discrimination was significantly higher compared to the normal hybrids and genotypes of coconut.

IDT7-117 | Temperature induction response technique: A physiological approach to identify thermotolerant genotypes in mungbean

Srikant[1], Rameshraddy[1], Shankar A. G.[1]*, Aftab Hussain[1], Bindumadhava H[2], Nair R. M.[2]

[1]University of Agricultural Sciences, GKVK, Bengaluru, Karnataka, India
[2]AVRDC-The World Vegetable Centre, ICRISAT, Hyderabad, India
*****E-mail: ambara8@hotmail.com

Temperature and drought are the major abiotic stresses which affect a broad spectrum of cellular components and metabolism of the crop plants, and are injurious at all the developmental stages, resulting in severe loss of productivity. The change in climate is expected to worsen abiotic factors globally, and adaptation strategies need to be established for target crops by inherent basal level tolerance as well as acquired tolerance, depending upon the response of plants to the rate of changes in temperature, its intensity and duration. Based on the acquired tolerance, initially 40 mungbean germplasm lines were screened for temperature tolerance. Temperature induction response (TIR) technique has been used for standardizing lethal (48oC for 3 h) and sublethal (28-42oC for 3 h) temperatures to identify thermotolerant genotypes. The identified thermotolerant and susceptible contrast lines were tested for their capacity to withstand water stress at seedling level (PEG8000) and whole plant level (withholding irrigation for seven days). Results revealed that those lines which are identified as themotolerant are also showing tolerance to moisture stress at seedling level, and maintain high relative water content (RWC) and low Malondialdehyde (MDA) content. This infers that TIR technique is a novel technique to understand the physiology of crop plants under stresses and can be used as a potential tool to identify and select temperature tolerant lines at seedling level, which also show tolerance to moisture stress both at seedling level and whole plant level.

IDT7-118 | Assessment of rice (*Oryza sativa* L.) for drought tolerance with SSR markers

Thakur P.[1]*, Prasad K.[2], Pande A.[2], Kumar S.[2] , Chaudhary V.P.[3], Prasad L.C.[1]

[1] Institute of Agricultural Sciences, B.H.U., Varanasi-221005, Uttar Pradesh, India
[2]Ranchi Agriculture College, B.A.U., Kanke, Ranchi-834006, Jharkhand, India
[3]International Crops Research Institute for Semi- arid Tropics, Patancheru-502324, Hyderabad, Telangana, India
*E-mail id: padma.13291@gmail.com

Drought remains a major constraint in rice (*Oryza sativa* L.) for productivity in rainfed environments, leading to huge economic loss. Molecular marker technology helps in identifying genomic regions influencing the response of yield and its components to water deficits, which will aid in our understanding the genetics of drought tolerance and development of more drought-tolerant cultivars. Investigation was carried out in rain out shelter at Birsa Agricultural University, Ranchi, Jharkhand with the aim to identify superior F3 segregants having drought-tolerant QTLs, from 100 randomly selected segregants of a cross between drought-tolerant (DT) parent *Birsa Gora* 102 and drought-susceptible (DS) parent BPT 5204. Check parents *Vandana* (DT) and IR 20 (DS) were used. Plant height, panicle length, number of tillers, number of effective tillers, grains per panicle, panicle weight, seed yield per plant and test weight were the traits under investigation. Seventeen segregants were identified as superior, with yield higher than 7.03 g/plant. The parents were analyzed with 19 SSR markers, out of which 14 markers were found to be polymorphic. These polymorphic markers were used to analyze the randomly selected segregants. None of the segregants were found to be homozygous at entire 14 loci. Seventeen identified segregants were found to have the drought tolerant QTLs. The genomic regions flanked by the polymorphic markers have been reported to be associated with several drought resistance component traits. Hence, the segregants identified in the early generation can be advanced further to develop drought tolerant cultivar.

IDT7-119 | Effect of drought stress on antioxidant enzymes activity and gene expression and physiological response in Wheat (*Triticum aestivum* L.)

Thakur V[1], Sheoran S[2], Pandey G.C[1], Sharma V[1]*

[1] Department of Bioscience and Biotechnology, Banasthali University, Rajasthan, India
[2]Indian Institute of Wheat and Barley Research, Karnal, Haryana, India.
*E-mail: vinaysharma30@yahoo.co.uk

Antioxidant enzyme activities and gene expression patterns were investigated in the leaf of wheat (*Triticum aestivum* L.) under drought stress. Two drought-tolerant genotypes (C306 and AKAW3713) and two drought-sensitive genotypes (HD2687 and PBW343) were subjected to medium (75% of field capacity) and severe stress (45% of field capacity) for 10 days at tillering and anthesis stages. The drought treatment resulted in reduction in thousand grain weight and grain yield. The genotypic variations in drought tolerance were found to have a significant effect on physiological traits. Malondialdehyde content increased while the relative water content and chlorophyll index decreased significantly in all the genotypes in severe drought stress. The transcript level of copper/zinc superoxide dismutase (Cu/Zn SOD) and Peroxidase (POX) was significantly higher at day 10 in C306, compared to well watered condition. The highest increase in transcript level of *manganese-superoxide dismutase* was observed at the 10th day of severe stress in C306 (42.8%) as compared with control condition, and significantly decreased in HD2687 at 1d and 10d. The highest decrease was found in the transcript level of Fe-SOD at day 10 in C306 (38.7 %). The enzyme activities of SOD and POX were more in drought-tolerant genotypes. CAT activity decreased in the tolerant genotypes but increased in sensitive ones at 10 day of severe stress anthesis stage. The genotype level information on drought stress responses can be useful for breeding programs to create drought resistant varieties.

IDT7-120 | Deciphering the genetics of drought tolerance through comprehensive genomic approaches in maize.

Nepolean T[1]*, Shikka M[1], Kanika A[1], Pooja B[1], Mallikarjun MG[1], HS Gupta

[1]ICAR-Indian Agricultural Research Institute, New Delhi, India-110012
*E-mail: tnepolean@gmail.com

Breeding for drought tolerance is a challenge due to low heritability of the trait. The trait also shows high degree of environmental interaction which adds an additional dimension to the complexity. In fact, drought tolerance *per se* is not a trait, but a cumulative function of different primary and secondary component traits and their interaction with each other and with the environment. The complex nature of these traits makes it difficult to understand the crucial mechanisms involved in drought tolerance. A series of whole genome experiments was employed in maize to understand the genetics of drought tolerance. Whole genome association mapping identified 61 significant SNPs that are linked to many functional traits, including flowering, root development, physiological traits such as regulation of stomata and water potential. Genome estimated breeding values from Bayesian models proved the importance of these SNPs in drought tolerance. Simultaneously, an RNA-Seq assay, using a set of contrasting maize inbreds, identified genes and *cis*-regulatory elements involved in the above-mentioned functional traits during drought stress. Post-transcriptional regulation of these genes was controlled by a group of drought-responsive microRNAs. Genes of association mapping and expression assay were co-mapped with QTLs identified from bi-parental crosses. The results generated from multiple genomic approaches identified target genes controlling key functional traits involved in tolerance. These genes are deployed in genomic-assisted breeding program to improve the tolerance of maize hybrids.

IDT7-121 | Selection of donor cultivars for breeding drought resistant rice (*Oryza sativa* L.)

Torres R[1], Henry A[1]*, Kumar A[1], Vera Cruz C[1], Sta. Cruz MT[1]

[1]The International Rice Research Institute, Los Baños, Laguna, Philippines 4031
* E-mail: A.Henry@irri.org

Traditional rice cultivars must have had particular adaptations to the local environment conditions to be continuously used by farmers. Therefore, they are potential sources of traits such as tolerance to drought and disease, which can be incorporated to modern high-yielding varieties. Experiments were conducted in three consecutive dry seasons from 2014 to 2016 at IRRI with a different set of 100 cultivars each season to screen potential lines for use in crossing. The cultivars were selected under drought stress at either seedling or reproductive stage in lowland and upland environments based on grain yield, crop uniformity, biomass, and seed appearance. Cultivar entries were tested with bacterial strains that cause bacterial leaf blight (BBL) and blast.
Selected from the lowland were Mudgo, MTU1010, Micochu, Hegra, Dumai, Dular, Dhan, Dhala Shaita, DGI-81 and Aus 196 under drought stress during seedling stage, and Camponi Sml, Da 28, Mahadethe, Makalioka 34, Micochu and Dumai with drought stress at the reproductive stage. In the uplands, Gopal, Soloi, Tchampa, and Wanni Dahanala were selected under drought treatment either at seedling stage or reproductive stage. The most resistant were Uquihua, Aus 257, Epeal 102, Icta Pazos, PSBRC 18, DZ 78, E Kha Keha, PTB 1, Benong 130A, Kaukhmwe and NP 125 against blast, Glenteng, Wanni Dahanala, Boder, MTU1010, IR64 against BBL, and Dular against both blast and BBL. Donor cultivars have been identified for breeding rice resistant to drought at seedling and reproductive stages in upland and lowland environments together with their reaction to diseases.

IDT7-122 | Expression analysis of genes associated with drought tolerance vis a vis impact of GA3 in sugarcane (*Saccharum* spp. hybrids)

Tripathi P[1, 2], Chandra A[1]*, Jain R[1], Pathak A D[1], Prakash J[2]

[1] Division of Plant Physiology and Biochemistry, ICAR- Indian Institute of Sugarcane Research, Lucknow-226002, India
[2] Amity Institute Of Biotechnology, Amity University Lucknow-226028, India
*E-mail: amaresh_chandra@rediffmail.com

Drought is one of the serious environmental factors limiting the production of sugarcane in recent times worldwide. No fixed patterns of changes in gene expression have been reported, indicating operation of a complex mechanism rendering drought tolerance. In view of this, a set of prominent genes including transcription factors associated with drought tolerance have been utilized in the present investigation to visualize their spatial and temporal expressions. A set of sugarcane varieties was subjected to progressive water deficit by withholding water. Parameters such as RWC, SLA, proline and MDA contents, SOD, POD, and P5CS enzyme activities along with expression patterns of 36 genes were recorded. To understand the impact of growth hormone on drought, GA3 was sprayed on drought initiated plants. Results demonstrated a significant reduction in RWC and chlorophyll content; and increased accumulation of osmoprotectants such as proline in stressed plants. The activities of SOD and CAT increased substantially in CoLk94184 and CoPK05191 varieties *vis a vis* quantitative expression of three SOD isoforms. Favorable changing patterns of these attributes caused by GA3 on drought-stressed plants suggest that it might mitigate the adverse effects of drought. Differential expression of some genes observed under drought, and especially expression of OAT that is involved in proline biosynthesis was found to be higher in drought-tolerant variety compared to drought-susceptible variety. Also, OAT expression increases with days of water stress. As expected, expression of TF1 was higher in drought-tolerant varieties (CoLk94184 and CoPK05191) over drought susceptible (CoLk8001). These shall be discussed in detail.

IDT7-123 | Growth and transpiration rates as potential proxy traits to track yield QTL in wheat under drought

Tura H*[1], Garcia M[1], Shahinnia F[3], Edwards J[2], Parent B[4], Kalambettu P[1], Sznajder B[1], Mather D[1], Langridge P[1], Fleury D[1]

[1] Australian Centre for Plant Functional Genomics, Adelaide, SA 5064, Australia
[2]Australian Grain Technologies (AGT),Adelaide, SA 5064, Australia
[3] Leibniz Institute of Plant Genetics and Crop Plant Researach (IPK), StalDTSeeland, Germany
[4]Laboratory of Plant Ecophysiological responses to Environmental Stresses, Montpellier, France
*E-mail: habtamu.tura@acpfg.com.au

Yield results from the cumulative effect of many traits interacting with the environment throughout the plant cycle. Targeting traits strongly associated to yield as a proxy for yield phenotyping under controlled environments could potentially help identify loci associated with yield under drought stress, and to study the mechanisms underlying drought tolerance in wheat. A QTL for plant growth and transpiration rate was detected on chromosome 1B in Drysdale/Gladius recombinant inbred lines (RIL) in the high throughput imaging platform of The Plant Accelerator (TPA) under drought and well-watered conditions. A total of 242 Drysdale/Gladius RIL recombinant in this 1B QTL region were phenotyped under well-watered and drought conditions in a semi-controlled rain-out shelter at Urrbrae, University of Adelaide, Australia, in 2014 and 2015. A QTL was detected under drought for seeds/spikelet and seeds/spike which partially overlapped with the QTL for growth and transpiration rate. Fine mapping of the QTL region using wheat genome sequencing data of the parental lines and high-density SNP maps revealed a co-location with a yield QTL under drought conditions detected previously in RAC875/Kukri double haploid population. The co-location of these different QTL indicate that the underneath gene would affect yield by controlling growth and transpiration rate. Physical mapping onto the wheat genome and the study of near-isogenic lines are being undertaken to progress in the QTL cloning.

IDT7-124 | Field evaluation of yield and yield component traits of breeding lines of maize over two seasons in a derived Savannah agro-ecology

Uba. C.U[1]*., Agbo C.U[1]., Chukwudi P.[1], Efusie A[1], Moujiama S[1].

[1]University of Nigeria, Nsukka.
*E-mail: Charlesuba192@gmail.com

Twelve maize genotypes were collected from the International Institute for Tropical Agriculture (IITA), along with seven landraces to identify contribution of different traits to yield improvement in the seasons. The experiments were carried out in two different seasons (early and late season) in a randomized complete block design with three replications. The results showed that 'TZE - Y -POR STR QPM CO' and 'TZE- Y - POP DT STR QPM' had significantly ($p < 0.05$) shorter number of days to tasselling and silking. One of the landraces, *Ugwuachara*, gave significantly higher grain yield in both seasons. Early-season planting had a higher grain yield when compared to late season, with 27.81% increase in grain yield of 3.02 tons/ha over late season. The number of ears per plant and shelling percentage were not influenced by seasonal effects. Grain yield had positive correlation with plant height, ear height, ear length, number of ears per plant, shelling percentage and ear weight in both seasons. Furthermore, ear weight had the highest correlation coefficient with grain yield in both seasons. Ear weight, followed by days to tasselling, showed the highest direct positive effect on grain yield in early season, while ear weight followed by shelling percentage exerted the highest direct positive effect on grain yield at late season. The genotypes, *'Ugwuachara'* and ''TZE- Y - POP DT STR QPM'' could be selected for late season planting because of their higher significant grain yields. Selection of genotypes with higher ear weight increased grain yield in both seasons.

IDT7-125 | Combining ability studies in drought tolerant groundnut (*Arachis hypogaea* L.) genotypes

M.Vaithiyalingan[1]*

[1]Oilseeds Research Station, Tindivanam- 604 002, Tamil Nadu, India
*E-mail: mvaithiyalingan@gmail.com

Groundnut (*Arachis hypogaea* L.) is a major oilseed and legume crop in India, accounting for 20% of oilseed area and 23% of oilseed production in the country. Combining ability analysis was carried out for 24 hybrids developed by 10 genetically diverse groundnut genotypes that were crossed in a line x tester mating fashion to obtain 24 hybrids. The lines, *viz*., JL 777, GPBD 4, PBG 6040, JL 839, R 2001-3, and Kadiri 9; and testers identified as donor for drought tolerant genotypes, *viz.,* JDR 65, JDR 66, R 2001-2 and RG 426; are involved in crossing. A total of 24 hybrids were evaluated along with their parents in a randomized block design with two replications at the Oilseeds Research Station, Tindivanam, during *rabi* 2014-15. Non-additive gene action was predominant for all the characters studied, such as on plant height, branches per plant, pods per plant, root length, SPAD chlorophyll meter reading, dry matter production, harvest index and single plant yield. Based on the mean, *gca* effects parent *viz*., JL 777, RG 426, and JDR 66 could be selected for crossing programs to obtain yield improvement. Among the crosses, R 2001-3 x R 2001-2 registered significant *sca* effects along with mean. Hence, pedigree breeding method could be adopted to isolate desirable recombinants. Crosses JL777xR 2001-2, JL777xRG 426 could be exploited for recombination breeding.

IDT7-126 | Evaluation of chilli (*Capsicum annuum var annuum* L.) genotypes for pod yield and quality under rainfed conditions of Tamil Nadu

Vanitha A* and Jansirani

Tamil Nadu Agricultural University, Coimbatore-641003, Tamil Nadu.
*E-mail: ajjanvanitha@gmail.com

An experiment was conducted during 2013-14 to study the yield and quality characteristics of 74 chilli accessions under rainfed conditions of Tamil Nadu in a randomized block design with two replications, with an objective to identify the most appropriate chilli genotype with high pod yield and quality suitable for rainfed conditions. The location under evaluation is unique to cultivating chilli under rainfed conditions that depend on monsoon rains only, wherein the productivity of chilli is 300-500 kg per hectare. Among the growth characters studied, the highest plant height was recorded in CA 31(100.98 cm) and the highest number of branches per plant was recorded in CA 14 (7.38); while the accession CA 74 recorded the highest root length (18.08 cm) and root volume (42.50 cc). The biochemical characters of 74 chilli accessions showed that CA 42 recorded the highest chlorophyll stability index (80.5%) and proline content (454.39 $\mu g\ g^{-1}$), whereas the accession CA 3 (157.4 µg/g) recorded the highest nitrate reductase activity. The accession CA 74 recorded 447.1 $\mu g\ g^{-1}$ of proline and 151.1 $\mu g\ g^{-1}$ of nitrate reductase activity. Among yield and quality characters studied, the number of pods per plant (233), fresh (1033.4 g per plant) and dry pod yield per plant (225.06 g) were found to be the highest in the accession CA74, whereas the capsaicin (0.655%) and oleoresin content (11.8%) were the highest in CA 74. From the present investigation, it may be concluded that the genotype CA 74 was observed to be the best genotype to get higher dry pod yield and quality under the specific rainfed area of southern Tamil Nadu.

IDT7-127 | Exploiting African rice germplasm to breed for drought tolerance

R.Venuprasad, M. Fofana, A. Shaibu, F. Adegbehingbe, S. Afeez

Africa Rice Center (AfricaRice), Ibadan, Nigeria
*E-mail: R.Venuprasad@cgiar.org

Rice, a major food crop of the world, is mainly cultivated in rainfed ecology in Africa. Drought is a major limitation to production, both in the rainfed upland and lowlands. Breeding for drought tolerance is an important objective of most breeding programs in the region. Efforts to introduce drought-tolerant breeding lines from Asia have not been successful so far. There is a need to exploit the available local rice germplasm for this purpose. In the past four years, at AfricaRice we have screened the O. sativa (more than 700 lines including landraces and breeding lines), O. glaberrima (~2000 accessions) and over 600 interspecific lines for drought tolerance in upland and lowland ecologies. Drought-tolerant lines have been identified in all these three groups. Three lines with exceptionally high level of tolerance are being used in breeding and genetic analysis. They showed at least 30% yield gain over tolerant checks from Asia under severe reproductive-stage drought. New breeding populations have been derived using these germplasm as donors. QTL analysis of the newly derived populations is ongoing. Results of germplasm characterization, breeding, phenotyping and QTL analysis will be presented during the meeting.

IDT7-128 | Exploration of landraces for future climate resilient wheat improvement

Prashant Vikram[1]*, Juan-Anders Burgueño[1], Carolina Paola Sansaloni[1], Guillermo Fuentes[2], Javier Ireta[2], Ernesto Solís Moya[2], Velu Govindan[1], Navtej Singh Bains[3], Achla Sharma[3], Vaibhav Kumar Singh[4], Sanjay Singh[4], Ashwani Kumar[5], Gyanendra Pratap Singh[6], Jose Crossa[1], Mohammad Reza Jalal Kamali[7], Sridhar Bhavani[8] , Sukhwinder Singh[1]

[1]International Maize and Wheat Improvement Center, México
[2]Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, INIFAP, México
[3]Punjab Agriculture University, Ludhiana, India
[4]Indian Agriculture Research institute, Pusa, new Delhi
[5]CSK Himachal Pradesh Krishi Vishwavidyalaya
[6]Indian Institute of Wheat and Barley research, Karnal, India.
[7]International Maize and Wheat Improvement Center, Tehran, Iran
[8]International Maize and Wheat Improvement Center, Nairobi, Kenya
*****E-mail: p.vikram@cgiar.org

Landraces represent an important resource of the genetic diversity stored in the wheat GeneBank (WGB). Wheat landraces available as 'on farm' and in 'GeneBank' germplasms should play a significant role in the development of next-generation wheat varieties. As part of the seeds discovery project of the International Center for Maize and Wheat Improvement (CIMMYT), over 10,000 landraces have been characterized genotypically and phenotypically. Using high density genotyping-by-sequencing data of 8416 Mexican bread wheat landraces, unique and rare alleles have been identified from drought-prone environment (Durango state of Mexico). Similarly, over 2403 Iranian landraces are being evaluated for capturing their value for heat and/or drought tolerance. Efforts are underway to characterize the well-known drought-tolerant '*Sardari*' landraces of Iran. Landraces identified through focused identification of germplasm strategy (FIGS) were also characterized thoroughly under drought stress situation at CIMMYT's experimental station. Till date, Mexican and Iranian wheat landrace core sets have been formulated using phenotypic and genotypic datasets (including drought stress evaluation data) capturing ~90% rare allelic variations of the original population. These germplasm sets have been utilized by scientists in Mexico, India, China, Iran and Kenya upon request. Potential donors for heat tolerance have been identified in the Mexican landrace core set and validation is continued. The trait and allele donors identified so far in the seed project can be successfully utilized in breeding pipelines of South Asia, Africa and Americas. The project aims for large-scale mobilization of landraces for climate-resilient wheat varietal improvement.

IDT7-129 | Genotype x environment interactions and trait donors for drought stress among Asia-adapted maize inbred lines

Vinayan, MT*,[1]; PH Zaidi[1], K. Seetharam[1], BS Vivek[1] and Dang Ngoc Ha[2]

[1] International Maize and Wheat Improvement Center, ICRISAT campus, Patancheru-502324, Hyderabad India
[2]National Maize Research Institute, Ha Noi, Vietnam
*E-mail: m.vinayan@cgiar.org

Drought stress is identified as one of the major challenges for maize in Asian tropics, where the crop is largely (~80%) is grown as rainfed crop. One of the major challenges in breeding for drought tolerance is high genotype x environment interactions, which significantly affects the selection efficiency for tolerance. In the present study an association mapping panel involving about 400 Asia-adapted advanced generation maize lines were testcrossed with two to three CIMMYT testers (CML-451, CML-286 and CML-474) and evaluated at four managed drought stress (Udaipur, Hyderabad, Rajedranagar, Nhatrang) and three well-watered environment (Udaipur, Hyderabad, Nhatrang). Across-location data analysis showed a large variation in terms of performance of test crosses with grain yields ranging from zero to 5.0 t/ha under managed drought stress. Incomplete line x tester analysis of grain yield under managed drought stress revealed significant GCA (general combining ability) and SCA (Specific combining ability) variances, implicating the importance of both additive and non-additive gene action for grain yield under drought stress. Lines such as CIL1218, ZL112675, VL1017544, CAL1485, CIL1256 and CAL1440 were found with good combining ability effects across locations under managed drought stress. Keeping in view the across-location performance these lines could be used as trait donor in drought breeding program. In addition, the study also identified promising crosses viz ZL112675/VL1055, CAL1480/VL1036, CIL1256/VL1036 with high SCA effects.

IDT7-130 | Development of high-yielding varieties for dry, direct seeded aerobic conditions utilizing marker-assisted breeding

Vipparla. AK[1], Jain. A[1], Singh. UM[1], Ramaya. J[1], Priyadarshi. R[1], Yadav. S[2], Dixit. S[1], Naik. S[1], Mallikadevi. N[1], Mamatha. P[1] and Kumar. A[1,2]*

[1]International Rice Research Institute, South Asia Hub, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad- 502324, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
*E-mail: a.kumar@irri.org

Rice consumes fresh water resources of the world, accounting for withdrawal of about 24%-30% of total fresh water and consumption of about 34%-43% of the total irrigation water. Moreover, recent trends in climate change predict high incidence of water deficit in rice-growing areas. To overcome these situations, development of dry direct seeded rice (DSR) cultivation technologies, which can support rice yield with less consumption of irrigation water and labor, is in demand with savings of 12%-35% of irrigation water as compared to flooded transplanted systems. The varieties developed under transplanted situations have shown drastic yield declines of about 8%-28.5% under DSR technologies in India. Research efforts were made to develop rice varieties tolerant for early uniform emergence ($qEUE_{3.1}$, $qEUE_{11.1}$) anaerobic germination ($qAG_{9.1}$, $qAG_{9.2}$), early vegetative vigor ($qEVV_{9.1}$), higher nutrient uptake ($qNR_{5.1}$) through higher root length density, lodging resistance ($qLDG_{3.1}$, $qLDG_{4.1}$) and grain yield ($qGYDS_{1.1}$, $qGYDS_{6.1}$, $qGYDS_{9.1}$, $qGYDS_{10.1}$) along with tolerance to drought. Parental polymorphism was done using 126 SSR primers for targeted gene/traits. Foreground selection was carried out using PCR-based molecular markers to identify the target genes at their respective generations; further, intercrossings were made to stack all the nine traits into the single recurrent parent. The results of the present study exemplify the utility of marker-assisted breeding (MAB) for targeted improvement of multiple traits in rice.

IDT7-131 | A new water-saving and drought-resistant rice variety 'Huhan61'

Feiming Wang [1], Xinqiao Yu[1],[2], Guolan Liu [1], Anning Zhang [1], Lijun Luo [1]*

[1]Shanghai Agrobiological Gene Center, Shanghai 201106,China
[2]Zhuanghang Integrated Experiment Station, Shanghai Academy of Agricultural Sciences, Shanghai 201415,China
*E-mail: lijun@sagc.org.cn

Huhan61, a new japonica conventional rice variety, had been bred by the Shanghai Agrobiological Gene Center. It had passed the investigation of Shanghai province variety examination and approval committee in 2016, and its cultivar registration number is 'Hu Shen Dao 2016005'. Huhan61 is suited for planting as single-cropping, late rice in Shanghai. The whole growth period of Huhan61 is 161.6 days, which is 0.5 days more than Xiushui134 (the control). The plant height of Huhan61 is 95.1 cm, and the ear length is 14.3 cm. Huhan61 has medium number of tillers, high percentages of ear-bearing tiller, large spikes, high seed setting rate and medium grain shape. The variety was also characterized as having moderate plant architecture, uniform growth, dark green leaf, beautiful colouring at mature period and strong lodging resistance. Through the field survey, we found that the damage by pathogens to Huhan61 was very low. The survey also showed that the Huhan61 had good resistance to stripe leaf blight, and medium resistance to rice blast. In 2016, a green planting experiment and exhibition of Huhan61 was carried out in Nanlu village Jinshan county of Shanghai province. Based on the results of this experiment, compared with Xiushui134, the consumption of irrigation water and fertilizer of Huhan61 reduced by 53.3% and 16.4% respectively, but its theoretical production increased 5.4% and its carbon emissions decreased 80%. Huhan61, as a good water-saving and drought-resistant rice variety.

IDT7-132 | Glycolipids remodeling involved in the drought-induced leaf senescence in maize

Wang SW[1,2]*, Deng XP[1,2], Yin LN[1,2],

[1]State Key Laboratory of Soil Erosion and Dryland Farming on the Loss Plateau, Institute of Soil and Water Conservation, Chinese Academy of Science and Ministry of Water Resources,
[2]Institute of Soil and Water Conservation, Northwest A&F University
* E-mail: shiwenwang@nwsuaf.edu.cn

Membranes lipids modifications may also play a role in the leaf senescence response induced by drought. However, although a number of studies have proved that drought stress can induce changes in plant membrane lipids and modulated membrane lipids could improves drought stress tolerance, little is known about the role of membranes lipids remodeling in the senescence response to drought stress of crops. Here, a comparative study was carried out using two maize cultivars differing in drought-induced leaf senescence to investigate the function of membranes lipids remodeling in the drought-induced senescence response in crops. The lipid and fatty acid compositions changes were studied during drought and subsequent re-watering. In the present study, the MGDG, DGDG content and the DGDG/MGG ratio were significantly higher in LY66, in which thylakoid membranes stay intact and leaf displayed much delayed drought-induced leaf senescence, than in LY99 under drought stress and after recovery. The expression of the transcripts of MGDG synthase (MGD, *ZmMGD1*, *ZmMGD2*, and *ZmMGD3*) and DGDG synthase (DGD, *ZmDGD1*), two enzymes involved in the biosynthesis of galactolipid, in both cultivars were up-regulated by the drought stress. And the expression level of these transcripts was much higher in LY66 than in LY99 under both control and drought stress conditions. Thus our results suggest that the higher lipids content and profoundly modified lipid composition, especially the galactolipid, are associated with the delayed leaf senescence response to drought. The regulation of galactolipid remodeling could be the basis for a novel stay-green strategy for drought adaptation.

IDT7-133 | Harnessing the hidden genetic diversity for improving multiple abiotic stress tolerances in rice *(Oryza sativa* L.)

Xu JL[1,2], Ali J[3], Gao YM[1,2] , Li ZK[1,3]

[1]Institute of Crop Sciences, Chinese Academy of Agricultural Sciences (CAAS), Beijing, China
[2]Agricultural Genomics Institute at Shenzhen, CAAS, Shenzhen, China;
[3]International Rice Research Institute, Philippines (IRRI), Philippines
*E-mail: xujlcaas@126.com

Low and unstable productivity from multiple abiotic stresses are characteristic of rice production of most rainfed areas of Asia and Africa. In 2007, we initiated backcross (BC) breeding procedure for improving yield and tolerances to multiple abiotic stresses. Using eight BC1 populations derived from a widely adaptable and high yielding recipient, and eight donors plus two rounds of phenotypic selection, we were able to develop 496 introgression lines (ILs) with significantly improved yields under drought and salt stress conditions. From these ILs, six new varieties were released for the rainfed and irrigated areas of Philippines and Pakistan, and many more are in the pipeline for future release. Genetic characterization by SSR markers reveal three interesting aspects of donor introgression in the selected BC1F2 plants and BC1F3 lines: i) introgression frequency in BC progenies was characteristic to specific crosses; ii) donor introgression at different genomic regions of the selected ILs varied considerably across the genome resulting at least partially from strong selection for target traits; iii) there was greatly reduced heterozygosity in the selected BC progenies, particularly with selection under drought and salinity. The strong phenotypic selection for abiotic stress tolerances at early segregating generations appeared to advantageously integrate one or more abiotic stress tolerances into elite backgrounds, and be able to achieve quicker homozygosity in the selected progenies. The trait specific ILs are good materials for discovery of genes/QTL underlying the target and non-target traits and for highly efficient development of Green Super Rice by designed QTL pyramiding.

IDT7-134 | Translational research to develop drought tolerant wheat cultivar

Arun Yadav[1]*, Crispin Howitt [2], Greg Rebetzke [2], Susanne von Caemmerer[1] and Barry Pogson [1]

[1]ARC Centre of Excellence in PEB, Australian National University, ACT, Australia
[2]Commonwealth Scientific and Industrial Research Organization, ACT, Australia
*E-mail: arun.yadav@anu.edu.au

SAL1, a nucleotidase/phosphatase, has been implicated as a negative regulator of drought tolerance in a model plant, *Arabidopsis thaliana* (Wilson et al., 2009). During drought and high light stress, 3′-phosphoadenosine 5′-phosphate (PAP), a substrate of SAL1 enzyme, functions as a chloroplast retrograde signal and regulates expression of many stress-responsive genes (Estavillo et al., 2011). Furthermore, endogenous and exogenous manipulation of SAL1-PAP can modulate abscisic acid (ABA)-mediated stomatal closure (Pornsiriwong et al., under review). What is less clear is whether this research can be translated into cereal crops such as wheat to develop a drought-tolerant variety. As a first step to addressing this question, we investigated the role of SAL1 in an Australian wheat variety, Chara: our analyses led to the identification of seven SAL1 homologues and assignment of their chromosomal locations in wheat. We PCR-screened heavy ion mutant population and identified 10 wheat lines harboring deletions in two out of seven SAL1 homologues. In rainfed conditions, three of these SAL1mutantshave showed either similar or improved grain yield and harvest index when compared with wild type plants. When subjected to different water stress regimes in controlled environments, mutants have shown no growth penalty and better maintenance of leaf turgidity. Furthermore, we found negligible biochemical and mesophyll conductance limitations on the photosynthesis among wheat SAL1 nulls. Collectively, our results demonstrate the maintenance of growth and yield in SAL nulls under moisture limited conditions and SAL1 can be established as a marker for selection of drought-tolerant wheat cultivars.

IDT7-135 | Drought tolerant maize for Asian tropics - what worked and what is challenging?

P.H. Zaidi[1]*, M.T. Vinayan[1], K. Seetharam[1], Raman Babu[1], Ramesh Kumar[2], Salahuddin Ahmed[3], Do Van Dung[4], Dang Ngoc Ha[4], Art Salazar[5], K. Muralikrishna[6]; R.B. Dubey[7] and B.S. Vivek[1]

[1]CIMMYT-Asia Maize Program, ICRISAT Campus, Patancheru-502324, Hyderabad, India.
[2]Indian Institute of Maize Research, PAU Campus, Ludhiana (Punjab), India
[3]Bangladesh Agricultural Research Institute, Gazipur, Bangladesh
[4]National Maize Research Program, Ha Noi\s, Vietnam
[5]Institute of Plant Breeding, University of Philippines-Los Banos, Philippines
[6]ANG Ranga Agriculture University, Hyderabad, India
[7] Maharana Pratap University of Agriculture & Technology, Udaipur, Rajasthan, India
*E-mail: phzaidi@cgiar.org

About 80% of the maize in Asian tropics is cultivated as rainfed crop and, hence, prone to climatic variability and associated weather extremes that lead to deficit moisture (or agricultural drought) at critical crop stages. CIMMYT's Asian regional maize program, based in ICRISAT campus, Hyderabad, India, in partnership with public and private sector maize programs in the region, has been focusing on development of drought-tolerant maize germplasm, trait donors and high-yielding, drought-tolerant maize hybrids for current climate, and maintain a germplasm base and product pipe-line to effectively feed the requirement of future climatic situations. The accelerated development and deployment of drought-tolerant maize hybrids is based on carefully undertaken field-based precision phenotyping through managed-stress screens, understanding the genetic architecture of the target trait, coupled with application of modern breeding tools, including genome-wide association studies (GWAS), genomic selection (GS), and double haploid (DH) technology, and effective partnerships with committed national programs and seed companies in the region for effective deployment and delivery of drought-tolerant cultivars. Good progress has been made and promising drought-tolerant hybrids are being licensed to the partners for large-scale deployment and scaling-out of drought tolerant hybrids in stress-prone agro-ecologies. However, in view of the climate change-mediated weather variability/uncertainty the biggest challenge is to achieve an improved-stable performance across locations/years. This needs a further intensified and concerted efforts to minimize genotype x environment interaction effects to develop maize germplasm with improved-stable performance.

IDT7-136 | Agro-morphological and physiological evaluation of common bean (*Phaseolus vulgaris* L.) germplasm under water stress

Sajad Majeed Zargar[1]*, Sufia Farhat[2]

[1]Division of Biotechnology, SKUAST-K, Shalimar, Srinagar, J&K, India
[2]NRCPB, New Delhi, India
*E-mail: smzargar@gmail.com

Common bean (*Phaseolus vulgaris* L.) is an important legume crop. It is considered the second most important source of calories after maize. It is an important source of protein, essential vitamins and minerals, soluble fiber, starch, and phytochemicals, and has low fat content. Since common bean is affected by various biotic and abiotic stresses that cause huge losses in yield, identification of resistance sources is a must. In order to identify the resistance sources for water stress tolerance, we have screened 51 diverse common bean genotypes under rainfed conditions to assess their performance. The genotypes were assessed under both irrigated (control) as well as rainfed (water stress) conditions. Various morphological parameters (number of pods per plant, pod length, pod width, seed weight per plant and plant height) and physiological parameters (chlorophyll content, RWC, and stomatal density) were recorded. We observed significant variations among genotypes as well as between conditions (treatments i-e: irrigated and water stress). As such, this study helped us identify water stress tolerant genotypes of common bean.

Poster Theme VIII

Agronomic Management/Cropping Systems for Water-Limited Environments, Broad Approaches

IDT8-001 | Contribution to the interaction between Arbuscular Mycorrhiza Fungi (AMF), (*Rhizophagus irregularis*) NPK and drought tolerance to yield of NERICA in northern Nigeria.

Abubakar ZA[1], Hussain A[2], Nzeako A[2], Muhammed NY[2], Muhammad M[2], Abdul Hameed A[2],*

[1]Gombe State University, PMB 127, Gombe, Nigeria
[2]Abubakar Tafawa Balewa University (ATBU), PMB 0248, Bauchi, Nigeria
[3]University of Aberdeen, AB24 3UU, Scotland, United Kingdom
*E-mail: gesunnam@yahoo.com

The study was conducted to evaluate the response of New Rice For Africa (NERICA) cultivar exposed to drought at 0%, 5% and 10% doses of *Rhizophagus irregularis* (Arbuscular Mycorrhiza Fungi (AMF);) and at 0 kg/h, 90 kg/h and 180 kg/h NPK respectively. Root and shoot mass and yield (100 grain) were measured. Higher NPK significantly increased yield in the irrigated treatment, but not root and shoot mass. The results showed that NPK and AMF significantly increase yield at 5% AMF colonization in all the NPK doses (0, 90 and 180 kg/h).The results of this study call for further studies to determine the appropriate levels of NPK that requires 5% *R. irregularis* to enhance yield in NERICA. It further recommends that this methodology be applied in other rice cultivars.

IDT8-002 | Effect of growth stages on community dynamics of Bambara groundnut (drought-tolerant crop) rhizospheric bacteria

Ajilogba, C.F.[1], Babalola, O.O.[1]*, Habig, J[2]

[1]Food Security and Safety Niche Area, Faculty of Agriculture, Science and Technology, North-West University, Mmabatho, Mafikeng 2735, South Africa
[2]Agricultural Research Council, Plant Protection Research Institute, Private Bag X293 Queenstown 0001, South Africa.
*E-mail: olubukola.babaloa@nwu.ac.za

The overall results of plant-rhizosphere microbe interactions are a higher microbial density and their metabolic functions in the rhizosphere. The functions of microbial communities differ from one growth stage to another. The functional diversity of the rhizospheric bacterial in growth stages of Bambara groundnut can be used to assess its impact on crop production with little or no water/rainfall. Bambara groundnut was grown during planting season in Mafikeng, South Africa. Soil samples were taken after every four weeks. Microbial diversity was determined by Community Level Physiological Profiling (CLPP) using BIOLOG GN2 plates. The soil microbial richness and abundance was measured using the Shanon-Weaver (H) and Evenness (E) diversity indices. Results showed that bacterial abundance and diversity were more pronounced after four weeks of planting, compared to the original soil. Carbon sources utilized by bacterial communities from all samples were uridine, bromosuccinic acid, acetic acid, D-glucosamic acid, succinic acid mono methyl ester, dextrin, glycogen, tween 80 and L-arabinose. Glucuronamide, L-pyroglutamic acid and L-glutamic acid were utilized by microbial communities from samples after four weeks of planting while D-serine was not utilized by any of the samples. The highest activity with microbial diversity, H= 4.05 and E=0.89, was in the soil sample after four weeks, while the lowest value was in one of the soil samples before planting (H=1.92 and E=0.56). This implies that the soil samples after four weeks were richer in diversity of microbial species and their abundance, making the soil important in crop production.

IDT8-003 | *In situ* rainwater conservation for enhancing productivity of maize (*Zea Mays* L)-chick pea (*Cicer arietinum*) cropping system on *Vertisol* region

Ashoka P [1]*, A B Khoth [2], G.V.Dasar [3]

[1]ICAR,KVK,H matti-581115,UAS,Dharwad,Karanataka
[2]AICRP on Water Management, Belvatagi (P),UAS, Dharwad
[3]AICRP on Water Management, Belvatagi (P), University of Agricultural Sciences, Dharwad, Karnataka State, Pin-582208,
*E-mail: ashokapuas@gmail.com

Water is the major limiting factor for crop production in black soil regions of semi-arid tropics in India, which have low rainfall and erratic rain distribution. Unpredictable occurrence of drought of different intensities from year to year and within individual crop-growing seasons results in lower productivity. In addition, the presence of black soils with high clay content and low infiltration rate results in 10% to 30% rainwater runoff and loss of fertile top soil. Under such conditions, *in situ* rainwater conservation plays a vital role in maintaining and/or increasing crop productivity. Rainwater conservation measures are part of agronomic practices in the rainfed production systems, and are adopted to suit a particular climate, soil, crop and cropping system by the resource poor farmers. The production of most rainfed crops averages between 400 and 900 kg ha^{-1}, with appropriate resource conservation and management techniques. Results of management in maize (*kharif*)-chick pea (*rabi*) from large-scale demonstration in famers fields in *Vertisol* region during 2013-14 were evaluated. The results indicate that treatment with compartment bunding with mulching between rows @5 t/ha was superior, with higher maize equivalent yield (134.2 q/ha), WUE (20.6 kg/ha-mm), gross income (68,000 Rs/ha), net income (52,000 Rs/ha)and B:C ratio (4.30). This technology conserves rainwater *in situ,* recharges soil profile uniformly, an d reduces runoff and soil and nutrient losses, and increases crop yields on a sustainable basis and at low cost. It can be adopted by the farmers easily in areas with deep black soils.

IDT8-004 | Charred rice husk to improve soil moisture retention and nutrient management in rainfed groundnut (*Arachis hypogaea* L.)

Balasubramanian P[1], Chinnamuthu C.R.[2], Babu R[3]., Rajesh Kumar A[4].

[1] Department of Agronomy, AC&RI, TNAU, Madurai, Tamil Nadu, India.
[2]Department of Agronomy, AC&RI, TNAU, Madurai, Tamil Nadu, India.
[3]Department of Farm Management , AC&RI, TNAU, Madurai, Tamil Nadu, India.
[4]Department of Agronomy, TNAU, Coimbatore, Tamil Nadu, India.
*E-mail: agribalatnau1991@gmail.com

A field experiment was conducted at the Department of Agronomy, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai, Tamil Nadu, during 2014-2015 *rabi* season. The investigations aimed to study the effect of adding charred rice husk and other organic amendments to improve soil moisture retention and nutrient management under rainfed conditions. The treatment includes charred rice husk, biochar, lignite and farm yard manure, which are enriched with the recommended dose of nitrogen (10 kg ha-1) and phosphorus (10 kg ha-1) fertilizer; and charred rice husk, biochar, lignite and farm yard manure without the recommended dose of nitrogen and phosphorus. These were compared with the absolute control and recommended dose of fertilizer (10:10:45 kg NPK ha-1). The different organic amendments were applied to a groundnut field at the rate of 5 tons/ ha-1 and incorporated into the dry soil during land preparation. The mixture was incubated 45 days under dark conditions at room temperature. The experiment was laid out in a randomized complete block design with ten treatments replicated thrice with groundnut variety VRI 2. The total amount of rainfall received during the entire crop growth period was 179mm in 2014-2015. The structural morphology of organic materials was studied using Scanning Electron Microscope (SEM) at low and high resolutions. The main results showed that enriched farm yard manure, followed by enriched charred rice husk, gave the highest value for vegetative growth attributes (plant height upto harvest stage) and pod yields and its components (number of pods per plant, number of matured pods per plant, peg to pod conversion percentage, and hundred pod weight) as well as biological yield compared with the control treatment. Water saved due to increase in the water retention capacity of charred rice husk was higher, with corresponding pod yield, when compared to the control. The results indicated that pod yield and its components were significantly increased by application of enriched farm yard manure (2190 kg/ha,) followed by enriched charred rice husk (1983 kg/ ha).

IDT8-005 | Combining ability for drought tolerance and yield components of highland tropic adapted potato in Ethiopia

Hirut BG[1],[2]*, Shimelis HA[1], Mengistu F[3], Bonierbale MW[4], Gastelo M[4], Asrat A[5]

[1]University of KwaZulu-Natal, Pietermaritzburg, Private bag X01 Scottsville 3209, KwaZulu-Natal, South Africa
[2]International Potato Centre (CIP) – Ethiopia, Addis Ababa, c/o ILRI, P.O. Box 5689, Ethiopia
[3]Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, P.O. Box 2003, Ethiopia
[4]International Potato Centre, Lima, P.O. Box 1558, Peru
[5]International Institute of Tropical Agriculture, Ibadan, PMB 5320, Nigeria
*E-mail: H.Getinet@cgiar.org

Recurrent drought and late blight disease are the major limiting factors to potato productivity in the north-west Ethiopian highlands. The objectives of this study were to determine combining ability effects and gene action for yield, yield components and drought tolerance in clones from late blight resistance breeding population and identify promising parents and families for cultivar development. Sixteen clones were crossed in two sets using a North Carolina Design II. The resulting 32 families were evaluated together with 17 clones in a 7 x 7 lattice design with two water regime and two replications. The experiment was carried out under well-watered and terminal water-stress conditions with drought imposed at the tuber bulking stage. Results showed highly significant differences among families and clones for the assessed traits. Traits including marketable tuber yield, marketable tuber number, average tuber weight and groundcover were positively correlated with tuber yield under both moisture stressed and fully watered conditions. Significant general combining ability (GCA) and specific combining ability (SCA) effects indicated the contribution of additive and non-additive genes in the expression of all traits. GCA effects were more important than SCA effects for total tuber yield, marketable tuber yield, average tuber weight, plant height and groundcover under stress conditions and chlorophyll content under well-watered conditions. This study identified the parents and families with best GCA and SCA effects, respectively for both tuber yield and drought tolerance traits, represent valuable genetic resources for improving potatoes adaptation to multiple stress environment.

IDT8-006 | Microbes bio-fortify rice

Sutradar M[1], Bharathprasad CT[1], Kavya Hp[1, 2], Vinutha Dn[1], Shashidar He[1]*

[1]University of Agricultural Sciences, GKVK, Bengaluru-560 065, Karnataka, India
[2]Madurai Kamaraj University, Palkalai Nagar, Madurai-625 021, Tamil Nadu, India
*E-mail: heshashidar@gmail.com

Aerobic rice (*Oryza sativa* L.) cultivation is an eco-friendly method which encourages soil microbes in the rhizosphere, beneficial for plant growth and development, as well as micro nutrient uptake from soil. A comparative study was carried out to understand the micro floral population as well as micro nutrient content in rice grown under aerobic and wetland conditions among the five different rice accessions: ARB 6, AM 65, AM 72, IR 64 and *Jeerigesanna*. The results showed wide range of unique bacteria, fungi and *Azotobacter* population in aerobic conditions compared to wetland in the case of ARB 6, AM 72, AM 65 and IR 64 genotypes. The results also showed increased micronutrient content of Zn and Fe in aerobic conditions compared to wetland in case of ARB 6 (28.4ppm and 15.9ppm), AM 72(33.4ppm and 16.4ppm), AM 65(32.2ppm and 16.4ppm) and IR 64(28.1ppm and 22.3ppm) genotype. A significant variation was noticed among the different microbial populations which might be either due to the differences in the environmental conditions (aerobic and anaerobic), or differences among the genotypes (ARB 6, IR 64, AM 72, AM 65 and *Jeerigesanna*). It could be due to interaction between the G x E conditions, where the microbial population was isolated. A highly significant variation was also noticed for micronutrient content among different rice accessions, which is due to the microbial population under aerobic condition that led to bio fortification of Fe and Zn in rice grains. The results were confirmed in a detailed study with one of the genotypes.

IDT8-007 | Assessment of common bean (*Phaseolus vulgaris*) genotypes for farmer's preferences and acceptance through participatory bean breeding approaches

Binagwa P.H.[1]*, Magdalena W.[2], Mbiu J. P.[2], Zakayo E.[1], Nestory S.M.[1]

[1]Selian Agricultural Research Institute P.O.Box 6024, Arusha, Tanzania
[2] Maruku Agricultural Research Institute, P.O.Box 127 Bukoba, Kagera.
*E-mail: hongera1984@yahoo.com

It is estimated that over 75% of rural households in Tanzania depend on beans for daily subsistence. Recently, farmers have been increasingly looking for improved bean varieties which meet specific market demands and/or adapted to local agro-ecologies. To achieve this, it is important to involve farmers through farmers' participatory variety selection process. This approach gives farmers an opportunity to assess and select varieties from a range of near finished materials in the breeding process. As part of the farmers' participatory variety selection process, 17 participants, of who 46% were women, were selected to participate in a focused group discussion. Through the discussions, farmers revealed that beans and their by-products have multiple uses: they are a source of food, cash for household incomes, while the crop residues are used as livestock feeds and to improve soil fertility. Eight bean genotypes (KG98, F8 drought, KATB9, F9 Kidney, KATB1, Lyamungu 85, JESCA and Local check) were involved in selection process at Karatu, Babati and Bukoba districts in Tanzania. The bean genotypes were evaluated using absolute, matrix and pair-wise rankings methods. Farmers preferred two genotypes of KATB1 and KATB9, based on early maturing seed type, marketability and high demand by bean traders in Tanzania and neigbouring countries. The release of the two selected bean genotypes by the national seed committee through national certifying institution will improve farmers' livelihood at large as well as other bean value chain actors.

IDT8-008 | Higher productivity in pearl millet (*Pennisetum glaucum* L.) with conservation furrow and supplemental irrigation

Ravindranatha Reddy B[1]*, Madhusudhan Reddy K[1], Shanthi P[1], Sahadeva Reddy B[1]

[1]Agricultural Research Station, Ananthapuramu-515001,
Acharya N.G. Ranga Agricultural University, Andhra Pradesh, India
*E-mail: b.ravindranathareddy@gmail.com

Pearl millet (*Pennisetum glaucum* L.) is an important cereal crop in arid and semi arid regions of the world. Due to low and uneven distribution of rainfall, and loss of rainwater through runoff, the crop undergoes moisture stress at critical stages, leading to low and unstable productivity. Rainwater conservation and supplemental irrigation is the only way of increasing the productivity of pearl millet. Field experiments were conducted with four main plots (rainfed, rainfed with conservation furrow, two supplemental irrigations with 20 mm and one supplemental irrigation with 10 mm) with two pre-release hybrids, ABH-1 and ABH-6, in sub plots in large-sized plots during the 2016 *kharif* season, at ANGRAU, ARS, Anathapuramu, Andhra Pradesh, India. An amount of 265.6mm rainfall was received in 12 rainy days during the crop season. Conservation furrows were formed with a small tractor-drawn (15HP) inter-cultivator-cum-conservation furrow at 33 days after sowing. Formation of conservation furrows helped in availability of moisture for a relatively longer time and increased the grain yield by 11.8% and 12.9% in ABH-1 and ABH-6 respectively, compared to rainfed crop. Two supplemental irrigations coupled with conservation furrows increased the grain yield by 176% and 130% in ABH-1 and ABH-6 respectively compared to rainfed crop. A single supplemental irrigation of 10mm by sprinkler irrigation at vegetative stage increased the grain yield of pearl millet by 96% and 72% in ABH-1 and ABH-6 respectively compared to rainfed crop without conservation furrows.

IDT8-009 | A protocol combining statistical and crop growth modelling to evaluate phenotyping strategies useful for selection under different drought patterns

Bustos-Korts D.[1 2]*, Malosetti M.[1],Boer M.P.[1], Chapman S.C.[3], Chenu K.[4], van Eeuwijk F.A[1]

[1]Biometris, Wageningen University and Research Centre, The Netherlands
[2]C.T. de Wit Graduate School for Production Ecology & Resource Conservation (PE&RC), The Netherlands, E-mail: daniela.bustoskorts@wur.nl
[3]CSIRO Agriculture and Food, Brisbane, Australia
[4]The University of Queensland, CPS, Queensland Alliance for Agriculture and Food Innovation, Toowoomba, Australia
*E-mail: daniela.bustoskorts@wur.nl

Genomic prediction of the final state of complex traits, say yield, benefits from accounting for the dynamics of those traits as well as from including information on correlated component traits. Statistical criteria for which yield components to include in the prediction model concern the heritability of the component traits and their genetic correlation with yield. Not all component traits are easy to measure. Therefore, it may be attractive to include proxies to yield components, where these proxies are measured in (high throughput) phenotyping platforms. We simulated phenotypes for a spring wheat diversity panel of about 1000 genotypes segregating for a set of APSIM parameters regulating phenology, biomass partitioning and the ability to capture environmental resources. In the multi-trait prediction models for final yield, we included proxies to biomass, water use, canopy cover and phenology as observed over the growing season. Various drought stress scenarios were evaluated. Each scenario triggers different adaptive mechanisms and, therefore, the importance of components traits differs between drought scenarios. Therefore, multi-trait genomic prediction models for yield require scenario-specific correlated traits. The combined use of crop growth models and multi-trait genomic prediction models provides a protocol to assess the efficiency of phenotyping strategies.

IDT8-010 | Promising sulphur oxidizing bacteria as a remedy for unavailable sulphur in dryland areas of India

Chaudhary S[1]*, Dhanker R[1], Tanvi[1] and Goyal S[1]

[1]Department of Microbiology, CCSHAU, Hisar-125004, Haryana, India
*E-mail: kesarsuman21@gmail.com

Sulphur (S) is recognized as the fourth major nutrient in addition to nitrogen (N), phosphorus (P) and potassium (K). Sulphur is best known for its role in the synthesis of proteins, oils, vitamins and flavored compounds in plants. Nowadays, sulphur deficiency is becoming a common problem in many countries. Its availability may prove an important gateway for many crops such as mustard. Two promising sulphur oxidising bacteria were isolated from different districts of Haryana (India). The two isolates, SSD15 and SSLP6, showed maximum sulphate production, i.e. 2.432 and 2.145mM respectively. Cultural conditions were also optimized for sulphate production by these two isolates. Glucose was found to be the best carbon source and ammonium chloride was the best nitrogen source. It was observed that 30ºC was the optimum temperature for sulphate production by isolate SSD15 and SSLP6. Sulphate production by SSD15 and SSLP6 was maximum after 7 days of incubation; and at pH 6 and pH 5 respectively. They also had the highest sulphide oxidase activity i.e. 30.6 U/ml (SSD15) and 27.8U/ml (SSLP6). On the basis of morphological and biochemical tests, the promising isolates probably belonged to genera *Xanthobacter* sp. (SSD15) and *Pseudomonas* sp. (SSLP6).

IDT8-011 | Advances in chickpea crop improvement for improved productivity and resilient cropping systems in Ethiopia

Chichaybelu M.[1]*, Eshete M.[1], Korbu L.[1], Mohammed R.[1], Girma N.[1], Bekele D.[1], Geleta T.[1], Fikre A.[2], Ganga Rao N.V.P.R[3], Ojiewo C.[4], Monyo E.[3], Gaur P.M.[5],Varshney R.K.[5,6],

[1]DebreZeit Agricultural Research Center, Ethiopian Institute of Agricultural Research (EIAR), DebreZeit, Ethiopia,
[2]Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia,
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya,
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Addis Ababa, Ethiopia,
[5]International Crops Research Institute for the Semi-Arid Tropics (ICRISATPatancheru, Hyderabad, India
[6]CGIAR Generation Challenge Programme (GCP), CIMMYT, Mexico DF, Mexico
*E-mail: chichemekasha@gmail.com

Chickpea (*Cicer arietinum* L.) is an important food legume in Ethiopia. Its production is challenged by low productivity of landraces, poor farming practices, and biotic and abiotic stresses, among others. To address these challenges, EIAR has partnered with CGIAR centers and developed improved chickpea varieties, along with integrated crop management technologies that have increased productivity. Central to these efforts is the Tropical Legumes Projects (TL) funded by the Bill and Melinda Gates Foundation. Since the inception of the Tropical Legume project in 2007, six '*kabuli*' and five *'desi'* chickpea varieties have been released. TL project also supported efforts to avail high-quality seed of improved varieties to many small holder farmers through participatory variety selection and demonstration activities. Eighteen farmers' seed producer associations have been established to fill up supply gaps for high quality seed. Seed production of improved chickpea varieties from 2008 to 2015 amounts to 50t breeder, 788t basic and 14,495.47t certified/Quality Declared Seed. The national average production and productivity of chickpea has increased by 60% and 51%, respectively, over the same period coupled with 16% growth in export volume. Chickpea improvement program is currently focusing on disease resistance, drought and heat tolerance, mechanical harvesting and herbicide tolerance to cope up with the changing climate and the need of specific production corridors.

IDT8-012 | The effects of cultivation methods and water regimes on root systems of one drought-tolerant (RD6) and one drought-sensitive (RD10) rice varieties of Thailand

Datta A[1]*, Ullah H[1]

[1]Agricultural Systems and Engineering, School of Environment, Resources and Development, Asian Institute of Technology, Pathum Thani 12120, Thailand
*E-mail: datta@ait.asia

In this study, we have attempted to investigate the effect of different water-saving cultivation techniques on root systems of two Thai rice varieties. The variables were two rice varieties (RD6 and RD10), two cultivation methods (dry direct seeding and transplanting), and two soil moisture regimes (field capacity [FC] and 50% FC). RD6 variety had higher root number, root length, and root length density compared with RD10 under transplanting method at FC. At flowering stage and at FC, the number of roots for RD6 and RD10 raised through transplanting method was 543 and 392 per plant respectively, compared with root number of 415 and 362 per plant for RD6 and RD10 respectively, raised through dry direct seeding method. Root dry matter was the highest for RD6 cultivated through dry direct seeding method, compared with transplanting method at FC for both tillering and flowering stages. RD6 variety resulted in 25% and 50% higher root dry matter at FC for dry direct seeding than transplanting, at tillering and flowering stages, respectively. The performance of RD10 was poor under 50% FC and dry direct seeding method. With proper selection of variety, dry direct seeding method could be a better alternative for sustainable rice cultivation under water-limited environments.

IDT8-013 | Impact of municipal sewage sludge on physicochemical characteristics and heavy metal accumulation in soil in accordance to its agricultural uses

Dhanker R[1]*, Chaudhary S[1], Tanvi[1] and Goyal S[1]

[1]Department of Microbiology, CCSHAU, Hisar-125004, Haryana, India.
*E-mail: rinku1989d@gmail.com

Under semi-arid conditions, soil is more prone to lose its fertility rapidly. This could be improved with the application of sewage sludge generated from wastewater treatment plants. Municipal sewage sludge is a rich source of various nutrients (N, P, and K) and organic matter vital for plant growth, and has drawn greater attention in the light of its potential for improving soil properties. The characteristics of sludge generated from different treatment plants vary, depending on the treatment, the area from which the sludge has been generated and the variable nature of pollutant inputs to wastewater. The goal of this study was to analyze the fertilizer potential and heavy metal risk of sewage sludge intended for agricultural application. In this work, soil was amended with different rates (0.5 to 4%) of sewage sludge collected from wastewater treatment plants in Rohtak (Haryana) and analyzed for a range of physico-chemical characteristics, including nutrients, organic matter, pH, cation exchange capacity and trace elements. The potential risk of heavy metal toxicity was also evaluated. Application of sewage sludge showed the buildup of organic carbon, nitrogen, phosphorous, microbial biomass, dehydrogenase, alkaline phosphatase and urease activities. Accumulation of heavy metals in sewage-amended soil was also below the permissible EC limits. The research results indicate a positive outcome for the wastewater treatment plants that currently keep large piles of unused dried sludge within their premises.

IDT8-014 | Intercropped woody species in the sahel to resist drought: Hydraulic lift and crop water relations

Teamrat A Ghezzehei, R. Dick[1]*, M. Sene[2], N. Bogie[3], F. Kizito[4], M. Dragila[5], I. Diedhiou[6]

[1]Ohio State University, USA.
[2]Sciences du Sol, Institut Sénégalais de Recherches Agricoles (ISRA)/ CERAAS, Thiès, Sénégal.
[3]University of California at Merced, USA 5USAID/ Sénégal, Dakar, Sénégal.
[4]California Water Board, Davis California, USA.
[5]Oregon State University, Department of Crop and Soil Sciences, Corvallis, OR USA.
[6]Unversity of Thiès, Thiès, Sénégal"
*E-mail: dick.78@osu.edu

The amount and timing of water availability in semi-arid environments such as the Sahel are the most important factors in controlling crop productivity and crop failure. This is of utmost importance for subsistence farmers in the Sahel, where combined with degraded soil and erratic precipitation they are under constant threat of food insecurity. Additionally, a common occurrence in the Sahel is short in-season drought periods that can significantly reduce yields or even cause crop failure. Our research in Senegal, over 15 years, has shown that intercropping annual crops with 2 native shrubs, *Guiera senegalensis* and *Piliostigma reticulatum* can mitigate crop failure and greatly increase crop productivity and as will be presented here; water relations are an important factor in this response. The early studies determined that hydraulic redistribution, or the diurnal movement of water via tap roots along a water potential gradient from wet sub-soil to dry surface soil, releases water by surface roots. This phenomenon is likely why we measure higher soil moisture levels, year around, in soil beneath shrubs over soil outside the influence of shrubs. Furthermore, water balance studies showed that *G. senegalensis and P. reticulatum* do not compete with crops for water and promote groundwater recharge. Our recent research is focusing on answering the question whether this hydraulically lifted water can actually be transferred to adjacent crops and whether shrubs can assist crops through seasonal drought periods. The research has been on the major food crop for the Sahel, *Penisetum glaucum* (Pearl Millet). To address this, millet intercropped with *Guiera senegalensis* in a replicated (3 reps) field trial was subjected to a simulated drought using drip irrigation in the dry season. Sixty eight days after sowing, irrigation was stopped for half of the treatments (with and without the presence of shrubs) from late flowering till end of the cropping season. Within 10 days the soils in the non-irrigated treatments became extremely dry with water potentials ranging from -0.5 Mpa to -3.0 Mpa at 20cm depth. Ten days after this, isotopically enriched deuterium was injected into shrub roots at a depth of 1.0 m followed by sampling of aboveground shrub and the surrounding millet tissues one to two times per day for four days. The leaf tissue of shrubs were first labeled with elevated deuterium after 24 hours and 12 hours later a highly enriched pulse of deuterium was measured in millet plants growing directly adjacent to the injection shrubs. The treatments with shrubs subjected to drought continued to maturity and produced harvestable millet product, whereas non-shrub plots resulted in crop failure. From this we conclude that *Guiera senegalensis* can transfer water from the subsoil to adjacent millet that is high enough to significantly buffer against drought – a truly profound finding!

IDT8-015 | Intercropped woody species in the sahel to resist drought: Beneficial microorganisms and common Mycorrhizal hyphal networks to reduce water stress.

R Dick[1], M Bright[1]*, S. Debenport[1], I Diedhiou[2] , A. Badiane[3], S Diedhiou[4], K Assigbetse[5]

[1]Ohio State University, USA.
[2]Sciences du Sol, Institut Sénégalais de Recherches Agricoles (ISRA)/ CERAAS, Thiès, Sénégal.
[3]University of California at Merced, USA 5USAID/ Sénégal, Dakar, Sénégal.
[4]California Water Board, Davis California, USA.
[5]Oregon State University, Department of Crop and Soil Sciences, Corvallis, OR USA.
[6]Unversity of Thiès, Thiès, Sénégal"
***E-mail:** dick.78@osu.edu

The Sahel is experiencing landscape and soil degradation that reduces food and economic security of rural, underprivileged communities. Recent research of the largely unrecognized system of intercropping the woody shrubs (*Piliostigma reticulatum or Guiera senegalensis*) the Sahel has shown dramatic yield response. Our previous research showed that shrubs perform hydraulic lift (movement of water from wet sub-soil via deep roots to dry surface soils) which could be important for microorganisms. Therefore, the objective was to investigate whether soil beneath shrubs increased microbial diversity and beneficial microorganisms in the rhizosphere soil of millet plants. The first study in Senegal showed that soil beneath *G. senegalensis* and *P. reticulatum* had greater diversity (bacterial and fungal DGGE gene sequences, and PLFA) and biomass, and activity (enzyme N mineralization) that was maintained in the dry season – in all likelihood due to hydraulic lift, and augmented by litter inputs, and root turnover that provided C inputs. A second determined whether hhis response was translated to the rhizosphere soil of millet using deep sequencing of DNA to profile microbial communities. Here again there was greater diversity in millet rhizosphere soil and enrichment of genera known to have plant growth promoting properties, with OTU enrichment ranging from 30 to 1000 fold increases. This included bacteria belonging to *Chitinophaga* and to 8 fungal genera (*Aspergillus, Coniella, Epicoccum, Fusarium, Giberella, Lasiodiplodia, Penicillium,* and *Phoma*). A second area of research is the beneficial fungus mycorrhizal (AM). This organism could promote crop growth in 2 ways – one is by its infection of crops roots and therefore through its extensive hyphae increase nutrients and water retrieval to the host plant; and secondly, specific to our system, whether a common mycorrhizal network (CMN) forms between the roots of shrub and of an associated crop such as millet. A field scale study of AM on millet across the major cropping region of Senegal showed that AM hyphal infection rates of millet roots were greater in the presence of *G. senegalensis*, which would contribute improved millet growth. We also performed an isotopic tracking study during a simulated drought field experiment, where we injected deuterium to *G. senegalensis* roots at 1 m depth and then tracked deuterium into millet plants inside root exclusion microcosms. A deuterium signal was found in both shrubs inside and outside microcosms confirming the profound outcome that shrubs transfer hydraulically lifted water to adjacent crops. In summary, these results are that shrubs control the recruitment of AM and potentially other beneficial microorganisms to the root zone of millet, which in part contribute the dramatic yield response we have shown for shrub intercrop systems. And furthermore, hydraulic lift and enhanced AM infection would be expected to contribute to the ability of shrub-intercropping to buffer against in-season drought. This optimized shrub systems therefore offers a truly local and biological resource that subsistence farmers in the Sahel can take advantage of.

IDT8-016 | Synergistic agronomic practices for improving soil functions and agricultural sustainability

Dubey Rama Kant[1], Abhilash P.C.[1], Singh H.B.[2]

[1]Institute of Environment & Sustainable Development, Banaras Hindu University, Varanasi 221005
[2]Institute of Agricultural Science, Banaras Hindu University, Varanasi 221005
*E-mail: ramakant.sls@gmail.com

Enhancing food production and reducing trace gas emissions from agroecosystems is an important step towards agricultural sustainability. Therefore, the present study was aimed at testing the hypothesis that the synergistic effects of mulching and no-tillage practices alter the soil functions and reduce the soil CO_2 efflux, compared to conventional agro-practices. These differences might depend on specific soil-water relationships, including soil physicochemical, biological, aggregation and enzymatic activity. A field experiment was carried out with *Brassica juncea, Cicer arietinum, Vigna mungo* and *Zea mays* crops, with mulching and no-tillage practices. The crops were grown in randomized complete block design in 2×2 m^2 plots. Periodic soil sampling and plant harvesting were done from each amended and control plot, and analysed for plant growth, biomass, and N, P and K contents. Diurnal variation in soil and microbial respiration were monitored using closed chamber method and soil incubation experiments, and data were correlated with soil moisture and temperature. Results showed significant ($p<0.05$) increase in soil quality and reduced rate of microbial and soil respiration (from 80.35±11.79 to 84.60±11.78 mg/m^{-2} hrs^{-1}) under synergistic practices, compared to the control (from 92.17±15.09 to 102.81±7.35 mg/m^{-2} hrs^{-1}). Soil samples were collected periodically and analysed extensively for soil physicochemical, biological and soil enzymes. Field data showed significant difference ($p<0.05$) in moisture content, organic carbon, microbial activity and diversity, dehydrogenase, α; β glucosidase activity between practised and control soil. Thus, the application of above mentioned practices improvess the soil fertility with multipurpose benefits to the global agroecosystems.

IDT8-017 | Tropical legume project impact on groundnut improvement research outputs in Nigeria

Echekwu C.A.[1]*, Alhassan U.[1], Mohammed S.G.[2], Motagi B.[3], Ajeigbe H.A.[3], Ahmed B.[1]Vabi M.[3]

[1]Institute for Agricultural Research (IAR) Samaru,Ahmadu Bello University,
[2]Centre for Dryland Agricultural, Bayero University Kano, Nigeria
[3]International Crop Research Institute for the Semi-Arid Tropics,Kano Station, Nigeria
*E-mail: candyechekwu@gmail.com

Groundnut is an important component of the farming systems in the dry savannas of Nigeria. It is planted on 34% of cultivated area and contributes to 54% of household cash in the country. Groundnut production in Nigeria has suffered from major setbacks; fungal and bacteria diseases, aflatoxin contamination and weak seed system. However, considerable progress had been made by IAR, ICRISAT and several partners to overcome these setbacks through the development and deployment of improved groundnut varieties and associated crop management systems. Earlier released Rosette resistant varieties, RMP12 (SAMNUT10) and RMP91 (SAMNUT11), were late maturing varieties. With climate change resulting in shortened growing season, the need for early-maturing, disease- and drought-tolerant varieties became urgent. Collaborative efforts of several partners resulted in the official registration and release of medium duration: SAMNUT21 (UGA2), SAMNUT22 (M 572, 801), and early-maturing varieties SAMNUT23 (ICGV-IS 96894) in 2001. With the arrival on the scene of the Tropical Legume Project (TL), along with the excellent research and development support, Samnut-24 and Samnut-25 and Samnut-26, were released. These varieties are part of the achievements from TL activities during 2012-13 and are our pride. These varieties are making a difference in the lives of farmers, improved the sustainability of the systems and also increased the cultivation of groundnut even in the dry season. TL project in Nigeria took the unique opportunity to partner with USAID-Groundnut up-scalling project to build capacity of farmers and awareness of improved production technologies and make seeds of improved varieties available.

IDT8-018 | Drought impacts on fungal and mycotoxin contamination of small-scale maize from the North-West province of South Africa

Ekwomadu TI[1]*, Gopane RE[1], Mwanza M[1]

[1]North-West University, Mafikeng campus, South Africa
*E-mail: 23115394@nwu.ac.za

Drought stress and high temperatures are two environmental factors that directly impact maize and other grains. Prevalence varies geographically, as does the risk of mycotoxin contamination of grains. Often climate extremes may alter the composition of fungal species infecting maize, which invariably could alter the mycotoxins contaminating infected grains. Contamination of foods by fungi and mycotoxins has been linked to various health and economic implications to both man and animals. This study evaluates the incidence of fungal species and mycotoxins contaminating small-scale maize from North West province of South Africa. A total of 100 maize samples were randomly collected from small-scale farmers across the province. Samples were investigated for fungal contamination using conventional and molecular methods to identify fungal species. Mycotoxin analysis was done using IAC, TLC, HPLC and ELISA. Percentage incidence of different genera revealed the predominance of *Fusarium* (82%), *Penicillium*, (63%) and *Aspergillus* species (33%). Among the species, *Fusarium verticilloides* had the highest incidence of 76% while *P.digitatum* had 56% total incidence and *Aspergillus fumigatus* (27%). Mycotoxin analysis revealed that FB_1 was the most contaminant mycotoxin, with incident rate of 100%. Aflatoxins contamination occurred in 26.7% while OTA had a high incident rate of 97.8% and ranged from 3.60 to 19.44 µg/kg cereal. None occurred in 50% of samples. Results showed that maize from small-scale farmers may contribute to dietary exposure to mycotoxins. Although little can be done to influence weather, farmers can make agronomic management decisions to minimise the impact of drought on maize quality.

IDT8-019 | Animal manure: a remedy for dryland crop production

NseAbasi NsikakAbasi Etim[1]*

[1]Akwalbom State University, P.M.B. 1167, Uyo, Akwalbom State, Nigeria
*E-mail: etimbobo@yahoo.com

This paper reviews the importance of animal manure in dry land crop production. Lack of water and nutrients are among factors limiting crop production, especially, during drought. Animals are a crucial link in nutrient cycle; they facilitate the transfer of nutrients from grazing land to cropping land, through deposition of manure and urine, returning nutrients to the soil in the form that plants can readily use. Animal manures are vital fertilizers, since few small-holders can afford enough mineral fertilizer. Moreover, intensification of manure production all year round, using litter, has been observed to be effective for maintaining soil organic matter. Dung and urine contain several nutrients such as nitrogen, phosphorus and potassium and the solid fraction contains organic matter that is important to maintain soil structure, fertility, water-holding capacity of coarse textured sandy soils, and reduce water erosion among other benefits. The nutrient content of manure and other organic fertilizers varies according to quality of feed and the way they are stored or handled. Dry matter content of manure also varies widely: in cows on lush pasture it can be less than 15%, but in sheep on dry forage, it can be higher than 50%. Furthermore, the chemical and physical properties of the soil affect how much manure can be safely applied to land. Dry matter accumulation and rain use efficiency can increase as manure application rate increases. Thus, livestock and poultry manures are key fertilizer in organic and sustainable soil management for sustainable crop production, especially, in dry land.

IDT8-020 | Innovative approach on common bean based technology generation and promotion for improvement of the livelihood at lowland areas of ethiopia

Berhanu Amsalu Fenta[1]*, Kassay Negash[1], Kidane Tumssa[1], Endeshaw Habte[1], Tigist Shiferaw[1], Dagmawit Tsegaye[1], Rubyogo Jean Claude[2], Clare Mugisha Mukankusi[3], Stephen E. Beebe[4]

[1]Ethiopian Institute of Agricultural Research, Melkassa research centre, P.O.Box 436, Ethiopia
[2]Pan Africa bean Research Alliance (PABRA), CIAT Africa, C/O Selian Agricultural Research Institute P.O. Box 2704, Arusha
[3]Center for International Tropical Agriculture (CIAT), P.O.Box 6247, Kampala, Uganda
[4]Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia
*E-mail: berhanufenta@gmail.com

The common bean research program in Ethiopia aims at contributing to the improvement of the livelihoods of smallholder farmers through generation and promotion of improved demand driven and climate-smart common bean based technologies and information thereby enhancing foreign currency earnings of the country. To achieve these goals, the breeding program utilized different approaches which include, hybridization and selection from advanced lines introduced from CIAT and other partners to fast-track variety evaluation and registration. The program focuses on four major seed market classes that include, small/large white beans, speckled/sugar bean, small/large reds and yellow beans which feed into the local, regional and international markets. During variety generation and testing, stakeholders along the value chain are involved in planning, trait prioritization and genotype evaluation to include their preference. At the end of this demand led process, user preferred bean verities with wider choice, which are adaptable to lowland agro-ecologies have been developed. Moreover, complimentary bean management technologies and information have also been generated. In addition to technology generation, there is a deliberate effort to promote these bean based technologies using multi stakeholders approaches which bring bean farmers and their cooperatives unions, exporters and traders, public and private extension, inputs suppliers, public policy makers, public and private seed enterprises producing quality declared seed (QDS) and certified to deliver large quantity of seed to millions of small holders. The engagement of stakeholders from the beginning of technology generation to promotion has contributed to wider technology uptake. This synergetic and innovative technology generation and promotion has transformed bean productivity. For instance, in the last 12 years, yield has more than doubled (from 0.7 to 1.5t/ha) and production area expanded up more three times (less than 150, 000 ha to 520,121 ha and total production almost five fold to 568,243. The use of improved early maturing varieties has also allowed two crop seasons per year from only season. The increased production has contributed to increased bean up to 130 million USD per annum (2015). These significant enhancements in the productivity, area of production and market in beans has impacted the livelihood of bean growers in the country. The demand led breeding and value chain approach using bean innovation platform can be used as a model system for other crops.

IDT8-021 | Effect of plastic mulch on yield and yield attributes of cauliflower and tomato in inland and coastal regions of Bangladesh

Ferdous Z[1], Datta A[1]*

[1]Agricultural Systems and Engineering, School of Environment, Resources and Development, Asian Institute of Technology, PathumThani 12120, Thailand
*E-mail-datta@ait.asia

Vegetable-based cropping system in currently underutilized lands could substantially benefit smallholder farmers and make considerable contributions to regional food security. In Bangladesh, malnutrition is a serious problem in women and children in rural areas, occurring mainly due to lack of vegetable consumption, and nutrition security is a burning issue in the country. Average yields of vegetable crops are low in Bangladesh and this is primarily attributed to lack of innovative technology and poor management practices. The objective of this study was to improve vegetable productivity of smallholder farmers, using plastic mulch. On-farm trials were conducted in two districts in Bangladesh to compare the effectiveness of innovative technology in cauliflower and tomato during 2014–2015. Twenty farmers in each location were selected to conduct the trials, in which cauliflower was selected as a test crop in Rajbari and tomato in Patuakhali district. Data on yield and its components were collected, and the gross return and gross margin were calculated. Cauliflower yielded more than 8.3 t ha^{-1}with plastic mulching, compared to without plastic mulching at Rajbari location, which was nearly a 19.5% yield improvement. Similar trends were observed with tomato at Patuakhali. Gross margin was higher in plots maintained under plastic mulch, compared to without plastic mulch at both locations. The results indicate that productivity and profitability of vegetables crops can be improved, using innovative technological management practices. Promotion of these more remunerative technologies would enable smallholders to manage all of their farms in an efficient way toward improved agricultural sustainability.

IDT8-022 | Response of quinoa to different water management strategies: field experiments and SALTMED model application results

Rachid Fghire[1]*, Fatima Anaya[1], Oudouissa Ali[1], Ouafae Benlhabib[2], Ragab Ragab[3] Said Wahbi[1]

[1]Laboratoire de Biotechnologie et Physiologie Végétales, Faculté des Sciences Semlalia, BP2390, Marrakech,
[2]Département Production, Protection et Biotechnologies végétales Institut Agronomique et Vétérinaire Hassan II Rabat, Maroc,
[3]Centre for Ecology and Hydrology (CEH), Wallingford, United Kingdom
*E-mail: r.fghire@gmail.com

Given the current water shortage in North Africa, improving water management to produce more crops per drop is vital. In addition, the introduction of drought-tolerant, less water-consuming crops such as quinoa is of great interest. To understand the response of quinoa to water stress in terms of biomass and grain yield under various irrigation management strategies, the SALTMED model was employed using field measurements during the cropping seasons of 2011 and 2012 at a site in the Marrakech region, south Morocco. Quinoa showed its ability to grow in the south of Morocco and give a good yield under full irrigation. However, the experimental and modelling results showed that under rainfed and deficit irrigation, the grain yield was lower than under the full irrigation treatment, and was dependent on water deficit level. The study revealed that a reasonable grain yield of quinoa can only be obtained if it was subjected to moderate water stress conditions. The results indicated that the SALTMED model is able to simulate the quinoa biomass and grain yield under various water deficit levels and that the model can be used in the evaluation of different irrigation strategies.

IDT8-023 | Rhizobacterial endophytes contribute to moisture stress tolerance in senescent genotype of sorghum [*Sorghum bicolor* (L.) Moench]

Govindasamy V[1], [2] *, Priya G[2], Aher L[2], Raina SK[2], Kumar M[2], Rane J[2], Annapurna K[1], Minhas PS[2] , Vittal KPR[2]

[1]ICAR-Indian Agricultural Research Institute, New Delhi, India
[2]ICAR-National Institute of Abiotic Stress Management, Baramati (Pune), India.
*E-mail: govindasamy@iari.res.in

A diverse group of bacteria colonize the exo- and endo-rhizospheres of this crop and play a critical role in its tolerance to drought and other abiotic stresses. We isolated 280 endophytic rhizobacteria from the endo-rhizosphere of sorghum cultivars and subjected them to *in vitro* screening for their plant growth promoting traits. Functional diversity grouping of all these isolates indicated one isolate having five PGP traits and two isolates having four PGP traits; and two and 29 isolates having three and two PGP traits, respectively. The 16S rRNA gene based identification of the isolates of single and multiple PGP traits revealed phylogenetic dominance of *Firmicutes*; *Acinetobacter*, *Bacillus*, *Enterobacter*, *Geobacillus, Lysinibacillus, Microbacterium, Ochrobactrum, Paenibacillus* and *Pseudomonas* which were the major genera present in the endo-rhizosphere of sorghum. Four rhizobacterial endophytes namely; *Ochrobactrum* sp. EB-165, *Microbacterium* sp. EB-65, *Enterobacter* sp. EB-14 and *Enterobacter cloacae* strain EB-48, have been evaluated for stress tolerance imparting ability under both *in vitro* experiments using ½-MS media + 15% PEG, and *in vivo* experiment using sterile soilrite mix base with imposed low moisture stress conditions in sorghum (R-16), a non-stay green and senescent genotype. These rhizobacterial endophytes were successful not only in imparting better cellular osmotic adjustment in leaves, but also in favourable physiological responses such as RWC and MSI to plants under imposed water stressed conditions. Changes in expression of selected stress-responsive genes were also observed in the endophytes-bacterized plants compared to non-bacterized plants. This work provides the basis for the selection of an effective endophytic rhizobacterium or its consortium for moisture stress alleviation in sorghum.

IDT8-024 | Bio protectant potential, abiotic stress tolerance and phytopathogenic properties of *Azotobacter tropicalis*KOP-11 strain isolated from paddy soils

Chennappa G[1]*, Nagaraj H[1], Amaresh Y.S[1], Mahadevaswamy[3], Sreenivasa M.Y[1]

[1]Dept. of Studies in Microbiology,University of Mysore, 570 006, Karnataka, India
[2]Dept. of Plant Pathology,College of Agriculture, UAS, Raichur –584104, Karnataka, India
[3]Dept of Agril.Microbiology, College of Agriculture, UAS,Raichur-584104, Karnataka, India
*E-mail: chinnagurikar@gmail.com

Azotobacter tropicalis KOP-11 strains were isolated by serial dilution method and colonies were pale, milky white to dark in color on Jenson's N-free agar. Morphological, biochemical and molecular studies showed characteristic features of *A. tropicalis* (KF470808). The isolates were further tested for their ability for nitrogen fixation; indole acetic acid and gibberllic acid production; and phosphate solubilization. *A. tropicalis*is efficient in fixation of the highest amount of N_2 (13.5μgN/ml/day), produced IAA (18.78μg/ml), gibberllic acid (17.25μg/25ml) and formed larger P solubilizing zone (9.4mm). *A. tropicalis* produced siderophore and hydrogen cyanide and was positive for ammonia production. Antifungal activity of *A. tropicalis* was tested against *Fusarium* species by dual culture method, and *A. tropicalis* inhibited the mycelial growth (18.33mm) of *Fusarium* on modified media. *A. tropicalis* isolates were also studied for tolerance to abiotic stress, against salt (0-10%), temperature (4-55ºC) and pH (5.0-10). *A. tropicalis* was found to be tolerant to a maximum of 6% NaCl at a temperature of 35-45ºC and upto pH 8. The studies revealed that the *A. tropicalis* strains not only influenced plants by producing plant growth promoting substances, but are also tolerant to abiotic stresses. Growth and survivability were tested in different formulations such as farm yard manure, lignite and talc. *A. tropicalis* recorded the highest population in talc and lignite (3.33 and 3×10^5). Talc formulation maintained a steady population throughout the year. Overall, it is confirmed that talc is the best carrier material for bio-fertilizer production to support viable population of *Azotobacter* for a longer shelf life.

IDT8-025 | Seed bioprotectant efficacy of *Azotobacter salinestris* and *Azotobacter* species (JX 262164) against phyto pathogenic *Fusarium* associated with cereal grains.

Nagaraja H[1], Chennappa G[1], Nayak MK[2], Sreenivasa M Y*.

[1]University of Mysore, Manasagangotri, Mysore- 570 006 Karnataka, India.
[2]University of Agriculture Sciences, Raichur – 584 104, Karnataka, India
*E-mail: sreenivasamy@gmail.com

Antifungal efficacy of *Azotobacter salinestris* and *Azotobacter* species (JX 262164) against phytopathogen *Fusarium* species such as *F. sporotrichioides, F. crookwellense, F. graminarium, F. poea, F. sambusinum, F. culmorum, F. acuminatum. F. avinacium, F. nivale* and *F. equeseti* associated with maize, sorghum and wheat was investigated. Challenge inoculation of *Fusarium* sp to three cereals showed 100% infection incidence. Maize recorded the highest vigour index against *F. acuminatum* (1859.715), in sorghum against *F. graminearum* 1470.84, and in wheat against *F. nivale* (2804.123). Percent germination was 76% in maize, 69% in sorghum and 68% in wheat when treated with *A. salinestris*. The efficacy of *Azotobacter* species (JX262164) results showed increased root length/shoot length of 13.81±2.25/11.28±2.70, 17.18±1.89/11.33±1.84 and 20.64±2.85/12.15±1.78 compared with control as 6.88±1.68/6.1± 0.86, 9.90±0.88/8.60±0.76 and 14.93±2.4cm in maize, sorghum and wheat respectively. The 100% germination was observed in maize, sorghum and wheat as compared to 60% and 80% of germination in untreated and control respectively. The growth enhancing ability of *Azotobacter salinestris* in green house experiments revealed the highest shoot length/root length recorded on 45th day in maize was (155.70/70.0) cm, in sorghum (165.90/48.0) cm and in wheat (77.85/56.0) cm. The highest root mass was 17.53 g in maize, 4.52 g in sorghum, and 1.90 g in wheat. In the case of *Azotobacter* (JX262164) the maximum shoot length was 151.40±10.62 in maize, 144.10±12.57 in sorghum, and 157±11.53 in wheat respectively. Root length/root mass was 86 cms/13.63 g in maize, 44cms /1.20 g in sorghum and 51cms/1.24 g. This study strongly confirmed that *Azotobacter* is a beneficial tool in agriculture and could be used as alternate bio control in crop protection.

IDT8-026 | Applications of Enclass® system and managed stress environment for characterizing and developing drought-tolerant products in corn

Hegde S[1]*, Gangashetti M[1], Kodappully V[1], Pandravada A[1],

[1] Pioneer Hi-Bred Pvt Ltd, Hyderabad, India
*E-mail: shridhar.hegde@pioneer.com

Drought stress is the single most important environmental factor affecting maize productivity and yield stability in main corn markets. DuPont Pioneer is the leader in the development of drought-tolerant corn hybrids through a multi-phase approach that delivers total product performance, minimizing risk and maximizing productivity on every acre.

The EnClass® system is a tool for classification of crop environments. It uses crop modeling technologies that integrate genetics, environment and management information to describe environmental variation. Statistical classification methods further cluster environmental information as integrated by crop models to determine environment classes that differentiate hybrid performance. This technology helps predict how products will perform in various environments. EnClass uses crop modeling and historical weather data (shown) to estimate the long-term frequency of weather environments expected at given locations. Managed stress Environment (MSE) is a testing location in which major environmental factors are managed to allow maximum expression of genetic variation in target stress in a repeatable manner. Key requirements of a managed stress environment location is no rainfall during growing season, precision irrigation, uniform temperature, uniform soils, few insect and disease interactions, and high yield potential when irrigated. In our experiment at Dupont Pioneer, we have tested 150 hybrids under managed stress environment with three treatments *viz.,* flowering stress, grain fill stress and well-watered or control treatment. Irrigation was given using subsurface drip system and the soil moisture availability was tested using moisture probes. With precision stress treatments, we could estimate differential yield loss of test hybrids under flowering and grain fill stress conditions.

IDT8-027 | Coinoculation with *Bradyrhizobium japonicum* NU1 and *Pseudomonas putida* NUU8 to improve growth and nodulation of soybean under drought condition

Jabborova D[1],[2]*, Davranov K[2], Turakulov Kh[1]

[1] Uzbekistan Academy of Sciences, Institute of Genetics and Plant Experimental Biology
[2]Faculty of Biology, National University of Uzbekistan
*E-mail: dilfuzajabborova@yahoo.com

Drought stress is the major abiotic factor limiting crop production. Inoculation of plants with beneficial plant growth promoting rhizobacteria improves plant growth and increases drought tolerance in arid or semiarid areas. Soybean is a major source of high-quality protein and oil for human, which is also sensitive to drought stress. Co-inoculation of drought-stressed legumes with nodulating rhizobia and root-colonising, plant growth promoting rhizobacteria improved the root and the shoot growth, formation of nodules and nitrogen fixation capacity in soybean. The objectives of this research were to observe if the co-inoculation of soybean (*Glycine max* L. (Merr.) with *Bradyrhizobium japonicum* NU1 and *Pseudomonas putida* NUU8 can enhance drought tolerance, nodulation and plant growth under drought condition. The results showed that co-inoculation of with *B. japonicum* NU1 *and P. putida* NUU8 gave more benefits in nodulation and plant growth of soybean compared to plants inoculated with *B. japonicum* NU1 alone and uninoculated control. Under drought condition, co-inoculation of *B. japonicum* NU1 with *P. putida* NUU8 strains significantly improved the shoot dry weight by 100% and the root dry weight by 30% in soybean compared with the uninoculated control. Co-inoculation of with *B. japonicum* NU1 and *P. putida* NUU8 significantly increased the shoot length by 45% , the root length and the number of nodulation by 82%, compared with the single inoculation with *B. japonicum* USDA110. The synergistic use of *B. japonicum* NU1 and *P. putida* NUU8 also improved on plant growth and nodulation of soybean under drought stress. The results suggested that these strains could be used to formulate a biofertilizer for sustainable production of soybean under drought stressed field condition.

IDT8-028 | Evaluating response of groundnut to crop geometries and growth promoting substances

Jat R. A.[1]*, Solanki R.[1], Thumbar B.[1]

[1]ICAR-Directorate of Groundnut Research, Junagadh, 362 001 Gujarat, India
* E-mail: rajatagron@gmail.com

A field experiment was conducted during *kharif* 2015 to identify suitable crop geometry in groundnut (variety TG 37 A) to facilitate mechanical interculturing to reduce cost on weed control, improve moisture conservation and enhance productivity; and also to evaluate the response of groundnut to growth-promoting substances. For mechanical interculturing with mini-tractor or bullock-drawn implements, wider spacing (at least 45 cm between rows) is required, but wider spacing reduces yield due to reduced plant stand. Therefore, suitable crop geometry needs to be identified to facilitate mechanical interculturing without yield penalties. The experiment was laid out in split plot design with three replications. In the main plot, five treatments of crop geometries, *viz.,* 30x10 cm, 45x10 cm, 45/10x10 cm, 45/15x10 cm, and 45/20x20 cm spacing, while in sub plots four treatments of growth promoting substances *viz*., control (only *Rhizobium*), plant growth promoting Rhizobia (PGPR), *Amrit pani*, and PGPR+*Amrit pani* , were tested.

The response of groundnut to crop geometries and growth-promoting substances was found to be significant. Sowing of groundnut at of 30x10 cm spacing, being on par with 45/10x10 cm spacing, gave significantly the highest dry matter per plant, pod and haulm yield, and net returns. Sowing with 45/10x10 cm spacing was also found to have the highest soil moisture content, but the least number of weeds. While the lowest pod and haulm yield, and net returns were found with crop geometry of 45x10 cm spacing. Seed treatment with PGPR significantly improved plant height, dry matter per plant, pod and haulm yield, and net returns of groundnut over control. Foliar spray of Amrit *pani* improved pod and haulm yield of groundnut, but differences were not significant at 5% probability.

IDT8-029 | Improvement of flower yield and physiological traits of saffron (*Crocus sativus* L.) under drought stress via different planting dates and corm sizes

Ghorbani Javid M[1],*, Ghobadi F[1]

[1]University of Tehran, Tehran, Iran.
*E-mail: mjavid@ut.ac.ir

Drought stress is a major factor limiting of yield of plants. Saffron is the most expensive spice in the world and it is an autumn plant that is semi resistant to water stress. Although Iran has the largest area under cultivation of saffron, its yield is low under drought stress conditions when compared with global production. In order to evaluate the effect of different planting dates and the corm size on improvement of yield, and some physiological characteristics of saffron under drought stress, an experiment was conducted as factorial in a randomized complete block design with three replications at the research farm of College of Abouraihan, University of Tehran, which is located in a dry plain with annual rainfall less than 100 mm. Four planting dates, 10 June, 7 September, 27 September and 12 October, and two corm sizes of 5-8 g and 10-14 g were considered as treatments. The evaluated physiological traits, which include proline and protein content in leaves; and yield traits which include number of flowers and dry weight of stigma; were measured in a square meter and the starting date of flowering was recorded. The results of this research showed that cultivation of large saffron corms (10-14 g) on the planting date of 10 June had maximum yield, with production of 62.7 flowers and 0.299 grams of dry weight of stigma in a square-meter plot. Leaf proline concentration of small saffron corms (5-8 g) on the planting date of 12 October and leaf protein concentration of small saffron corms (5-8 g) on the planting date of 10 June were higher than the other planting dates. Increasing proline concentration increased plant resistance under drought and cold in corms planted on 12 October, particularly with small corms. In general, these results indicate that improvement of flower yield in the first year is more influenced by corm size, and planting of large corms (10-14 g) on 10 June will have a suitable production.

IDT8-030 | SWOT Analytical Framework of Innovation Platforms (IPs) for promoting the adoption of improved Groundnut seed in Northern Ghana

Jinbaani AN*[1], Oteng-Frimpong R[1], Nutsugah SK[1], Adogoba DS[1], Nyuor A[1], Lamini S[1] and Wiredu AN[2]

[1]CSIR-Savanna Agricultural Research Institute (SARI), Tamale, Ghana
[2]International Institute of Tropical Agriculture, Nampula, Mozambique
*E-mail: alhassanjinbaani@gmail.com

The main objective of the study was to identify internal strengths and weaknesses as well as external opportunities and threats in sustaining Innovation Platforms (IPs) for improved groundnut seed delivery in Northern Ghana. This study employs the strengths, weaknesses, opportunities and threats (SWOT) analytical framework of existing IPs on groundnut established under the Tropical Legume III (TLIII) project in the 3 regions of Northern Ghana; Upper East, Upper West and Northern Regions. A total of seven IPs were surveyed using Focus Group Discussions (FGDs). From the results of the study, presence of seed producers, an IP composed of well identified actors and regular financial contributions by IP members were identified as key strengths of the IPs. Weaknesses identified included poor consultation among IP members and lack of clear cut procedure on resolving disagreements. Key opportunities identified in the study were the presence of credit lending financial institutions and Non-Governmental Organizations (NGOs) implementing agricultural projects at the district and community levels. Drought, insect attack, high cost of borrowing as well as high default rates among borrowers were identified as threats facing Innovation Platforms. SWOT analysis of internal strengths and weaknesses as well as external opportunities and threats is important for sustaining IPs. The study recommends that groundnut seed producers within the IPs should be trained on how to produce certified groundnut seed. Also, Savanna Agricultural Research Institute (SARI) and the Ministry of Food and Agriculture (MoFA) should work together to address the threats identified in the study.

IDT8-031 | The weeds flora of grain sorghum (*Sorghum bicolor* (L.) Moench) in Senegal (West Africa): characterization of flora and species harmfulness

Ka SL[1], [2], Mbaye MS[2], Gueye M[1], Noba A K[2]

[1]Service Agronomie, Senegalese Institute of Agriculture Research/CRZ, Kolda, Senegal
[2]Cheikh Anta Diop University of Dakar, SENEGAL
*E-mail: kasam74@gmail.com

Senegal is a Sahelian country where agriculture employs nearly 70% of the active population (Kane, 2014). However, agricultural production is limited by several constraints, the most important are water, soil fertility and weeds flora pressure. Therefore, the improvement of agricultural production, including sorghum, requires a good knowledge of the structure of the weeds. This study was realized in southern Senegal at the experimental station of the Senegalese Institute of Agriculture Research from 2015 to 2017. It aims to study the weed flora of sorghum, to determine the yields and the critical periods, and to propose a technical weeding route. This study focuses only on the characterization of weed flora. Thus, phyto- sociological surveys were carried out in sorghum fields on station and in numerous rural areas in Upper Casamance. It appears from this study that the weed flora of sorghum consists of 120 species, 75 genera and 26 families. This flora is dominated by dicotyledons that are 76.92% of the species. Five families are more than 50% of the species : *Fabaceae*, *Poaceae*, *Convolvulaceae*, *Cyperaceae* and *Malvaceae* (8.33%). Therophytes dominat ewith 72.5% of the flora, while perennials represent 27.5% of the flora. The African species dominate, followed by the pan-tropical species. Started last year, the inventory is ongoing and a study of weed competition is installed on station to determine a weeding calendar of sorghum.

IDT8-032 | Water-saving irrigation to maximize rice production in Colombia

Deshmukh V[1], Kamoshita A[1]*, Lorena Lopez-Galvis[1], Dario Pineda[2], Gabriel Garces[2], Nelson Amezquita[2]

[1]University of Tokyo, Tokyo, Japan
[2] FEDEARROZ, Colombia
*E-mail: akamoshita@anesc.u-tokyo.ac.jp

Two levels of water-saving irrigation by lengthening irrigation interval (small saving and risky saving as W2 and W3, respectively) were compared with conventional frequent irrigation (W1) for rice productivity together with 5 levels of N fertilizer application methods (220 N with 5 splits, 180 N with 5 splits, 140 N with 5 splits, 180 N with 3 splits of mixture of slow release, 0 N) and among 8 rice genotypes (Fedearroz60, Fedaerroz174, Fedaerroz473, CT21375, Fedearroz67, Fedearroz733, IR64, IR64_Dro1) in Central Colombia in 2 seasons from 2015 to 2016. Grain yield was linearly reduced from W1 (1247 mm) to W2 (1161 mm) and W3 (908 mm) as more irrigation water was saved in the first growing season from May to Sep 2015 where evapotranspiration was higher with higher cumulative solar radiation. Yield was reduced only in W3 (with 683 mm) but not in W2 (693 mm) compared with W1 (1047 mm) in the second growing season (Feb to June 2016) where evapotranspiration was lower and yield potential was smaller due to high temperature during the first 2 months and consequent shortened vegetative period, resulting in higher water productivity (total water basis) in W2 (0.61 kg m^{-3}) than W1 (0.43 kg m^{-3}) and W3 (0.49 kg m^{-3}). The magnitude of water-saving (i.e., compared with W1) during the first 2 month was larger in the 2015 experiment than the 2016 experiment, and it was smaller in W2 than W3 in the 2016 experiment. N treatments had in general small effects except for 0N treatment, indicating possibility of saving of N from the conventional level (180 N). Fedearroz473, Fedearroz174, Fedaerroz67 yielded higher with higher water productivity than Fedaerroz60. Prospect for water-saving irrigation is to be discussed.

IDT8-033 | Soil water conservation strategies effects on maize yields in farmer managed trials in the central highlands of Kenya

Kiboi MN[1]*, Ngetich KF[1], Diels J[2], Mucheru-Muna M[3], Mugwe J[3], Mugendi DN[3]

[1]University of Embu, Embu, Kenya
[2]K.U.Leuven, Leuven, Belgium.
[3]Kenyatta University, Nairobi, Kenya
*E-mail: milka.kiboi@gmail.com

Farmers in the central highlands of Kenya have experienced a decrease in crop yields in recent decades as a result of low water availability in the area, caused by low and erratic rainfall, low inherent water storage (by the soils) and poor water harvesting techniques. On-farm trials were set up to determine the effects of soil water conservation strategies (mulching (MC), tied ridging (TR) and minimum tillage (MT) on maize yields. The research was carried out in Mbeere South and Meru South sub-counties for four consecutive cropping seasons: short rains 2011, long rains 2012, short rains 2012, and long rains 2013. The experimental design was an incomplete randomized complete block design with the SWC treatments replicated four times and a control (CT) practised by each farmer. Data was subjected to analysis of variance using general linear model in SAS 9.2 and mean separation done using least significant difference at p=0.05. Compared with the CT, results showed that in Mbeere South grain yields significantly increased under TR and MC during LR12, SR12 and LR13 seasons. In Meru South, yields significantly increased under all the tested SWC strategies during SR11, LR12 and SR12 seasons. Maize grain yields were more stable under TR and MC, with residual variances of 0.107 and 0.183 Mg ha^{-2}, respectively in Mbeere South. Mulching, MT and TR strategies indicated yield stability with residual variances of 0.017, 0.039 and 0.155 Mg ha^{-2}, respectively, in Meru South. Findings highlight the importance of SWC strategies for stable maize yields.

IDT8-034 | Performance of marker assisted backcross breeding (MABC) elite chickpea lines under drought conditions in Kenya

*Paul Kimurto[1], Moses Oyier[1], Richard Mulwa[1], Sarah Songok[1], Bernard Towett[1], Erick Cheruiyot[1], Rajeev Varshney[2], Pooran Gaur[2], Thudi Mahender[2], Gangarao Rao[3], Said Silim[3] and Moses Siambi[2]

[1]Dept of Crops, Horticulture and Soils, Egerton University, P.O. Box 536, Egerton Kenya
[2]ICRISAT, Eastern and Southern Africa Regional Office, Nairobi Kenya
[3]ICRISAT, Headquarters, Pantancheru, India
*E-mail: kimurtopk@gmail.com

Drought is the most important constraint affecting production of chickpea and other crops as well. Quantitative traits like drought tolerance are multigenic and their inheritance is difficult to predict hence the need to explore more precise breeding techniques like maker assisted selection. The aim of this study was to introgress the identified root trait QTLs into Kenyan adapted cultivar to enhance drought tolerance through marker assisted backcrossing. Four varieties *Chania Desi* 1 (ICCV 97105), ICCV10, ICCV 92318, and *Saina K*1 (ICCV 95423) were selected as a recurrent parents for improvement among ten agronomically superior elite cultivars after exhibiting high polymorphism with SSR markers. Five molecular markers (CaM1903, CaM1502, TAA 170, NCPGR21 and GA11) were validated for use in MABC deployed in this study. Crosses were made between the four parents and ICC 4958 followed by marker screening of the F1 seedling progenies for the QTL of interest. Identified true heterozygotes were used as donors and backcrossed to the recurrent parent to obtain BC1F1 seeds. The process was repeated to obtain BC2F1 and finally BC3F1 with molecular marker identification of seedlings carrying the QTL region at each step. Results of evaluation in one trial site in Kenya semi-arid area (Koibatek ATC) of MABC lines for the four parents ICCV10 (24 lines), ICCV 92318 (8lines), ICCV 97105 (12 lines) and Saina K1-ICCV 95423 (10 lines) showed that the best progenies with higher levels of drought resistance and yield were ICCMABCD-21, 9, 20, 23, 15, 22, 5, 14, 16, 19 and 6 with yields > 2.5 tons/ha. The results indicated that it is possible to transfer QTL that confers drought tolerance using MABC. The best progenies are undergoing further evaluation to validate the contribution of the introgressed QTL in improving drought tolerance and yield.

Key words: Marker Assisted Backcross (MABC), Drought tolerance, Donor parent, Recipient parent, Quantitative trait loci (QTL)

IDT8-035 | Best Management Practices in sunflower for maximizing yield in dry lands

Kumar GDS[1]*, Aziz Qureshi A[1], Sudhakara Babu SN[1], Hareesh kumar S[1],

[1] ICAR- Indian Institute of Oilseeds Research (IIOR-ICAR), Hyderabad, India
*E-mail: gd.satishkumar@icar.gov.in

In India, sunflower is cultivated in an area of 0.55 m ha with a production of 0.42 m t (2014-15) mainly under rainfed conditions. The productivity is highly fluctuating due to vagaries of monsoon. The researchers involved in the All India Coordinated Research Project (AICRP) on sunflower developed several technologies suitable to specific agro-ecological situations to manage drought and excess moisture. But, awareness and adoption of these technologies among farmers is far less than anticipated. Hence, effective and efficient technology transfer models are required to transfer the existing technologies from research system to the farmers' fields in order to realize immediate gains to the individual farmers and long term gains in enhancing the knowledge of farmers. The present project was implemented to demonstrate the potential of Best Management Practices (BMPs) of sunflower developed by the researchers. Two States Karnataka and West Bengal which represent traditional and non- traditional States for sunflower cultivation were selected. Based on the climate, soils, water availability and the scope and potential of sunflower, two potential districts each representing high spread-low productivity and low spread-high productivity in the two states were identified. In consultation with stakeholders (farmers, researchers and officials of agriculture department) BMPs identified for each district/region in sunflower were demonstrated in farmers' fields on a large contiguous areas at each site. The paper discusses the results of the demonstrations conducted on 272 farmer's fields and their perception of the technologies in managing the variation in rainfall.

IDT8-036 | Selection of *Trichoderma* spp. for plant growth promotion and abiotic stress tolerance

Kumar A[1]*, Jain AK[1], Tripathi SK[1], Tiwari RK

[1]JNKVV, College of Agriculture, Rewa M.P., India
*E-mail: ashishashish2612@gmail.com

Trichoderma is a genus of filamentous fungi that include strains used as biocontrol agents in agriculture due to their antagonistic abilities against phytopathogenic fungi and oomycetes. The biocontrol mechanisms are based on the production of antibiotics and/or hydrolytic enzymes as well as competition for nutrients. In addition, *Trichoderma* strains are also able to stimulate defense responses in plants, inducing resistance to biotic and abiotic stresses, and promote plant growth. In recent years, the use of indigenous *Trichoderma* isolates has been suggested as a method to counter some of the factors responsible for inconsistency in performance. Keeping this in view, a study was conducted to identify the abiotic stress-tolerant isolates of *Trichoderma* spp. from Madhya Pradesh and further use the selected isolates for plant growth promotion and biological control. In the present investigation, a total of 177 soil samples were collected from cultivated (121) and non-cultivated (56) farmers fields of Madhya Pradesh and 40 isolates of *Trichoderma* spp. was isolated from 40 different locations of 62 blocks from 14 districts of Madhya Pradesh. The isolated *Trichoderma* spp. represented not only the different locations of Madhya Pradesh but also the non-cultivated and cultivated fields of different crops like chickpea, chilli, guava, kodo millet, maize, mango, mungbean, pigeonpea, rice, sesame, soybean, tomato, wheat and sugarcane. All isolates were subjected to high- and low-temperature stress; and colony characteristics and radial growth was observed. Among the 40 isolates, two isolates of *Trichoderma* were recorded as tolerant to high temperatures. The selected isolates were also tested for plant growth promotion in tomato under green house conditions. Maximum root and shoot length was recorded in seed treatment with T_4 isolate of *Trichoderma*. Further, all the isolates were evaluated for their antagonistic potential under *in-vitro* conditions against different plant pathogens and differential reactions were recorded. The study confirmed the significant root growth promotion which will help in improved plant growth under drought stress. High-temperature-tolerant isolates of *Trichoderma* spp. coupled with better antagonistic potential and plant growth promotion activity will open new avenues for crop growth under biotic and abiotic stress conditions.

IDT8-037 | Potential application of aldose reductase homolog from a resurrection plant for abiotic stress tolerance

Kumar D[1,2]*, Singh P[1], Sarin NB[1]

[1] School of Life Sciences, Jawaharlal Nehru University, New Delhi, India.
[2]Department of Plant Sciences, Central University of Jammu, Jammu
*E-mail: deepakinjnu@gmail.com; deepakkumar@cujammu.ac.in

Drought and salinity exert osmotic stress on terrestrial plants, causing water deficit, which consequently affects plant growth and development. Therefore, these stresses are recognized as among the most serious challenges to crop production worldwide. Different environmental stresses imposed on plants may result in similar responses at the cellular and molecular level. It has been demonstrated that the level of methylglyoxal (MG), a cytotoxic compound, increases upon exposure of plants to various abiotic stresses, in addition to ROS. Methylglyoxal is mainly catabolized by two major enzymatic pathways. The first is the ubiquitous detoxification pathway, the glyoxalase pathway. An alternate pathway involves aldose reductase that converts methylglyoxal into acetol in a NADPH-dependent two-step reaction. It is this pathway that we have exploited in our study. A detailed functional validation of aldose reductase homologue *ALDRXV4* was first carried out in a model plant, tobacco, and subsequently used for the transformation of a recalcitrant pulse crop, *Vigna mungo*. Studies with the model plant and crop plant revealed that over-expression of *ALDRXV4* in transgenics were more tolerant not only to osmotic stress, but also salinity stress. The increased aldose reductase activity, higher sorbitol content and less accumulation of the toxic metabolite methylglyoxal in the transgenic lines under non-stress and stress conditions resulted in increased protection through maintenance of better photosynthetic efficiency, higher relative water content and less photo-oxidative damage. Together, these findings suggest the potential of engineering aldose reductase levels for better performance of agriculturally important crop plants growing under stress conditions in future.

IDT8-038 | Efficacy of *Jatropha* seedcake on growth, photosynthesis and yield of *Camelina sativa* under water-limited conditions

Kumar S[1], Reddy A. R.[1]*

[1]University of Hyderabad, Hyderabad-500046, Telangana, India.
*E-mail: attipalli.reddy@gmail.com

Camelina (Camelina sativa L. Crantz) is a non-food oilseed crop which holds promise as an alternative biofuel energy resource. We designed a study to investigate the effect of increasing the concentration of *Jatropha* seedcake on growth, photosynthesis and reproductive yields of *Camelina sativa* (cv. Celine). A field-based trial was performed in a randomized block design and five different treatments of seedcake (control: T_0; 1 t ha^{-1}: T_1; 2 t ha^{-1}: T_2; 3 t ha^{-1}: T_3; 4 t ha^{-1}: T_4) were applied (soil application) after one week of sowing of seeds of *Camelina* in four experimental plots. A separate positive control plot was maintained and treated with basal application of inorganic fertilizer (NPK). All the treatments were subjected to two different watering schemes, well-watered (WW) and drought (D). The *Camelina* plants at T_3 and T_4 treatment provided the best economic outcomes, in terms of the highest improvement in growth and seed yield under both WW and D, with the yields better in WW conditions when compared to D. The seed yield increment was mainly due to enhanced number of siliques and secondary branches per plant when compared to the control. The treated plants displayed better photosynthetic leaf gas exchange characteristics, higher chlorophyll contents and possessed dark green leaves which were photosynthetically active for a longer period and facilitated higher photoassimilation than the respective controls in both WW and D conditions. Our study elucidates that *Jatropha* seedcake can be a potential organic fertilizer to achieve better growth and seed yield from *Camelina* under water-limited environments.

IDT8-039 | Adaptation of seven quinoa (Chenopodium quinoa Willd.) cultivars to agroecological conditions of Kinshasa (DRC)

Lutonadio G.S.*

University of Kinshasa, Kinshasa, Democratic Republic of the Congo" and
*E-mail: geniespiroulutonadio01@gmail.com

Recognized as a highly nutritious food and a crop of great value in terms of tolerance to abiotic stresses, quinoa constitutes an alternative and a strategic crop that can adapt to diverse soil and climatic conditions; to large altitude and latitude ranges; and to marginal agricultural production systems. This makes it important for diversification of future agricultural systems in this time of climate change. In a preliminary study conducted at the University of Kinshasa, (DR Congo), seven quinoa cultivars were evaluated over two consecutive cropping seasons (dry season and wet season in 2016) for their adaptation. Three high-ranking cultivars(Pasankala, Puno and Titicaca) selected on the basis of their survival in the local environment were evaluated, based on agronomic traits and production potential in a replicated field trial.There were significant differences among the three cultivars for growth and development ($P<0.05$), with respective mean values of plant height of 18.50 cm, 15.05 cm and 17.53 cm. Differences among cultivars for production parameters were found to be significant ($P>0.05$) with respective mean values for seed weight per plant of 140.26 g, 96.64 g and 180.03 g; the above-ground biomass mean values were 243,46 g, 170,14g and 280,03 g respectively. Cultivars such as Blanca of Junin, Blanca de Soraca, Choclito and Salcedo did not survive due during the experiment due most probably to photoperiod sensitivity and/ordamping-off in wet season, which resulted in death of seedlings.

IDT8-040 | Potential contribution of maize (*Zea mays*) in the estimation of croplands' carbon fluxes under climate variability using static chambers in Kenya

Macharia J.M[1]*, Ngetich F.K[2] , Shisanya C.A[1]

[1]Kenyatta University, P.O Box 43844-00100, Nairobi, Kenya
[2]UniversityofEmbu, P.O Box 6-60100, Embu, Kenya
*E-mail: machariamjoseph@gmail.com

Agricultural crop production will be significantly affected by changes in climate due to rising carbon dioxide (CO_2). Sub-Saharan Africa heavily depends on rainfed agriculture, thus making the region one of the most vulnerable regions to climate change. Adaptation to climate variability in the region is, thus, critical not only because of the existing poverty but also because of the large uncertainty on the effects and the magnitude of climate variability. Carbon sequestration by cropland has been suggested as an option for mitigating rising CO_2 levels. However, the carbon fluxes' estimations during the maize crop growth are not well understood. Thus, this study aims to determine the carbon fluxes rates in fields under maize crop in Embu County of Kenya. The study involves experimental designs under research type with experiments set up in the ASALs of Mbeere South Sub Counties. Experimental data will be analyzed using ANOVA, and means separated using least significant difference (LSD) by means of R software. Results will be presented using tables and figures. The initial results indicate that application of urea at 60kgNha^{-1} had the highest fluxes at 1670 mgCO$_2$/m^2/ha. It is envisaged that the findings of this study will provide an adaptation guideline to the smallholder farmers on timely preparation of farmland, mobilisation of seed/crop, and manpower, and most likely reduce the risk of planting and sowing too late or too early. The findings will also assist the Kenyan government in tracking and accurately reporting carbon emissions from the land sector.

IDT8-041 | LHCSR3 impairs photosynthetic membrane complex assembly of *Chlamydomonas reinhardtii*under drought stress

Madireddi SK[1], Bag P[1], Nama S[1], Subramanyam R[1]*

[1]University of Hyderabad, Hyderabad, Telangana 500046 India.
*E-mail: srgsl@uohyd.ernet.in

Photosystems (PSI and PSII) run photosynthetic processes that convert light energy to chemical energy by carbon fixation. This process is affected by abiotic stress factors leading to the compromised photosynthetic yield that affects plant growth and eventually leads to loss of crop yield. Earlier reports suggest that photosynthetic yield is decreased under water deprived conditions due to stomata closure which causes limited supply of carbon dioxide, impairs ATP synthesis, hampers sucrose metabolism and damages photosynthetic apparatus. The present work represents the consequences of drought stress on photosynthetic efficiency in turns of assembly of photosynthetic assembly. By using biochemical and biophysical approaches such as lpBN-PAGE, PAM, and Circular-dichorism, we studied physiological, morphological, structural and functional changes in photosynthetic apparatus in *C. reinhadrtii,* under Poly Ethylene Glycol (PEG)-induced artificial drought conditions. Significant findings of this work are: (i) in contrast to previous observations, under drought, there is negligible damage to protein content of photosystems, but there is significant decrease in electron transport rate (ETR) and photosynthetic yield. (ii) there are intact core complexes in both photosystems, but assembly of core with peripheral antenna to form functional super/mega complexes of PSII is affected. (iii) significant expression of LhcSR3in drought stress indicates role of this protein in disassembly of photosynthetic complexes. Hence, we propose that alteration in assembly of photosynthetic membrane complexes under drought is one of the reasons for decreased photosynthetic yield. Expression of LHCSR3 coupled with impaired assembly of PSII super and mega complexes under drought indicates the photo-protective adaptation under high light.

IDT8-042 | Determination of suboptimal irrigation rates through drip for maize (*Zea mays* L.) under southern peninsular region of India

Kadasiddappa Malamasuri[1]*, Praveen Rao V[2], Yella Reddy K[3], Ramulu V[2], Uma Devi M[2], Narender Reddy S[2] and Ashvathama V.H[1].

[1]University of Agricultural Sciences Dharwad, India
[2]Water and Land Management Research and Training Institute (WALAMTARI), Hyderabad, India
[3]Prof. Jayashankar Telangana State Agricultural Universities, Hyderabad, India
*E-mail: kadasiddappa.m@gmail.com

Maize is one of the most efficient field crop in producing higher dry matter and grain yield per unit quantity of water applied among the cereals. Presently, all agricultural producers are facing decreasing water supplies and are becoming increasingly aware of the need for conservation of limited water resources. An alternative way to address these concerns is to utilize new irrigation technologies such as drip irrigation. Hence, increased and efficient use of water and nutrients can be achieved under water stress and resource constraint situations along with the higher yield levels. In this context, a field investigation was carried out in two successive *rabi* seasons to determine the suboptimal rate of irrigation through drip. The study consisted of five levels of irrigation through drip (40%, 60%, 80%, 100% and 120% Epan) based on pan evaporation and a surface irrigation at IW/CPE=1. The result shows that, when irrigation was applied at suboptimal level (80% Epan) the crop performed statistically at par (8215 kg/ha) with that of 100% (8456 kg/ha) and 120% (8189 kg/ha) Epan irrigation levels. Further, the yield levels obtained at 60% Epan (5914 kg/ha) was able to produce equivalent growth and yield parameters with that of surface irrigation applied at IW/CPE=1 (6003 kg/ha). This indicates that crop grown under southern peninsular region can produce analogous yield with suboptimal levels of water than fully irrigated crop and helps in saving water to the tune of 20-30%, yield levels 35-40% compared to surface irrigation and also energy consumption. Therefore, such perceptive physiological performance of the crop not only helps in realizing higher yield but also helps in saving of precious water under this climate change scenario and further helps in increasing the irrigation area to sustain and achieve the food security of the country.

IDT8-043 | Efficacy of polymer coated cotton seeds on crop productivity under moisture stress conditions

S. Deepika, Manonmani V , Ambika. S

Tamil Nadu Agricultural University, Coimbatore-641003, Tamil Nadu, India
*E-mail: vmano_2004@yahoo.com

Cotton is the world's leading natural fibre crop. India is the second largest cotton producer in the world. Cotton seed is susceptible to water stagnation as well as severe drought, and seed germination is highly influenced by moisture status of the substrate. In order to get better establishment under very low and very high moisture status, polymer coating technology is highly useful. Hence, assessing the germinability of the coated seeds at different water-holding capacities will be useful for stress management. A field experiment was conducted to assess the efficacy of polymer coating on growth and productivity of cotton under moisture stress conditions. The cotton seeds were polycoated with various polymers *viz.,* Genius coat 171, Genius coat 172, Arcus, Myconate and Quick roots, and tested along with the untreated control. The polymer-coated seeds were raised in the field by creating stress at 50% flowering stage, boll formation stage, and at both 50% flowering and boll formation stages, along with normal irrigation. The results showed that cotton seeds coated with Quick roots recorded higher field emergence (99%), early flower initiation and lesser days for 50% flowering than the untreated control seeds. Seeds coated with Quick roots recorded higher plant height (138.3 cm), and increased number of bolls per plant, boll weight, number of seeds per boll, kapas yield (1749 g/ plot) and seed yield (627 g /plot) under stress at boll formation stage, than with stress at both 50% flowering and boll formation stages. Seeds coated with Quick roots increased the physiological parameters *viz.,* leaf area index (2.38), relative water content (73%), chlorophyll stability index (74%), soluble protein content (7.7 mg g^{-1}) and nitrate reductase activity (35.7 $\mu g\ NO_2\ g^{-1}\ h^{-1}$) under stress at boll formation stage when compared to stress at both 50% flowering and boll formation stages.

IDT8-044 | Dissemination and adoption of drip irrigation among smallholder farmers in Svosve-Wenimbi, Marondera, Zimbabwe

Pisa C[1], Ngezimana W[1], Chipomho J[1], Tatsvarei S[1], Mapope N[1], Mupeti S[1], Chimsoro T[2], Masuka BP[1]*

[1] University of Zimbabwe Marondera College of Agricultural Sciences and Technology, Marondera, Zimbabwe
[2]Pedstock Corner Alpes and Harare Drive Harare
*E-mail: trimasuka@gmail.com

Smallholder farmers in Zimbabwe produce maize as a staple food crop and other field crops including groundnuts, cowpeas and millets under rainfed conditions while supplementary irrigation is provided for high value horticultural crops. Production is mostly in marginal areas with poor soils, where yields are low due to frequent droughts and low fertilizer use. Yield of staple and pulse crops has declined over the years. Low yield due to frequent drought and limited water in reserves raised the need to efficiently utilize water and improve productivity in the field to improve food security and conserve available water. Drip technology is used widely in urban areas and on commercial farms. With drip technology smallholder farmers can irrigate small land areas (500- to 5000 m^2) to produce vegetables off season and supplementary irrigate maize during the rainy season for food security. To disseminate drip technology to smallholder farmers and evaluate adoption, UZMCAST, AGRITEX and Pedstock trained 75 farmers from Svosve-Wenimbi on drip irrigation in March 2016, encouraged adoption and linked farmers to suppliers. Technical support was given by trainers on contact, ICT (whatsapp platform) and upon request. All trained farmers expressed willingness to adopt but cited cash flow challenges. Six months post-training, 5.3% trained farmers had purchased and installed the drip system each on about 1000 m^2. This enabled off season production and cut down energy usage, labour and water requirements by up to 90%. With training adoption of technology is promising and can improve food security even with limited water resources.

IDT8-045 | Intercropping pigeonpea [*Cajanus cajan* (L.) Millspaugh] with maize (*Zea mays* L.) to enhance food security, sustainability and profitability of smallholder farmers in semi-arid South Africa

Mathews C*, Van Averbeke W, Dakora FD

Tshwane University of Technology (TUT), Pretoria, 0001, South Africa
*E-mail: cherianm47@gmail.com

Although South Africa is considered food-secure based on aggregate food availability, 35% of its rural households remain food insecure due to poverty and inherently low crop yields. A field experiment was conducted at Nelspruit, South Africa, for three seasons (2007-2009) to evaluate different cropping systems on plant growth, biomass accumulation and grain yield of a long-duration pigeonpea genotype (ICEAP00040) intercropped with maize. The study revealed significant differences in above-ground biomass accumulation (7.5 to 13.5 t ha^{-1}) of pigeonpea, with significant reduction in biomass and grain yield under intercropping compared to sole cropping. Intercropped pigeonpea showed greater shelling percentageand100-seed mass. Protein content of maize grain was significantly increased under intercropping although its above-ground biomass and grain yield remained unaltered. The intercropping treatments were found to be more efficient based on land equivalent ratio (LER), area time equivalent ratio (ATER) and economic aspects such as monetary value, gross margin and cost-benefit ratio. Although the ^{13}C isotope study did not show any significant influence of cropping systems on water-use efficiency, the lower ^{13}C isotope ratios recorded at later growth stages, suggest pigeonpea's ability to adjust under changing climate. The study indicated that intercropping pigeonpea with maize under the semi-arid environment of South Africa can improve food security in a sustainable and profitable manner. Additionally, enhanced protein content of cereal grain and the greater carbon sequestration potential observed in the current study would go a long way in reducing the negative effect of extreme weather patterns anticipated under a climate change scenario.

IDT8-046 | Advances in groundnut (*Arachis hypogaea*) breeding for resilient cropping systems in Burkina Faso

A. Miningou[1]*, A.S. Traore[1]

[1]Institut de l'Environnementet de RecherchesAgricoles / CREAF de Kamboinsé 01 BP 476 Ouagadougou 01 Burkina Faso
*E-mail: miningou_amos@yahoo.fr

Groundnut is the second major legume crop in Burkina Faso after cowpea. The national production increased steadily during the last 10 years, but yields remain stable, showing that the production increase is counted for mostly by expansion in the growing areas.The need to develop, release and promote high-yielding varieties of groundnut with resistance/tolerance to different stresses (drought, foliar diseases and aflatoxins) cannot be overemphasized. New groundnut varieties were introduced from ICRISAT- Mali in 2013, screened and evaluated in a multi-location design for three years in four regions (Central-Eastern, Center-North, Center-West and South) of Burkina Faso. Six best bet varieties have been selected and chosen by farmers (60% of who were women) during the field days, organized two each for tolerance to aflatoxins, foliar diseases and drought: two aflatoxin-tolerant varieties (ICGV 91317, ICGV 93305); two foliar disease-tolerant varieties (ICGV 86015, ICGV 01276); and two drought-tolerant varieties (ICIAR 19BT, Kiema). The pod yields of these new varieties are superior (above 1.5t.ha^{-1}) to the yields of the released varieties (700-900kg.ha^{-1}) in farmers' fields. Farmers will have to follow recommended practices, including optimal crop density and timely planting in order to benefit from these yields improvements. Awareness creation through training and demonstrations on these practices is necessary. The challenges are to train farmers and provide groundnut seeds in quantities and at lower price to them to increase yields and groundnut productiondurably, in Burkina Faso.

IDT8-047 | The potential of cowpea in marginal cropping areas of South Africa

Mofokeng M.A.*, Shargie N.G. and Mashingaidze K.

Agricultural Research Council, Grain Crops Institute, Private Bag X 1251, Potchefstroom, 2520, South Africa
*E-mail: MofokengA@arc.agric.za

Cowpea is one of the most important pulses grown in South Africa. It grows in environments considered marginal for other crops. Its nutritional value and ability to withstand drought makes it an important crop for food and nutritional security in the sub-Saharan Africa. The objectives of the study were to evaluate cowpea genotypes for grain yield and identify best performers for screening under drought conditions and get farmer's variety preferences. The studies were conducted over two seasons 2012/13 and 2013/14 in North West, Limpopo and Mpumalanga Provinces. The survey was conducted using semi-structured interviews and questionnaires in 16, 6 and 12 villages of Mpumalanga and Limpopo Provinces, respectively. The yield data were analysed using analysis of variance and treatment means were separated by Least significant difference test in GenStat 17 version. Top twenty cowpea lines with high yield were selected and tested in Potchefstroom, Taung and Casteel villages in 2014/15 season. The best five cowpea lines identified were 99K-494-6, 98K-476-6, ITOOK-1263, CH47 and Bechuana White. The data across locations showed that ITOOK 1263 as the best for both grain and fodder yield. ITOOK 1263 can be recommended for farmers in North West, Limpopo and Mpumalanga Provinces for food and fodder. The interviewed famers indicated that they prefer cowpea cultivars with good yielding ability for both grain and leaves as well as resistance to insect pests. Cowpea can serve as the best pulse in farmer's fields.

IDT8-048 | Gender and climate change adaptation among bean farming systems in Uganda

Mubuka AS[1]*, Bonabana JW[2], Katungi E[3]

[1]Makerere University, Kampala, 256, Uganda
[2]1Makerere University, Kampala, 256, Uganda
[3] International Centre for Tropical Agriculture (CIAT), Kampala, 256, Uganda
*E-mail: asmubuka@gmail.com

The impact of climate change on agricultural activities in developing countries is increasing, with higher temperatures and decreasing precipitation levels depressing crop yields. This is particularly true of low-income countries where agriculture is rain-fed and adaptive capacities are low. Production of highly vulnerable food crops that are important for food security and incomes, such as the common bean, is expected to be severely affected.

The study aimed at estimating the effect of intra-household gender parity on the choice of production strategies to adapt the bean crop to climate change, gender-based perceptions of climate change, and awareness of existing adaptation strategies. A multi-stage random technique was used to select locations and respondents. Primary data was collected from 360 randomly selected households from Sironko, Kapchorwa, Lira and Oyam districts using a semi-structured questionnaire and focus group discussions.

Preliminary results using descriptive statistics provided insights into farmers' perception of climate change, perceived, types of adaptation strategies to climate change, and barriers to adaptation strategies. Multivariate probit results confirm that gender parity, literacy status, farming experience, family size, farm size, access to credit, access to media, extension contact, income, livestock ownership and access to training have a significant impact on choice of climate adaptation strategies. Therefore, future policy should focus on awareness creation on climate change, using different sources such as mass media and extension, facilitate the availability of credit, and promote participation of different gender categories in climate change adaptation activities.

IDT8-049 | Women's production capacities enhancement and gender yield gap reduction in groundnuts in Uganda

Johnny Mugisha[1], Christopher Sebatta[1], Kai Mausch[2]

[1]Department of Agribusiness and Natural Resource Economics, School of Agricultural Sciences, Makerere University, Kampala, Uganda
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Nairobi, Kenya
*E-mail: jomugisha@agric.mak.ac.ug

Literature shows that women in many African farming communities are more involved in agricultural production activities than men, but their capacities, including access to key farm resources and markets are lower, leading to gender differentials in productivity or yield gaps. In Uganda, women make up 53% of the agricultural labor force, but reportedly manage plots that are 20-30% less productive than plots managed by the men. This study analyses groundnut production differences among female and male farmers in Uganda. Yield gaps between the male and female farmers are considered at two levels; differences between actual and potential yields, and differences between expected and actual yields. A total of 240 randomly selected farmers (58% females) were interviewed using a pre-tested questionnaire. Using regression analysis, factors that contributed to groundnut yield gaps among and between female and male farmers were determined. Results show that both female and male farmers experience a yield gap ranging from about 20% to 37%. The results further indicate that more men than women use improved seed, fungicides, and carry out timely weeding; the crucial factors that affect groundnut output and yield. Majority of farmers, especially women, use home saved seeds and fewer improved technologies due to high cost, leading to low production. Other factors contributing to the yield gap are socio-demographic, economic and institutional factors including less access to extension services by women, less access to and/or control over land, lower affordability of labor and other key inputs.

IDT8-050 | Groundnut gendered yield gap analysis in Tanzania: social and economic implication

Mwakimata., R. G[1]*, J.P Hella[2]

[1]Agricultural and Applied Economics, Sokoine University of Agriculture, P.O. Box 3007 Morogoro,Tanzania
[2]Sokoine University of Agriculture, P.O. Box 3007, Morogoro, Tanzania
*E-mail: mwakimata@gmail.com

Tanzania is the sixth largest producer of groundnut in the world, which is grown for both food and income generation. However the average yield stands at 0.96 tons/acre compared to the world average of 1.5 tons/acre. This paper explores gender-related factors in groundnut production in Tanzania. The study is based on survey data collected from farmers randomly selected in the main producing regions of Shinyanga, Dodoma, Songwe and Mtwara, and it thus encompasses the socio-cultural and climatic differences. Data was analyzed using "gendered" stochastic frontier production function to establish factors affecting groundnut production across gender divides. The results revealed that groundnut is the most important crop for all age groups and across gender divides. Participation in farm activities across locations is mostly by women and youth, particularly at the marketing stage. Female-headed households recorded lower productivity than male-headed households. The difference is attributed to factors related to differences in ownership of productive resources such as land, labour, improved seed and recommended production techniques. The paper recommends gender-specific support to close the yield gap, which will ensure equal income distribution and, hence, reduce poverty, especially in female farmers.

IDT8-051 | Agronomic options in sorghum for improved water use efficiency across semi arid areas of Tanzania

Mwenda, E.T[1] *

[1] Ilonga Agricultural Research Institute (ARI- Ilonga), Kilosa, Morogoro, Tanzania.
*E-mail: emmamwenda@yahoo.com

Sorghum (*Sorghum bicolor)* is the third important crop after maize and rice in Tanzania, and is mostly cultivated in the semi-arid areas for food, feed and brewing. Semi-arid areas are characterized by periodic droughts, low and erratic rainfall, and high evaporation rates that exceed the amount of annual rainfall. Water scarcity, to some extent, is the result of climate change and variability, and partly a result of increased competition for limited water resources. This paper attempts to briefly review several researches conducted in Tanzania, which can stimulate more agronomic research on increasing water use efficiencies (WUE) critical to enhancing sorghum production. There is a wide range of agronomic options available in semi arid areas of Tanzania cropping systems for increasing WUE at the field level, resulting from the existing variation in climate, soil and technological innovation. Both soil and water management options have been developed and tested. Current practices employed to capture more water and use it more effectively involve thoughtful management of prior crops and fallows (e.g. crop sequence, weed control options, residue management). About 14.5% of farmers adopted *in situ* water conservation measures such as tillage practices, small basins, pits and tie-ridging. Practices such as mulching with crop residues increase efficiency by 10%–25% through reduced soil evaporation. However, the effect of soil and water management options such as the use of conservation tillage and ridging should be further investigated, to allow a clear assessment of the potential of such systems for bringing improvements in WUE. It is important also to note that improvement of water use efficiency at the field level depends equally on the use of the best agronomic practices and better genotypes.

IDT8-052 | Resilient agronomic practices to cope with seasonal drought in *Sali* rice grown in North Bank Plain Zone of Assam, India

Prasanta Neog, P.K Sarma, M.K. Sharma, P. Borah, D. Sarma, G.Ravindra Chary[2], Ch. Srinivasa Rao[1]

All India Coordinated Research Project for Dryland Agriculture, Biswanath Chariali Center, Assam Agricultural University, Assam, India
All India Coordinated Research Project for Dryland Agriculture, CRIDA, Hyderabad, Telangana, India
[1]ICAR- Central Research Institute for Dryland Agriculture, Hyderabad, Telangana, India
*E-mail: neogprasanta@rediffmail.com

The intermittent dry spells during growing season of winter or *Sali* rice, cultivated in the North Bank Plain Zone (NBPZ) of Assam, India, is the major weather risk causing widespread damage to crop. Yield reduction in *Sali* rice was observed up to 100% due to seasonal drought, particularly when cultivated on uplands and medium lands of the zone. From 2011 to 2015, an on-farm study was undertaken in Chamua village (27°02'18" N, 93°52'46"E and 83 to 90 m) in NBPZ, covering 132 ha involving 120 farmers, with an aim to cope with seasonal drought in *Sali* rice by introduction of short- and medium-duration varieties of *Sali* rice and crop diversification in *Sali* rice. Except in 2012, *Sali* rice in all other years was affected due to delayed onset of monsoon, and/or mid-season/terminal drought coinciding with tillering, panicle initiation and grain-filling stages of crop. Improved short-duration varieties such as *Dishang* and medium-duration varieties such as *Basundhra,* when evaluated under upland and medium land situations, performed consistently better than the traditional or long-duration improved varieties. As against the average rice grain yield of 1800 kg/ha and 3000 kg/ha of the traditional varieties, *Dishang* and *Bashundhara*/TTB-404 gave 3220 kg/ha and 4000 kg/ha under upland and medium land situation respectively. Growing of alternate crops such as turmeric, ginger, and pigeionpea; or crop diversification with rice, rapeseed, potato, maize, tomato, cabbage, cauliflower, cucumber, summer and winter vegetables resulted in an increase in rice equivalent yield, net income, and B:C ratio from 2700 kg/ha to 9800 kg/ha; Rs. 6500 to 617926/ha and 1.31 to 2.70 respectively. Similarly, adoption of physiography-specific double cropping system resulted in higher rice equivalent yield (kg/ha) and net income (Rs/ha) of 7400 and 34727; 21600 and 114660; and 15100 and 110075 with rice (*Dishang*) + *toria* (TS-36); rice (*Dishang*) + potato (*Kufri phokhraj*) and rice (TTB-404) + maize (All rounder), respectively. The five-year on-farm study indicated that to cope with seasonal drought in *Sali* rice, introduction of resilient varieties and or alternate crops/cropping systems is the pivotal need towards climate resilient rainfed agriculture in NBPZ of Assam, India.

IDT8-053 | Research and development partnerships for a large-scale diffusion of technologies for sorghum and millet systems in Mali

Nzungize J[1]*., Badolo F[1]., Ba M. N[1]., Tabo R[1].

[1]International Crops Research Institute for the Semi-Arid Tropics, Bamako, Mali
*E-mail: j.nzungize@cgiar.org

The objective of this work is to improve production systems based on sorghum and pearl millet in the Mopti and Sikasso regions of Mali, by strengthening research and development partnerships for large-scale utilization of proven technologies with potential for improving nutrition, benefiting women and children, and enhancing the sustainability of smallholder agriculture. At the farm level, the focus has been to improve production by increasing access to selected new technologies, and enhancing awareness and 'know-how' for the use of existing technologies to enhance sorghum and millet production. In the Mopti and Sikasso regions of Mali, the major technologies targeted for dissemination include: i) the use of seed treatment such as Apron Star 42WS, ii) seed of improved varieties of pearl millet, sorghum (both hybrid and open pollinated varieties), groundnut and cowpea adapted to the Sahelian environmental conditions, iii) integrated *Striga* and soil-fertility management practices; and iv) biological control of the millet head-miner. Seed treatment of pearl millet with Apron Star significantly reduced the incidence and severity of diseases. Grain yield was 20% higher when seed was treated. Further, the practice increases yield by 39% relative to farmers' current practice.

IDT8-054 | Sowing dates affect pumpkin fruit yield and quality

Oloyede F. M[1]*

[1]Department of Agronomy, Osun State University, Ejigbo Campus, Osogbo, Nigeria
*E-mail: funmilayooloyede@yahoo.co.uk

Climate change is a major challenge to the world today, especially the African continent, with significant threat to food security, human health and economic stability. In Sub-Saharan Africa, where rainfed agriculture is still the primary source of food and income, two-thirds of the working population still make their living from agriculture. Pumpkin (*Cucurbita pepo* Linn.) can be a good crop to meet the challenge of climate change. The fruit of *C. pepo* has a shelf life of three to six months (an index of its high antioxidant concentration), and the crop has been found to be drought-resistant. There are a number of agronomic practices that can be adjusted or manipulated in the quest for finding a remedy for the adverse effects of climate change, especially drought associated with changes in rainfall pattern. Hence, in 2007 and 2008, the effect of sowing dates on the yield and quality of pumpkin fruit was evaluated at the Teaching and Research Farm, Obafemi Awolowo University, Osun-State, Nigeria. In the study were four sowing dates (01 April, 15 April, 01 May, and 15 May). As the sowing dates were delayed, pumpkin fruit yield and nutrient contents diminished significantly (P=0.05). Adaptation to climate change involves deliberate adjustments in cropping systems. Time of sowing could be adjusted and or a range of sowing dates could be used so that food insecurity mediated by rainfall shortage could be mitigated.

IDT8-055 | Flowering responses of selected cassava genotypes to plant growth regulator application under screen house and field conditions in Uganda

Mikidadi, A[2, 3], Setter, T[1], Baguma, Y[3], Gibson, P[2], Edema, R[2], Pariyo, A[3], Hyde, P[1], Mukasa, S[2]

[1] Cornell University, Ithaca, New York
[2] Makerere University, Kampala, Uganda
[3]National Crops Resources Research Institute, Kampala, Uganda
*E-mail: sbmukasa@caes.mak.ac.ug / sbmukasa@yahoo.com

Shy flowering behavior of cassava limits cassava hybridization. Enhancing flowering through foliar application of plant growth regulators helps in synchronization of flowering dates and enables timely production of sufficient seeds. This study investigated flowering response of the selected cassava genotypes to the application of plant growth regulator treatment under screenhouse and field conditions. Two experiments were conducted, one in the screen house and the other in the field at NaCRRI in Uganda. The experiments were laid out in split plot design with genotype as main plot and plant growth regulator treatment as subplot. Plants were foliar sprayed at two weeks interval. Each plot consisted of five plants. The number of plant branches, number of male flowers and the number of female flowers were recorded on monthly basis. The data was analyzed using Gen stat 14th edition. Results showed that flowering responses of cassava genotypes to plant growth regulator application under screen house was significantly different from the flowering response in the field conditions. At nine months after planting, the number of flowers were significantly ($P<0.001$) different among plant growth regulators. Magana, NASE 14 and TME 204 planted under the screenhouse did not flower, whereas the same genotypes, NASE 14 and TME 204 planted in the field flowered. These results suggest that flowering response of cassava genotypes to plant growth regulator application under the screenhouse is different from the response in the field and that it is possible to enhance flowering in cassava by foliar application of plant growth regulators.

IDT8-056 | Market access and the impact of adaptation to climate change among bean farmers in Uganda

Onzima B[1]*, Bonabana-Wabbi J[1], Katungi E[2]

[1]Makerere University, Kampala, Uganda
[2]International Centre for Tropical Agriculture, Kampala, Uganda
*E-mail: benardonzima@yahoo.com

Climate change is probably the greatest challenge in the 21st century. The main exposure to climate change in Uganda is likely to come from changes in temperature, which in some cases could reach a 1.5 to 2°C annual average increase by 2030, higher than the temperature increase observed during the past six decades. New bean models project production decreases of 40% or more and decline in suitable areas of 30-50% in the 21st century in eastern Africa, without adaptation. In Uganda, bean production is projected to decline most in northern Uganda as a result of temperatures exceeding the optimal and marginal maximum temperatures at which beans can grow. This study used quantitative and qualitative cross-sectional data collected from 480 bean farmers in northern and central Uganda and employed the multivariate probit (MVP) technique to model simultaneous and interdependent adoption decisions by farm households in a random utility framework. The MVP simultaneously models the influence of the set of explanatory variables on each of the different strategies adopted, while allowing the unobserved and unmeasured factors (error terms) to be freely correlated. One source of correlation may be complementarities (positive correlation) and substitutabilities (negative correlation) between different strategies. The impact of adaptation to climate change on bean yield was modelled using instrumental variable regression because of the potential endogeneity of the adaptation decision. Access to extension information and weather information were used as instruments.

IDT8-057 | Endophytic bacteria endow solace to drought-stressed peanut

Pal KK[1]*, Dey R[1], Sherathia DN[1], Chakraborty K[2], Rathnakumar AL[1], Mahatma MK[1], Ajay BC[1], Devidayal[3], Shamsudheen M[3], Arvind Kumar[4], Mandaliya VB[1], Bhadania RA[1], Patel MB[1], Maida P[1], Mehta DH[1], Nawade BD[1], Patel SV[1], Lokesh Kumar T[1], Singh V[1]

[1]ICAR-Directorate of Groundnut Research, Junagadh 362001, Gujarat, India
[2] ICAR-Natioanl Rice Research Institute, Cuttack 753006, Odisha, India
[3] ICAR-Central Arid Zone Research Institute, RRS-Kukma, Bhuj 37001, Gujarat
[4]ICAR-Central Soil Salinity Research Institute, Karnal 132001, Haryana
*E-mail:kkpal9426476749@gmail.com

Each of the nearly 300,000 known plant species is host to one or more endophytes. It is believed that endophytes co-evolved with plants and helped them to acclimatize to terrestrial ecosystems. Endophytic bacteria have been reported to alleviate abiotic stresses in many crops by modulating the production of ROS alleviating enzymes and signalling pathways; modification of root growth; helping plants for osmotic adjustment and stomatal regulation; and production of anti-oxidants. Endophytic bacteria isolated from internal tissues of root, stem and seeds of groundnut (TG37A), such as *Bacillus firmus* J22, *Pseudomonas pseudoalcaligenes* SEN29, *Bacillus subtilis* REN51, etc. were applied in field-grown groundnut as seed treatment with cultivar TG37A, during summer months, without application of supplementary irrigation after sowing. These endophytes significantly improved the root length, biomass, and volume; K uptake; physiological parameters such as reduction in stomatal aperture and loss of water through transpiration; modulated the production of ROS scavenging enzymes such as catalases, peroxidases, superoxide dismutase, glutathione and reductase, when soil moisture at 0-15cm and 15-30cm was 12% and 15%, respectively. With the reduction in the moisture level further, these endophytes helped groundnut in better uptake of water, maintaining turgidity, enhancing WUE, improving leaf RWC, and reducing transpiration by stomatal modulation, besides enhancing the transcripts of the enzymes of carboxylation and decarboxylation modules. Application of endophytic strains J22 and SEN29 alleviated drought and prevented the loss of pod and haulm yield of groundnut (TG37A) by 15%-25% over control. Thus, endophytes would help in horizontal spread of groundnut in drought-prone areas.

IDT8-058 | Soil moisture conservation measures in cotton (*Gossypiun hirsutum*) under high density planting system to sustain drought condition

Pandagale A. D.[1]*, Baig K. S.[1] and Waskar D. P.[2] and Venugopalan M. V.[3]

[1] Cotton Research Station, Nanded – 431 604, MS, India
[2] Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani – 431 402, MS, India
[3]Central Institute for Cotton Research, Nagpur – 441 108, MS, India
*E-mail : arvindpandagale@yahoo.co.in

An experiment was conducted to standardize soil moisture conservation method and to optimize the nutrient requirement of cotton under high density planting system through TMC MM I 1.4 project. The experiment was conducted at Cotton Research Station, Nanded (Maharashta, India) in monsoon 2014 -15 and 2015-16 seasons under rainfed condition. Experiment was laid out in split plot design with three replications. Three soil moisture conservation techniques in main plot and five nutrient level treatments were evaluated in sub plot. Cotton variety NH 615 (non Bt) was sown after receipt of monsoon at 60 x 10 cm spacing (1.66 lakh plants `ha^{-1}). Deficit rains to the extent of 48.0 and 36.5 per cent, respectively over average were received during both years.

On the basis of pooled mean, sowing on broad bed and furrows (BBF) was found to give highest seed cotton yield (1339 kg/ha) and was significantly superior over flat bed (1177 kg/ha). The BBF and opening of furrows at 30 DAS recorded 13.76 per cent and 11.47 per cent increased yield over flat bed, respectively. The BBF and opening furrow treatments recorded significantly higher yield contributing characters, monetary returns over flat bed. Both the moisture conservation techniques were found to be statistically remunerative over flat bed. Significantly more moisture in sowing on BBF and opening furrow treatments than flat bed was recorded at 60 DAS to 120 DAS. Increase in yield contributing characters and seed cotton yield ha^{-1} were recorded with increased level of nutrients. The level of 150% RDF was found to be significantly profitable and higher seed cotton yield (1374 kg/ha) over 100% RDF. Application of 125% RDF, 125% RDF + sec. micronutrients and 150% RDF were on par in terms of NMR and B:C ratio.

IDT8-059 | Effect of ethephon and gibberellic acid on productivity and juice quality of sugarcane (*Saccharum officiarum* L.)

Praharaj S[1]*, Singh D[1], Guru S K[1], Bhatnagar A[1]

[1]G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India
*E-mail: praharaj93@gmail.com

Sugarcane is the most important sugar crop in tropical and subtropical countries. However, poor agro-techniques have led to sub-optimal productivity and juice quality of sugarcane. The goal of the present study was to improve root growth for better drought avoidance, along with higher cane productivity and juice quality in sugarcane. Overnight soaking of sets with 50 ppm as well as 100 ppm ethephon solution resulted in faster as well as higher emergence. This fast emergence can be useful in late spring planting conditions of India, as the fast emerged seedlings will attain enough growth to utilize the monsoon rainfall. Ethephon was also found to improve the root growth of sugarcane, thus imparting better drought avoidance mechanism to the crop. At the later stage, the crop was sprayed with 35 ppm gibberellic acid solution at 90, 120 and 150 days after planting, which further improved the stem length. Treatment comprising a combination of overnight soaking of sets with 100 ppm ethephon and foliar application of gibberellic acid at 90, 120 and 150 days after planting was found to be the best treatment, as it resulted in the highest cane yield as well as improved juice quality parameters *viz.* sucrose percentage and commercial cane sugar (CCS) production. It was interesting to observe that the treatment improved cane weight along with sucrose content, thus showing no dilution effect. Due to better root system, this agro-technique may be highly useful under water limiting environment for producing higher cane yield as well as commercial cane sugar.

IDT8-060 | Identification and characterization of drought tolerant CLP producing fluorescent *pseudomonads* in maize (*Zea mays* L.)

Radhajeyalakshmi R[1], Sethuraman K[1], Kumari Vinodhana N[1], Ganesan KN[2] and Viswanathan R[3]

[1]Maize Research Station, Vagarai-624613, Palani, Tamil Nadu Agricultural University, Tamil Nadu, India
[2]Agricultural Research Station, Bhavanisagar-638451, Tamil Nadu Agricultural University, Tamil Nadu, India
[3]Sugarcane Breeding Institute, Coimbatore-641007, Tamil Nadu, India
*E-mail: radhajeyalakshmi@hotmail.com

Cyclic lipopeptides (CLPs) with antibiotics-producing fluorescent *Pseudomonads* were isolated from maize rhizosphere grown in sandy loam soils at the Maize Research Station, Vagarai, TNAU. Approximately 20 fluorescent *Pseudomonads* from sandy loam soils were isolated, using two different growth media. The strains were distinguished based on their growth, CFU/g, fluorescence, and pigment production. Growth inhibition of maize pathogens by CLP producing fluorescent *Pseudomonads* strains were studied by dual culture experiments. The impact of flurorescent *Pseudomonads* strain (CLP) on the zoospores of Downy mildew pathogen of maize was studied by direct microscopy and encysted zoospores were observed. *In vitro* biochemical experiments confirmed the presence of CLP-producing strain among the fluorescent *Pseudomonads* isolates, in terms of utilization of C, N sources. The particular strain was able to colonize the roots of maize and improved maize growth when applied as seed treatment ($5X10^7$ cells). Germination, seedling vigour and disease resistance were assessed. Field experiments were conducted to test the performance of CLP-producing *Pf* strains in maize crop for disease resistance and growth during water stress conditions prevailing in MRS, Vagarai in summer.

IDT8-061 | Comparison of water use, growth and ^{15}N recovery among Flooding, SWD and Non-flooding water-saving irrigation practices under lowland paddy field

Shah Moinur Rahman[1], Ken-Ichi Kakuda[3], Yuka Sasak[2], Ho Ando[3]

[1]Hajee Mohammad Danesh Science and Technology University, Dinajpur-5200, Bangladesh
[2]Yamagata Field Science Centre, Faculty of Agriculture, Yamagata University,Tsuruoka 997-0369, Japan
[3]Course of Safe and Reliable Agricultural Production, Faculty of Agriculture, Yamagata University, Tsuruoka 997-8555, Japan
*E-mail: nurhstu@gmail.com

Water and nitrogen (N) play a vital role in rice production aimed at high N use efficiency and water-saving irrigation. Water-saving management might affect the soil condition (oxidiation and reduction) and the soil condition, in turn, affects the fate of N in paddy soil also. Therefore, we designed three irrigation regimes: conventional irrigation (flooding), shallow water depth (SWD), and non-flooding, in our study. The fate of N and growth of rice were not different among treatments during early growth stage by water management. Root activity of rice during middle growth stage was high in SWD, and this might affect above-ground biomass during middle growth stage of rice. We found that the recovery efficiency, N uptake and above-ground biomass at heading stage were higher in SWD than the other two treatments. Despite water stress under non-flooding water management at vegetative stage, yield did not differ from flooding and can save much irrigation water during rice growing period.

IDT8-062 | Physiological efficiency and drought tolerance ability of Buckwheat (*Fagopyrum esculantum* L.) under hill slopes of North Eastern Himalayan region

Krishnappa R[1], Dipjyoti R, Meghna H, Anjan K. S, Uday S. S, Kaberi M, Nishant A. D, Anup D.,Ganga R. A., Subhash B, Thoithoi D, Prabha M and Ngachan S V

[1]ICAR Research Complex for NEH Region, Umiam-793103, Meghalaya, India
[2]ICAR Research Complex for NEH Region, Medziphema-797106, Nagaland, India
[3]Assam Agriculture University, Jorhat-785001, Assam, India
[4]ICAR Research Complex for NEH Region, Lembucherra-799001, Tripura, India
*E-mail: krishphysiology@gmail.com

Hill Agriculture in North Eastern Himalayas is highly challenging due to various crop production constraints. Even though the region receives high rainfall (≈2000mm per annum), intermittent and terminal drought during non-monsoon rabi season. Evaluation of crop(s) with wider adaptability such as buckwheat is urgent need. In view of these, a field study was undertaken during 2012-13 to examine the physiological efficiency and cultivation of buckwheat round the year, revealed that sowing of buckwheat between mid-September to mid-December exhibit improved physiological efficiency which in turn enhance grain yield (1100 kg ha^{-1}). But the crop can be sown and grown successfully round the year for higher green biomass (1800 – 4320 kg ha^{-1}) utilized as quality fodder and soil incorporation. In order to understand the physiological mechanisms and stress tolerance ability of Buckwheat under moisture stress, few important physiological and biochemical traits have been investigated during rabi season reveals enhanced root growth and proliferation with increased root length and root surface area to the tune of 15% and 35% respectively, significantly improved leaf characteristics, altered stomatal adaptations and varied epicuticular wax deposition. The rate of water loss was significantly low due to its well regimented stomatal and non stomatal transpiration regulation secured to retain more water for cellular metabolism and resilient crop growth under hilly ecosystems of Himalayan region. The stress tolerance of buckwheat is also imparted by synthesis of compatible osmolytes like proline, retention of higher soluble leaf protein and sugar content with increased metabolic activity. Buckwheat can be a potential resilient crop to cultivate under stressful conditions of changing climate of the region with better morpho-physiological and biochemical traits which are essential for achieving increased food security of NEH region.

IDT8-063 | *Lactobacillus plantarum* MYS44 as potential biological tool to control aflatoxigenic *Aspergillus parasiticus*

Poornachandra Rao K[1], Sreenivas M Y[1]*

[1]Department of Studies in Microbiology, University of Mysore, Manasagangotri, Mysore-570006, Karnataka, India.
*E-mail: sreenivasamy@gmail.com

In the current study, among seven isolates of lactic acid bacteria (LAB), *L. plantarum* MYS44 showed maximal suppression of *Aspergillus parasiticus* MTCC411 in standard *in-vitro* techniques, suggesting the antifungal property of the strain in minimizing aflatoxin production and fungal growth. The inhibition of *A. parasiticus* by the supernatant (CFS) of MYS44 on peanuts confirms the ability of the strain in bio-preservation, and its activity chiefly depends on favourable acidic conditions. The concentration of 40 µL of 10^6 cells/mL of *L. plantarum* MYS44 and 80 µL of CFS showed visible inhibition of *A. parasiticus* and it was measured as MIC. Analyzed antifungal components in CFS of MYS44 were identified as oleic acid, octanoic acid, butanamide, and dodecanoic acid by GC-MS. In poultry feed sample, the live cells and CFS of MYS44 reduced the level of aflatoxin content by 34.2% and 42.2% respectively. On the other hand, the strain was potent enough in resisting acidic pH along with mixed response to the microbial inhibitors (antibiotics), binding capability to chicken crop epithelial. Findings from this study suggest *Lactobacillus plantarum* MYS44 as a potential antifungal agent capable of reducing aflatoxin production in conjugation with its probiotic property, which could be used in poultry.

IDT8-064 | Genotype and environment interaction in the Tunisian dairy flocks

Ressaissi Y.[1]*, Ben Hamouda M.[2]

[1]Departement des Sciences Animales, Institut National Agronomique de Tunisie, 43 Avenue Charle Nicolle 1082-Tunis-Mahrajène-Tunisie
[2] Institution de Recherches et de l'Enseignement Supérieur Agricole, Ministère d'Agriculture, 30 Rue Alain Savary-1002 Tunis Belvédère-Tunisie
*E-mail : yos.re@hotmail.fr

In the dairy cow, fluctuations in the productivity of flocks are defined by the genetic material and also the environmental circumstances in which the animals are supposed to produce. This study aimed to quantify the contribution of the environmental factors related to husbandry conditions, climate change, and food and water supply in dairy cows raised in the Tunisian conditions, and to genetically assess flocks for 305-days milk yield. The study involved 23,280 Holstein cows which belonged to 307 herds and were calved between 2006 and 2011. A total of 32,688 lactation performances were computed according to 8-monthly records and standardized to 305 days. The cows were divided into eight flock size groups according to which the variance analysis of the 305-days milk yield was performed by a fixed linear model. The genetic evaluation was carried by a uni-trait animal model with permanent effect. Raw average milk yield reached 4975 kg (± 2708 kg) while the average standardized performance was about 5770.67 kg (± 2396 kg), with respective maximums of about 16,064 kg and 14,838 kg. Heritabilities and repeatabilities ranged respectively between 0.02 and 0.07, and 0.20 and 0.38 by group of flock. High permanent environment variance components were observed compared to the additive genetic merit, especially in small flocks. The 305-days yield was found to be deficient in the Tunisian Holstein flocks, highlighting a limited genetic potential expression and unstable environment that reflects difficult conditions in the Tunisian husbandry of dairy cows.

IDT8-065 | Evaluating the potential of increasing atmospheric CO_2 to promote chickpea (*Cicer arittinum* L.) production in semi-arid region of northern India

Saha S[1]*, Sehgal VK[1], Chakraborty D[1], Pal M[1], Singh SB[2]

[1]Indian Agricultural Research Institute, New Delhi, 110012, India,
[2]ICAR Research Complex for NEH Region, Mizoram Centre, Kolasib, 796081, Mizoram
*E-mail: sauravs.saha@gmail.com

An open top chamber experiment was conducted for two years (2010-11, 2011-12) to evaluate elevated CO_2-induced changes in crop water relations and canopy radiation interception in a research farm of the Indian Agricultural Research Institute, New Delhi. Chickpea (Pusa-1105 genotype) was grown under an atmospheric CO_2 enrichment level of 580±20 ppm, as compared to the ambient level of 397±10 ppm of atmospheric CO_2. Elevated CO_2 resulted in a significant increase in canopy temperature and leaf water potential in chickpea. Increase in Normalized Difference Water Index (NDWI) values and relative leaf water content were indicators of improved plant water status under elevated CO_2 treatment. Our results signify that an increase in plant water content promotes an increase in canopy temperature due to elevated CO_2-induced hindrance in transpiration process. Besides, significant increase in Leaf Area Index (LAI) due to CO_2 fertilization effect cannot compensate the reduction in leaf level stomatal conductance. Although water use efficiency (WUE) significantly increased by 22.3% under enriched CO_2, the canopy conductance value remained unchanged when compared to ambient CO_2 treatment. Thus our results suggest that it is possible to improve the plant water status with enhanced biomass production, and the same amount of cumulative crop water use under elevated CO_2 conditions rather than ambient conditions. Our results signify the possible beneficial impact of atmospheric CO_2 enrichment on water use efficiency of chickpea and its improved performance r under water-limited dryland conditions.

IDT8-066 | Innovative rainwater management technology to cope with climate variability and sustainable productivity of rainfed groundnut (*Arachis hypogaea* L.)

Sahadeva Reddy B[1]*,PadmalathaY[2], Madhusudhan Reddy K[1], Radha Kumari C[1],Ravindranatha Reddy B[1] , Gopal Reddy B[3]

[1]Agricultural Research Station, Ananthapuramu-515001 , Acharya N.G.Ranga Agricultural University, Andhra Pradesh, India
[2]Agricultural Research Station, Reddipalli--515701, Acharya N.G.Ranga Agricultural University, Andhra Pradesh, India
[3]Regional Agricultural Research Station, Nandyal-518502, Acharya N.G.Ranga Agricultural University, Andhra Pradesh, India
*E-mail: sahadevardd@gmail.com

The low productivity of groundnut (*Arachis hypogaea* L.), the important food legume, is mainly due to its cultivation in rainfed production systems with prolonged dry spells during critical stages of the crop growth period. Rainwater harvesting refers to all techniques involving both *in– situ* and *ex–situ* rainwater conservation measures, where rainwater is collected to make it available to cope with drought situation. But the combined effect of *in–situ* and *ex–situ* rainwater conservation measures in bringing more resilience to rainfed groundnut crop during varied drought situations is not known. Hence, field experiment were conducted during the 2016 *kharif* season, with three main plots (rainfed, two supplemental irrigations each with 10 mm and 20 mm) and six sub plots (conservation furrows with 45 ,60,120 cm apart at time of sowing and each at 30 days after sowing) in large sized groundnut plots at ARS, Ananthapuramu, ANGRAU, Andhra Pradesh, India. Since the formation of moisture conservation furrows after crop establishment has some practical problems, they were formed at sowing time itself with an innovative technique of attaching shovels to the seed covering blade so that sowing, covering the seed and formation of moisture conservation furrows could be done simultaneously to maintain the required sub-plot treatments. An amount of 265.6mm rainfall was received in 12 rainy days during the crop season and the crop was subjected to dry spell at pegging and pod development stages. Conservation furrows formed at the time of sowing in between every two crop rows with inter-row spacing of 45 cm recorded 7.5% higher pod yield with 3.52 kg hamm^{-1} rainwater use efficiency, compared to conservation furrows formed at alternate rows with inter-row spacing of 30 cm. Two supplemental irrigations (each at pegging and pod development stage) with 10 and 20 mm increased the pod yields by 12% and 26% respectively, compared to rainfed crop. Integration of *in-situ* conservation furrows at the time sowing with 45-cm inter-row spacing coupled with supplemental irrigation with 20mm during dry spells increased the productivity of rainfed groundnut by 60%, compared to conservation furrows at 60 cm interval, formed at 30 days after sowing.

IDT8-067 | Response of sorghum drought tolerance to application of film-forming antitranspirants over the reproductive stage

Samaila JT[1]*, Crook M[1], Grove IG[1], Kettlewell, PS[1].

[1]Crop and Environment Sciences, Harper Adams University, Newport, TF10 8NB, England, United Kingdom.
*E-mail: jsamaila@harper-adams.ac.uk

Sorghum is a drought-tolerant crop grown under rainfed conditions in Africa and Asia where water deficit is common. Significant reductions in yield have been reported when the plant was subjected to water stress at the rooting to flowering stages. Four glasshouse and one field experiments were conducted at Harper Adams University-UK, to evaluate the responses of sorghum drought tolerance to application of film-forming antitranspirants. All the experiments consists of two factors, and four treatment combinations. The four glasshouse experiments were laid out in a randomized complete block design, while the field experiment was in a split-plot design. In the four glasshouse experiments, all plants were irrigated to between 'head in flag leaf' to 'tip of head visible' stages and film antitranspirants were applied onto the sprayed treatments, while irrigation was suspended for the droughted treatments. In the field experiment under fixed rain-out shelters, all plants were irrigated up to '5 leaves unfolded' stage, and irrigation suspended for the droughted treatments. Later film antitranspirants were sprayed onto the sprayed treatments, between the 'flag leaf' to 'tip of head visible stages'. Data was collected on physiological and yield parameters and results were analysed using factorial ANOVA. Results showed that there is potential for film-forming antitranspirants to improve drought tolerance in sorghum, with the right timing of drought imposition being critical in determining the effectiveness of the antitranspirants in increasing grain yield of droughted sorghum. This suggests that film-forming antitranspirant application is another agronomic technique that could enhance sorghum drought tolerance.

IDT8-068 | Variation in total soluble sugars and protein content in the leaves of downy mildew resistant and susceptible pearl millet genotypes

Pooja Sangwan[1] and Kushal Raj[2]

[1,2]Department of Plant Pathology, CCS Haryana Agricultural University Hisar, Haryana, INDIA
E-mail: choudhary.shweta737@gmail.com

Downy mildew of pearl millet incited by *Sclerospora graminicola* (Sacc.) Schroet is the most widespread and destructive disease of pearl millet in India and other pearl millet growing areas of the world. This disease is a major factor limiting full exploitation of high yield potential hybrids in India. Sugars are precursors for the synthesis of phenolics, phytoalexins, lignin and callose. Hence, play an important role in defense mechanism of plants against invading pathogens. In the present study, total soluble sugars and protein content were estimated at 30, 40, 50 and 70 days after sowing (DAS) in leaves of resistant HHB 223 and susceptible 7042 S pearl millet genotypes. Total soluble sugars in healthy resistant genotype were higher at each stage of the crop in comparison to susceptible diseased plant. At 30 DAS, resistant genotype exhibited higher level of total soluble sugars (10.64 mg glucose equi./g) whereas in susceptible it was only 2.21 mg glucose equi./g. As the disease progressed depletion of sugars was maximum in resistant genotype in comparison to susceptible genotype. In susceptible genotype protein content was higher (25.20% and 27.30%) at 30 and 40 DAS but less (20.30% and 19.60%) at 50 and 70 DAS as compared to resistant genotype (25.03% and 21.88%) at 50 and 70 DAS.

IDT8-069 | Plant ideotype suitable for adaptation to water limited environment and *per se* yield enhancement in rainy season in soybean (*Glycine max* L. Merill)

Satpute GK[1]*, Arya M[1], Gupta S[1], Devdas R[2], Ratnaparkhe MB[1], Bhatia VS[1]

[1] ICAR - Indian Institute of Soybean Research, Indore, 452001, Madhya Pradesh, India
[2]ICAR - National Research Centre for Orchids, Pakyong, 737106, Sikkim, India
*E-mail: gksatpute@yahoo.co.in

Soybean is the principal oilseed crop of rainfed farming systems in India. Occurrence of drought, particularly during seed-fill stage, is frequent, limiting its production. In a 2014 summer trial comprising 323 high-yielding breeding lines in F_5 generation which possessed >50 pods /plant, low canopy air temperature differential trait (δT^0C) was found to express well in 148 lines under water-limiting environment. During *per se* yield evaluation of these lines in augmented trial in the 2014 rainy season, two yield-attributing traits *viz.* number of pods/ plant and plant height, were shown to possess high heritability in broad sense (78.08%, 92.11%) as well as high expected genetic advance (76.13%, 65.47%), respectively. Interplay of correlations between δT^0C (summer) and yield attributing traits (rainy season) set a framework for an ideotype with characteristic adaptation to water-limiting environment and simultaneous seed yield enhancement under rainy season. Such an ideotype was determined to possess $\delta T^0C < -7.3^0C$ with number of pods/ plant >90.1 and plant height taller than 61.1cm. A medium value of 100-seed weight (9.8-12.9gm) would strike a balance between number of nodes/ plant (>14.6) and seed yield (>15gm/ plant) under such conditions. Fourteen advance breeding lines, which conform to the defined plant ideotypic trait(s), were identified from three populations of crosses *viz.* (JS 90-41xJS 97-52), (JS 97-52xNRC 37), and (JS 71-05xC-2797). These lines will be further confirmed for terminal drought tolerance and high-yielding traits under strict water limiting environment in rainout shelter and under rainfed and irrigated conditions.

IDT8-070 | Effect of mannitol-mediated water stress on chlorophyll content and scavenging enzyme activity in rice genotypes

Vanisri. S.*[1], Sreedhar. M[2], Jeevan. L[1], Pavani. A.[1], Anurag Chaturvedi.[2], Aparna. M.[2], Pavan Kumar. D.[2], Aruna. K.[1], Durgarani. Ch.V.[1]

[1]Institute of Biotechnology, Prof. Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad – 500030, Telangana, India.
[2]Quality Control Laboratory, Prof. Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad – 500030, Telangana, India.
*E-mail: vanisree_dhar@yahoo.com, vanisreedhar1994@gmail.com

In an effort to determine the biochemical markers for identifying genotypes for drought tolerance, changes in chlorophyll content and activities of scavenging enzymes were determined in the seedlings of 20 rice genotypes, each with different genetic background. Water deficit conditions were induced by treating with mannitol. The 14th day seedlings of 20 rice genotypes were selected for stress treatment with mannitol at 20% concentration, which was added to the supporting medium. Control with cultivar *Vandana* was taken by using the same micro nutrient medium Yoshida. The estimation of chlorophyll content and activity of scavenging enzymes in the leaf tissue was carried out after 24 hrs exposure to stress. The results of the present study revealed a significant increase in the activity of SOD and POD in rice genotypes exposed to a water-limiting situation. These findings indicated increased antioxidant activity in correspondence with raised levels of free radicals. The observed increase of SOD and POD of the antioxidant system indicated that increase in oxidative stress caused by drought might have been overwhelmed by this enzymatic system. The leaf SOD activity of *Rajendra* (34.39), *Vandana* , IR 64(31.48), *Anjali* (30.38) and *Varalu* (30.23) at 20% mannitol was higher than that of the check *Vandana* at no mannitol stress. Genotype *Rajendra* was superior to check *Vandana* at 20% mannitol stress. The results have clearly indicated the free radical scavenging ability of these varieties under the influence of drought stress by correspondingly enhancing the production levels of SOD. The POD activity in *Vijetha* (138.60), MTU 1010 (133.40), *Vandana* (136.50), BPT 5204 (127.77), IR 64 (112.90), *Prasanna* (114.30), B 133 (114.80) and *Azucena* (102.50) was found to be desirable and had reflected an increased ROS scavenging capacity of these genotype. Significant reduction in leaf chlorophyll content was also observed under mannitol stress. The study indicated that chlorophyll b was found to be more sensitive than chlorophyll a for water stress conditions. The data showed that the status of scavenging enzymes and chlorophyll could provide a meaningful tool for depicting drought tolerance of a rice genotype.

IDT8-071 | Building drought resilient agri-systems in semi arid tropics through the intervention of TEK (Traditional Ecological Knowledge): The Kachchh case study

Sharma S B[1]*, Thakkar M G[1] and Thivakaran G A[2]

[1]Department of Earth and Environmental Science, KSKV Kachchh University, Mundra Road, Bhuj 370001, Gujarat, India.
[2]Gujarat Institute of Desert Ecology, Bhuj, Gujarat, India.
*E-mail: seemabhargavsharma@gmail.com

The semi arid tropics are resource-scarce in agriculture, in terms of soil quality and rate of precipitation, and sustainability of agro ecosystems is an important issue. Kachchh is a unique ecological terrain of western India, with low and erratic rainfall, droughts, seismic instability and harsh climate. Traditional ecological knowledge (TEK) refers to the knowledge, innovations and practices of indigenous and local communities around the world. In India, there is enormous wealth of TEK, but it is being lost and is surviving only in bits and pieces. The present four-year study was undertaken in earmarked agricultural fields of this terrain, based on amendment practices. The two amendment systems were demarcated on the basis of agricultural inputs used *viz*. A1 (organic inputs and practices based on TEK) and A2 (chemical inputs). The physico-chemical and microbiological characteristics of the soil were analysed for three crop phases *viz.* pre-sowing, mid phase and post harvest phase, for six cropping seasons. Better soil structure, improved physico-chemical attributes, higher count of beneficial microorganisms, especially phosphate solubilising microorganisms (PSM), and novel stress-tolerant microbes with diversified profile are important attributes of TEK-based systems, and this is evident even during stress periods of droughts in two out of six seasons. The present study proves to be a milestone in research related to TEK based agro-sustainable solutions for the semi-arid tropics and agri-sector of similar areas or elsewhere, where scarcity of natural resources remains a big question.

IDT8-072 | Identifying suitable rice hybrids for rainfed ecosystem using AMMI analysis

Sheeba. A[1]*, P. Vivekanandan[1]

[1]Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India
*E-mail: sheebateddy@gmail.com

Rice farmers in rainfed ecosystems need improved genotypes that are high yielding, tolerant to abiotic stress and responsive to better management, with stable yield across environments. Forty hybrids obtained from crossing four TGMS lines with ten drought-tolerant short-duration testers were studied for their adaptation under three different environments *viz*., managed stress, rainfed and irrigated condition. The mean data on single plant yield for the three environments studied were subjected to stability analysis by Additive Main Effect and Multiplicative Interaction (AMMI) model. ANOVA for AMMI analysis of G x E interaction (GEI) for the trait single plant yield indicated that genotypes, environments and GEI components were significant. The AMMI 1 biplot for yield clearly indicated that the three environments had differed in both main and interaction effects. The hybrids GD 98049/*Varappukudanchan*, GD 99017/PM 01010, GD99033/*Varappukudanchan*, GD 99036/PM 01011, PM 99036/PMK 2 and GD 99036/*Norungan* showed IPCA 1 score close to zero with high main effects for single plant yield; and these hybrids were considered as stable and found to have general adaptability at all environments studied. The crosses GD98049 PMK3, GD 98049/*Norungan*, GD 99017/ PMK 2, GD 99017/*Varappukudanchan*, GD 99033/ PMK 3, GD 99036/PMK 3 and GD 99036/IR 36 and the environment rainfed had negative IPCA 1 score and they were adjudged as suitable hybrids for rainfed ecosystem.

IDT8-073 | Crop geometry and nitrogen managementto combat water scarcity and yield maximization in extra early rice

Silambarsan M[1]*, Subramaniyan E[1], Arunachalam P[1], Babu R[1]

[1]Agricultural college and research institute, TNAU, Maduri, India
*E-mail: silambutnau@gmail.com

Very early rice varieties which are of less than 100 days duration may be suited for delayed sowing, especially during the first season. They can fit well in delta regions to catch the second-season rice. Drought avoidance mechanisms are noticed due to lesser field duration. These varieties can also be used as a contingent crop when there is delayed release of canal water. In extra early rice, yield barriers have been observed due to reduced field duration.Towards realizing the objective and reducing the yield gap in extra early rice, field experiments were conducted with four crop geometries (133, 66, 50 and 44 hills m^{-2}) and four N management levels (100 kg of nitrogen four equal splits at basal, AT, PI, flowering ; and 100 kg four split and five part at 1/5basal, 2/5AT, 1/5PI, 1/5flowering and 100 kg four splits six parts 1/6 basal, 2/6AT, 2/6 PI, 1/6 flowering and 120 kg four equal splits and 120 kg four splits five parts 1/5 basl,2/5 AI,1/5 PI,1/5 flowering and 120 kg four splits six parts1/6 basal,2/6 AI,2/6PI, 1/6 flowering). Among the crop geometry, closer spacing of 66 hills m^{-2} produced higher yield of 6.3 t ha^{-1}. Nitrogen at 120 kg four splits six parts 1/6th basal,2/6th AI,2/6th PI,1/6th at flowering realized higher yield when compared to the recommended N application of four equal splits. Hence, in extra early rice varieties, closer spacing with N at varying level as per the growth stages of rice has to be followed for yield maximization in rice.

IDT8-074 | Performance of polymer coated CORH 3 hybrid rice seed on productivity under moisture stress conditions

Ambika S[1*], Bhaskaran M[2], Manonmani V [3], S. Deepika S[4]

[1]Tamil Nadu Agricultural University, Coimbatore.
[2]Tamil Nadu Open University, Chennai.
[3] Tamil Nadu Agricultural University, Coimbatore.
[4]Tamil Nadu Agricultural University, Coimbatore.
*E-mail: ambikasingaram@gmail.com

A field experiment was carried out at the Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore, to know the effect of polymer seed coatings on growth and productivity of CORH 3 hybrid rice seed under various moisture stress conditions *viz.,* stress at panicle initiation stage, stress at grain filling stage, and stress at both panicle initiation and grain filling stages, along with normal irrigation. The experiment comprising six seed treatments (untreated control, Genius coat 171, Genius coat 172, Arcus, Myconate and Quick roots), with three replications, was laid out in split plot design. The results of the present investigation revealed that seeds coated with Quick roots were significantly superior in growth and yield parameters, *viz.,* plant height (95 cm), took less days for 5% and 50% panicle emergence (50 and 60 days, respectively), and had higher plant population (100%), nil pest incidence, higher number of productive tillers per plant (35), more number of grains per panicle (125), and grain yield (7166 kg/ha); and physiological parameters, *viz.,* leaf area index (3.2), relative water content (81%), chlorophyll stability index (74%), soluble protein content (7.71 mg g^{-1}), and nitrate reductase activity (0.616 µmol NO_2 g^{-1} h^{-1}), when under stress at grain filling stage, compared to stress at panicle initiation stage and stress at both panicle initiation and grain filling stages.

IDT8-075 | Effect of spacing and fertiliser dose on dry and sprouted seed sown aerobic rice (*Oryza sativa* L.)

Laxman Sunkaliker[1]*, Prabhakar Reddy, T.[2], Joseph B[2]

[1] Regional Agricultural Research Station (RARS), PJTSAU, Polasa - 505 529, Jagtial, Telangana, India
[2]Regional Sugarcane & Rice Research Station, Rudrur – 503 188, Nizamabad, Telangana.
*E-mail: laxman_agridoctor@yahoo.com

A field experiment was conducted during *kharif* 2015 at the Regional Sugarcane and Rice Research Station, Rudrur, of Professor Jayashankar Telangana State Agricultural University, to assess the response of aerobic rice to three levels of fertiliser (100%, 125% and 150% RDF,) and two spacings (20x10 cm and 30x10 cm). The treatments were replicated thrice and were tested in randomized block design. The main objective was to grow rice crop with less water and save water. Dry seeds and sprouted seeds were used. Land was prepared perfectly till fine tilth was obtained. Seeds were sown in lines manually under saturated soil moisture conditions. Crop was irrigated as and when small hair line cracks were observed in the soil, and the soil was kept at saturated moisture conditions throughout the crop period. Standing water was not allowed at any stage of crop growth. A common dose of zinc sulphate and iron sulphate were applied each @ 50 kg/ha as basal. The data revealed that levels of RDF significantly influenced the grain yield of aerobic rice. However, it was not significantly influenced by spacing treatments and their interaction with levels of nitrogen. In both the experiments, aerobic rice applied with 150% RDF (150-75-60 kg N-P_2O_5-K_2O ha^{-1}) resulted in higher grain yield, which was on par with 125% RDF and significantly superior over 100% RDF. 125% RDF recorded 12.6% and 12.2% increase in grain yield over 100% RDF in both dry seeded and sprouted seeded, respectively. Thus it is concluded that 125% RDF (125-62.5-50 kg N-P_2O_5-K_2O ha^{-1}) under 20x10 cm spacing is suitable for dry direct seeded aerobic rice grown under Telangana conditions for getting more yields.

IDT8-076 | Enhanced root activity and nitrification under SRI system improves nitrogen nutrition of rice

P.C. Latha[1], R.Mahender Kumar[1], D.Vishnu Vardan Reddy[2], T.Ramesh[2], S. Praneeth Kumar[1,2]*

[1] Indian institute of rice research (IIRR) , Hyderabad, India
[2] Professor Jayashankar Telangana State Agricultural University, Hyderabad, India
*E-mail:suvarnapraneeth@gmail.com

System of rice intensification (SRI) makes rice production more sustainable by increasing yields by 20%-40%, and simultaneously reducing water utilization by 25%-50%. The scientific reasons for the observed yield increases are yet to be elucidated. This study presents the hypothesis that SRI method of cultivation induces nitrification, reduces aerenchyma formation and improves root nutrient uptake from the rhizosphere, leading to better yields. Nitrification rate in SRI soils increased by a factor of 1.13, which also maintained higher level of NO_3-N compared to NTP. The increased nitrification rate leads to rhizosphere acidification during the conversion of NH_4-N to NO_3-N. Rhizosphere acidification creates an environment which is favourable for root elongation, resulting in increased root surface area and thereby enhancing the absorption of nutrients. Greater nitrate content in the rhizosphere of SRI system leads to improved nitrate uptake, as evidenced by higher concentration of nitrate in the xylem sap. Increased expression of nitrate transporters is known to influence pH buffering capacity of the plant and results in enhanced nitrogen use efficiency and grain yields. Better soil aeration under SRI system reduces the formation of aerenchyma tissue in rice roots compared to NTP. This reduced aerenchyma allows better uptake of nutrients due to improved translocation use efficiency. Hence, SRI method of rice cultivation by mediating changes in the plant morphology, soil nitrate concentration and microbial nitrification brings together a combination factors that ultimately lead to increased grain yield and nutrient uptake.

IDT8-077 | Development of an index to characterize and monitor agricultural droughts

Swain S[1]*, Reddy MJ[1]

[1] Indian Institute of Technology Bombay, Mumbai, India
*E-mail: sabyasachiswain16@gmail.com

Drought is amongst the most complicated and incomprehensible natural events; often attributed to persistence of precipitation deficit. For India, the rising frequency of protracted and pervasive droughts, leading to exacerbating socio-economic effects, is thought-provoking. This paper proposes an index for identification and monitoring of agricultural droughts. The hydro-meteorological data requirements of this index are precipitation, evapotranspiration and soil moisture content at daily time steps. The methodology is analogous to the Standardized Precipitation Index (SPI), which is ubiquitously used for characterizing meteorological droughts. The difference is that in place of raw precipitation, only the portion of precipitation contributing to evapotranspiration demand and moisture content of soil is considered. As the part of precipitation contributing to surface runoff has no direct role to play for agricultural droughts and the index is computed at a finer (daily) scale, it can capture the onset and persistence of drought conditions. Having two-third of population with agriculture as their primary occupation, this study will be helpful to track drought events and hence, to develop better adaptive strategies.

IDT8-078 | Evaluation of cotton genotypes and standardization of agrotechniques for high density planting in rainfed alfisols of Telangana

Thatikunta R[1]*, Santhosh B[1], Janakiramulu Y[1], Lavanya B[1], Gourishankar V[1], Hussain SA[1], Reddy DVV[1]

[1]College of Agriculture, Professor Jayashankar Telangana State Agricultural University, Rajendranagar-500030.
*E-mail: thatikuntaramesh@gmail.com

Cotton crop in Telangana is predominantly cultivated in shallow to medium soils under rainfed conditions in 17 lakh ha. Seed Cotton Yield (SCY) is limited by the occurrence of terminal stress. Hence, high SCY from long-duration varieties or Bt hybrids could not be harnessed. Besides, farmers invest sizable amounts of money on purchase of hybrid seed every year. Cultivation of varieties that give high SCY and are amenable for mechanized picking reduces the cost of cultivation. To improve SCY, the concept of high density planting system (HDPS), popularly known as ultra narrow row (UNR) cotton, with suitable varieties offers a viable alternate approach *vis a vis* conventionally planted cotton. Towards identification of HYVs, an experiment has been conducted with nine genotypes with three spacings (45 x 10, 60 x 10 and 75 x 10) in split plot design during *kharif* 2015-16 and 2016-17. The genotypes have been characterized at three stages viz., square, flowering and boll formation for physiological, morphological and enzymatic parameters. Deltapine 9121 at 75 x 10 cm recorded superior performance for earliness in square initiation (41 days), leaf area (3489 cm^2), sympodials (15.2), bolls per plant (7.9), boll weight (2.5g), SCY (16.2 g $plant^{-1}$ / 18.8 q ha^{-1}), proline content (614 $\mu g\ g^{-1}$ fresh weight), catalase activity (227 μ mol H_2O_2 mg $protein^{-1}$ min^{-1}), peroxidase activity (0.89 mg soluble $protein^{-1}$ min^{-1}) and polyamines. WGCV 48 showed high values for TDM (130 g $plant^{-1}$) and SCMR (43.9). Deltapine 1921 hybrid and WGCV 48 are performing better.

IDT8-079 | *Pseudomonas putida* modulates morphophysiological, biochemical and molecular responses in chickpea (*Cicer arietinum* L.) during drought stress and recovery

Tiwari S[1,2], Ram Jatan[1,3], Lata C[1,*]

[1]CSIR-National Botanical Research Institute (CSIR-NBRI), Lucknow, India
[2]University of Lucknow, Lucknow, India
[3]Academy of Scientific and Innovative Research (AcSIR), New Delhi, India
*E-mail: charulata@nbri.res.in

Among abiotic stresses, drought is one of the most devastating environmental stress factors that maximally affect plant growth and yield. However, some plant growth promoting rhizobacteria (PGPR) are known to improve plant health and promote growth during abiotic stresses. The present study suggested the potential role of *Pseudomonas putida* MTCC5279 (RA) in drought stress amelioration in two contrasting chickpea varieties namely, cv. BG-362 (*desi*) and cv. BG-1003 (*kabuli*) under both *in-vitro* and greenhouse conditions. Drought stress significantly affected various growth parameters, membrane integrity, osmolyte accumulation, reactive oxygen species (ROS) scavenging ability and stress responsive gene expressions at all given stress durations, which were positively modulated upon application of NBRIRA in both chickpea cultivars. In comparison to the control, both chickpea types showed better improvement after recovery in RA inoculated plants. Quantitative (qRT) PCR analysis showed differential expression of genes involved in transcription regulation (*DREB1A* and *NAC1*), stress response (*LEA* and *DHN*), ROS scavenging (*CAT*, *APX*, *GST*), ethylene biosynthesis (*ACO* and *ACS*), and salicylic acid (*PR1*) and jasmonate (*MYC2*) signalling in both chickpea cultivars subjected to drought stress and recovery with or without RA. Our results thus indicate that RA confers drought tolerance in chickpea by altering various morpho-physiological and biochemical parameters, as well as by regulating differential expression of at least 11 stress responsive genes. To the best of our knowledge, this is the first report on detailed analysis of plant growth promotion and stress amelioration in one month old *desi* and *kabuli* chickpea subjected to short-term drought stress and subsequent recovery.

IDT8-080 | New drought-tolerant groundnut varieties for Bac Binh District, Binh Thuan Province, Vietnam

Nguyen Thi Hoai Tram[1], Tran Thi Phuong Nhung[2]

[1] Center of Incubation and Technology Transfer, Hue University, Vietnam
[2] Research Institute for Oil and Oil Plants, Vietnam
*E-mail: hoaitramnt@gmail.com

Climate-resilient varieties are needed to address issues arising in agriculture from climate change. Local varieties are not well-suited to face unpredictable wide fluctuations in climatic conditions. A varietal evaluation was conducted in the summer season of 2015 in Bac Binh district to identify drought-tolerant, high-yielding groundnut varieties, which will be adapted to local agro-ecological conditions. From this evaluation, three new groundnut varieties, VD1, VD2 and VD 01-1, were identified, which mature in 79-85 days and have yield potential ranging from 3.9 tons to 4.2 tons per hectare. These varieties yield 23.1% to 28.6% more than the local varieties. In addition to their drought tolerance, these varieties are also tolerant of major pests of groundnut in the province. Farmers of the district have adopted the new varieties for cultivation to meet the requirement of raw material for the development of the district.

IDT8-081 | Differential effect of AMF (*Glomus intraradices*) and endophytic fungus (*Piriformospora indica*) on finger millet [*Eleusine coracana* (L.) Gaertn] under the drought stress

Tyagi J[1], Varma A[1], Pudake RN [2,*]

[1]Amity Institute of Microbial Technology, Amity University Uttar Pradesh, Noida, UP, 201 313, India
[2]Amity Institute of Nanotechnology, Amity University Uttar Pradesh, Noida, UP, 201 313, India
*E-mail: rnpudake@amity.edu

The aim of this work was to investigate the impact of AMF (*G. intraradices*) and endophytic fungus (*P. indica)* on the growth of finger millet plant under drought stress. Plant growth parameters such as leaf water status, chlorophyll content, malondialdehyde (MDA) content, electrolyte leakage, enzymatic (catalase CAT, superoxide dismutase SOD, guaicol peroxidase G-POX and polyphenol oxidase PPO), non-enzymatic antioxidants (ascorbic acid, glutathione, total phenols and flavonoids), and osmolytes (proline and total soluble sugars) were studied in pot culture under three soil moisture regimes (well-watered, moderate, and severe stress). Fungal-inoculated seedlings showed better growth as compared to non-inoculated plants. AM fungus was found to be more efficient in alleviating the detrimental effect of water stress by improving the plant biomass and growth characteristics. *P. indica*- inoculated plants have higher proline, relative water content and photosynthetic content under severe stress. Total soluble sugars accumulated more in AM-inoculated seedlings. Consequently, mycorrhiza-treated plants showed lower accumulation of ions, MDA and H_2O_2 at all stress levels. Secondary metabolites (phenol, flavonoid) and ascorbate-glutathione redox status was improved in *P. indica* treatments. AM fungus was more efficient in improving the antioxidant enzymatic activity under water stress condition, except *P. indica* showing their positive effects in improving the PPO activity under drought stress.

In conclusion, our findings indicated that inoculation with both of these fungi increased water stress tolerance of finger millet plant through a stronger antioxidant defence system. But both of the fungi may differ in their drought stress tolerance mechanisms.

IDT8-082 | Prospects of new chickpea varieties in Andhra Pradesh

V. Jayalakshmi[1], A. Trivikrama Reddy[1], N.Kamakshi[1], S. Khayum Ahammad[1], P. Munirathnam[1], P.M. Gaur[2] , S. Srinivasan[2] Y. Padmalatha[1] and B. Gopal Reddy[1]

[1]Regional Agicultural Research Station, Nandyal 518502, Andhra Pradesh, India.
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Telangana, India
*E-mail: veera.jayalakshmi@gmail.com

Andhra Pradesh is an important chickpea growing state in southern India, with spectacular increase in chickpea area from 120,000 ha in 1997/98 to 638,000 ha in 2007/08. The chickpea revolution in Andhra Pradesh has improved the prospects of many resource-poor, small land holding and rainfed farmers of Andhra Pradesh. However, the growing season of chickpea in Andhra Pradesh is warm and short (90-110 days), and drought is the foremost factor responsible for significant yield losses. Rainfall in major chickpea-growing regions is quite uncertain and erratic, resulting in poor yields. The Regional Agricultural Research Station of Acharya N G Ranga Agricultural University, Nandyal, Andhra Pradesh, India is the lead centre responsible for location-specific research in chickpea in Andhra Pradesh. With support from ICRISAT and ICAR, the centre has initiated crop improvement programmes during 2004 and has released four promising chickpea varieties for commercial cultivation. Three *desi* varieties viz., *Nandyal Sanaga* 1(NBeG 3), *Dheera* (NBeG 47), and *Nandyal Gram 49* (NBeG 49) released for Andhra Pradesh and one large-seeded *kabuli Nandyal Gram 119* (NBeG 119) released for the southern zone comprising Andhra Pradesh, Karnataka and Tamil Nadu, are cutting across chickpea growing regions of Andhra Pradesh. *Nandyal Sanaga 1*, released in 2012, is a bold-seeded *desi* variety tolerant to drought and heat; *Dheera* released during 2015 is also a *desi* variety and the first of its kind in India, suitable for mechanical harvesting. *Nandyal Gram 49* released during 2016 is a high-yielding *desi* variety with attractive seeds; whereas *Nandyal Gram 119* is early bold-seeded *kabuli* variety released during 2015. These varieties have clearly demonstrated their advantage (10%-15 % increase over popular varieties of the tract) in farmers' holdings in large-scale demonstrations and are being preferred by farmers of not only Andhra Pradesh, but also Karnataka, Tamil Nadu, Odisha and Maharastra. Efforts are underway to promote large-scale adoption of these varieties to maximize long term productivity of chickpeas in rainfed vertisols.

IDT8-083 | Strip intercropping system for sustainable crop production under rainfed ecosystem

Vijayaprabhakar A , Jayanthi C[1]

[1]Tamil Nadu Agricultural University (TNAU), Coimbatore, 641003, Tamil Nadu, India
*E-mail: a.vijayp@ymail.com

Strip intercropping system is one of the options to address crop failure in rainfed ecosystem due to prolonged dry spell and uneven distribution of rainfall. It is the practice of producing two or more crops in narrow strips located throughout the length of the field. The strips are wide enough so that each can be managed independently, and yet narrow enough so that each crop can influence the microclimate and yield potential of adjacent crops (Cruse, 2008). Strip intercropping is a highly sustainable system under rainfed ecosystem by its very nature. Strip intercropping offers raising different crops simultaneously with different traits for drought tolerance, and moisture-sensitive crops will secure the minimum income for farmers by avoiding entire crop failure (Dutta and Bandyopadhyay, 2006). The diversified nature of strip intercropping reduces pest infestation and rate of pesticide usage from the monoculture (Gurr and Wratten, 2003). Growing legume crops and deep-rooted crops in strips strongly increases soil fertility by fixing atmospheric nitrogen and reducing soil erosion (Jakhar, 2015). Accumulation of more crop residues that increase humus content and physical characteristics of soils leads to increased population of soil flora and fauna, which results in improved soil health and safeguards the environment. Also, strip intercropping is acceptable to farmers as it facilitates simultaneous growing of different crops such as food grain, oil seed, fiber and sugar crops. Strip intercropping is also highly suitable for modern concepts of agriculture, such as conservation agriculture, eco-friendly farming and organic farming. Further research and better understanding of strip intercropping system will help heighten its benefits under rainfed conditions.

IDT8-084 | Phosphorus influence on nitrogen uptake, nutrient and yield attributes of finger millet in semi-arid region of Kenya

Wekha N.W.[1, 2*], Korir N.K[1], Ojulong H.F[2], Gweyi-Onyango J.P[1]

[1]Kenyatta University, P O Box 43844-00100, Nairobi, Kenya
[2]ICRISAT, ICRAF house, UN Avenue, Gigiri, PO BOX 39063-00623, Nairobi, Kenya
*E-mail: nelwaf@gmail.com

An understanding of P efficiencies of finger millet is very important in soil management and selection of varieties adaptable to P-deficient soils. Therefore, on-station experiments were conducted at the ICRISAT-Kiboko research station to evaluate the effect of differential levels of P on nitrogen uptake, nutrient content and yield. There were four P levels (0, 12.5, 25 and 37.5 kg ha^{-1} P_2O_5) and three varieties (U-15, P-224 and Ekalakala). Ekalakala was the local check while 0 kg/ha P_2O_5 was the control. The trial was laid out in a randomized complete block design in factorial arrangement with three replicates. Soil analytical results showed moderately available P but very low N, organic carbon and zinc. Significant differences *($P<.05$)* were observed between the phosphate levels on the nitrogen contents, where the control had the lowest with 4.95% and 4.90% for the short and long rains respectively; while the 25 kg ha^{-1} P_2O_5 rate had the highest, with 5.66% in the short rains and 5.14% in the long rains. The protein content significantly increased with phosphorus application, peaking at 11.00 g/100 g on the 25 kg ha^{-1} P_2O_5treatment. The newly released variety (U-15) responded positively to P supplemented at 25 kg ha^{-1} P_2O_5, with a maximum grain yield of 3,410 kg ha^{-1}. It can, thus, efficiently utilize N in soils with low N and is highly recommended. The application of P beyond 25 kg ha^{-1} P_2O_5 would not be translated into profitable yields, but losses to the farmer.

IDT8-085 | Exploitation of grasspea (*Lathyrussativus* L.) potential for food and fodder security in dry areas of central India

V. K. Yadav[1]*, M.M. Das[1], P. Sharma[1], Pradeep Singh[1], M. K. Srivastava[1], P.K. Ghosh[1]

[1]ICAR- Indian Grassland & Fodder Research Institute, Jhansi, Uttar Pradesh-284003, India
*E-mail: vijayyadav777@gmail.com

Lathyrus or grasspea (*Lathyrus sativus* L.), an important crop in South Asian countries and China, is grown for human food, animal feed and soil health improvement. In India, grasspea is grown in about 521,100 ha, mainly in Chhattisgarh, Bihar, Jharkhand, Maharashtra, Orissa, Assam, West Bengal, and eastern Uttar Pradesh. As grasspea has an ambivalent reputation due to ODAP content in its plant parts, efforts are on to develop low-ODAP or ODAP-free grasspea varieties with high biomass, for dual purposes of human food and animal feed. In Bundelkhand region, demonstrations were conducted with low-ODAP and high-biomass varieties, *Nirmal* and *Ratan*, covering an area of more than 200 ha. Nutritional analysis of hay, straw and grain was conducted. Feeding trials were also conducted on small ruminants to understand the effect of feeding of grasspea fodder and grain-based concentrates.On an average, improved varieties with site-specific production technologies provided 39.61% higher seed yield than the local cultivar and farmers' practice. Field performance on biomass showed excellent fodder and seed production. The variety *Nirmal* had slightly higher biomass yield at 50% flowering stage compared to the variety *Ratan*, which ranged from 250 to 278 q/ha. Fodder analysis at 50% flowering showed crude protein content between 14.80% and 16.48%, which was on par with superior legume fodder, *viz*. Egyptian clover and *Stylosanthe*s. The most important parameter to decide the usability as fodder, the ODAP content, was below detectable limits (<3.5 ppm), indicating the suitability and safety of grasspea for use as fodder. The effect of use of grasspea solely and in combination was also studied in lamb diets for a period of 90 days. The study indicated that grasspea hay was found to be on par with hay prepared from Egyptian clover. The study proves the potential of utilizing grasspea as food and fodder crops in drought-prone areas of Bundelkhand.

Poster Theme IX

Genomics, Biotechnology and Molecular Breeding

IDT9-001 | Engineering dehydration stress tolerance in sesame: use of sodium tungstate, as ABA inhibitor, to overcome problems associated with overexpressing of *LOS5/ABA3* gene in sesame

Al-Shafeay AF[1], Nesiem MR[2] and Tawfik MS[1]*

[1]Agricultural Genetic Engineering Research Institute (AGERI); Agriculture Research Center
[2]Plant Physiology Sec., Faculty of Agriculture, Cairo University, Giza, Egypt
*E-mail: amal.alshafeay@gmail.com

In an effort to engineer dehydration stress tolerance in sesame (*Sesamum indicum* L.), de-embryonated cotyledons were selected as explant source and were transformed using *Agrobacterium* strain LBA4404 harboring the LOS5 gene (it encodes a molybdenum cofactor sulfurase (MCSU), which catalyzes the generation of the sulfurylated form of MoCo, a cofactor required by aldehyde oxidase to function in the last step of ABA biosynthesis, leading to ABA accumulation in tissues) under a constitutive promoter (three copies of the octopine synthase enhancer in front of the manopine synthase promoter). Unexpectedly, all regenerated, PCR positive T_0 plantlets showed small rooting systems that lacked root hairs, their leaves showed some degree of vitrification, and they also had incomplete vascular differentiation at the root-to-shoot interface, resulting in the plantlets' failure to acclimatize successfully in a Conviron® unite. All the above mentioned observations could be a consequence of overproduction and accumulation of ABA in sesame tissue. In an attempt to overcome the above mentioned obstacles, sodium tungstate, a known ABA inhibitor *via* antagonizing molybdenum, either by competing or substituting Mo in the cofactor enzymes), was used at various concentrations (0.0, 0.005, 0.05 and 0.1 mM). Low concentration of 0.005 mM significantly supported and restored the differentiation and regeneration of normal looking transgenic sesame plantlets. The plants also reflect a highly drought-tolerant phenotype and this was studied also by enzymatic analysis.

IDT9-002 | Overexpression of *Sorghum bicolor* vacuolar H+- pyrophosphatase (SbV-PPase) to improve salt and drought stress tolerance in peanut (*Arachis hypogaea* L.)

Amareshwari P[1], Venkatesh K[1], Kavi Kishor PB[1] and A. Roja Rani[1]

[1]Department of Genetics and Biotechnology, Osmania University, Hyderabad-500007, Telangana State, India.
*E-mail: anupallirr@gmail.com

Groundnut is a good source of edible oil, dietary proteins, resveratrol, fiber, folic acid, vitamins, and minerals. India is one of the world's largest producer of groundnut. Groundnut production is threatened by the changing environments, and predominantly drought and salt stresses are the major abiotic stresses which limit the normal growth, development, production and quality of groundnut. Therefore, there is need to develop stress-tolerant peanut varieties which can be cultivated in drought-prone and salinity-affected areas. Genetic transformation has been suggested to be an effective approach for improvement of stress tolerance in plants. One of the strategies to improve drought- and salt tolerance in plants is to increase solute concentration in the vacuoles of plant cells. In the present study, a vacuolar pyrophosphatase gene (*SbV-PPase*) from Sorghum bicolor was introduced into groundnut (*Arachis hypogaea* L.) by the Agrobacterium tumefaciens mediated genetic transformation. Putative transgenic plants produced were confirmed by molecular methods such as PCR, Southern blot analysis, and RT-PCR. Under drought and salt stress the transgenic plants showed better growth than untransformed controls. Na^+ and K^+ contents were higher in transgenic leaves than in untransformed leaves in saline conditions. The transgenic plants exhibited higher total chlorophyll and relative water content, accumulated more proline than untransformed plants under drought and salt stress conditions. Physiological analysis of transgenic lines showed higher shoot and root biomass compared to untransformed control plants. To conclude, our study suggests that the transfer of *V-PPase* gene in groundnut resulted in enhanced salt and drought stress tolerance.

IDT9-003 | Identification and characterisation of drought responsive microRNAs in cardamom

Anjali N[1], and Sabu K K[1]*

[1]Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI), Palode, Thiruvananthapuram 695562, India
*E-mail: sabu@jntbgri.res.in

Plant microRNAs are found to be present throughout the genome and they regulate gene expression either by cleaving mRNA or inhibiting the translational process at the post transcriptional level. Drought is one of the major limiting factors that negatively affect productivity of plants. Cardamom cultivation is having good production potential but the plants are vulnerable to biotic and abiotic stress factors. To date, nothing is known about the regulatory roles of miRNAs in response to drought stress in cardamom. Ion Torrent sequencing of two small RNA libraries prepared from control (C) and treated (T) plants raised under well irrigated and drought stressed treatments respectively created 3,938,342 and 4,083,181 primary reads. A total of 150 conserved and 20 novel microRNAs were identified from both the control and treated libraries. Discovery of 17 differentially expressed miRNAs under drought stress suggests that these miRNAs might have involved in various biological processes to improve plant tolerance to water stress. Several target genes for drought stress regulating miRNAs were identified including miR156l and miR169c which cleave the target mRNA involved in response to water deprivation. miR530b and miR156a target mRNAs which respond to water deprivation and inhibit the translational process. The expression patterns of some of the miRNAs were validated by qRT-PCR. This study is the first report of drought responsive miRNAs and their targets in cardamom. The outcome of this research could provide insights into the miRNA based regulatory mechanisms in response to drought stress in monocot plants.

IDT9-004 | Studies on genetic relationship in pigeon pea under drought stress using SSR markers

Anuradha Chetukuri*, Siddiq E.A

Institute of Biotechnology, Professor Jayashankar Telangana State Agricultural University, Rajendranagar, Hyderabad-500030, Telangana, India.
*E-mail: anu_dna@rediffmail.com

Pigeonpea, *Cajanus cajan* [L] Millsp. is one of the most important legume grown in the tropics and sub tropics as a rich source of protein for humans and is also as good source of fodder. Among the various abiotic factors, drought is the major stress affecting the crop production. Molecular markers are useful tools for assessing genetic relationship of various crops and among them simple sequence repeats (SSRs) are popular as they reveal more variation, co-dominant and have wide genomic distribution.

In the present study a total of 54 SSR primers were used for establishing the relationship of 40 pigeonpea genotypes, in which 22 SSR primers were found to be polymorphic. A total of 60 alleles were obtained using 22 SSR primers with an average of 2.727 alleles per primer The number of alleles amplified for each primer ranged from 2 to 4. The polymorphic information content (PIC) for these primers ranged from 0.609 to 0.929. The similarity coefficient among the genotypes ranged from 0.204 to 0.820 indicating that the genetic diversity among the genotypes was quite wide. 40 genotypes were grouped into 7 clusters clearly differentiating the drought tolerant and susceptible. In addition to displaying the existing variability among cultivars for drought tolerance, this study also provides valuable information on target trait availability for successful breeding programs.

IDT9-005 | Development of chalcone synthase locus specific CAPS marker to screen abiotic stress tolerant mulberry genotypes from a recombinant population

Arora V[1], Gangopadhyay G[1]*

[1] Bose Institute (Main Campus), Kolkata – 700009, West Bengal, India
*E-mail: gaurab@jcbose.ac.in

Mulberry (*Morus* spp.) is a commercially valuable plant as its foliage is the sole food of the silkworm (*Bombyx mori* L.). Hence, the yield and quality of mulberry leaf play a determinate role in the sericulture industry. Various abiotic stress conditions, such as moisture, salinity and alkalinity can cause 50 to 60% yield loss in mulberry. Hence, there is a need to produce qualitative mulberry foliage that can adapt to different climatic conditions. Flavonoids have been reported to play a decisive role in the plant responses when exposed to various abiotic and biotic stresses. Chalcone synthase (CHS) is an essential enzyme in the phenylpropanoid pathway that catalyzes the first step in flavonoid biosynthesis in plants under various environmental stress. It makes the chalcone synthase gene a strong candidate to develop a gene-based marker. We have used CHS as a candidate gene in mulberry and developed Single Nucleotide Polymorphism (SNP) based co-dominant Cleaved Amplified Polymorphic Sequence (CAPS) marker associated with the CHS locus. Screening of the marker in F1 recombinant population, derived from a hybridization program between two mulberry genotypes, showed polymorphism for the CHS locus. Differential CHS activity of the recombinants was correlatable with the segregation pattern of the marker. Bioinformatic analyses, homology modelling and docking studies of the identified CHS alleles substantiated differential CHS activity in the parents and recombinants.

IDT9-006 | Metabolic activity in breeding lines favoring drought tolerance in soybean (*Glycine max* (L.) Merrill)

Arya M*[1], Satpute GK[1], Gupta S[1], Devadas R[2], Ratnaparkhe M[1], Bhatia VS[1]

[1]ICAR-Indian Institute of Soybean Research, Indore, 452001, MP, India
[2]ICAR-National Research Centre on Orchids, Pakyong-737106, Sikkim, India
*E-mail: mamta.gpb@gmail.com

Soybean is an important oilseed crop cultivated under varying agro-climatic conditions across India. Rapid growth of soybean in terms of area and production has resulted in crop exposed to many biotic and abiotic stresses of which drought has been a major constraint resulting in huge losses. There are few varieties and exotic germplasm accessions in India which have shown tolerance to drought stress and which are being utilized in breeding program to develop suitable genotype(s) that can perform well in terms of yield under water limiting environment. Twenty six breeding lines in their F8 generation from three crosses involving JS 97-52, JS 90-41 and NRC 37 were evaluated under terminal drought stress conditions induced in rain out shelter at R5 stage with two checks NRC 7 (tolerant) and NRC 2 (susceptible). There is a significant contribution of leaf RWC towards increased tolerance which is further correlated with leaf chlorophyll content. Proline, an osmoprotectant, scavenges ROS, thus checking H2O2 concentration as a result of oxidative damage. This in turn indicates higher catalase and reduced peroxidases activities. Above trend has been followed in the study and based on that, few lines viz., 107-4, 104-62, 104-35, 108-86 and 104-31 were found superior which in turn has been confirmed with field screening based on yield performances under water limiting conditions.

IDT9-007 | Rhizoscope phenotyping tools: validation under natural condition.

Dardou A.[1], Ba M. [2], Audebert A.[1,2*]

[1]CIRAD, UMR AGAP, Montpellier F34098 France
[2]ENSA-Ceraas, BP 3320 Thiès Senegal
*E-mail: alain.audebert@cirad.fr

Cirad set up a high-throughput system for roots phenotyping, named “Rhizoscope” (Courtois et al, 2013). The system is based on the use of 2-D “Nail board rhizoboxes” filled up with transparent glass beads and connected with a nutrient solution irrigated system. The transparent glass bead substrate allows to study root growth and development under uniform mechanical impedance with mineral nutrient constraint. The objective of this work was to validate the Rhizoscope system with field measurements.

Three contrasted rice varieties were used. The Rhizoscope data used come from different previous studies (Sandhu et al, 2016): During the 2016 rainy season, these three varieties were grown in favorable condition in the Isra Bambey station in Senegal. Root phenotyping was done at the same growth stage than in Rhizoscope (30-40 days). Two field root phenotyping methods were used to obtain the same roots variables: (i) the “monoliths method” which consists in extraction of the complete soil volume containing the entire root system. The roots are separated from the soil by washing without injury to them (Kücke et al, 1995) and (ii) the “trench profile” which consists in counting intersections between thick and fine roots on a soil profile with spatial location of their position (Chopart et al, 2008; Dusserre et al, 2010).

Results showed that the description of the rice root architecture systems were equivalent in both environment, and at least that the discrimination between genotypes were equivalent between environments. These results confirmed the Rhizoscope as a representative tool for roots architecture studies.

IDT9-008 | Developing a resource of wild cultivated chickpea introgression lines for climate resilience

Balcha L[1*], Besha D[1], Dinegde K[2], Lindsay D[3], Mir Rouf R[4], Mamo B[5], Sani G[5], Vance L[5], Bergmann E[5], Tar’an B[3], Woldemedhin A[1], Penmesta V[5] and Cook D[5]

[1]Ethiopian Institute of Agricultural Research, DebreZeit Agricultural Research Center, DebreZeit, ETHIOPIA,
[2]Ethiopian Institute of Agricultural Research (EIAR), Melkasa Agricultural Research Center, Nazareth, ETHIOPIA,
[3]University of Saskatchewan, Department of Plant Sciences, Saskatoon, CANADA.
[4]Sher-E-Kashmir University of Science & Technology-Jammu, Division of Plant Breeding and Genetics, INDIA,
[5]University of California, Department of Plant Pathology, Davis, USA.
*E-mail: lijupeace@gmail.com

The use of crop wild relatives has been a component of cultivar improvement programs since 1920s and 1930s, after Vavilov recognized their value as a source of increased variation. Reduced genetic diversity in elite varieties of modern crop plants derives from a combination of an early domestication bottlenecks and subsequent focus on fewer improved genotypes during modern breeding. As a result, the prospect for sustainable genetic gain from elite germplasm is increasingly limited. By contrast, the wild ancestors of crop plants typically possess high levels of genetic diversity and an expanded range of adaptive traits that may be of agricultural relevance. Chickpea (Cicer arietinum L.) is one of the most valuable global crops and suffers from a lack of genetic diversity. With the goal of increasing genetic diversity in chickpea, we initiated a novel and systematic introgression from wild Cicer species into cultivated elite germplasm. The approach combines (1) systematic survey of wild diversity, (2) introgression of a representative set of genotypes, and (3) marker-assisted normalization of phenology among segregating progeny. Twenty diverse wild founders of C. reticulatum were selected from 270 wild accessions based on a combination of their genomic sequence information and the ecology of their origin sites. Each of the 20 founders was crossed to elite cultivars of India, Ethiopia, Canada and Turkey. Early generation segregant populations will be phenotyped for climate resilient traits at multiple sites in Ethiopia and India. This resource of introgressed populations will serve as a platform for gene discovery through genomics, modeling and phenotyping, and for the development of tools for marker-assisted selection for breeding.

IDT9-009 | Over-expression of gene encoding hydrogen peroxide generating germin-like protein induces thermo-tolerance in potato

Baniekal Hiremath Gangadhar[1,8,*], Kappachery Sajeesh[1,2], Jelli Venkatesh[1,3], Venkidasamy Baskar[1],
Kumar Abhinandan[4], Raghvendra Kumar Mishra[5], Akula Nookaraju[6,7], Jae Woong Yu[1]

[1]Department of Molecular Biotechnology, Konkuk University, Seoul, 143701, South-Korea
[2]School of Applied Biosciences, Kyungpook National University, Daegu. South-Korea, 702-701
[3]Department of Plant Science and Vegetable Breeding Research Center, Seoul National University, Seoul, South Korea
[4]Department of Biological Sciences, University of Calgary, Calgary, AB, Canada, T2N 1N4
[5]Amity Institute of Biotechnology, Amity University Madhya Pradesh, Gwalior, India
[6]Department of Biological Sciences and School of Forest Resources and Environmental Science Michigan Technological University, USA
[7]Kaveri Seed Company Ltd. India Kaveri Seed Company Ltd. India
[8]Department of Biotechnology and Crop Improvement, University of Horticultural Sciences, Bagalkot, India
*E-mail: gangubhm@gmail.com

Germins and germin-like proteins (GLPs) belong to cupin super-family have been reported to be involved in plant responses to several biotic and abiotic stresses involving production of hydrogen peroxide (H2O2), but their role in mitigating heat stress is poorly understood. In the present study, we examined the ability of a Solanum tuberosum L. GLP (StGLP) gene isolated from the yeast expressed cDNA library generated from a heat stressed potato plants (Gangadhar et al., 2014a), and characterized its role in imparting innate and/or acquired thermo-tolerance to potato thorough genetic transformation. The transgenic plants exhibited enhanced tolerance to severe heat and drought stress in terms of maximal cell viability, minimal ion leakage and reduced chlorophyll breakdown. Further, three (G9, G12 and G15) StGLP transgenic lines exhibited enhanced production of H2O2, which was either reduced or blocked by inhibitors of H2O2 under normal and heat stress conditions. This tolerance was mediated by up-regulation of antioxidant enzymes (catalase, ascorbate peroxidase and glutathione reductase) and other heat stress responsive genes, StHSP70, StHSP20 and StHSP90 in transgenic potato plants. These results demonstrate that H2O2 produced by over-expression of StGLP in the transgenic potato plants triggered the reactive oxygen species (ROS) scavenging signaling pathways controlling antioxidant and heat stress responsive genes imparting tolerance to heat stress in transgenic plants.

IDT9-010 | Genome wide analysis of the family of genes encoding SET-domain containing proteins in *Triticum aestivum*

Batra R[1], Gahlaut V[1], Gautam T[1], Vasistha NK[1], Balyan HS[1], Gupta PK[1]*

[1]Department of Genetics and Plant Breeding, Ch.Charan Singh University, Meerut-250004, UP, India.
*E-mail: pkgupta36@gmail.com

The proteins containing SET-domain are involved in methyl transferase and other catalytic activities including histone lysine methylation, which alters chromatin structure and regulates transcription of genes involved in various developmental and physiological processes. We performed a genome-wide analysis of genes encoding SET domain containing proteins in wheat and identified 142 *TaSET* genes. These genes are distributed on all the 21 wheat chromsomes with maximum genes present on group 2 chromosomes (28) and minimum on group 4 chromosomes (11). The length of genes (1631-21525 bp) and cDNA sequences (867-6976 bp) varied considerably. For individual genes, the number of exons varied from 1 to 24 while the number of transcripts varied from 1 to 14. Similarly, variation was observed at the protein level also; the length of the proteins encoded by individual genes ranged from 191-2028 aa, the pI ranged from 4.44 to 9.28, molecular weight ranged from 22.22 to 221.14 KDa, aliphatic index ranged from 60.07 to 97.78, and Grand Average of Hydropathy (GRAVY) ranged from -0.813 to -0.016. TaSET proteins encoded by most of the genes in wheat were unstable, except for the following: TaSET025, TaSET033, TaSET059, TaSET074, TaSET079, TaSET081 and TaSET138. TaSET. Phylogenetic analysis classified *TaSET* genes into different classes. *In silico* expression analysis revealed differential expression of *TaSET* genes under conditions of heat, drought and heat+drought stress. The results of the present study are being used for designing wet-lab experiments, which will facilitate an understanding of the mechanism of epigenetic regulation of abiotic stress tolerance in wheat, particularly that involving histone modifications.

IDT9-011 | Using the allelic diversity platform at syngenta for identifying optimized alleles of drought tolerant loci

Chintamanani S[1*], Williams T[3], Warner T[2], Prest T[1], Caton H[1], Magwire M[4], White K[4], Bensen R[2]

[1] Syngenta Seeds, Inc., Slater, Iowa, United States of America
[2] Syngenta Seeds, Inc., Stanton, Minnesota, United State of America
[3] Syngenta Seeds, Inc., Clinton, Illinois, United States of America
[4] Syngenta Crop Protection, LLC, Research Triangle Park, North Carolina, United States of America
*E-mail: satya.chintamanani@syngenta.com

Conventional breeding, when combined with molecular genetic approaches such as genome-wide association mapping and genomic selection, have enabled an increased rate of genetic gain for yield under water limited conditions. These approaches have focused on driving improvements by manipulating the limited genetic diversity that is available in commercial breeding germplasm. Redesigning maize for improved tolerance may be further enhanced by the introduction of novel alleles from a broader base of germplasm. In order to facilitate the identification of desirable alleles from a broader base of germplasm, the proper reagents need to be created, evaluated and transferred into commercial germplasm. Towards this end, Syngenta has developed an Allelic Diversity (AD) platform. Under this platform the genomes of 134 diverse lines (including 65 inbred lines and 69 landraces) have been backcrossed into two lines (one stiff stalk and one non-stiff stalk line). Over 65,000 back-cross derived near isogenic lines (NIL's) were created as a part of this platform. We are currently utilizing this platform to identify optimal alleles of Quantitative Trait Loci (QTL) that have been associated with yield under drought stress in maize. Our results have demonstrated that the AD platform can be successfully used to identify significantly improved allelic versions of QTLs associated with yield performance in water limited conditions.

IDT9-012 | Heat tolerance in groundnut is associated with efficient strategies of physiological adaptation and early induction of small HSPs

Chakraborty K[1,2], Bishi SK[1*], Mahatma MK[1], Kalariya KA[1,3], Goswami N[1], Zala PV[1], Singh AL[1]

[1]ICAR-Directorate of Groundnut Research, Junagadh, Gujarat, INDIA
[2]ICAR-National Rice Research Institute, Cuttack, Odisha, INDIA
[3]ICAR-Directorate of Medicinal and Aromatic Plants, Anand, Gujarat, INDIA
*E-mail: sujitbishi@gmail.com

In the long run, the global climatic change could negatively affect agriculture in terms of production and productivity of many crops including groundnut (*Arachis hypogaea* L.). In areas where temperatures are already close to the physiological maxima for crops, global warming will impact yields more immediately. Thus, a field experiment was conducted to understand the metabolic processes associated with heat tolerance taking four groundnut genotypes (ICGS 44, GG 7, AK 159, DRG 1) having different thermo-tolerance ability, and grown under varying temperature regimes by staggered sowing (D_1, D_2, D_3) with 20 days interval. At the time of sampling (at 50% flowering), variability of 2.0-2.5 and 3.0-3.5 °C in mean day and night temperatures respectively was observed between each date of sowing. A distinct difference (20-25%) in membrane stability index (MSI) was observed between tolerant (ICGS 44, GG 7) and sensitive genotypes (DRG1, AK 159) under highest temperature regime (D_3). Higher MSI and pollen viability at 4.0-6.0 °C higher temperature than that of the optimum temperature proved to be the key factor responsible for heat tolerance in groundnut. Changing sugar accumulation pattern in leaf indicated faster degradation of storage carbohydrates (sucrose) under high temperature, while increased content of the breakdown products may have direct role in thermo-stability of tolerant groundnut genotypes under elevated temperature. Short-term induction of high temperature stress (5 °C above ambient) in growth-chamber study revealed early induction of small heat-shock proteins (HSPs), particularly HSP-17, which seems to be associated with heat tolerance behaviour of tolerant genotypes.

IDT9-013 | Comprehensive expression study on microRNA sand their targets transcripts under different heat stress treatments in contrasting rice cultivars

Sailaja B[1], Mangrauthia SK[1]*, Vishnu Prasanth V[1], Agarwal S[1], Voleti SR[1], Sarla N[1], Subrahmanyam D

[1]ICAR-Indian Institute of Rice Research, Hyderabad, India
*E-mail: skmdrr@gmail.com

High temperature has emerged as an important abiotic stress in a changing climate scenario. Heat-tolerant genotypes have more efficient gene regulatory networks to reorient the metabolic processes to sustain during the high temperature stress. In addition to protein coding transcripts, the expression dynamics of non-coding regulatory microRNAs (miRNAs) is of great significance, considering their crucial role in gene regulation. Very limited information is available on miRNAs expression at different stress treatments in susceptible and tolerant rice genotypes. Keeping this in view, the miRNAs study on genome wide identification of miRNAs was conducted through deep sequencing in tolerant (Nagina 22) and susceptible (Vandana) rice cultivars by constructing 16 cDNA libraries representing root and shoot of 13-days-old seedlings under different heat stress treatments. Small-RNA sequencing of 16 libraries generated ~271 million high-quality raw sequences. One hundred and sixty two known miRNA families were identified in which miR166, miR168, miR1425, miR529, mR162, miR1876, and miR1862 were found to be highly expressing in rice tissues. Expression of osa-miR1436, osa-miR5076, osa-miR5161, and osa-miR6253 was observed only in stressed tissue of both the genotypes, indicating their general role in heat stress response. Expression of osa-miR1439, osa-miR1848, osa-miR2096, osa-miR2106, osa-miR2875, osa-miR3981, osa-miR5079, osa-miR5151, osa-miR5484, osa-miR5792, and osa-miR5812 was observed only in N22 during high temperature, suggesting specific role of these miRNAs in heat stress tolerance. By using stringent criteria, novel miRNAs were also predicted. This study provides differentially regulated miRNAs expressed in root and shoot of heat susceptible and tolerant rice genotypes under heat stress treatments and recovery.

IDT9-014 | Genetic variation, marker validation and water use efficient lines identification in recombinant inbred lines of rice (*Oryza sativa* L.)

Boranayaka MB[1*], Lokesha R[1], Sheshshayee MS[2], Jiwan JR[1], Mahanth Shivayogayya K[3] and Rajendragouda Patil[1]

[1]University of Agricultural Sciences, Raichur-584104, Karnataka (India)
[2]University of Agricultural Sciences, GKVK, Bengalure-560065, Karnataka (India)
[3]AICRP (Rice), Agricultural Research Station (ARS), Gangavati-583227, Karnataka (India)
*E-mail: mbboranayak@gmail.com

Water Use Efficiency (WUE) and root traits play a key role in breeding for drought tolerance in crop plants. A study was undertaken with 188 Recombinant Inbred Lines (RILs) derived from the cross between Swarna x WAB450 and 54 genotypes of rice along with checks were selected based on mean data of grain yield and their attributing traits. These selected RILs along with checks were phenotyped for various root traits and Water Use Efficiency (Δ^{13}) and genotyped using 88 Simple Sequence Repeat (SSR) markers. The Δ^{13}C of the leaf samples were determined using the Isotope Ratio Mass Spectrometer (IRMS) and single marker analysis was performed to tag and confirm potential SSR markers associated with various root traits and WUE. Root length (RL) ranged in between 21.0 cm and 92 cm with mean of 44.72 cm at reproductive stage in genotypes SW-L49 and WAB450 respectively. The lowest carbon-13 (Δ^{13}C) isotope composition recorded in SW-L38 (16.837) followed by SW-L130 (16.903), SW-L163 (17.579) and SW-L15 (17.858). The RILs SW-L38 and SW-L130 were identified as Water Use Efficient. The markers RM518 and RM224 were found to be associated with WUE trait with highest phenotypic variance explained. The results provide a useful reference for further dissecting the genetic and physiological basis of WUE in rice and new varieties that produce high grain yields under water-saving technologies such as AWD and the aerobic rice systems should be developed.

IDT9-015 | Enhancing stress tolerance of mungbean (*Vigna radiata*) through the use of genetic diversity and molecular breeding

Breria CM[1, 3], Hsieh CH[1], Wang YM[2], Yen JY[3], Ramakrishnan N[4], Schafleitner R[3*],

[1] Department of Tropical Agriculture and International Cooperation, National Pingtung University of Science and Technology, Pingtung 912, Taiwan
[2] Soil and Water Engineering – Department of Civil Engineering, National Pingtung University of Science and Technology, Pingtung 912, Taiwan
[3] Biotechnology/Molecular Breeding, World Vegetable Center, Shanhua, Tainan, Taiwan 74151
[4] World Vegetable Center South Asia, ICRISAT Campus, Patancheru 502 324, Hyderabad, Telangana, India
*E-mail: roland.schafleitner@worldveg.org

Mungbean (*Vigna radiata*) is mainly grown in South and Southeast Asia totaling up to 6 million hectares worldwide. Short duration, low input requirement and high global demand make mungbean an ideal rotation crop for smallholder farmers with good tolerance to drought and heat. Till present, investment in mungbean varietal improvement has been very low. Current mungbean varieties lack key traits to cope with some virus diseases and salt stress. The World Vegetable Center holds a collection of more than 8,000 mungbean accessions. To improve access to diversity by sourcing new traits, a mini-core collection comprising 296 accessions representing a large portion of the diversity was established. The International Mungbean Improvement Network funded by the Australian Centre for International Agricultural Research (ACIAR) made this collection available to several countries in Asia for multi-location trials. In conjunction, the collection is submitted to genotyping by sequencing (GBS) to produce a large number of molecular markers. Marker-trait association will provide insight into the genes underlying key traits and facilitate molecular breeding approaches for the genetic improvement of mungbean. Here we report the first results on variation of salt tolerance present in the mini-core collection and on an association genetics study pinpointing candidate genes underlying this trait. The study produced a large number of single nucleotide polymorphism markers for the mini-core collection. This will be available to the International Mungbean Improvement Network and its partners to characterize mungbean lines. Thus, resilient varieties with high nutritional value and greater stress tolerance will be developed.

IDT9-016 | Chickpea transcription factor, CaTLP1, modulates ROS accumulation and promotes ABA-mediated stomatal closure

Chakraborty N[1]*

[1]National Institute of Plant Genome Research, Jawaharlal Nehru University Campus, ArunaAsaf Ali Marg, New Delhi-110067, India
*E-mail: nchakraborty@nipgr.ac.in

Water-deficit or dehydration is the most crucial environmental constraint on the plant growth and development, and agricultural productivity. To understand the underlying mechanism of dehydration tolerance, we screened the dehydration-responsive extracellular matrix proteome of chickpea and identified a tubby-like protein (TLP), referred to as CaTLP1. We demonstrated that CaTLP1 participates in osmotic stress response, and might be associated with ABA-dependent network. Molecular genetic analysis showed differential expression of CaTLP1 under normal and stress conditions, and its preferential expression in the nucleus. Overexpression of CaTLP1 in transgenic tobacco plants conferred multivariate stress tolerance along with improved shoot and root architecture. Complementation of the yeast *yap1* mutant with CaTLP1 revealed its role in ROS scavenging. Furthermore, complementation of Arabidopsis *attlp2* mutant displayed enhanced stress tolerance, indicating the functional conservation of TLPs across the species. The presence of ABA-responsive element along with other motifs in the TLPproximal promoters established their involvement in stress signalling pathways. The CaTLP1 promoter driven GUS expression was restricted to the vegetative organs, especially stem and rosette leaves. Immunoprecipitation assay revealed that protein kinases are most likely to interact with CaTLP1. This study suggests, for the first time, that the TLPs act as module for ABA-mediated stomatal closure possibly via interaction with protein kinase.

IDT9-017 | A transcriptomic study to understand the combined effect of waterlogging and salinity stress in rice

Koushik Chakraborty*, Soham Ray, Anuprita Ray, JoshithaVijayan, Kutubuddin Ali Molla, Krishnendu Chattopadhyay, Ramani K. Sarkar

ICAR-National Rice Research Institute, Cuttack – 753 006, Odisha, INDIA
*E-mail: koushikiari@gmail.com

During its growing period rice faces multiple abiotic stresses either simultaneously or in tandem. For example, in coastal-saline belts it often faces combined stresses of waterlogging and salinity during different phases of growth. To assess the physiological and metabolic changes in rice associated with waterlogging and salinity stresses, a transcriptome profiling was performed in two waterlogging tolerant rice genotypes, Varshadhan (salinity susceptible) and Rashpanjor (salinity tolerant). Transcriptome analysis in leaf sheath at reproductive stage revealed that in response to waterlogging stress a total of 1489 and 1028 genes were differentially expressed in Vashadhan and Rashpanjor, respectively. Interestingly, combined stress of waterlogging and salinity (WS) resulted in fewer number of differentially expressed genes (748 and 840 in Vashadhan and Rashpanjor, respectively) in both the genotypes. Although both the studied genotypes were tolerant to waterlogging stress, but the transcriptome data primarily indicated existence of differential tolerance mechanisms in them. Varshadhan showed up-regulation of hormonal biosynthesis pathway genes (ethylene and gibberellic acid) and triggers NADPH oxidase activity pointing towards ethylene dependent aerenchyma formation, while Rashpanjor showed up-regulation of genes related plant growth (SPL 8, SPL 16 etc.) as stress induced response. The combined stress (WS) showed up-regulation of Ca^{2+}-dependent signalling (Ca^{2+}-ATPase, CAX etc.) in both the genotypes, but the induction was more pronounced in Rashpanjor. Changes in the expression level of key K^+-transporters (up-regulation of HAK5 and down-regulation of AKT1) emphasized better K^+-retention ability in Rashpanjor under salinity stress contributing towards its salt-tolerant behaviour as compared to Varshadhan.

IDT9-018 | Maker-assisted recurrent selection (MARS) and genome-wide association study (GWAS) for enhanced drought tolerance in cowpea

Chamarthi SK[1], Belko N[1], Togola A[1], Fatokun C[2], Boukar O[1*]

[1] International Institute of Tropical Agriculture (IITA), Kano, Nigeria.
[2]International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria.
*E-mail: O.Boukar@cgiar.org

Cowpea (*Vigna unguiculata* (L.) Walp.) is an important legume crop grown in the semi-arid tropics for its protein-rich leaves, pods and grains for both human and livestock. The crop is relatively well adapted to marginal lands although it is facing more intense and frequent environmental stresses due to climate change with potentially negative impacts on its productivity especially in sub-Saharan African farmers' fields. Marker-assisted recurrent selection (MARS) is being deployed in cowpea breeding programme at IITA with an objective to develop improved cowpea varieties with enhanced drought tolerance. Favorable alleles for drought tolerance are being pyramided using crosses between elite lines IT84S-2246 and IT98K-1111-1, with high yield and drought tolerance, respectively. Seven QTLs have been identified for high grain yield, drought tolerance and stay green in an $F_{2:3}$ generation. These favorable alleles have been fixed following one cycle of recurrent selection and seven rounds of selfing. Homozygosity of the favorable alleles are need to be checked with QTLs flanking markers. Currently, F_7 generation is being evaluated under post-flowering drought and well irrigated conditions in the field. Further, 268 mini-core accessions of cowpea were genotyped using GBS and phenotyped for drought and heat tolerance, striga and aphid resistance under field and screen-house conditions. Genome-wide association study (GWAS) will be performed using TASSEL to identify marker-traits associations. It is anticipated that cowpea lines selected through MARS and GWAS will be characterized by higher productivity in the face of multiple stresses.

IDT9-019 | Transcriptomic analysis of tolerant and susceptible tea cultivars during drought stress

Nalina M[1], Shivashankara KS[2], Ramya L[3], Rajashekar B[3], Radhakrishnan B[1], Chandrashekara KN[1*]

[1]United Planters Association of Southern India Tea Research Foundation Tea Research Institute (UPASI TRF TRI), Valparai 642 127, Coimbatore, Tamil Nadu, India
[2]Indian Institute of Horticultural Research (IIHR), Hessarghatta 560 089, Bangalore, Karnataka, India
[3]Genotypic Technology Pvt. Ltd., R. M. V. Extension 560094, Bangalore, Karnataka, India
*E-mail: knchandu1@gmail.com

The tea plant [*Camellia sinensis* (L.) O. Kuntze] is an important commercial crop. Drought responsive gene expression profiles of drought-tolerant and susceptible cultivars remain largely unexplored. In this research, the transcriptome of a drought-tolerant (UPASI-9) and susceptible tea cultivar (TRF-1) was studied using mRNA-Seq, and important metabolites related to quality of tea under control and drought stress condition. A total of 55.02 million reads from tolerant and 52.68 million reads from susceptible cultivar were produced from transcript sequence of RNA libraries. *C. sinensis* gene assembled and annotated for UPASI-9 (50,018) and TRF-1 (55,247), number of unigenes 30,182 and 34,603 respectively. Differential gene expression between two conditions (control and drought) showed that at least 2,218 and 2,557 statistically significant, functionally known, non-redundant differentially expressed genes (DEGs) from tolerant and susceptible libraries. Drought stress has up-regulated 6,598 and 3,022 DEGs and down-regulated 4,877 and 2,965 DEGs respectively in tolerant and susceptible libraries. The effects of drought stress on the phenotype, physiological characteristics and major bioactive ingredients accumulation of *C. sinensis* leaves were studied. The results from HPLC and LC-MS analysis indicated that during extended drought, there was significant decrease in the phenolic acids, flavonoids, free amino acids and increased levels of osmolytes. Our study concluded that extended drought stress severely decreased the quality and quantity of tea leaves. Tolerance of the plant largely depends on its genes interactions and metabolite flux. However, as more and more knowledge about the complex networks and the cross talk during drought is available, more options will be revealed.

IDT9-020 | NGS-based Identification of heat stress responsive genes in seabuckthorn (*Hippophae* sp.)

Chaudhary S, Sharma PC*

University School of Biotechnology, Guru Gobind Singh Indraprastha University, New Delhi, India
*E-mail: prof.pcsharma@gmail.com

Heat stress causes significant loss to crop production every year worldwide. High temperature effects growth and development of crop plants, which subsequently decreases crop yield. Identification of candidate genes for thermo-tolerance from a plant adapted to harsh environments is an important step towards development of heat tolerant crops. We have generated comprehensive transcriptome data for a medicinally and ecologically important plant seabuckthorn (*Hippophae* sp.), adapted to high altitude regions. In total, 86,253,874 high quality short reads were obtained using Illumina Hiseq2000 platform from stem and root tissue libraries of seabuckthorn. The high quality reads were further assembled into 88,297 putative unigenes. On the basis of Gene Ontology (GO-annotation) term assigned to unigenes, 602 transcripts were grouped under category "response to abiotic stimulus", indicating that a large number of transcripts are expressed in response to environmental stresses. Among abiotic stress responsive genes, 52 were identified as heat stress responsive. Genes coding for heat shock proteins and proteins with chaperone activity were found to be most abundant. Further, 10 genes coding for unknown proteins were also found which were designated as seabuckthorn specific response to heat stress. Although heat responsive genes in seabuckthorn need further validation, the data generated provide valuable resources for gene discovery and development of functional molecular markers related to heat tolerance in seabuckthorn and other crop plants.

IDT9-021 | *In silico* comparison of HSF family genes in *Solanum tuberosum* and *Solanum lycopersicum*

Chauhan SS[1]*, Misra P[2]

[1]Department of Molecular and Cellular Engineering, JSBB Sam Higginbottomn Institute of Agriculture, Technology & Sciences, Allahabad, U.P- 211007
[2]Department of Molecular and Cellular Engineering, JSBB Sam Higginbottomn Institute of Agriculture, Technology & Sciences, Allahabad, U.P- 211007
*E-mail: shubhendra.schauhan@shiats.edu.in

Heat shock transcription factors are one of the important transcription factors involved in heat stress and several other abiotic stresses like drought and cold. HSF regulates expression of HSPs and controls high temperature stress, damage and biological process. In this study we identified the HSF genes in potato and tomato and compared their gene structure, evolutionary relationship, motif and domains with the help of several bioinformatics software. 17 members of potato and 24 members of tomato were identified from Plant Transcription Factor database. Potato and tomato genes were distributed unevenly in 9 and 10 chromosomes of 12 chromosomes respectively. In terms of Gene structure, potato HSF genes retain 1 intron except 2 genes while in tomato 9.3% of genes consist 2 intron which suggests gain of intron during evolutionary process. Comparative phylogenetic analysis of HSF genes revealed 4 groups with several orthologous and paralogous genes. Time of divergence was also examined to understand evolutionary concepts. Conserved domains and cis-regulatory elements were also searched for both species of solaneaceae family. Segmental duplications were found to be involved in family expansion and evolution. Our comparative study may be helpful in understanding of HSF genes in solaneaceae family and evolutionary pathways of HSFs in potato and tomato.

IDT9-022 | Engineering of sugarcane for enhanced water deficit stress tolerance

Augustine SM, Ashwin Narayan J, Manoj VM, Subramonian N, Appunu C*

ICAR-Sugarcane Breeding Institute, Coimbatore 641007, Tamil Nadu, India
*E-mail: cappunu@gmail.com

Sugarcane is a high water demanding crop. Drought is one of the most limiting factors for sustainable sugarcane production and contributing up to 50 % yield loss in India. Over a period of 25 years (1970-71 to 2004-05) sugarcane yields per hectare have fallen from 115 to 60 tonnes due to lack of water availability for irrigation in drought prone areas in India (World Bank report 42946-1N). To enhance the sugarcane water deficit stress tolerance, *EaDREB2, EaHSP70* (isolated from *E. arundinaceus*, a wild relative of sugarcane) and *PDH45* genes were overexpressed in a popular sugarcane variety (Co 86032) of tropical India. *Agrobacterium* mediated or biolistic bombardment method was followed to generate transgenic events. Transgenes were driven by a constitutive port ubi2.3 promoter isolated from *P. coarctata* and *hpt* or *bar* as selection marker. Transgene integration was confirmed through gene specific PCR and also the promoter specific forward primer and the gene specific reverse primers. One hundred events (25 events /construct) were screened in replicated CRD design for soil moisture stress tolerance at the formative phase of V_1 transgenics by withholding irrigation for 10 days under potted conditions. Physiological (photosynthesis rate, stomatal conductance, transpiration rate, relative leaf water content, cell membrane stability, chlorophyll content, photosynthetic efficiency), molecular (upregulation of abiotic stress responsive genes *viz.*, ERD, ERF, LEA, COR, RD29, BRK) and morphological parameters (leaf and tiller numbers) were used to assess water deficit stress tolerance. Overexpression of EaDREB2 and EaHSP70 genes resulted in enhanced water deficit stress tolerance in transgenic sugarcane.

IDT9-023 | Genetically transformed chickpea (*Cicer arietinum* L.) carrying transcription factor, *AtDREB1a* improves drought tolerance through modifying water relation and photosynthesis

Das A[1*], Thakur S[1], Singh P[2], Chaturvedi SK[3], Sheshshayee M S[4], Bansal KC[5], Singh NP[1]

[1]Division of Plant Biotechnology, ICAR-Indian Institute of Pulses Research, Kanpur-208 024
[2]Division of Basic Sciences, ICAR-Indian Institute of Pulses Research, Kanpur-208 024
[3]Division of Crop Improvement, ICAR-Indian Institute of Pulses Research, Kanpur-208 024
[4]Department of Crop Physiology, University of Agricultural Sciences, GKVK Campus, Bangalore 560 065
[5]National Research Centre on Plant Biotechnology, PUSA, New Delhi 110 012
*E-mail: adas@icar.org.in

Drought tolerance is a polygenic character resulting from expression or upregulation of genes modifying the response of crops to drought stress. *AtDREB1A* are an important APETALA2 (AP2)/ ethylene responsive factor (ERF) group of plant transcription factors that induce set of abiotic stress tolerant genes involved in various absicic acid (ABA) dependent as well as independent regulatory mechanisms. Transgenic chickpea lines harbouring the transcription factor, *AtDREB1A* gene driven by stress inducible promoter *rd29a,* were developed and phenotyped under *dry down* conditions. The results revealed modification of many physiological processes in genetically modified chickpea variety, DCP 92-3, which have cumulatively affected the water relation characteristics. These transgenic lines exhibited higher relative water content (RWC) and longer chlorophyll retention capacity, under declining soil moisture at root zone (approx. 7% closer to wilting point), as compared to control non transformed cultivar, DCP 92-3. Some of the transgenic lines exhibited higher osmotic adjustment, which was inherently lacking in the chickpea cultivar, DCP92-3. The enhanced osmotic solute accumulation imparted tolerance through higher membrane stability as evidenced by intact membrane bound photosynthetic electron transport preventing photo inhibition at high irradiance levels with reduced minimal fluorescence (*Fo*) and maintained enhanced quantum yield (Fv/Fm). Based on precise phenotyping, involving non-invasive chlorophyll fluorescence imaging, followed by carbon isotope discrimination ($\Delta^{13}C/^{12}C$), osmotic adjustment and membrane stability, it can be concluded that *AtDREB1A* transgenic chickpea lines are physiologically better adapted to water deficit.

IDT9-024 | Isolation and characterization of stress inducible promoters from *Pennisetum glaucum* and their role in abiotic stress adaptation

Divya K, Reddy PS*, Bhatnagar-Mathur P, Vincent Vadez, Kiran K. Sharma

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502 324, Telangana, India
*E-mail: p.sudhakarreddy@cgiar.org

Abiotic stresses including drought, salinity, oxidative stress, extreme temperatures and a combination of these stresses cause immense loss to agricultural crop production. These losses could be immensely reduced if the crops were able to tolerate these above mentioned conditions. This can be overcome by developing transgenic plants with stress inducible promoters with specific genes. Stress-inducible promoters have previously been identified, but there is a shortage of efficient promoters for gene expression that display favorable characteristics in their native plants as well as in xenogeneic species. In the present study five stress inducible promoters PgApx, PgDhn and PgHsc70, PgLea, PgHsp10 were isolated and functionally validated in the tobacco plants. Five stress inducible promoters were isolated using genome-walking method. Further, all five promoters were subjected to *cis*-motif analysis and identified several stress inducible and tissue specific *cis*-acting elements. These five full-length promoters were fused with *uid*A gene in plant transformation vector pMDC164 and transferred to tobacco. Putative transgenic positive plants were confirmed by PCR and positive plants advanced for T1 and T2 generations. Homozygous T2 transgenic plants were analysed for their tolerance to these stresses. The PgApx pro, PgDhn pro, PgHsc70, PgLea, PgHsp10 pro offers advantages over constitutive promoters to produce genetically modified tolerant crops to these adverse conditions. In summary, PgHsc70 pro is active in high temperatures, PgDhn pro in heat, cold and drought and PgApx pro in drought stress, PgLea pro in heat and drought, PgHsp10 pro in control, heat, cold, salt and drought stress treatments.

IDT9-025 | Identification and expression profiling of stress-related transcription factors involved in drought stress response in sesame: Case of DREB, HSF and WRKY

Dossa K[1,2,3], Li D[1], Wei X[1], Fonceka D[2,4], Zhang Y[1], Wang L[1], Yu J[1], Diouf D[3], Boshou L[1], Cissé N[2], Zhang X[1]*

[1]Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences, Key Laboratory of Biology and Genetic Improvement of Oil Crops, Ministry of Agriculture, No.2 Xudong 2nd Road, 430062 Wuhan, Hubei, China
[2]Centre d'Etudes Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), BP 3320 Route de Khombole, Thiès, Sénégal
[3]Laboratoire Campus de Biotechnologies Végétales, Département de Biologie Végétale, Faculté des Sciences et Techniques, Université Cheikh Anta Diop, BP 5005 Dakar-Fann, Code postal 107000, Dakar, Sénégal
[4]CIRAD, UMR AGAP, F-34398 Montpellier, France
*E-mail: zhangxr@oilcrops.cn

Sesame (*Sesamum indicum* L.) is an ancient crop, termed as the queen of oil seeds because of its high oil quality and quantity. It is mostly grown under rain-fed conditions in arid and semi-arid areas where it is prone to terminal and intermittent droughts. Transcription factors (TFs) are known to regulate a set of targeted genes under their control and consequently enhance the stress tolerance of plants. The goal of this study was to identify DREB, HSF and WRKY as abiotic stress related TFs in the whole genome of sesame and investigate their expression changes under moderate drought stress through qRT-PCR and RNA-seq analyses. In total, 41, 30 and 64 DREB, HSF and WRKY were uncovered, distributed unevenly in the 16 linkages groups (LGs) of the sesame genome. They were further classified into functional groups including A1-A6, A-C and I-III for DREB, HSF and WRKY□ respectively. qRT-PCR analysis in drought tolerant sesame genotype revealed that 20, 27, 38 DREB, HSF and WRKY were drought responsive (> 2-fold rate increase or decrease in gene expression compared to the control), respectively. In addition, RNA-seq results were consistent with qRT-PCR, revealing 50%, 90% and 59 % of DREB, HSF and WRKY significantly and differentially expressed under drought stress ($P<0.01$), respectively. Results suggested that these up and down regulated TFs are involved in drought tolerance mechanisms in sesame and could be good candidates for genetic engineering and transgenic studies towards improvement and breeding for drought-prone environments.

IDT9-026 | Marker assisted selection and phenotyping of an inter-specific hybridization derived population towards development of sesame with synchrony in pod maturation for drought avoidance

Dutta D[1], Gangopadhyay G[1]*

[1]Bose Institute (Main Campus), Kolkata – 700009, West Bengal, India
*E-mail: gaurab@jcbose.ac.in

Cultivated sesame (*Sesamum indicum* L.) is a low-input oilseed crop that can grow under drought conditions and in extreme heat in general. However, in certain African countries and drought-prone regions in India, it often fails to sustain continuous drought if there is a lack of irrigation facilities. Under non-irrigated sesame production, fluctuation in rainfall, both in amount and distribution, exposes the crop to drought stress resulting in drastically reduced yield. Additionally, the asynchrony in pod maturation leading to shattering of seeds that is the characteristic of most of the cultivated sesame varieties further reduces the yield. We are developing early-maturing sesame with synchrony in pod-maturation to avoid prolonged drought condition. *S. prostratum* Retz is wild sesame that has remarkable synchrony in pod maturation. We have made inter-specific hybridization between one selected high yielding Indian sesame (*S. indicum*) and *S. prostratum*; and screened desired recombinants in F2 generation through phenotyping for plant architecture (branching type and synchrony in pod maturation). Phenotypic data revealed near 1:1 ratio between parental types and recombinants (population size 122, male type 27, female type 35, recombinants 60). The recombinants can be grouped further into three categories. No molecular marker linked to possible QTL (Quantitative Trait Locus) behind synchrony in pod maturation is available in sesame database till now. We have noticed one significant polymorphism between two parents using EST-SSR marker. At present, we are screening the population through this identified marker for establishment of an association between the molecular marker and the phenotype.

IDT9-027 | Marker assisted introgression of a major QTL, *qDTY3.1* governing reproductive stage drought tolerance into a popular rice variety Pusa 44 and their phenotypic assessment

Dwivedi P[1], Dhawan G[1], Gopala Krishnan S[1*], Ramawat N[2], Nagarajan M[3], Viswanathan C[4], Bhowmick PK[1], Dhandapani R[4], Kumar S[4], Singh M[4], Singh AK[1]

[1]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India
[2]Amity Institute of Organic Agriculture (AIOA), Amity University, Noida – 201303, Uttar Pradesh
[3]Rice Breeding and Genetics Research Centre, ICAR-IARI, Aduthurai 612 101, Tamil Nadu
[4]Division of Plant Physiology, ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India
*E-mail: gopal_icar@yahoo.co.in

The growing demand for essential uses has rapidly reduced available water for agriculture purposes, thereby, increasing the intensity of drought in rainfed ecosystem and aggravating water shortage in irrigated ecosystem. Rice (*Oryza sativa* L.) is vulnerable to drought stress, which has been predicted to occur more frequently due to climate change. Therefore, there is a need to develop and disseminate ecosystem-specific, water-saving technologies that can reduce water requirements of rice crop without a yield penalty. Pusa 44 (P44) is a popular rice variety due to its advantages of dwarfness, non-lodging habit, long slender grains and high yield of 8.0 t/ha. Marker assisted backcross breeding (MABB) was adopted to incorporate a major QTL for grain yield under drought, *qDTY3.1* from the donor IR81896-B-B-142 into the rice variety, P44 for enhancing grain yield under the drought stress at reproductive stage. Foreground selection was done the marker RM520, linked to *qDTY3.1* and polymorphic SSR markers were used for assessment of background recovery. Additionally, at each generation stringent selection for the recurrent parent phenome, grain and cooking quality characters was done. Advanced BC_3F_4 backcross progenies harbouring *qDTY3.1* are being evaluated for their agronomic performance under drought and irrigated conditions in both natural field conditions and phenomics facility which will help in identifying potential lines with drought tolerance as well as other desirable traits. The improved lines will also be invaluable source of drought tolerance in rice improvement.

IDT9-028 | *de novo* genome assembly and high dense SNP linkage map facilitate genetic dissection of drought avoidance possessed by the upland rice variety IRAT109

Feng FJ, Lou QJ, Xu XY, Yan M, Fan PQ, Wei HB, Chen L, Luo LJ, Mei HW*

Shanghai Agrobiological Gene Center, Shanghai, China
*E-mail: hmei@sagc.org.cn

Drought stress was the main limiting factor of rice production in both upland and rainfed lowland areas. Genetic differentiation of drought resistance existed between upland and lowland rice ecotypes. Typical upland rice varieties were used to develop populations, crossing to commercial lowland rice varieties, for genetic mapping or breeding concerning drought resistance. IRAT109 is an upland rice variety released in Cote D'Ivoire and other countries including China. This variety has been used as a donor parent of drought resistance in a series of genetic studies and breeding programs.

Using next-generation sequencing technology, a draft genome sequence of upland rice variety IRAT109 was *de novo* assembled. The contigs (377Mb) cover approximately 97% of the estimated genome size. A total of 34,198 protein-coding genes were annotated while 170Mb of TE sequences were identified, spanning 43.8% of the estimated genome size. Homology-based annotation of noncoding RNA sequences predicted 727 transfer RNA (tRNA) genes, 689 small nuclear RNA (snRNA) genes, 1387 ribosomal RNA (rRNA) genes and 771 microRNA (miRNA) genes.

Based on resequencing of a RIL population derived from the cross between IRAT109 and Zhenshan97, a high dense SNP linkage map (2498 bins) was develop. A total of five QTLs for the ratio of deep rooting (RDR) which was vital for plants' drought avoidance were identified as being located on chromosome 1, 2, 4, 4, and 6. The candidate genes discovered from this study may provide information for dissecting the genetic basis of drought avoidance in rice.

IDT9-029 | Genome wide association mapping of four agronomic traits in wheat (*Triticum aestivum* L.) under irrigated and rain-fed environments using 18K SNP

Gahlaut V[1], Jaiswal V[1,2], Mehar PK[3], Misra PC[4], Ellis M[5], Singh S[5], Wenzl P[5], Killian A[6], Rao AR[3], Balyan HS[1], Gupta PK[1*]

[1] Department of Genetics and Plant Breeding, Ch. Charan Singh University, Meerut, India
[2] CSIR-National Botanical Research Institute, Lucknow, India
[3] Centre for Agricultural Bioinformatics, Indian Agricultural Statistics Research Institute, New Delhi, India
[4]Jawaharlal Nehru Krishi Vishwavidyalaya, Zonal Agricultural Research Station, Powerkheda, India
[5] CIMMYT, Mexico DF, Mexico
[6]DArT Pty. Ltd., Yarralumla, Australia
*E-mail: pkgupta36@gmail.com

In bread wheat, GWAS was conducted for four traits (days to anthesis, grain filling duration, grain number/ear and grain weight/ear) relevant to drought tolerance. For this purpose, a spring wheat reference set (320 genotypes) was genotyped for ~18K SNPs using genotyping-by-sequencing (GBS), and phenotyped under irrigated (IR) and rain-fed (RF) environments. Four different models that were used for GWAS included the following: (i) single locus single trait (SLST) mixed linear model (MLM); (ii) SLST statistical machine learning (SML) approach, (iii) multi-locus mixed model (MLMM), and (iii) multi-trait mixed model (MTMM). A variable number of MTAs were identified for the four traits using two SLST approaches (543), MLMM (702) and MTMM (559); 15 MTAs were common among MTAs identified using different approaches. Together, only 57 MTAs (12 from SLST; 24 from MLMM and 21 MTMM) were stable in RF and IR+RF environments. The MTAs identified during the present study supplemented the available information on the genetic control of traits under IR and RF conditions. Stable MTAs may be exploited for improvement of drought tolerance in wheat using MAS. Seven candidate genes associated with stable MTAs and involved each in one of the following processes were also identified: transcription, transferase activity, protein processing, positive regulation of catalytic activity, lipid metabolic process, protein serine/threonine kinase activity and cytochrome P450 oxidase activity. Further studies involving these candidate genes for drought responsive traits may prove useful.

IDT9-030 | Detection of stay-green QTL in a sorghum recombinant inbred population based on cross (N13 × E36-1)

Gaikwad PS[1], Mehtre SP[1*], Vadez V[2], Hash CT[3], Deshpande SP[2]

[1]Department of Genetics and Plant Breeding, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, 413402, Maharashtra, India
[2]International Crop research Institute for the Semi-Arid Tropics, Patancheru, 502234, Hyderabad, India
[3]International Crop Research Institute for the Semi-Arid Tropics, Niamey, Niger
* E-mail: shivaji_pmehtre@rediffmail.com

The progress in genetic improvement of post-rainy sorghum for drought tolerance using traditional plant breeding practices has been slow, and selection has not been much effective due to complex interaction between genotype and environment. Identification of genetic factors involved in stay-green through molecular breeding approaches would provide the basis for genetic improvement for drought tolerance. In this experiment stay-green QTLs were mapped and the effect of environment on stay-green expression was observed. For this a sorghum Recombinant Inbred Line (RIL) population was field evaluated for 2 years during the post-rainy season of 2011 and 2012, under two water regimes, (stress and control). A set of 200 entries, including 180 RILs, parents and checks were sown in a plot of 2 rows of 2m in RCBD design with 3 and 2 replications for stress and control treatments, respectively. Data was recorded for percent green leaf area (%GLA) with a weekly interval basis (7 counts) with starting from 50% flowering till physiological maturity. This reveals significant genotypic variances along with high heritability. A genetic linkage map based on 176 RILs with 271 markers consisting of SSRs, DArT and two qualitative traits was developed. In total 45 QTLs were identified for seven %GLA scores in two seasons and two treatments. The phenotypic variation explained by each QTL ranged from 6.00 to 14.00%. In further across environment analysis, some QTLs may be environment specific and some may consistent across environment, such stable QTLs could be utilized through genomics approaches to improve drought tolerance of post rainy sorghum varieties.

IDT9-031 | Expression of *Pennisetum glaucum* translational initiation factor for enhancing drought and salinity tolerance in groundnut

Tata SRBR[1], Juturu VN[1], Mallu M[1], Reddy MK[2], Mallikarjuna G[1&2*]

[1]Agri Biotech Foundation, Hyderabad, Telangana State, India
[2]International Center for Genetic Engineering and Biotechnology, New Delhi, India
*E-mail: garladinnemarjun@gmail.com

Eukaryotic translational initiation factors belong to family of helicases which involved in multifunctional activities either in plants or animals. An eukaryotic translational initiation factor 4A was isolated from stress induced cDNA of *Pennisetum glaucum* and expressed in groundnut under the regulation of stress inducible *rd29A* promoter with *bar* as a selectable marker. The de-embryonated cotyledons of JL-24 variety were infected with *Agrobacterium* (LBA4404) and phosphinothricin resistant calli were produced from which the shoots were regenerated with high frequency. Molecular confirmation of these plants showed the gene integration and expression of eIF4A gene. The single copy integration was seen in T_0 transgenic plants. Predicted Mendelian ratio of segregation (3:1) was noted in single copy integrated plants. Quantitative PCR showed that higher transcript was accumulated in transgenic plants. Transformed *eif4A* groundnut plants exhibited 2-6 fold higher performance in all the phenotypic parameters like shoot length, tap root length and lateral root formation under simulated drought and salinity stresses compared to wild type. In addition, transgenic plants exhibited higher chlorophyll retention, enhanced membrane stability due to scavenging of ROS. Taken together our results confirm that the *eIF4A* gene expressing transgenic plants exhibited better adaptation to drought and salinity stresses.

IDT9-032 | Marker-assisted introgression of a major QTL for yield related traits to improve grain yield in wheat under drought

Gautam T[1], Gahlaut V[1], Saripalli G[1], Balyan HS[1], Gupta PK[1*]

[1]Molecular Biology Lab, Department of Genetics and Plant Breeding, Ch. Charan Singh University, Meerut-250004, India.
*E-mail: pkgupta36@gmail.com

A major QTL (*Qyld.csdh.7AL)* contributing to >20% higher yield per ear under stress environments (including drought stress) was introgressed from wheat genotype SQ1 into four popular Indian wheat varieties (HUW234, HUW468, K307 and DBW17) using marker assisted selection. A set of 62 BC_2F_4 progenies with desirable phenotypes were evaluated in randomized block design with two replications under irrigated and rainfed environments at Meerut (UP) and Niphad (Maharashtra) during 2015-16. Average decline in grain yield under rainfed environments at the two locations was 9% (Meerut) to 31% (Niphad), suggesting suitability of the rainfed environments for evaluation of the derived progenies. Under rainfed environments, six progenies in the backgrounds of HUW234, HUW468 and K307 at Meerut and four progenies in the background of HUW234 at Niphad gave significantly higher grain yield (8% to 59%) than their respective recipient genotypes. One of the higher yielding progenies in the background of HUW234 was common at both the locations. The high yielding progenies were also significantly superior for two or more of the following seven traits: grain number per ear, grain weight per ear, tiller number per m^2, harvest index, biomass, canopy temperature and chlorophyll content. All the progenies are being evaluated at three different locations under irrigated and rainfed environments during 2016-17. This will allow us to identify progenies with higher and stable grain yield and under rainfed environments constituting important material for release as high yielding drought tolerant cultivars of wheat.

IDT9-033 | Introgression of *arcelin* gene into advanced lines of common bean and validation using marker-assisted selection

Girsil TS.*[1], Melis R.[2],Sibiya J, Keneni G[3], Fenta BA[1],[4] Mukankusi CM[4]

[1]Ethiopian Institute of Agricultural Research, Melkassa Research Centre, Adama, Ethiopia
[2]African Center for Crop Improvement (ACCI), University of Kuazul Natal, South Africa
[3]Ethiopian Institute of Agricultural Research, Holeta Research Centre, Ethiopia
[4]International Center for Tropical Agriculture (CIAT), Kampala, Uganda
*E-mail: tshiferaw2006@gmail.com

Common bean (*Phaseolus vulgaris* L.) is the second most important grain legume in Ethiopia, contributing to food security and household income; and enhancing the national economy through exports. Production is, however, greatly curtailed by both field and post-harvest biotic and abiotic constraints. Among the post-harvest constraints, bruchids, particularly Mexican bean bruchid (*Zabrotes subfasciatus* Boheman) is a major problem for farmers, traders and exporters. In the warmer areas, this species is known to cause up to 38% to 60% grain loss after three to six months in storage. This study aimed to identify resistant genotypes among local and improved bean germplasm and introgress arcelin based resistance "*Arc* gene" into selected commercial varieties with the aid of molecular markers. From a set of 300 genotypes, only six RAZ (resistant to *Zabrotes*) and one MAZ (Marker Assisted *Zabrotes*) lines showed complete resistance. AnF_2 population was developed using one selected resistant line of Andean background, MAZ 200 and a small red bean SCR-15 (susceptible parent). DNA was extracted from 322 F_2 bean plants grown at CIAT-Uganda and analyzed using *Tm* shift SNP marker CB_00253 that is linked to *arcelin* gene. Thirty-two lines were found to be positive for arcelin marker giving a single peak at around 83°C.The F_2 population will be further phenotyped to study the expression of this resistance gene.

IDT9-034 | Marker assisted transfer of QTLs, *qDTY1.1* into Basmati rice variety "Pusa Basmati 1" and *qDTY3.1* into elite rice variety "Pusa 44" for enhancing grain yield under reproductive stage drought stress

Gopala Krishnan S[1*], Dwivedi P[1], Dhawan G[1], Nagarajan M[2], Viswanathan C[3], Bhowmick PK[1], Dhandapani R[3], Kumar S[3], Singh M[3], Singh AK[1]

[1]Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India
[2]Rice Breeding and Genetics Research Centre, ICAR-IARI, Aduthurai 612 101, Tamil Nadu
[3]Division of Plant Physiology, ICAR-Indian Agricultural Research Institute, New Delhi 110 012, India
*E-mail: gopal_icar@yahoo.co.in

Drought is one of the major abiotic stresses, which is gaining importance in India even under irrigated ecosystems, due to decrease in irrigation water availability resulting from declining ground water levels as well as fluctuating monsoons. *Pusa Basmati 1* (PB1), a semi-dwarf high-yielding Basmati rice variety, and Pusa 44 (P44) are highly popular in north western India even today due to their higher productivity, non-lodging habit and long slender grains. Since, they were bred for irrigated ecosystems with assured irrigation, both varieties are susceptible to drought, which limits yield and grain quality under drought stress. Marker assisted backcross breeding was adopted to incorporate QTLs, namely, *qDTY1.1* and *qDTY3.1* from *Nagina 22* and IR 81896-B-B-142 respectively for enhancing grain yield under drought stress at reproductive stage. Foreground selection was carried out at each backcross generation using QTL linked markers RM431 and RM520 respectively. Additionally, in each backcross generation, stringent selection for the recurrent parent phenome, grain and cooking quality was carried out to identify the best plant for further backcrossing. Advanced backcross progenies in BC_3F_4 harboring *qDTY1.1* in PB1 and *qDTY3.1* in P44 have been developed and are being assessed for their agronomic performance and grain quality under both under irrigated conditions and drought in field, as well as in a phenomics facility. This will help in identifying elite improved genotypes with drought tolerance as well as other desirable traits which can be further tested in multi-location trials for release as improved rice varieties with reproductive stage drought tolerance.

IDT9-035 | Discovery and validation of genomic regions associated with drought tolerance in tropical maize germplasm

Manje Gowda[1]*, Yoseph Beyene[1], Dan Makumbi[1], Jumbo Bright McDonald[1], Michael Olsen[1], Boddupalli Maruthi Prasanna[1]

[1]International Maize and Wheat Improvement Center (CIMMYT), P. O. Box 1041, Village Market 00621, Nairobi, Kenya
*E-mail: M.Gowda@cgiar.org

In Sub-Saharan Africa, drought is the most common cause of reduced maize yields. Further, climate change is predicted to exacerbate drought's impact. Identification of the genomic regions underlying drought tolerance in maize is of great importance in Sub-Saharan Arica, to develop drought-tolerant germplasm. Here we report a genome-wide association study (GWAS) of maize drought tolerance. Further, we also used linkage mapping and genomic selection (GS) to understand the architecture of grain yield under drought. Association mapping panel comprised 250 diverse maize inbred lines. Three bi-parental populations were used for quantitative trait loci mapping. All populations were evaluated in multiple environments under managed drought conditions, and fingerprinted with genotyping-by-sequencing. Phenotypic variation for grain yield and other agronomic traits under drought were significant and heritabilities were moderate to high. GWAS identified more than 25 significantly ($P< 5 \times 10^{-5}$) associated SNPs for grain yield under drought conditions. These SNPs are located within or adjacent to 15 candidate genes. Linkage mapping analysis identified many QTLs with minor effects distributed across chromosomes. The prediction accuracy within association panel encourages the application of GS in breeding for drought tolerance. Inclusion of drought tolerance linked markers into prediction models led further improved accuracy. Overall grain yield under drought tolerance is controlled by multiple loci with medium to small effect size. The QTLs identified by GWAS and linkage mapping can be used as potential candidates in breeding for drought tolerance.

IDT9-036 | Draft Genome based analysis of WRKY gene family in *Triticum aestivum* and their role in different abiotic stress

Saurabh Gupta, Pritish Kumar Varadwaj*

Department of Bioinformatics, Indian Institute of Information Technology, Allahabad-210012, India
*E-mail: rs159@iiita.ac.in

The WRKY Transcription Factors (TFs) acts as an essential component in growth and development of plant in abiotic stress. Although the draft genome of wheat plant has been released recently, the genome-wide information for WRKY gene family is yet to be annotated. This study intends to perform a genome-wide transcriptomic analysis of *TaWRKY* gene family with 173 genomic sequences of WRKY and their chromosome wise distribution through physical map analysis. The genomic sequences produce 403 transcripts sequences as result of alternative splicing in wheat genome. A set of 285 unique *TaWRKY* proteins, which includes characterized, uncharacterized and fragment proteins were been identified after systematic manual screening of downloaded sequence from all public and specialized transcription factor databases. Series of sequence alignments and phylogenetic analysis were carried out to classify the above set of proteins into three distinct groups viz. I, II and III, where majority of TaWRKY proteins were found to clustered in group-II. Domain analysis these proteins provide the details of WRKY motif and zinc finger-like structure along with other additional domain information. Further role of each *TaWRKY* TF in different abiotic stress were identified through Co-regulatory Transcriptional Network analysis. Finally the result was summarized to provide an insight into the functional annotation of uncharacterized/fragment protein and their targets under abiotic stress conditions.

IDT9-037 | Mapping the genomic regions governing chlorophyll content as a component trait of drought tolerance in peanut (*Arachis hypogaea* L.)

Hake AA[1], Patil Malagouda[1], Sukruth M[1], Bhat RS[1]*

[1]Department of Biotechnology, University of Agricultural Sciences, Dharwad – 580 005, India
*E-mail: bhatrs@uasd.in

Peanut is an important edible crop worldwide for its oil and nutritive value. Peanut productivity is severely affected by drought and moisture stress. With an objective of improving drought tolerance in peanut, an effort was made to map SPAD chlorophyll meter reading (SCMR), which is an important component trait of water use efficiency and drought tolerance. TMV 2-NLM, a mutant from TMV 2, is highly drought tolerant. The parents differed significantly for SCMR, specific leaf area (SLA) and relative water content. TMV 2 had relatively high SLA (238.87 cm2/g) and relative water content (92.0%), and low chlorophyll content (24.59 μg/cm2), while TMV 2-NLM had low SLA (189.28 cm2/g) and relative water content (84.41%), and high chlorophyll content (44.56 μg/cm2). A mapping population consisting of 432 recombinant inbred lines derived from TMV 2 and TMV 2-NLM was evaluated for SCMR during the rainy season of 2016. The RILs differed significantly for SCMR, and showed a normal distribution for SCMR. Among the RILs, SCMR ranged from 19.55 to 44.55 with a mean value of 34.13. SCMR showed a high PCV (44.42) and moderate GCV (17.59) with a low heritability (15.67) and genetic advance (4.89). Pod yield (kg/ha) showed a positive association with SCMR. RILs were genotyped with 105 Arachis hypogaea miniature inverted-repeat transposable element (AhMITE) markers. The genetic linkage map of 1205.66 cM with 20 linkage groups was constructed using 91 mapped markers. Single marker analysis (SMA) and QTL analysis were carried out to identify the genomic regions governing chlorophyll content in peanut. A total of 16 markers showed significant association with SCMR. Twelve QTL regions were detected by composite interval mapping for SCMR with a LOD score of more than 3.00, however all were found to be minor QTL regions contributing for SCMR.

IDT9-038 | Evaluation of drought tolerance selection indices in chickpea genotypes

Uday Chand Jha[1]*, Parthasarathi Basu[1], and Narendra Pratap Singh[1]

[1]Indian Institute of Pulses Research, Kanpur, 208024
*E-mail: uday_gene@yahoo.co.in

Drought or soil moisture stress remains one of the most important abiotic stresses, limiting chickpea production worldwide. In order to identify drought tolerant chickpea genotype, 34 genotypes including 4 checks were evaluated under irrigated and moisture stressed condition in randomized complete block design with three replications during 2013-14. Six drought tolerance indices viz, mean productivity (MP), geometric mean productivity (GMP), yield index (YI), tolerance index (TOL), stress susceptibility index (SSI), and superiority measures (SM) were implicated on the basis of grain yield in moisture stress (Ys) and well irrigated (Yp) conditions. Genotypes viz. FLIP03-100, FLIP05-123C, FLIP03-98C, IPC2009-102 and IPC2009-186 were found to be more drought tolerant based on drought tolerant indices used. Highest significant positive correlations were recorded between MP and GMP (1**), MP and YI (0.984**) and GMP and YI (0.984**) indices. Principal component analysis lowered the six indices into two components first and second component justified 97.9 % of the variations between criteria (84.63 and 13.34 % for PC1 and PC2, respectively).Further, the genotypes were grouped into 4 groups by two ways cluster analysis (using Ward's method) based on Yp, Ys and drought tolerance indices. Importantly, the results of correlation, 3D graphs, bi-plot and cluster analysis reveals that the most suitable indices to screen chickpea genotypes in drought stress conditions were MP, GMP and YI. Therefore, these indices may be useful for selection of drought tolerant chickpea genotypes.

IDT9-039 | Elucidation of differentially expressing genes in roots experiencing different levels of moisture stress using NGS in sorghum (*Sorghum bicolor* L.)

Kadam SR[1,4], Fakrudin B[2,4]*, Kavil SP[3,4]

[1]KRC College of Horticulture, Arabhavi (UHS, Bagalkot) – 591310, Karnataka, India
[2]College of Horticulture, (UHS) GKVK Post, Bengaluru - 560 065, Karnataka, India
[3]University of Greenwich, Kent – ME44TB, United Kingdom
[4]Institute of Agricultural Biotechnology, UAS, Dharwad – 580005, Karnataka, India
*E-mail: sandeepkadam15@gmail.com

Sorghum [*Sorghum bicolor* (L.) Moench], a member of C4 grass family, is an often cross pollinated diploid has more drought enduring capacity. In order to elucidate gene networks in response to moisture stress, a global overview of transcriptome was obtained by generating RNA-Seq libraries. Out of 136.9 million reads that were generated across the sorghum genome for mild, moderate and severe stressed and control treatments, 94.7 million reads aligned uniquely to the sorghum genome. A total of 34,569 gene models in each treatment could be resolved. 4,728 unique genes were classified as differentially expressed genes, which were characterized in three main gene ontology *viz;* biological class, molecular function and cellular component. Of which 1604 genes were upregulated and 3,124 genes were downregulated among all treatments as compare to control treatment. The upregulated genes that were categorized under response to abiotic stress, their fold change of expression has been compared in mild, moderate and severe, between mild and moderate stress, between moderate and severe stress and for the genes which are uniquely upregulated in moderate and severe stress. In total, we revealed the transcriptomes of the sorghum cv. M35-1 to reveal the overall transcriptional landscape in moisture stress at maximal resolution.

IDT9-040 | Mapping of quantitative trait lociin pearl millet (*Pennisetum glaucum* (L.) R. Br.) and relating to the water stress environments

Kakkera A[1], Baddam R[1], Vadez V[1]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Hyderabad, 502324, Telangana, India
*E-mail: v.vadez@cgiar.org

Pearl millet, [*Pennisetum glaucum* (L.) R. Br.], is commonly grown in the dry environments of north west India, characterised by erratic rainfall that results in highly variable yields. Therefore, identification of plant types to a target environment is a big challenge. In this study, we are interested in traits that help improve yield when the crop is grown under control, mild, moderate and severe water stress based on the mean seasonal rain fall variations (460, 305, 252 and 139 mm in 1988) observed in dry environments of Rajasthan. We used F_7 progenies of the RIL cross H 77/833-2 × PRLT 2/89-33. LG 2 was associated with grain yield components i.e. grain mass, grain number of all water stress environments, tiller number (mild water stress) and PHI (severe water stress). Stover yield and flowering time were majorly associated with LG 4 and LG 6 (mild and moderate water stress). QTL interactions revealed that under well-watered conditions, a combination of two H 77/833-2 alleles enhanced yield by 21%. Under mild water stress interaction of two PRLT 2/89-33 alleles, one H 77/833-2 allele enhanced the yield by 29%. Under severe water stress, combination of three PRLT 2/89-33 alleles enhanced yield by 8%, but when this severe stress was interrupted by rain, then interaction of two PRLT 2/89-33 alleles with one H 77/833-2 allele enhanced the yield to 18%. This QTL study and their interactions elucidated the adaptability of lines to design environment-specific ideotypes.

IDT9-041 | Fine mapping studies identified a 113 kb region within "*QTL-hotspot_a*" for seed weight and drought related traits in chickpea

Kale SM[1], Jaganathan D[1,2], Roorkiwal M[1], Thudi M[1], Purushothaman R[1], Praveenkumar M[1,2], Krishnamurthy L[1], P B Kavi Kishor[2], Gaur P[1] , Varshney RK[1, 3,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, Telangana, India.
[2]Osmania University, Hyderabad, 500007, Telangana, India.
[3]The University of Western Australia, Crawley, 6009, Australia.
*E-mail: r.k.varshney@cgiar.org

A "*QTL-hotspot*" region of 7 Mb size for drought component traits was identified on CaLG04, using a recombinant inbred line (RIL) population (ICC 4958 × ICC 1882) in chickpea. Further, skim-based genotyping by sequencing (GBS) approach with large SNP markers delimited the "*QTL-hotspot*" region into two sub-regions; viz, "*QTL-hotspot_a*" of 139.22 kb and "*QTL-hotspot_b*" of 153.36 kb, on the *kabuli* draft genome sequence. In order to validate and identify more recombinations in the sub-regions for further refinement, a fine mapping population with 1,911 lines was developed. Flanking markers of the two "*QTL-hotspot*" sub-regions were converted to KASPar assays and used to screen the fine mapping population consisting of 1,911 lines. As a result, 19 $F_{2:3}$ recombinant families were identified. These families were phenotyped for seed weight and other drought-related traits. Comparison of genotype and phenotype data identified a genomic region of ~113 Kb size within "*QTL-hotspot_a*" responsible for 100 seed weight (100SDW) and other drought-related traits in chickpea. Subsequently, a syntenic study between the refined "*QTL-hotpsot*" region and desi genome identified a 2 Mb region on Ca_LG_4 pseudomolecule. Whole genome re-sequencing (WGRS) analysis of selected lines from each recombinant family identified several non-synonymous and InDel mutations within important candidate genes. Functional validation of these genes will help decipher the mechanism of drought stress tolerance in chickpea.

IDT9-042 | High throughput phenotyping and advanced genotyping reveals QTLs for plant vigor and water saving traits in a "*QTL-hotspot*": New opportunities for enhancing drought tolerance in chickpea

Sivasakthi K[1,2], Thudi M[1], Tharanya M[1,2], Kale SM[1], Kholová J[1], Halime MH[1], Jaganathan D[1], Baddam R[1], Thirunalasundari T[2], Gaur PM[1], Varshney RK[1], Vadez V[1] *

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru 502 324, Hyderabad, Telangana, India
[2]Bharathidasan University, Tiruchirappalli 620 024, Tamilnadu, India
*E-mail: v.vadez@cgiar.org

Terminal drought stress leads to substantial yield losses in chickpea (Cicer arietinum L.). Water conservation at vegetative growth (canopy conductivity and canopy size and development) allow plants to increase soil water extraction during grain filling and are hypothesised to help chickpea adaptation to water limited environments. Plant vigour and water saving traits were phenotyped in 232 recombinant inbred lines (RILs), derived from a cross between ICC4958 and ICC1882, at 28 days after sowing under well water conditions using a high throughput phenotyping platform. Different density genetic maps (241-SSR-Low density, 1007-SSR+SNPs-High density and 1557-SNPs-Ultra high density) were used for QTLs identification. Several major QTLs (M-QTLs) for plant vigour traits (3D-leaf area, shoot biomass, plant height and growth related traits) were identified on CaLG04, and co-mapped with previously identified and fine mapped major drought tolerance QTL-hotspot region on CaLG04 (~300Kb).The canopy conductance trait (e.g Transpiration rate) had a M-QTL mapped on CaLG03 using ultra-high density bin markers. Plant vigour traits on CaLG04 and canopy conductance related traits on CaLG03 provide opportunity to manipulate these loci to tailor recombinants having lower transpiration rate and high plant vigour. This ideotype might be enhancing the water stress adaptation in chickpea. To test this hypothesis, a subset of 40 RILs contrasting for vigour and water use traits was tested in lysimeters and field under different water stress treatments. High vigour low water use lines had higher seed yield under severe water stress treatments than high vigour and high water use lines, validating the hypothesis.

IDT9-043 | Optimization of sand hydroponics system and transcriptional studies on the putative high affinity nitrate transporter gene in guar

Kaur N.[1] and Randhawa G. S.[1]*

[1]Indian institute of Technology Roorkee, Roorkee, Uttarakhand, India, 247667
*E-mail: Sharnfbs@iitr.ac.in

Sterilized seeds of guar (Cyamopsis tetragonoloba) variety RGC - 1066 were kept in dark for 3-5 days for germination. Germinated seedlings were transferred to the pots filled with sand. A small hole was made at the base of each pot and pots were placed in trays containing 5 L Hoagland medium. The plants showed optimal growth with proper root and shoot development up to 28 days. The seedlings were grown in full strength Hoagland medium up to 15 days for studying the effect of various nitrogen concentrations on the plant. After 15 days, twenty guar plants were transferred to Hoagland medium with limited nitrogen supply and named as experimental plants. Another twenty plants were transferred to full strength Hoagland medium and labelled as control plants. Expression analysis of an orthologue of Glycine max putative high affinity nitrate transporter gene (NRT2) in guar was carried out in root and shoot tissues of experimental and control guar plants. This gene has been reported to be involved in efficient nitrogen uptake from the soil in limited nitrogen supply in Arabidopsis. Higher expression of this gene in root and shoot tissues of experimental guar plants in medium with limited nitrogen supply indicates that NRT2 gene in guar may also be involved in efficient nitrogen uptake from the soil in limited N supply.

IDT9-044 | Phenotypic and marker-assisted selection for drought tolerance in potato

Karin Köhl[1]*, Christina Schumacher[2], Heike Sprenger[1], Manuela Haas[1], Katharina Rudack[3], Jürgen Gremmels[1], Ellen Zuther[1], Sylvia Seddig[3], Rolf Peters[4], Dirk Walther[1], Joachim Kopka[1], Dirk Hincha[1], Renate Horn[2]

[1]Max Planck Institute of Molecular Plant Physiology, 14476 Potsdam, Germany
[2]University of Rostock, 18051 Rostock, Germany
[3]Julius Kühn Institute for Resistance Research and Stress Tolerance, 18190 Sanitz Germany
[4]Agricultural Research Station Dethlingen, 29633 Munster, Germany
*E-mail: koehl@mpimp-golm.mpg.de

Climate models predict an increased likelihood of seasonal droughts for many areas of the world. Potato produces more food energy per water volume than other crops, but it is drought-sensitive. Assessment of drought effects on tuber starch yield in controlled environments and field trials revealed a significant variation in drought tolerance within the group of tetraploid European *Solanum tuberosum* ssp. *tuberosum* cultivars. For this population, we developed a tolerance prediction model based on metabolite and transcript levels in leaf samples that were derived from pot and field experiments. This model predicts drought tolerance with an accuracy of 90% from leaves sampled in different agro-environment. We developed a population segregating for drought tolerance and genotyped it with SSR and AFLP markers. From this population, we selected a tolerant sub-population based on yield data from a limited set of trials plus a tolerant and a sensitive sub-population employing our marker model. These populations were phenotyped for yield, drought tolerance, leaf metabolite and transcript levels in pot and field experiments conducted on three sites for three years. Tuber yield data indicated that lines with high drought tolerance and high tuber yields under drought stress are over-represented in both sub-populations selected for drought tolerance. Yield, metabolite and transcript data are used to identify QTL regions. Selected QTL regions will be sequenced to identify SNP markers for drought tolerance in potato and to elucidate the physiological basis of tolerance to intermittent drought.

IDT9-045 | Root transcriptome analysis to reveal the genetic mechanism of deep rooting in rice

Lou QJ[1], Chen L[1*], Zhong Y[2], Li TM[1], Wei HB[1], Feng FJ[1], Mei HW[1], Luo LJ[1]

[1]Shanghai Agrobiological Gene Center, Shanghai, China
[2]Fudan University, Shanghai, China
*E-mail: cl@sagc.org.cn

Drought is the most serious abiotic stress limiting the rice production. Deep root mainly decided the plants' ability to avoid drought stress. In this study, the transcriptomes of 74 roots samples from 37 rice varieties were surveyed by RNA-seq. About 306G bases clean data were obtained. Meanwhile, using 12 microarrays, the accuracy of the RNA-seq was verified. Basing on the whole transcriptomic information, the samples were clustered into 2 big groups: one containing all the shallow and most median rooting varieties, while the another one containing all the deep rooting varieties. The differentially expressed genes (DEGs) with FDR<0.05 were identified according to two levels' comparisons: deep rooting varieties vs shallow rooting varieties (got 13242 DEGs); and deep roots vs shallow roots from the same plant (got 1052 DEGs). Seventy-five DEGs of deep roots VS shallow roots were known genes controlling roots architecture. The expression patterns of these 75 DEGs among RNA-seq, microarray and quantitive real-time PCR were similar. Ten QTTs (quantitative trait transcript) were detected to be related to the distribution of roots. Through WCGNA analysis of DEGs, eighteen hub genes were detected. Half of them functioned in the metabolism of energy, and all these genes expressed higher in deep roots than in shallow roots. Four DEGs were chosen to qRT-PCR test in 14 rice varieties, and their expressions were in accordance with their profile in RNA-seq. Our results provided a lot of reliable candidate genes to improve deep rooting in rice, and strongly suggested the importance of energy metabolism for the development of deep roots.

IDT9-046 | Development of salt tolerant transgenic cultivated tomato by constitutive over expression of HSP24.4 gene

Upender Mahesh[1,4], Praveen Mamidala[1,2]*, PJM Rao[4], Hari Yadla[4], Francisco JL Aragao[3], Harinder Reddy P[1], P.B.Kirti[5] and Rama Swamy Nanna[1]

[1]Plant Biotechnology Research Group, Department of Biotechnology, Kakatiya University, Warangal-506 009, Telangana, India
[2]Department of Biotechnology, Telangana University, Nizamabad – 503322, Telangana, India
[3]Gene Expression Laboratory, National Centre for Genetic Resources and Biotechnology, EMBRAPA-CENARGEN, Brasilia, Brazil
[4]Biotechnology Research Laboratory, Prof. Jayashankar State Agricultural University, Regional Agricultural Research Station, Warangal – 506 007 (Telangana State), India
[5]Plant Molecular Biology and Genetic Engineering Research Laboratory, Department of Plant Sciences, School of Life Sciences, University of Hyderabad, Hyderabad-500046, India
*E-mail: pmamidala@gmail.com

Tomato (*Solanum lycopersicum* L.) is sensitive to high salt conditions at almost all the stages of its growth and development. Considering the important role of heat shock proteins in imparting tolerance against high salt to the cells and tissues, for the first time, we isolated small *HSP24.4 (MasHSP24.4)* cDNA from wild banana (*Musa accuminata*) and introduced into the cultivated tomato cv PKM1 via *Agrobacterium tumefaciens.* Stable integration and expression of the transgene in the tomato genome was demonstrated by southern, northern and western blot analyses. The genetic analysis of the transgenic T_2 tomato lines showed the Mendelian ratio in transgene segregation. The *MasHSP24.4* showed expression in root, shoot and stem tissues at 200 mM and 250 mM NaCl treatments and conferred tolerance to high salt stress by showing increased seed germination, healthy vegetative growth and normal fruit and seed setting. The transgenic tomato plants showed significantly the best growth performance in the recovery phase following the salt stress.

IDT9-047 | Comparative analysis of miRNA in oxidative stress response in cultivated sugarcane and its wild species

R. Manimekalai*, Jini Narayanan, Gokul, M. Selvi, A, Gomathi, R.

Sugarcane Breeding Institute, Coimbatore, 641007, India
*E-mail: rmanimekalaiicar@gmail.com

Sugarcane crop is exposed to oxidative stress, which inevitably is the result of all primary biotic and abiotic stresses. Molecular study of sugarcane genome in oxidative stress was carried on through miRNA profiling for the first time. Hydrogen peroxide (H2O2) was used to induce oxidative stress in sugarcane and wild species. The small RNA was sequences through illumine platform. Although Erianthus arundinaceus and Saccharum spontaneum share only a small number of common miRNA (6.2% control and 2.4% treated samples), the miRNA which were significantly differential during the stress, followed the same expression pattern. 38 such miRNA were found to be differentially expressed and 10 miRNA were further filtered for their significant differential expression. While the miRNA sbi-miR5568g-3p, sbi-miR5567, ghr-miR393, pab-miR3711 and mdm-miR7121e were down-regulated during the oxidative stress in wild types and up-regulated in Co86032), miRNA rgl-miR5139 remained neutral in wild type but up-regulated in Co86032. miRNA osa-miR1848, tae-miR9774, osa-miR5072, and sbi-miR396e were found to be up-regulated in wild types but down-regulated in Co86032. miRNA gma-miR166k was found to be expressed abundantly only during the stress condition in all the three types. miRNA ata-miR166c-5p and gma-miR166c-5p were found to be expressed only in wild type varieties in control samples, while miRNA mtr-miR166e-5p was found after stress. Cultivated variety Co86032 however had more unique miRNA both in control and treated samples. The expression of miRNA cpa-miR166d, sbi-miR5568g-5p, sbi-miR5568f-3p and osa-miR1561-3p in control samples and miRNA sbi-miR171f, aly-miR 845a-3p, sbi-miR396d, vvi-miR3630-3p and ath-miR172a in treated samples, were significant.

IDT9-048 | Functional characterization of With No Lysine (WNK) kinase in rice under abiotic stress condition

Manuka R[1] and Kumar K[1]*

[1]Birla Institute of Technology & Science Pilani. K. K. Birla Goa Campus, Goa-403726, India
*E-mail: kundan@goa.bits-pilani.ac.in

Eukaryotic protein kinases represent one of the largest gene families involved in diverse regulatory functions. WNK (With No Lysine) kinases are members of ser/thr protein kinase family, which lack conserved catalytic lysine (K) residue at protein kinase subdomain II and is replaced by either asparagine, serine or glycine residues. In plants the role and expression of WNK genes is largely unknown. However 11 WNK kinases have been reported in Arabidopsis thaliana and few of them were characterized under abiotic stresses. In the present study, we have identified 9 members of WNKs in rice. The transcript analysis of OsWNKs under various abiotic stresses viz. salinity, drought, cold and heat revealed differential regulation pattern of OsWNK genes at different time points, suggesting their probable role in various abiotic stresses. Among OsWNKs, OsWNK9 revealed highly differential regulation pattern under abiotic stress conditions. Further OsWNK9 gene was heterologously overexpressed with constitutive promoter in Arabidopsis thaliana and generated various overexpression lines. The overexpressed lines showed the better growth in terms of shoot, fresh weight and root length under salt and dehydration stress compared to wild type Arabidopsis. Tissue specific localization of OsWNK9 was performed by fusing promoter region of OsWNK9 with GUS and transformed in rice by Agrobacterium. The preliminary GUS assay showed that OsWNK9 was expressed in callus, shoot and roots. The sub cellular localization studies of OsWNK9 showed that OsWNK9 is localized in nucleus In conclusion, we found that rice OsWNK9 gene was playing a role under abiotic stress conditions. Key words: Serine threonine kinase, salt stress, dehydration stress, abiotic stress, *OsWNK*

IDT9-049 | Harnessing the power of social media to reach the unreached: knowledge dissemination for greater impact of tropical legumes

Nilesh Mishra[1]*, Emmanuel S Monyo[2], Rajeev K Varshney[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Nairobi
*E-mail: m.nilesh@cgiar.org

Tropical Legumes III (a project supported by Bill & Melinda Gates Foundation, led by ICRISAT and jointly implemented by CIAT, IITA and NARS partners) has developed several technologies, including best bet varieties (>163) and other pool of resources over 3 phases (2007-2016) of its implementation. However, it-faces the challenge of reaching the intended target populationat scale, putting our mission of availing International Public Goods (IPG's) in jeopardy.ICRISAT being majorly funded by public money is a firm supporter of global open access and considers technologies, research results and data generated from different projects as IPGs to be shared with the global scientific community using different open source platforms and tools. Social media revolution has potential to address some of these challengesand so TL III marked its presence on four social media platforms: Facebook (500 followers), Twitter (230 followers), Slide-share (8,242 views), and Flickr (396 photos) and regularly uses them as a vehicle to reachfarmers and interested stakeholders.Technologies and varieties developed under TL III have been an eye opener for many in the agriculture sector, and small-holder farming in particular. Over the period of one year of the project phase III implementation, these four different platforms have shown different level of engagements, information dissemination and reach, which will be highlighted and discussed.

IDT9-050 | Extent of heterosis in CMS based hybrids of Pigeonpea [*Cajanus cajan* (L.) Millsp.]

Mohan N[1,3]*, Galian JL[2], Babu JDP[3], Sameerkumar CV[4], Rao VS[3]

[1]Institute of Agricultural Science, BHU, Varanasi, 221 005, Uttar Pradesh, India.
[2] Benguet State University, La Trinidad, Benguet, 2601, Philippines.
[3]Acharya N G Ranga Agricultural University, Guntur, 522 509, Andhra Pradesh, India.
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.
* E-mail: nidhimohan91@gmail.com

Endowed with several unique characteristics, pigeonpea [*Cajanus cajan* (L.) Millsp.] holds a prominent position in farm households of semi-arid and arid regions of the world. With the advent of hybrid pigeonpea technology, pigeonpea, once designated as orphan crop, has grown in importance as a commercial crop. Thus, development of more number of quality hybrid varieties has become imperative to meet the future demand. The present study was taken up to elicit the information on magnitude of the genetic variability, heritability, genetic advance as percent of mean, extent of fertility restoration and heterosis in newly developed CMS based pigeonpea hybrids. Twenty four pigeonpea hybrids along with four checks *viz., Asha, Maruti*, LRG 41 and BDN 711, were evaluated in *kharif* 2015 at ICRISAT, Patancheru. Analysis of variance showed significant differences among the hybrids for all the characters studied. High genetic variability coupled with high heritability and genetic advance as percent of mean were recorded for number of primary branches, number of secondary branches and pollen fertility percent. Fertility restoration studies showed that 15 out of 24 hybrids recorded high (>80 %) pollen fertility and exhibited better fertility restoration. High levels of heterosis *i.e.* over 50% in traits like number of pods per plant, pod weight per plant and grain yield per plant. were also recorded. ICPH 3762 and ICPH 4502, with high *per se* performance and high standard heterosis for grain yield per plant and for majority of yield attributes, were identified as promising hybrids.

IDT9-051 | MAGIC population in cowpea for facilitating gene discovery for drought tolerance related traits

Moukoumbi YD[1]*, Yunus R[2], Yao N[3], Gedil M[4], Togola A[1], Nouhoun B[1], Chamarthi SK[1] and Boukar O[1]

[1] International Institute of Tropical Agriculture (IITA), Kano, Nigeria
[2]Ahmadu Bello University, Zaria, Nigeria
[3]Biosciences eastern and central Africa - International Livestock Research Institute (BecA - ILRI) Hub, Nairobi, Kenya
[4] International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
*E-mail: Y.Moukoumbi@cgiar.org

Cowpea (*Vigna unguiculata* L.) is an important grain legume crop in the drier regions of West and Central Africa because of its high protein (25%), vitamin, and mineral contents. It has the advantage of adapting to different types of soil and inter-cropping systems and becomes an important economic crop in many developing regions in Sub Saharan Africa. Drought tolerant cowpea reference lines for West Africa were identified and most of them have been used separately in breeding for drought tolerance in cowpea to develop multiple introgression lines. The goal of this project is to develop at least 2,000 Recombinant Inbred Lines (RIL) derived from Multi-parent Advanced Generation Intercrosses (MAGIC) population that will be used for localizing QTLs for multiple traits within 3-5 cM of the related genes. Eight drought tolerant varieties were selected through morphological traits related to drought tolerance at seedling stage and molecular screening with 125 SSR markers distributed throughout the cowpea genome. F_1 (two way) were generated and they are being assessed genotypically and phenotypically. The work is still in progress and we expect that the novel allele rearrangements and greater genetic diversity in these MAGIC populations derived from mating cycles will facilitate the discovery and manipulation of new forms of allelic variability. Also, the highly recombined MAGIC populations may be used directly as source materials for the identification of breeding lines and varieties adapted to different drier environments in Africa and shared with NARS partners.

IDT9-052 | JcAKR, an aldo-keto reductase from *Jatropha curcas* L. and its role in drought and salt tolerance

Mudalkar S[1]., Reddy A. R. [1]*

[1]University of Hyderabad, Hyderabad - 500046, Telangana State, India
* E-mail: arrsl@uohyd.ernet.in

Jatropha curcas is known for its abiotic stress tolerance but the mechanism underlying such tolerance with respect to reactive carbonyls is not yet reported. Methylglyoxal (MG), an α, β-dicarbonyl aldehyde, is a by-product of oxidative stress and is highly toxic to plants. MG accumulation was observed in J. curcas under abiotic stress wherein the levels of MG increased with increased stress severity. AKRs are known for metabolism of aldehydes and ketones. In the current study, JcAKR from J. curcas was cloned and characterized to study its role in MG detoxification. JcAKR was heterologously expressed in E.coli BL-21(DE3) cells and the protein was purified with GST binding column. MALDI-TOF analysis was done to confirm the purified JcAKR protein. The recombinant protein had an enzyme activity and catalytic efficiency of 5.9 μmol mg^{-1} min^{-1} and 62.83 s^{-1} mM^{-1} respectively, in assays containing MG as the substrate. Protein modelling and docking studies showed that JcAKR had efficient MG binding site. The mRNA expression and enzyme activity of JcAKR was higher in leaves compared to roots, under progressive drought and salt stress. Further, enhanced bacterial and yeast tolerance was observed in cells expressing JcAKR towards PEG (5%), NaCl (200mM) and MG (5mM) treatments compared to controls. Our study on JcAKR showed its protective role under abiotic stress for the detoxification of MG and could be a potential target for plant breeding especially to drought and salt stresses.

IDT9-053 | Regulated expression of *AmNAC1* transcription factor by biotic and abiotic stresses in the mangrove plant *Avicennia marina* (Forsk.) Vierh

M Ashok Kumar, G. Ganesan*, G N Hariharan & Ajay K Parida

M.S.Swaminathan Research Foundation, Taramani, Chennai 600113, India
SRM University , Kattankulathur, Chennai 603203, India
*E-mail: ashokkumar.mb@gmail.com

NAC (NAM, ATAF1/2 and CUC2) a large family of transcription factors unique to plants which control growth, development and stress responses. Mangroves are a group of facultative and obligative halophytes, which naturally tolerates extreme conditions of high salinity (0-90 ppt) and high light intensity. Avicennia marina is a facultative halophytic mangrove tree species with modified root system (pneumatophores) and salt excretion glands in leaves as its one of the unique features to consider. In this study, a multiple stress responsive NAC transcription factor gene (AmNAC1) of Avicennia marina was analysed for its expression pattern under salt, drought, cold and biotic stress conditions using qRT-PCR. AmNAC1 expression pattern in leaves and root tissues of A. marina seedlings treated with 250mM NaCl for 10 days revealed a long term response of AmNAC1 to salt stress treatment. Interestingly, expression pattern of AmNAC1 subjected to drought stress is similar to the expression pattern obtained in salt stress experiment. Similarly, Cold stress (4ºC) experiments in A. marina seedlings showed an early and long term response of AmNAC1 to cold stress. Furthermore, in response to biotic stress (Insect infestation) occurred naturally in mangrove fields, AmNAC1 expression pattern was found to be approximately 3 fold higher than control. This was studied using northern hybridization. Hence to summarize that our results clearly suggests that AmNAC1 is highly responsive to multiple stress factors in A. marina seedlings under controlled and natural conditions.

IDT9-054 | Marker-assisted introgression of different traits in drought-tolerant rice variety *Sahbhagi Dhan*

Nachimuthu VV[1], Nagamallikadevi M[1], Singh UM[1], Dixit S[1], Ramayya PJ[1], Priyadarshi R[1], Venkateshwarlu CH[1], Alam S[1], Naik SM[1], Jain A[1], Kumar VA[1], Mamatha P[1] , Kumar A[1,2]*

[1]International Rice Research Institute-South Asia Hub, Building # 303, ICRISAT, Patancheru -502324, Telangana State, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
*E-mail: a.kumar@irri.org

The increasing frequency of climate extremes such as water deficit stress, high temperature and altered soil properties, along with higher incidence of pests and diseases, is posing a serious threat to rice farming. To face these challenges, crop scientists have started improving existing crops for traits providing tolerance to different stresses by utilizing modern, innovative technologies. As rice is the largest calorie provider for the global population of 7.4 billion, its production needs to increase by at least 30% by the year 2030 and by 50%-70% by 2050. Hence, breeding climate-smart rice varieties without yield and quality trade-offs serves as the primary objective of various breeding programs. *Sahbhagi Dhan*, one of the revolutionary drought-tolerant varieties, suffers from impaired growth under low temperature. Hence, the current study was framed to combine additional drought tolerance ($qDTY_{1.1}$, $qDTY_{3.1}$), cold tolerance (*qCTS4a, qCTS11*), bacterial blight (*Xa21*) tolerance and blast (*Pi9*) disease tolerance in *Sahbhagi Dhan* background, using a marker-assisted breeding approach. *Sahbhagi Dhan* was crossed with multiple donors conferring tolerance to a range of biotic and abiotic stresses, following a complex crossing scheme. Trait-based marker-assisted selection was practised in each generation to ensure the presence of genes/QTLs conferring tolerance. Several lines combining the genes for different targeted traits were developed and are being advanced.

IDT9-055 | Insights on host-pathogen interaction between groundnut (*Arachis hypogaea*) and *Aspergillus flavus*

Nayak SN[1], Agarwal G[1,2,3], Pandey MK[1], Sudini HK[1], Jayale AS[1], Purohit S[1], Bajaj P[1], Desai A[1], Wan L[4], Guo B[2], Liao B[4], Varshney RK[1,5]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Crop Protection and Management Research Unit, USDA-Agricultural Research Service, Tifton, USA
[3]University of Georgia, Department of Plant Pathology, Tifton, USA
[4]Oil Crops Research Institute (OCRI), Chinese Academy of Agricultural Sciences (CAAS), Wuhan, China
[5]The University of Western Australia, Crawley, Australia
*E-mail: r.k.varshney@cgiar.org

Aflatoxin contamination, caused by fungal pathogen *Aspergillus flavus*, is the major quality and health problem delimiting the trade and consumption of groundnut (*Arachis hypogaea* L.) worldwide. Three types of aflatoxin resistance mechanisms namely, resistance to in-vitro seed colonization (IVSC), pre-harvest aflatoxin contamination (PAC) and aflatoxin production (AP) have been reported in groundnut. Transcriptome sequencing approach was used to study the differentially expressed genes that differ in-vitro seed colonization (IVSC) in resistant (J 11) and susceptible (JL 24) genotypes. A total of 1,344 million raw reads with an average of 84 million reads per sample were generated from 16 libraries from four different stages of fungal infection. A total of 737.75 and 770.83 million reads were mapped on the progenitor genomes- *A subgenome* (*A. duranensis*) and *B subgenome* (*A. ipaensis*) of cultivated groundnut (*A. hypogaea*), respectively. In groundnut, defense related genes like senescence associated proteins, resveratrol synthase, seed linoleate 9s-lipoxygenases (9s-LOX), pathogenesis related proteins, peroxidases, glutathione-S-transferases, chalcone synthase, defensin and chitinases were differentially expressed. In *A. flavus*, the genes involved in growth and development of fungus, aflatoxin biosynthesis, binding and transporter proteins were found to be induced in compatible interaction. In addition to IVSC resistance, we have also carried out transcriptome sequencing for PAC and AP resistance. In summary, this study will provide greater insights on the resistance mechanisms and discovery of candidate genes for all the three mechanisms that can further be used as expression markers in genomics-enabled aflatoxin resistance breeding.

IDT9-056 | Iron acquisition and transport under aerobic and alkaline soil pH condition in rice (*Oryza sativa* L.)

Nisarga KN, Aftab Hussain IS, Sheshshayee MS, Udayakumar M*

University of Agricultural Sciences, GKVK, Bengaluru, 560065, Karnataka, India
*E-mail: udayakumar_m@yahoo.com

Iron (Fe) is an essential micronutrient for plant growth and development. Under aerobic rice cultivation Fe deficiency is a major problem resulting in low grain iron content and also under high soil pH condition iron acquisition is affected leading to iron deficiency chlorosis (IDC) resulting in substantial yield loss. To identify the superior rice genotype that adapts to aerobic cultivation system 24 different rice genotypes adapted to upland, low land and aerobic ecosystems were screened for shoot and grain Fe content and contrasts were identified. Further characterization of eight contrasting rice genotypes differing in shoot iron content under high pH (pH=8) condition showed chlorosis, reduction in growth and genetic variability for iron content was maintained. Similarly, these genotypes grown in agar media with high pH condition, extent of chlorosis were more than low and neutral pH conditions. Further in two contrasting rice genotypes JBT 37/128 (high type) and CTH-1(low type) the physiological and molecular mechanism of Fe acquisition, transport and plant responses to iron deficiency was studied. JBT 37/128 showed higher cholorophyll content, active iron (Fe^{2+}) content, photosynthetic rate and shoot iron content. The iron deficiency responsive genes OsIRO2, OsIRT1, NAS1, OsNAS2, OsYSL2 and OsYSL15 were strongly up-regulated in JBT 37/128 than CTH-1 genotype indicates more tolerance to high pH condition/ Fe deficiency. The study demonstrates that the genotype JBT 37/128 has better adaptation under Fe deficiency due to the induced expression of Fe deficiency responsive genes that are involved in maintaining the cellular homeostasis.

IDT9-057 | Development of the mungbean Nested Association Mapping (NAM) resource: transformation from opportunity crop into Queensland's most dynamic pulse

Noble T[1], Douglas C[2], Williams R[2], Williams B[1] and Mundree S[1]

[1] Queensland University of Technology (QUT), Brisbane, 4000, Queensland, Australia
[2] Department of Agriculture and Fisheries (DAF), Warwick, 4370, Queensland, Australia
*E-mail: t2.noble@qut.edu.au

Mungbean (*Vigna radiata*)**,** is established as the key rotation in tropical Australia's cereal-based cropping systems. It has a short duration, wide sowing window, a range of rotation benefits and is established as a high-value product for discerning international markets.

New varieties released by the National Mungbean Improvement Program have doubled production to 70,000 tonnes since 2003. Further industry growth, expansion into new tropical production environments, and progress towards a new industry target of 170,000 tonnes annual production requires the adoption of new breeding technologies and an understanding of traits and the physiological processes determining yield and response to abiotic and biotic stress. This project is delivering new genetic knowledge that will directly assist the breeding of better mungbean varieties for Australian growers. The NAM framework will be used to introduce genetic diversity including abiotic/biotic resistance and new adaptive traits into elite mungbean germplasm using bi-parental and backcross breeding. Five hundred and sixty mung bean, black gram and wild accessions have been genotyped as part of a genetic diversity study completed on cultivated and wild Australian germplasm. Thirty crosses have been made to Crystal forming the NAM population, including four interspecific crosses to Vigna var. *sublobata***.** For each population, sixty, F2 derived recombinant inbreed were fast tracked to the F5 generation using controlled environment and field increases. This population is a global resource and will aid in the study of complex traits such as drought and heat stress at flowering as well as disease resistance.

IDT9-058 | Genome wide analysis of sodium transporters and expression of Na^+/H^+-antiporter-like protein (*SbNHXLP*) gene in tomato for salt tolerance

Palavalasa HK, Narasu LN[2], Varshney RK[3], KaviKishor PB[1]*

[1]Osmania University, Hyderabad 500 007, Telangana, India
[2]JNTUH, Hyderabad 500085, Telangana, India
[3]ICRISAT, Hyderabad 502324, Telangana, India
*E-mail: pbkavi@yahoo.com

Salt stress is perceived by plants as ionic and osmotic stresses. Excess Na^+ and Cl^- instigate conformational changes in protein architecture and membrane depolarization leading to the ion toxicity perception. At cellular level, sodium toxicity can be sensed by plasma ion transporters, membrane proteins, and Na^+ sensitive enzymes. In the present study, a full-length cDNA homologue of salt overly sensitive1 (*SbNHXLP*) gene was isolated from *Sorghum bicolor,* and its overexpression in tomato plants lead to less Na^+ and more K^+accumulation in root and flower tissues indicating that it helps in proper ion homeostasis. Cambial activity and increased xylogenesis have been noticed under salt stress in transgenic root and stem tissues unlike that of untransformed controls. *In silico* protein-protein interaction studies of NHXLP revealed hypothetical interactions with several sodium proton antiporter (NHX and SOS) and cation proton antiporter (CHX) proteins. Co-immunoprecipitation followed by MALDI-TOF analysis showed that NHXLP protein interacts *in vitro* with one of the cation proton antiporter (CPA) family members CHX2, belonging to CPA1 family. Comparative genomics helped in knowing the evolutionary history by studying the phylogenetic distance, divergence and synteny of Sodium transporters between sorghum, maize and rice. This information would be useful in selecting candidate genes for functional validation in relation to abiotic stress tolerance during various developmental phases in crop species Thus, *SbNHXLP* gene appears to be associated with Na^+ exclusion at the plasma membrane and helps the tomato transgenics to ameliorate salt stress.

IDT9-059 | Heat induced differential proteomic changes reveal molecular mechanisms responsible for heat tolerance in chickpea

Parankusam Santisree*, Pooja Bhatnagar-Mathur and Kiran K. Sharma

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad-502324, Telangana, India
*E-mail: S.Parankusam@cgiar.org; santhikinnu@gmail.com

Understanding the molecular differences in plant genotypes contrasting for heat sensitivity can provide useful insights into the mechanisms that confer heat tolerance in plants. We focused on comparative physiological and proteomic analyses of heat sensitive (ICC16374) and tolerant (JG14) genotypes of chickpea (*Cicer arietinum* L.) when subjected to heat stress at anthesis. Heat stress reduced seed germination, leaf water content, chlorophyll content and membrane integrity with a greater impact on sensitive genotype than on the tolerant ones that had higher total antioxidant capacity and osmolyte accumulation, and consequently less oxidative damage. Comparative gel-free proteome profiles indicated differences in the expression levels and regulation of common proteins that are associated with heat tolerance in contrasting genotypes under heat stress. Several crucial heat induced and heat responsive proteins were identified and categorized based on ontology and pathway analysis. The proteins which are essentially related to the electron transport chain in photosynthesis, aminoacid biosynthesis, ribosome synthesis and secondary metabolite synthesis may play key roles in inducing heat tolerance. In addition, our study also provides evidence that the foliar application of nitric oxide (NO) donor can enhance heat and drought stress tolerance by modulating a number of proteins in chickpea. Understanding the active metabolic adjustments in tolerant genotype under stress and inducing the stress tolerance in sensitive genotype by exogenous NO application offers a comprehensive and systematic approach to tackle heat and drought stress in chickpea. This study potentially contributes to improved stress resilience by offering valuable insights on the mechanisms of heat and drought tolerance in chickpea.

IDT9-060 | Exploring the behavior of transporter proteins in response to abiotic stress through genomics and microarray analyses

Patil S[1,2], Prashant R[1,3], Kadoo N[1,2], Gupta V[1,2,*]

[1]CSIR – National Chemical Laboratory, Pune, India
[2]Academy of Scientific and Innovative Research (AcSIR), CSIR-IGIB Campus, New Delhi, India
[3]MIT School of Bioengineering Sciences and Research, MIT-Art, Design and Technology University, Pune, India
*E-mail: vs.gupta@ncl.res.in

Plants respond to stress conditions through various physiological mechanisms like redistribution of nutrients to critical tissues, production of metabolites for free radical scavenging, and osmotic adjustments. Transporter proteins are the key components of such processes and their diversity contributes to the plant's ability to survive under stresses. The Major Facilitator Superfamily is one of the largest superfamilies of secondary active transporters that transport diverse molecules such as sugars, sugar-alcohols, vitamins, amino-acids, oligopeptides and nucleosides. We identified members of this superfamily in *Arabidopsis thaliana* and *Vitis vinifera* through protein homology search and domain annotation, and classified them into 21 families based on the type of substrate they potentially transport. Analyses of microarray data revealed that 52% of them were transcribed in six different tissues, suggesting their role in cellular transport and distribution of metabolites across plant tissues. However, about 30% of these were differentially regulated under heat and salinity stress conditions; half of these comprised sugar porters and amino-acid transporters known for maintaining the osmotic balance and turgor pressure under water-stress. Surprisingly, we observed simultaneous up- and down-regulation of transporters of the same family in same tissue under same condition, suggesting contrasting effect of solutes of similar class of molecules, opposite transport directions of co-localized transporters or different behaviors of transporters in different cell types in a tissue. Further studies on these transporters with the combined implementation of transcriptomics and mutant studies could lead to better prediction of their roles in metabolic fluxes in a plant under abiotic stresses.

IDT9-061 | Next generation sequencing based transcriptomic studies for crop improvement in pigeonpea

Pazhamala LT[1], Saxena RK[1], Purohit S[1], Bajaj P[1], Kumar V[1], Garg V[1], Srikanth S[2], Hingane A[1], Kulshreshtha A[1], Krishnamurthy L[1], Sameerkumar CV[1],Verdier J[3], Varshney RK[1, 4,]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad502 324, India
[2]Nanyang Technological University, Singapore 639798
[3]INRA - Research Institute in Horticulture and Seeds (IRHS), 49071 Beaucouze, France
[4]School of Plant Biology and Institute of Agriculture, The University of Western Australia, 35 Stirling Highway, Crawley, WA, 6009, Australia
*E-mail: r.k.varshney@cgiar.org

Transcriptomic studies are rapidly evolving as a powerful tool with next-generation sequencing technology to understand gene functions and molecular mechanisms. RNA sequencing (RNA-seq) provides a dynamic range for transcript detection and a better quantification of expression levels.With the availability of genome sequence in pigeonpea, RNA-seq was used to link the sequence information to phenotypic traits resulting from specific developmental processes. In pigeonpea, three-line hybrid breeding system is well-established; however, it is technically demanding and cumbersome. In order to explore the possibility of a two-line hybrid breeding system, a coherent transcriptomic approach supported by physiological and cytological data has led to the identification of a temperature-sensitive male sterile (TSMS) line. This line has been characterized for critical (tetrad) stage and temperature (23°C), and the identification of candidate genes involved in abscisic acid signaling for fertility reversion. Furthermore, a gene expression atlas (CcGEA) has been developed and transcriptomic profiles generated for studying pod and seed development with a dataset of 590.84 and 342 million paired-end reads, respectively in pigeonpea. These data have been analyzed for genes with differential, specific, spatio-temporal and constitutive expression. In addition, CcGEA identified a gene network of 28 co-expressed genes, including two regulatory genes, a pollen specific SF3 and a sucrose-proton symporter to be involved in pollen fertility, which has potential implication in seed yield improvement. In summary, this study, especially identification of TSMS and development of CcGEA, will accelerate on-going efforts to enhance genetic gains in pigeonpea.

IDT9-062 | *In silico* analysis of candidate gene from identified QTL regions for drought stress tolerance in wheat

Phuke RM [1]*, Rao AR[2], Ambati D[1],Singh JB[1], Sai Prasad SV[1], Chaudhari GN[3], Manjunatha C[4] Verma P[5]

[1]Indian Agricultural Research Institute, Regional Station, Indore, India
[2] Indian Agricultural Statistical Research Institute, New Delhi, India
[3]College of Horticulture,Banglore, India
[4]Indian Agricultural Research Institute, Regional Station, Wellington, India
[5]Central Institute for Cotton Research, Nagpur, India.
*E-mail: rahulphuke18@gmail.com

Drought stress is a complex phenomenon, and many approaches are used to overcome drought stress in wheat. Availability of DNA markers closely linked to drought tolerance QTLs will make the job easier. The QTLs generally span the genomic region containing tens to hundreds of genes, and identification of the most promising regulatory genes within QTL interval will be more effective than using QTL-linked markers. In the present study, efforts were made to identify putative genes within QTL regions. The previously identified three QTLs for drought tolerance were selected between marker intervals *viz.,* xbarc 48 – xbarc 101(QTL1), xbarc 271 – Xgwm337 (QTL2) and Gdm 132 – cfd 42 (QTL3). *In silico* analysis of candidate genes from QTL regions was done, using gene finding algorithms such as FGENESH, GENESCAN and AUGUSTUS. Large numbers of genes were predicted for all three QTLs, which were quarried against *Arabidopsis thaliana* and maize genome in order to find high similarity between the sequences. Finally, three common predicated genes for QTL1 and QTL 2, and five predicted genes for QTL 3 were selected after comparison with FGENESH, GENESCAN, AUGUSTUS, *Arabidopsis*, maize and Genebank data. The selected genes' function was found out using the BLASTx annotation and the gene or protein was queried based upon Query coverage and E value. The identified candidate genes in all three QTLs were mostly governing their function in one or more stress conditions. Primer were designed using primer 3 plus an online primer designing software to validate the identified candidate genes' using qRT-PCR.

IDT9-063 | Improvement of Brinjal germplasm for root knot - nematode resistance using molecular markers

Kiran Babu T, Raghuprakash K.R, Sivaramakrishnan S, Varaprasad K. S*, Anuradha G# and Jayamma P

Institute of Biotechnology, PJTSAU, Rajendranagar, Hyderabad – 500030
*NBPGR Regional Station, Rajendranagar, Hyderabad – 500030
#Biotechnology Unit, ARI, Rajendranagar, Hyderabad - 500030
*E-mail: jayapunna@gmail.com

Institute of Biotechnology, PJTSAU, Rajendranagar, Hyderabad – 500030; *Principal Scientist, NBPGR Regional Station, Rajendranagar, Hyderabad – 500030;#Principal Scientist, Biotechnology Unit, ARI, Rajendranagar, Hyderabad - 500030 Brinjal or eggplant (*Solanum melangena* L.) being a poorman's vegetable has been affected with many biotic stresses. In the present study we have identified the root knot-nematode race prevalent in major vegetable growing areas of Telangana in India as *Meloidogyne incognita* race 2 using host differentials and 60 germplasm accessions including different varieties of brinjal were screened against the *Meloidogyne incognita* race 2. However, none of the accessions/varieties which were reported to be moderately resistant were proved so in the present study indicating that there was a probable escape in previous investigations. Further we also cloned resistant gene homologs from brinjal using degenerate primers designed based on the conserved NBS motifs. Out of 46 recombinant clones, five NBS sequences had high similarity with the known resistant genes namely, Chilli CaMi and Tobacco N gene. Further identification of these resistant gene homologs is underway. Cluster analysis using the deduced amino acid sequences of brinjal with the other reported analogous domains of known R- genes, classified brinjal sequences into two major groups. Isolation of full length genes from these resistant gene homologs would help in improving the genetic resistance of the available superior germplasm against root knot-nematodes. Plant disease resistance (R) genes are abundant in every plant species.

IDT9-064 | Next generation sequencing approaches for understanding genetic mechanism of drought tolerance in Valencia Peanut

N. Puppala[1]*, A. Xavier, V. Garg[2], S. Nayak[2], M. Pandey[2], R. Varshney[2], N. Layland[3], P. Payton[3], C. Holbrook[4]

[1]New Mexico State University Agricultural Science Center, Clovis-NM, USA
[2]International Crops Research Institute for the Semi-Arid Tropics, Patancheru-Telangana, India
[3]USDA-ARS, Cropping Systems Research Laboratory, Lubbock-TX, USA
[4]USDA-ARS, Crop Genetics and Breeding Research Unit, Tifton-GA, USA
*E-mail: npuppala@nmsu.edu

Valencia peanuts are highly susceptible to drought stress. The yield reduction due to stress can result in more than 50% reduction resulting in high aflatoxin contamination. In our present study we have compared Valencia-C genotype with a highly drought tolerant runner type peanut C76-16 using transcriptome sequencing to investigate tissue-specific gene expression and response to abiotic stress. We evaluated the two genotypes under field conditions under irrigated and stress plots in 4 replications. We found that genotype C76-16 outperformed yield compared to Valencia-C under drought stress conditions with only a 30 % reduction in yield while Valencia-C showed a higher loss of up to 70%. Each year the yield varied widely due to the environmental factors but C76-16 was consistently ranked among the top and suffered a minimal loss of yield suggesting that it is best suited for the erratic climatic conditions of southwest U.S. Leave samples were harvested from the control and stress conditions and used for RNA isolation and sequencing. A total of 340 million paired-end reads were generated and were used to find differentially expressed genes and transcripts between tolerant and susceptible genotypes. The pathways and candidate genes involved in drought tolerance will provide basic information and expression markers for drought tolerance in peanut. We will present our findings on genic content and tissue-specific gene expression and discuss the challenges and opportunities of unifying transcript sequence data for the peanut community.

IDT9-065 | A system biology approach to elucidate the network of proteins involved in NO^-_3 signalling and transport under multiple abiotic stresses in shoot and root of maize genotype (Zea mays L.)

Rafique S*[1] and Abdin M Z[2]

[1]Jamia Hamdard, Faculty of Science, New Delhi-110062, Delhi. India.
[2]Jamia Hamdard, Faculty of Science, New Delhi-110062, Delhi. India.
*E-mail: suphia123@gmail.com

In an era of global climate change and frequent occurrence of various abiotic stress, at different timings and with more intensity have pose a great challenge for the scientists. To cope with such a situation they have been working to select, identify, developed the germplasm which not only withstand in extreme weather but also efficiently reproduced with higher yields and nutrition. Among various abiotic stresses that is drought, waterlogging, salinity, heat they are not only detrimental itself for the growth and development of the plant but also effects the nutrient uptake, specifically nitrogen. NO-3 is the main source of inorganic nitrogen taken up by the roots and assimilated in the roots or the shoots of the plants while photosynthesis plays key role in nitrogen assimilation. In the present study during the screening for waterlogging, drought & low-N at vegetative stage, ten inbred genotypes, showed the efficient photosynthesis rate even in stressed condition and the effect of low-N was not obvious when compared with non stressed plants for various morpho-physiological parameters. Thus, to unravel the processes controlling the tolerance to multiple stress and in particular for low-N stress maize root and plasma membrane proteome profiling is done by nLC-MS and SDS-PAGE. Thus, a shoot and root system under multiple stress especially low-N respond to environmental signals and elucidate the network of proteins involved in nitrate uptake, assimilation along with the proteins of carbon and energy metabolism. The response of the plant for single stress is different than the combination of stresses.

IDT9-066 | Cloning and characterization of bacterial RNA chaperone genes (*CspA* and *CspB*) and their heterologous expression in rice confers drought and salt stress tolerance

G. Rajasheker[1]*, Madan Shekhar[2], A. R. Reddy[2] and P. B. KaviKishor[1]

[1]Department of Genetics, Osmania University, Hyderabad 500 007
[2]Department of Plant Sciences, School of Life Sciences, University of Hyderabad, Hyderabad 500 046
*E-mail: grajashekharou@gmail.com

The bacterial RNA chaperones or Cold Shock Proteins(CspA and CspB)possess conserved RNA binding domains (RNP1 and RNP2) like in eukaryotes.The CspS generally bind to single stranded RNA and prevent secondary structure formation, anti-terminationand enhance mRNA stability, and translation of proteins under stress.But, not much is known about the Csps of bacterial origin and their overexpression in plants for abiotic stress tolerance.In the present study, we cloned *CspA* and *CspB* from *Escherichia coli* strain K12, characterized and overexpressed in Indica rice using *in planta* method of transformation for drought stress tolerance. Phylogenetic analysis, domain structure of the proteins and characterization of the transgenic plants by PCR amplification and DNA blot analysis was carried out. Transgenics (T_1 generation) were exposed to the drought and salt (100 mMNaCl) stresses along with the wild-type plants. It has been found that the transgenics have the better ability to tolerate to abiotic stresses compared with wild-type plants. Further, antioxidant enzyme activities were higher in transgenics in comparison with wild-type plants. Ion analysis (Na^+, K^+, Ca^{2+} and Cl^-) indicate that not much differences exist between the transgenic lines and wild-type plants. The results point out the role of CspA and CspB impart salt and drought stress tolerance in rice.

IDT9-067 | Expression analysis of basal transcriptional regulators (TBP Associated Factors) under different stress conditions in finger millet

Rakshitha HC, Parvathi MS and Nataraja KN*

Department of Crop Physiology, University of Agricultural Sciences, GKVK, Bangalore-560065, India
*E-mail: nataraja_karaba@yahoo.com

Basal transcriptional regulators are critical for transcription initiation and activation of gene expression under normal and stress conditions. We evaluated the different basal transcription regulators, the TATA Box Binding Protein (TBP) Associated Factors (TAFs) associated with transcription pre initiation complex assembly, through e-northern analysis using the *Arabidopsis* and rice expression data from publically available databases. Based on this analysis, a few TAFs were shortlisted by examining their inductive responses under different stress conditions. We identified the homologs of the select TAFs from finger millet using transcriptome data generated earlier. The expression of the selected TAFs was analyzed in leaf tissue of finger millet exposed to different levels of drought stress by gravimetric approach. Further, the expression of these TAFs is also being examined in the finger millet seedlings exposed to NaCl-, Mannitol-, and methyl viologen- induced stresses. The response of the select TAFs to different stresses will be discussed. The role of the different stress responsive TAFs are being validated by functional genomics approaches.

IDT9-068 | Marker-assisted breeding for introgression of multiple QTLs/genes for drought and disease resistance in rice variety *Naveen*

Ramayya PJ[1], Singh UM[1], Priyadarshi R[1], Yadav S[2], Nachimuthu VV[1], Nagamallikadevi M[1], Alam S[1], Dixit S[1], Venkateshwarlu CH, Naik SM[1], V. Abhilash Kumar[1], Abhinav Jain[1], Raman. A[1], Arvind Kumar[1,2]*

[1] International Rice Research Institute-South Asia Hub, Building # 303, ICRISAT, Patancheru -502324, Telangana State, India
[2]International Rice Research Institute, DAPO BOX 7777, Metro Manila, Philippines
*E-mail: a.kumar@irri.org

Rice is one of the most important staple food crops in Asia. Its production and productivity is severely affected by several biotic stresses (bacterial leaf blight, blast, brown plant hopper and gall midge) and abiotic stresses including drought. A systematic QTLs/genes introgression program was initiated to improve the popular rice variety *Naveen* for resistance/tolerance to BLB (*Xa21*), blast (*Pi9*), gall midge (*Gm8*) and drought ($qDTY_{1.1}$, $qDTY_{2.2}$ *and* $qDTY_{4.1}$), using marker-assisted selection (MAS). A complex crossing scheme, starting from simple crosses *Naveen* × *Aganni* (gall midge), *Naveen* × IRBL9 (blast), *Naveen* × IRBB60 (BLB), *Naveen* × IR87707-445-B ($qDTY_{2.2}$ *and* $qDTY_{4.1}$) and *Naveen* × IR96321-1447-561-B-1 ($qDTY_{1.1}$), followed by crosses between F_1 possessing two and four genes, was attempted. The resulting complex F_1s were raised during the 2015 wet season and verified for presence of genes using gene-based markers and QTLs using peak and flanking markers. The $F_{2:3}$ plants were raised during the 2016 wet season. In all generations, foreground selection was exercised using QTL/gene-linked SSR markers. In the F_3 generation, out of 442 plants, 72 plants harboring four QTLs/genes and eight plants harboring five QTLs/genes were identified. In order to pyramid all the six QTLs/genes in a single line, intercrossing between introgression lines in different combinations have been attempted. The lines with all the six QTLs/genes will provide resistance/tolerance against all the above-mentioned stresses and will help in development of next-generation *Naveen* rice variety with enhanced resistance/tolerance against biotic and abiotic stresses.

IDT9-069 | Whole genome recovery and development of drought tolerant rice (*Oryza sativa* L.) through marker assisted backcross – inbreeding method

Ramchander S[1]*, Raveendran M[2], Robin S[3]

[1]Research Scholar, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University (TNAU), Coimbatore - 641003, Tamil Nadu, India.
[2]Professor, Department of Biotechnology, Centre for Plant Molecular Biology & Biotechnology, TNAU, Coimbatore -641 003, Tamil Nadu, India.
[3]Dean (SPGS), Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India
*E-mail: rubulochander_009@yahoo.co.in

Molecular breeding for drought tolerance was targeted through maximising recovery of a drought- tolerant genome through backcross-inbreeding method. The study involved the physiological and molecular characterization of 101 Backcross Inbred Lines (BILs) of rice derived from the cross combination of *Norungan* // TKM9/ *Norungan* (BC_1F_5 population). The population was developed through a single stage selection against the plant type (tallness) of the drought tolerant landrace, *Norungan*. The physio-morphological traits, *viz.,* plant height, panicle length, 1000 grain weight, panicle exertion, harvest index and other yield attributing characters, exhibited significant phenotypic variation among the parents and BILs under stress and control conditions. Parental polymorphism survey was performed with 167 markers, including three gene-specific markers for *sd1* locus, of which 31 markers exhibited polymorphism between two parents. Single marker analysis revealed that 21 markers were linked to at least one of the investigated traits and many markers were reported to be linked with more than one trait. The markers RM302 on chromosome 1 (*sd1*) had putative linkage with the traits, such as plant height, number of productive tillers and relative water content. Since the population was selected after selection pressure for semi-dwarfness, expectedly in chromosome 1, all the lines possessed introgression from TKM9 around the linked marker RM302 and GA20Oxi_2, except five lines which were clearly explained by graphical genotyping. The population was also screened for blast to infer the agronomic worthiness for further exploitation and the improvement of drought tolerance in locally adapted cultivars.

IDT9-070 | Functional validation of drought responsive genes in rice

Ramsankar C[1], Ghatbale PS[1], Shankarrao CN[1], Valarmathi R[1,2], Raveendran M[1]*

[1]Tamil Nadu Agricultural University, Coimbatore, India
[2]Sugarcane Breeding Institute, Coimbatore, India
*E-mail: raveendrantnau@gmail.com

Development of drought-tolerant rice cultivars is indispensable to meet the future demands of a growing world population, where the situation is predicted to be highly water-limiting. Understanding the molecular basis of drought tolerance in rice is a prerequisite to develop elite drought tolerant cultivars. The present study was focused on functional validation of two drought responsive genes viz. OsGASR9 and OsOLP, identified through our transcriptome analysis in a set of contrasting rice genotypes IR64 (drought susceptible) and Apo (drought tolerant). Full length cDNA of these genes were isolated from Apo and mobilized into plant transformation vector pCAMBIA 1301 under the control of CaMV35S promoter. Putative transgenic rice lines (ASD16) over-expressing OsGASR9 and OsOLP were generated through *Agrobacterium* mediated transformation and the integration of transgene was confirmed through PCR analysis. Transgenic rice lines engineered with OsGASR9 were found to maintain 15% to 20% higher RWC than non-transgenic ASD16 plants. Similarly, OsOLP engineered transgenic rice lines were found to exhibit delayed leaf rolling due to higher RWC status (16% and 22% higher than non-transgenic). Transgenic rice plants showed better drought recovery than NT-ASD 16 upon re-watering. *In vitro* seed germination assay revealed that two events of OsGASR9 could show higher vigour index than ASD 16 even at 150mM NaCl stress. Further physiological, biochemical and molecular experiment are being carried out to characterize the putative transgenic lines for their abiotic stress tolerance ability and to understand their role in providing abiotic stress tolerance in rice.

IDT9-071 | A novel strategy to tap the drought tolerance genes of *Aegilops tauschii* for bread wheat improvement

Rasool S[1]*, Srivastava P[1], Sandhu S[1], Bains N S[1]

Punjab Agricultural University (PAU), Ludhiana, 141004, India.
*E-mail: souliha.rasool@gmail.com

Among the wheat progenitor species, *Aegilops tauschii,* has the widest amplitude of genetic variation as well as the best prospects for ease of recombination and gene transfer. The conventionally used strategy for introgression of *Aegilops tauschii* genes depends upon bridge crosses with *Triticum durum* leading to formation of synthetic hexaploids which, in turn, are used in crosses with bread wheat. The present study explores an alternative route to gene transfer, based on direct crosses between *Aegilops tauschii* and bread wheat. The study evaluates the feasibility of this cross in reciprocal orientations with use of different growth regulators as well as embryo rescue strategies. The *Aegilops tauschii* donor subset was picked from a set of lines evaluated for drought tolerance and presence of drought-related genes. The outcome of the various crossing techniques clearly demonstrated that contrary to expectations, use of *Aegilops tauschii* as female parent was effective whereas crossability in *T.aestivum* x *Ae. tauschii* cross was found to be nil in all the 40 cross combinations performed over five seasons. The crosses with *Ae. tauschii* as female parent showed a crossability of 54% to 76% and no genotypic specificity with respect to the parental combination. The method offers good prospects for using the target recipient wheat in the primary crosses. A major constraint in these (*Ae. tauschii* x bread wheat) crosses however was observed for embryo regeneration frequency (9% to 12%). The caryopsis growth had to be supported through application of high dose of auxin (2,4-D, 100 ppm) administered 24 and 48 hours after pollination. The embryos were seen to be floating in the watery endosperm. A short *in vitro* culture phase to detached *Ae. tauschii* tillers (15 DAP) at low temperature improved embryo size and regeneration ability (20% to 25%). The direct cross F_1s show almost complete sterility. The options available for handling of these F_1s involve chromosome doubling or backcross or both. Seed set was obtained under both the above mentioned strategies. This step presents the only major bottleneck in gene transfer. Once backcross seed is obtained, almost complete fertility is restored and further gene transfer does not require any special intervention. The advantages of the direct cross approach (using *Ae. tauschii* as female) over the conventional bridge cross based approach are: i) quick recovery of recipient background; ii) no interference of the genetic input from the durum wheat A and B genomes, and iii) easy monitoring/tagging of genes of interest using molecular markers. The backcross derivatives generated in the present study have been evaluated using seedling assays and allelic variants for DREB 1, Wdhn 13, Wdhn 17 and the putative introgressed derivatives short listed for further studies.

IDT9-072 | Molecular and evolutionary studies of genes associated with drought tolerance in soybean

Ratnaparkhe MB[1]*, Kavishwar R[1], Rathod S[1], Jumrani K[1], Kumawat G[1], Satpute G[1], Arya M[1], Gupta S[1], Singh AK[2] and Bhatia VS[1]

[1]ICAR-Indian Institute of Soybean Research, Indore, India
[2]ICAR-National Institute of Abiotic Stress Management, Baramati, India
*E-mail:milind.ratnaparkhe@gmail.com

Drought is one the most important constraint which effects the yield in soybean. Yield reduction due to water stress depends on genotype, developmental stage, and severity of water stress. But during the flowering, seed formation and seed filling stages, the negative effects of drought stress is more obvious. Development of soybean genotypes/varieties with inbuilt climate resilience is very much needed to improve the crop yield. Abiotic stresses such as drought induced diverse physiological and molecular responses in plants. These responses include changes in gene expression. We are using RNAi and VIGS approach to identify the function of genes associated with drought tolerance in soybean. Genes and proteins associated with tolerance to drought, including chaperones, heat-shock proteins (HSPs), late embryogenesis abundant (LEA) proteins, ABA-responsive elements and various transcription factors were selected and are being studied using comparative and functional genomics approach. We have conducted genome wide analysis for selected gene families associated with drought tolerance. Phylogenetic analysis and genomic organization studies provide new insights into the evolution of the soybean gene families associated with drought tolerance.

IDT9-073 | Comparision of expression and sequence of SnfK and DREB2A transcript in heat tolerant lentil genotypes

Sen S, Sagolsem D, Roy A, Murmu S, Nagesh U J, Nath R, Roy A and Bhattacharyya S

Bidhan Chadra Krishi Viswavidyalaya, Mohanpur, PIN 741252, West Bengal, India.
*E-mail: somnathbhat@yahoo.com

To identify the heat tolerance lentil genotype, 190 genotypes were screened for consecutive two years following augmented design. They were sown in 18th November (normal sowing, NS) and also in 11th December (late sowing LS) with three popular cultivars as check in. Most of the late sown (LS) plants showed reduced vegetative phase than those of NS by four days. But eleven genotypes showed delayed flowering in LS condition and several of them also exhibited terminal heat tolerance ability. Mean seed weight/plant (g) varied from 1.04 to 6.5in NS whereas it varied from 0.04 to 3.78 in LS. Three lines showed only 20-30% reduction in yield as compared to 60% reduction in average. Degenerate primer pairs from known genes like DREB2A and SnfK from *M. truncatulata* were used for amplification and relative quantification of the transcript. Sequence of the analogous Genes from lentil were compared among the contrasting genotypes to identify SNPs. Part of a gene showed complete similarity with stress responsive ORF of chickpea.

IDT9-074 | Constructing improved chickpea genome assemblies using skimGBS

Pradeep Ruperao[1,2,3], Philipp Bayer[1,3], Chon-Kit Kenneth Chan[1,3], Satomi Hayashi[1], Manish Roorkiwal[2], Anu Chitikineni[2], Tim Sutton[4], Jacqueline Batley[1,3], Rajeev K. Varshney[2],[3], David Edwards[1,3,*]

[1]University of Queensland, Brisbane, Queensland, Australia
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana, India
[3]University of Western Australia, Perth, Western Australia, Australia
[4]South Australian Research And Development Institute, Adelaide, South Australia, Australia
*E-mail: Dave.Edwards@uwa.edu.au

Chickpea (*Cicer arietinum* L.) is the second most important grain legume after soybean and plays an important role in food security. The application of genomics provides the potential to increase the productivity and resilience of this important crop. We have developed a novel strategy to assess and improve the chickpea reference genomes. The quality of both chickpea *desi* and *kabuli* draft genomes were assessed using sequence data from flow cytometry isolated chromosomes to identify misplaced contigs. Using SNPs derived from whole genome sequence data of ICC 4958 x PI 489777, and skim sequence-based genotyping of this population, we could validate and correct the draft assembly. In addition to placing the misplaced sequence regions into corresponding chromosome positions, most of the previously unplaced contig sequences have now been incorporated into the pseudomolecules of the improved version. The total chromosome sequence length has increased from 124.38 Mb and 347.24 Mb to 375.06 Mb and 423.28 Mb for the *desi* and *kabuli* genomes respectively. Both genomes have been re-annotated. A total of 33,473 genes from *kabuli* and 31,419 genes from *desi* were predicted. Both improved genomes are available at http://cicer.info.

IDT9-075 | Molecular characterisation of rice genotypes for drought tolerance using microsatellite marker

Salam, S. A.[1]*, Sindhumole, P[1]., Waghmare, S. G.[1]

[1]Division of Plant Breeding and Genetics, RARS, Pattambi
*E-mail: shaheensalam121@gmail.com

Plant growth as well as productivity of rice (*Oryza sativa*), the major cereal and staple food of millions, is significantly affected by numerous biotic and abiotic stress inducing factors. Among these, drought stress is one of the major constraints for production and yield stability of rice in rainfed ecosystems. The main objective of the present study was molecular characterisation of some rice genotypes for drought tolerance, using microsatellite markers. Twenty one genotypes obtained from the Plant Breeding Division, RARS, Pattambi, were used for the study. Initially, drought tolerance in seedlings of various rice genotypes was assessed by conventional method employing PEG-6000 induced drought stress. Out of the 21 genotypes, only 14 genotypes were selected, based on seedling vigour index. Among these, 2RFU, 26RFU, 11M, *Aiswarya*, *Kanchana* and *Uma* exhibited high seedling vigor index. All the selected 14 rice genotypes were used for molecular characterisation by DNA extraction of samples by CTAB method, followed by PCR amplification with low specific SSR markers, *viz*, RM103 and RM212. Monomorphic upper and lower bands were observed with RM103 for all the 14 genotypes; hence it cannot be considered a suitable marker for drought tolerance in these genotypes. Polymorphic bands were observed in these genotypes for the marker RM212. A lower band (near 100bp) was observed in 2H, 12RFU, 26RFU, 3RN, 11M and Aiswarya, and was assumed to be linked with drought tolerance; while an upper band (between140-160bp) observed in 11H, 2RFU, *Kanchana, Harsha, Jyothi, Swarnaprabha* and *Uma* was assumed to be linked with drought susceptibility. Hence, RM212 could be considered as a better marker for the characterisation among these 14 rice genotypes. However, further research with other linked SSR markers must be carried out for marker assisted selection for drought tolerance in rice.

IDT9-076 | Pre-field screening protocols for heat tolerant mutants in rice

Sarsu F[1*], Ghanim AMA[1], Das P[2], Bahuguna R[2], Mbogo KM[3], Ashraf M[4], Pareek SLS[5], Pareek A[2], Forster BP[1,6], Ingelbrecht I[1]

[1]Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Plant Breeding and Genetics Section, Vienna, Austria
[2]Jawaharlal Nehru University, New Delhi, India
[3]Sokoine University of Agriculture, Morogoro, United Republic of Tanzania
[4]Nuclear Institute for Agriculture and Biology (NIAB), Faisalabad, Pakistan
[5]International Centre for Genetic Engineering and Biotechnology, New Delhi, India
[6]BioHybrids International Ltd, Reading, United Kingdom
*E-mail: f.sarsu@iaea.org

Global warming has a negative impact on plant development and hence on crop yield. This is particularly crucial to global rice production, rice being the major staple crop of nearly half of the world's population, and delivering 27% of dietary energy and 20% of dietary protein in the developing world. Developing heat tolerant rice is therefore an urgent objective. However, a major bottleneck in the breeding for heat tolerance is the current inability to screen and select putatively heat tolerant progeny of breeding programmes for further propagation. To facilitate such screening, we have developed simple protocols that may be used in mutation breeding programmes. Seedling establishment and flowering, two critical heat sensitive stages in the life cycle of rice, have been targeted, in which screening is based on simple phenotypic responses. These protocols involve: i) screening for heat tolerance at the seedling stage, with young seedlings exposed to heat temperature stress at 45°C/28°C (day/night) for 6/18 hours in a growth chamber for 4-6 days, and ii) evaluation of heat tolerant mutant lines at the reproductive (flowering) stage, with plants treated from the first day of anthesis at 35.0-39.0°C/28°C (day/night) for 6-4/18-20 hours for 6-4 days; spikelet fertility at maturity is used to assess the heat tolerance of the tested genotypes. These protocols may be adopted and applied to mutant populations also in other crops.

IDT9-077 | Towards defining heterotic pools for accelerating hybrid breeding in pigeonpea

Rachit K Saxena[1]*, Vikas Singh[1], Abhishek Rathore[1], Obarley Yu[2],Changhoon Kim[3], Vinay Kumar[1], Kishan Patel[1], Aamir Khan[1], Kuldeep Tyagi[4], Shaun An[2], Dong Seon[3], MS Kuruvinashetti[4], Jihun Kim[3], BellbullKim[3], Wei Zhang[2], CV Sameerkumar[1], S Muniswamy[6], KB Saxena[1], Jochen C Reif[7], Rajeev K Varshney[1]*

[1]Inetrnational Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Millennium Genomics Inc., Shenzhen, China
[3]MACROGEN Inc., Seoul, South Korea
[4]Krishidhan Seeds Pvt Ltd, Jalna, India
[5]Professor Jayashankar Telangana State Agricultural University, Hyderabad, India
[6]University of Agricultural Sciences, ARS-Gulbarga, Raichur, India
[7]The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany
E-mail: r.saxena@cgiar.org and r.k.varshney@cgiar.org

Recently released pigeonpea hybrids for cultivation in farmers' fields have shown their potential to elevate the yield levels. For instance, the world's first grain legume hybrid of pigeonpea ICPH 2671 showed 47% yield advantage over the check varieties. Generally, the development of such hybrids is based on selection efficiency of breeding program; breeders make thousands of random crosses between cytoplasmic male sterile (CMS) lines and tester lines. In order to enhance the selection efficiency, genomic diversity along with the phenotyping data have been used for predicting the best possible parental combinations. This approach has been successfully used in defining heterotic pools in many crop species such as maize, rice, sunflower, and rapeseeds.. With an aim to define heterotic pools in pigeonpea, a set of 104 parental lines (09 CMS, 13 maintainers and 82 restorers) have been re-sequenced following whole genome re-sequencing (WGRS) approach. WGRS yielded a total of 511 GB data with the coverage ranging from 5X to 10X. A total of 3.4 million SNPs have been identified across parental lines. Structural variations such as copy number and presence/ absence variations have been also identified. In parallel, these parental lines have been used to develop test crosses in factorial mating design. F_1 hybrids along with parental lines were phenotyped for yield and yield related traits at two locations in India, namely ICRISAT, Telangana State and ARS-Gulbarga, Karnataka. The availability of genome-wide SNP variations combined with the phenotypic data will be used for deploying genomic selection to define hetereotic pools in pigeonpea for accelerating hybrid breeding program.

IDT9-078 | Targeted genome mining, comparative modelling and protein structural motifs studies of Δ1-pyrroline-5-carboxylate synthetase (P5CS) in *Zea maize*

Shanker A.K*, Maddala. A, Divya Bhanu, Yadav S.K., Maheswari M

ICAR - Central Research Institute for Dryland Agriculture (ICAR - CRIDA), Hyderabad 500059, Telangana, India
*E-mail: arunshank@gmail.com

One of the chief concerns of climate change is an escalation in the frequency and severity of abiotic stresses. Proline plays an important in drought tolerance in plants. There are two pathways for proline and one of them is from glutamate, which is converted to proline by two successive reductions catalysed by pyrroline-5-carboxylate synthase (P5CS) and pyrroline-5-carboxylate reductase (P5CR), respectively. During stress, the expression of P5CS, but not of P5CR gene, is correlated with proline content. We hypothesize that it will be possible to associate candidate genes discovered in model species such as *Arabidopsis thaliana*, with corresponding loci in maize. In this study we took up an analysis of the complete maize genome for the similarity/ presence of P5CR protein product. We conducted targeted genome mining, comparative modelling and protein structural motifs studies of P5CS. The best homolog of P5CS protein in maize was identified based on significant sequence similarity. The target sequence was used to identify the close homolog in PDB with better resolution. A homology model was built according to the positive match protein sequence. A comprehensive search for templates was done in all publicly available structure databases of pdb structures solved by X ray crystallography or NMR. InterPro scan was done with other known protein families, domains, regions, repeats, and sites for identifiable features found in known proteins to be applied to the target protein sequence. The resultant putative P5CS protein was subjected to detailed bioinformatics analysis to ascertain it's structural and functional similarly to known P5CS.

IDT9-079 | Global transcriptome analysis of multiple genotypes to identify key regulator(s) involved in drought tolerance and genomic resource creation in tea [*Camellia sinensis* (L) O. Kuntze]

Parmar R., Singh G., Seth R., Bhandawat, A., Singh, P., Sharma, R.K.*

Molecular Genetics & Genomics Lab, Department of Biotechnology, CSIR-Institute of Himalayan Bioresource Technology, Palampur, Himachal Pradesh, 176061, India,
*E-mail: rksharma.ihbt@gamil.com

Abiotic stresses are the environmental conditions that reduces the growth and crop yield below optimum levels. Drought stress is one such primary cause which recorded significant crop loss and productivity, worldwide. Tea is a perennial evergreen plant of genus ***Camellia*** belongs to Theaceae family. It is an important non-alcoholic beverage consumed by people worldwide due to its numerous health benefits. Drought stress is one of most severe abiotic stress that limits growth, yield and geographical distribution of tea. To explore the genotypic behavior of tea during drought conditions and key molecular players engaged, transcriptome sequencing of four diverse genotypes, two each form tolerant and susceptible response to drought was carried out to create drought specific genomic resources in tea. After quality filtering, more than 100 million reads from tolerant and susceptible genotypes were obtained. *De novo* assembly results in total of 36,216 contigs with an average length of 847bp. Functional characterization with multiple public protein databases (NCBI's NR, TAIR10, Swiss-Prot, Plant-TFDb) annotated more than 73 % contigs. Overall, 34 critical pathways related to drought were identified. Differential gene expression analysis of various genes related to drought were compared in susceptible and tolerant genotypes for identification of key candidates of drought tolerance in tea. Exploration of genomic resources for ascertainment of functionally relevant sequence based markers identified more than 16,000 SSR's and over 40,000 non-synonymous SNPs. Outcomes of the present study, will help to elucidate the drought responsive key molecular players, also in gaining deeper understanding to expedite genetic improvement and productivity efforts in tea.

IDT9-080 | Marker assisted backcross breeding of recombinant 1BL.1RS chromosome for better root traits and bread making quality in wheat (*Triticum aestivum* L.)

Sharma A[1], Sheikh I[1], Sharma P[1], Kumar R[1], Vyas P[1] , Dhaliwal H.S.[1]*

Eternal University, Baru Sahib-173101 Himachal Pradesh INDIA
*E-mail: hsdhaliwal07@gmail.com

The 1BL.1RS translocation is known for disease resistance genes (*Lr26*, *Yr9*, *Sr31* and *Pm8*) on 1RS and enhanced yield of wheat cultivars. However, due to the presence of *Sec-1* loci on the 1RS arm, cultivars with the 1BL.1RS translocation possess sticky dough and absence of *Glu-B3/Gli-B1* of 1BS. Many QTLs useful for root traits have also been mapped on 1RS. In the present study, 28 genotypes were used to examine their micro SDS sedimentation value (MST) and high molecular weight glutenin subunits (HMWGS). PCR-based markers (ω- sec- P3/P4, Rye R3/F3, Psp3000, Sfr 43) were used to check the presence of *Sec-1*, rye translocation, *Glu-B3/Gli-B1* and *Pm8* respectively. Root traits were examined under hydroponic culture system supplemented with Hoagland medium. The integrated marker and the MST data suggest that MST values are not affected by the absence of *Glu-B3/Gli-B1*. Among the 1RS, *Sec*–ve lines, i.e. 1B+38, Hahn WR and 1RS44:38, had moderately high MST values, particularly Hahn WR, suggesting their high gluten strength. The HMWGS profiling of 1B+38 and 1RS44:38 showed *GluB1* encoding subunits 17+18 and *GluD1* encoding subunits 2+12 for their moderate gluten strength. In PBW550, HS240 and MAC2496 (*Sec*+ve cultivars) had high MST values suggesting that secalin is not the only factor responsible for poor gluten strength. The recombinants with 1RS fragment at their distal region (1B+38, 1RS44:38 and Hahn WR) showed better root traits (root length, branching and wet/dry root biomass) than most of the cultivars, proving their utility in drought conditions and future breeding programmes.

IDT9-081 | Selection of suitable reference genes for assessing gene expression in pearl millet under different abiotic stresses and their combinations

Shivhare R[1,2], Ram Jatan[1,2], Lata C[1, 2*]

[1]CSIR-National Botanical Research Institute, Lucknow, India
[2]Academy of Scientific and Innovative Research (ACSIR), New Delhi, India
*E-mail: charulata@nbri.res.in; charulata14@gmail.com

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is a widely used grain and forage climate-resilient crop of dryland regions of Asia and Africa. It is grown in areas frequented by one or more abiotic stresses, has superior drought and heat tolerance, and is considered a model crop for stress tolerance studies. Selection of suitable reference genes is a key requisite for quantification of stress-responsive gene expression under various abiotic stresses through quantitative real-time (qRT)-PCR analysis. In this study for accurate normalization of gene expression data in pearl millet through qRT-PCR, a total of 20 candidate reference genes, including both traditional housekeeping as well as new reference genes were analysed . However, only 10 of them namely, *ACT, EF-1α, eIF4A, GlutR, HSP90, MDH, PP2A, RPL20, TIP41* and *E2 (UBC-E2)* could amplify in a pair of contrasting genotypes under all stress conditions. All the 10 candidate genes were examined in various developmental tissues as well as under different individual abiotic stresses and their combinations at 1 h (early) and 24 h (late) of stress using geNorm, NormFinder and RefFinder algorithms. Result of this study showed *EF-1α* and *UBC-E2* as the reliable reference genes across all samples, which were further validated by evaluating the relative expression of a *PgAP2* like-*ERF* gene. Pairwise variation suggested use of these two reference genes is sufficient for accurate transcript normalization under different stress conditions. This is the first report on validation of reference genes under different stress combinations in pearl millet which can further facilitate fastidious discovery of stress-tolerance genes.

IDT9-082 | *NAC* gene from *Lepidium Latifolium* confers drought tolerance in transgenic tobacco plants

Singh S*, Grover A, Khalid H, Nasim M

Defence Institute of Bio-Energy Research, Haldwani, Nainital-263139, Uttarakhand, India
*E-mail: sadhnasingh1986@gmail.com

Nicotiana tabacum (tobacco) plants over-expressing *LlaNAC* gene, and co-transformed *npt*II gene, (four transgenic lines-NC2, NC7b, NC10 and NC18 in generations T2) along with wild-type (WT) plants were maintained in containment under controlled conditions of temperature (25 ± 2°C) and light (16/8 h photoperiod), and grown in soilrite. Plants of age ten weeks were exposed to 5 and 15% PEG-8000 solution at constant temperature (25 ± 2°C) and light (16/8 h photoperiod) for one week to simulate drought conditions. Regularly watered plants under optimum conditions of temperature (25 ± 2°C) and light (16/8 h photoperiod) for one week was considered as control. Specific activities of antioxidant enzymes superoxide dismutase, catalase and glutathione reductase was measured under drought stressed and control conditions. The accumulation of antioxidant enzymes showed an elevation of 2 - 3 fold among transgenic lines, when compared to the wild-type plants on induction of 5 and 15 % PEG8000. The *LlaNAC* transgenic plants were able to cope with the drought stresses, due to the ability of transgenic plants to fastly scavenge the highly reactive reactive oxygen species (ROS), whereas the wild type plants showed signs of withering, reduced growth or death.

IDT9-083 | Marker-assisted stacking of QTLs/genes for drought, blast and BLB into popular rice variety– Lalat

Singh UM[1], Yadav S[2], Dixit S[1], Ramayya PJ[1], NagamallikadeviM[1], Nachimuthu VV, Priyadarshi R, Shamshad A, Venkateshwarlu CH, Naik SM, Jain A, Vipparla AK, Mamatha P, Arvind Kumar[1,2]*

[1]International Rice Research Institute (IRRI)-South Asia Hub, ICRISAT campus, Patancheru, Telangana State, India
[2]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
* E-mail: a.kumar@irri.org

Achieving the desired increase in rice production to feed the growing population faces severe constraints due to varying climate patterns. In shallow, rainfed lowland ecosystems, drought, blast and bacterial blight are considered major constraints affecting rice yield. *Lalat* is a medium-duration, high-yielding, long slender grain variety rice, having resistance to gall midge, brown plant hopper, stem borer and sheath rot. But it is highly susceptible to drought, blast and bacterial blight. The present study aims to improve *Lalat* variety with introgression of major QTLs for grain yield under drought ($qDTY_{1.1}$, $qDTY_{3.1}$, $qDTY_{12.1}$), broad-spectrum blast resistance gene (*Pi9*) and durable bacterial blight resistance genes (*xa5, xa13, Xa21*). Different donors were used to combine the target traits by utilizing a complex crossing scheme. F_1s were tested for the presence of target genes/QTLs by gene-specific markers for gene or peak, as well as flanking markers in case of QTLs. At F_2 level, three-way strategies were adopted to develop double haploids with the required gene combinations, identify F_3 lines with homozygous and heterozygous gene combinations, as well as attempt backcrosses using *Lalat* as recipient and donor line with gene combinations. Several lines with the target traits combining good agronomic performance were selected at F_3 stage. F_3 double haploid lines as well as BC_1F_1 lines are being advanced to develop breeding lines with appropriate combination of genes.

IDT9-084 | Identification and validation of insertion–deletion polymorphisms in pigeonpea

Singh VK, Kale SM, Saxena RK, Sinha P, Parupalli S, Suryanaraya V, Obala J, Sameer Kumar CV, Varshney RK*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: r.k.varshney@cgiar.org

Completely sequenced plant genomes provide scope for designing a large number of genome wide insertion–deletion (InDel) markers, which are useful in various aspects of crop breeding and genetic analysis. With the objective of developing InDel markers from pigeonpea genome, the re-sequencing data of eight MAGIC parental lines were used to identify InDels using Dindel software. As a result, a total of 102,181 InDels were identified. Of these 70158 InDels were found unique. The higher number of InDels were found in intergenic (43%) followed by upstream (26%) and downstream (24%) regions. A total of 6.93 % of Indels were found in the genic region. Out of 70158 InDels, 2,426 (1032 Insertions and 1394 deletions) with ≥20 bp size among different parental lines were selected. Average distribution of selected 2426 InDels was found 220 InDels/LG with maximum number of InDels on CcLG11 (385 InDels) and minimum number of InDels on CcLG05 (70 InDels). A set of 293 InDels could assess genetic diversity and establish phylogenetic relationships among 16 parental lines of different mapping populations. Validation of these primer pairs on parental lines of different mapping population resulted in higher amplification success rate (≥83%) with almost 52.04% polymorphism rate among parental lines on 3% agarose gel. The number of alleles per locus ranged from 2 to 9 with an average of 3.8 alleles. Further, to track the genome of parents in complex funnel crossing scheme of pigeonpea MAGIC population at 28-two way, 14-four way and 7-eigth way stages, we have identified unique InDel primers for each of the 8 MAGIC parents. The result showed that InDel markers with their high polymorphic potential in comparison to SSR markers would be preferred candidate markers in various marker-based applications in pigeonpea genetics and breeding.

IDT9-085 | Development and characterization of transgenic pigeon pea plants carrying *OsRuvB* gene for drought and salinity tolerance

Singh R.* and Kharb P.

College of Basic Sciences and Humanities, CCSHAU, Hisar (125004) Haryana, INDIA
*E-mail: singhrakshita19@gmail.com

Environmental parameters such as drought, salinity, cold, freezing, high temperature and high light intensity which result in a disrupted metabolism in plants are termed as abiotic stresses. Drought stress and salinity stress further lead to osmotic stress through reduced availability of water required for vital cellular functions and maintenance of turgor pressure.DNA helicases like PDH 45, PDH 47 have been overexpressed in plants and found to play a role in abiotic stress tolerance (salinity tolerance in tobacco). However the role of overexpression of RuvB, another DNA helicase, in abiotic stress tolerance in plants has not been reported so far. Therefore we have developed transgenic pigeon pea plants carrying ***OsRuvB*** gene to see the effect of overexpression of this gene in alleviating the pleotropic effects of stresses such as salinity and drought. The transgene integration in putative T_0 plants has been confirmed through PCR analysis and transformation efficiency of 35-40% has been observed. The PCR positive transgenic plants are being analysed through southern hybridization and real time PCR to determine the transgene copy number. The expression of the transgene in T_1 and T_2 plants will also be studied by real time PCR amplification analysis. Further these plants will be exposed to drought and salinity stresses and physio-biochemical parameters such as relative water content, chlorophyll content, membrane stability test, proline content etc. will be studied to assess the tolerance level of the transgenic plants.

IDT9-086 | Identification of drought-responsive genes in *Cicer microphyllum* using high-throughput sequencing

Gupta K, Sinha R, Singh AK*

ICAR-Indian Institute of Agricultural Biotechnology, PDU Campus, IINRG, Namkum, Ranchi-834010, India
*E-mail: anils13@gmail.com

Yield of chickpea (*Cicer arietinum*) crop is significantly affected by drought stress. *Cicer microphyllum*, a wild relative of cultivated chickpea is a high altitude legume widely distributed in cold deserts of Ladakh and Lahaul and Spiti in India. Considering the *extraordinary tolerance* of this species to cold and drought, present study was undertaken to identify drought responsive genes from *C. microphyllum*. The seeds of *Cicer microphyllum* were germinated on MS medium and seedlings were transferred to pots after 15 days. *Plants were allowed to acclimatize in pots for three days and drought stress* was imposed. Total RNA was isolated and RNA-Seq libraries were prepared and sequenced using Illumina NGS platform. A total of 141,296,346 raw paired-end reads were generated which were subjected to quality filtering, resulting in 133,072,190 (94.17%) of high quality (HQ) reads. These HQ reads were subjected to *de novo* assembly using CLC genomics workbench resulting into 69,214 contigs with average length of 834 bp and N50 of 1100 bp. A total of 40,877 transcripts were annotated using gene ontology with prevalence of genes associated with response to abiotic stimulus, mRNA modification, response to stress, under biological process, while under molecular function, oxidation-reduction reaction, catalytic activities, protein binding, transferase activities, endonuclease activity were found in majority. Differential expression analysis has identified differentially expressed transcripts in response to drought stress. The drought-responsive genes identified in the present study may be used for engineering abiotic stress tolerance in plants.

IDT9-087 | Haplotype for drought responsive genes in pigeonpea

Pallavi Sinha[1], Rachit K Saxena[1], Vikas K Singh[1], Aamir W Khan[1], HD Upadhyaya[1], Aarthi Desai[1], CV Sameer Kumar[1], Varshney RK[1] *

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: r.k.varshney@cgiar.org

Pigeonpea is a resilient crop which is relatively drought tolerant compared to many other legumes. To understand the molecular mechanisms of this unique feature in pigeonpea, 51 genes were selected using the Hidden Markov Models (HMM). These genes were validated for their expression on parents of mapping populations (ICPL 151, ICPL 8755, and ICPL 227) segregating for drought tolerance. A total of 10 differentially expressed genes that showed ≥2-fold up-regulation in the higher drought tolerant genotypes was identified. Further analysis of the 10 genes revealed that they encode four different classes of proteins. These include plant U-box protein (four genes), universal stress protein A-like protein (four genes), cation/H(+) antiporter protein (one gene) and an uncharacterized protein (one gene). Subsequently, these 10 candidate genes were used for haplotype analysis in whole genome re-sequencing data of 292 lines. As a result, 10 to 56 haplotypes were identified for the selected 10 genes. In order to validate the haplotype results, a defined set of lines is being phenotyped for induced water stress using polyethylene glycol (PEG) at seedling stage along with the non-stressed control seedlings. Phenotyping data together with the haplotype information of the targeted candidate genes will be useful for the identification of superior haplotypes of genes. The lines possessing superior haplotypes of the candidate genes could be used in genomics-assisted breeding programs for development of more drought tolerant lines.

IDT9-088 | Development of transgenic tomato (*Solanum lycoperscicum* L.) by heterologous expression of osmotin-like protein (*OLP*) and chitinase (*Chi11*) genes for salt and drought stress tolerance

Somanaboina AK[1], Narasu LN[2], Varshney RK[3], KaviKishor PB[1*]

[1]Osmania University, Hyderabad 500 007, Telangana, India
[2]JNTUH, Hyderabad 500085, Telangana, India
[3]ICRISAT, Hyderabad 502324, Telangana, India
*E-mail: pbkavi@yahoo.com

Tomato (*Solanum lycopersicum* L.) is the second most produced and consumed vegetable, next to potato. Pusa early dwarf (PED) variety of tomato is sensitive to salinity and drought which reduces the yield and fruit quality in tomato. In the present study, tomato transgenics were developed with osmotin-like protein (*OLP*) and chitinase (*Chi11*) genes *via in vitro* and *in planta* transformation methods. Transgene integration and transcript levels were confirmed by multiplex PCR, DNA blot, and multiplex reverse transcriptase PCR. Homozygous T_2 transgenics, when evaluated for salt and drought stress, showed enhanced tolerance compared to wild-type plants. Transgenics showed enhanced root biomass under normal conditions. Transformants also displayed higher proline content, K^+, relative water content, chlorophyll fluorescence, total biomass, vascular conductivity, and fruit yield compared to the wild-type plants under stress conditions. Co-immunoprecipitation revealed that Chi11 co-expresses with phosphofructokinase2 (PFK2), which may play a role in enhanced root biomass. qPCR analysis resulted in higher transcript levels of *OLP*, *Chi11,* and *PFK2* in transgenics as compared to the wild-type plants.

IDT9-089 | Molecular mapping and tagging of *Fusarium* wilt resistance in chickpea (*Cicer arietinum*)

Soregaon C. D.[1]*, Ravikumar R. L.[2], Thippeswamy S [3]

[1]College of Agriculture, Vijayapur-586101, University of Agricultural Sciences, Dharwad, Karnataka, India
[2]GKVK campus, University of Agricultural Sciences, Bangalore, Karnataka, India
[3]Regional Agricultural Research Station (RARS), PJTSAU, Polasa - 505 529, Jagtial, Telangana, India
*E-mail: soregaoncd@uasd.in

Chickpea (*Cicer arietinum* L. 2n=2x=16), is the third most important cool season food legume in the world, after dry beans and peas. Productivity of chickpea has not yet been significantly improved due to *Fusarium* wilt caused by *Fusarium oxysporum* f.sp. *ciceri*. Eight races of the pathogen have been reported and race 1A is more prevalent in India and it causes significant yield losses. The resistance genes to all identified races of *Fusarium* wilt have been identified and mapped, except the H_2 locus of race 1A. The present study emphasizes on validation and mapping of molecular marker ($A07C_{417}$) linked to H_2 locus of *Fusarium* wilt using $F_{9:10}$ recombinant inbred lines (RILs) obtained from an intraspecific cross of JG62 x WR315, segregating for both H_1 and H_2 loci; and K850 x WR315 segregating for H_2 locus alone respectively. A partial linkage map was developed using 31 polymorphic markers with 5.72 cM marker density.

Single marker analysis (SMA) based on linear regression identified four markers, *viz.* H_4G_{11}, SSR14, $A07C_{417}$ and OPK9 which contributed substantially to variance for *Fusarium* wilt. SMA also identified markers associated with agronomic and productivity traits. QTL mapping using composite interval mapping (CIM) identified three QTLs for *Fusarium* wilt, out of which one major QTL (OPK9- $A07C_{417}$, H_4G_{11}) for *Fusarium* wilt was identified with the phenotypic variance ranging from 13.5% to 17.4% and tightly linked to $A07C_{417}$ and H_4G_{11} (72.4 cM) on LG_3. H_4G_{11} is an SSR marker and hence it will be very useful in routine chickpea breeding programs.

IDT9-090 | Marker assisted pyramiding of QTLs for yield under drought and root morphology into a popular rice cultivar ADT 45

Suresh, R[1]*, Reena S[2], Ashish R[2], Bharathi A[2], Helan BT[2], Chandra Babu R[2]

[1]Tamil Nadu Rice Research Institute, Tamil Nadu Agricultural University, Aduthurai, Thanjavur, India
[2]Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, India
*E-mail: sureshpbg@gmail.com

Rice is cultivated under diverse ecosystems ranging from rainfed uplands to submerged deep water conditions (Singh, 2009). In the Indian State of Tamil Nadu, rice is grown in an area of 17.9 lakh hectares and most part of the rice-growing regions are prone to drought stress at different stages of crop growth. Predicted climate change and shift in rainfall patterns are expected to aggravate this situation and are, thereby, considered to be an important yield limiting factor. Therefore, the goal of the present study was to pyramid QTLs for yield under drought and root morphology from CT 9993 into the high-yielding popular rice variety of Tamil Nadu, ADT 45. Initially, the drought-susceptible high-yielding, early-maturing recurrent parent, ADT 45, was hybridized with donor parent and true F_1 plants were fixed, based on the polymorphic marker data. Subsequently, true F_1 plants were hybridized with the recurrent parent and 79 BC_1F_1 plants were produced. BC_1F_1 plants were genotyped using the markers for yield under stress and basal root thickness respectively. Out of 79 plants, 41 plants were identified to co-segregate with the marker genes, and were further hybridized with the recurrent parent and BC_2F_1 population with 115 plants were generated. BC_2F_1 population is being genotyped and the plants with the marker genes will be further hybridized to develop BC_3F_1s and foreground and back ground selections will be performed to improve the yield potential of ADT 45 under drought stress.

IDT9-091 | Fine mapping of stay-green QTLs on sorghum chromosome SBI-10L – An approach from genome to phenome

Usha Kiranmayee K N S[1]*, Hash C T [3], Kavi Kishor P B[2], Ramu P[4], Sivasubramani S[1], Sakhale S A[1], Santosh P Deshpande[1]

[1] International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2] Department of Genetics, Osmania University, Hyderabad, India
[3] International Crop Research Institute for the Semi-Arid Tropics, Niamey, Niger
[4] Cornell university, Ithaca, New York, United States
*E-mail: knskira@gmail.com

Sorghum is the fifth most important C_4 cereal crop grown globally in arid and semi-arid climatic conditions. Drought is the major cause for loss of productivity worldwide. Delayed senescence of plants leads to adaptation to drought stress conditions by staying-green and giving high yields. In order to identify and dissect the stay-green genomic regions we have developed a high resolution fine mapping population from introgression line cross RSG04008-6 (stay-green) × J2614-11 (shoot fly resistant). Nearly 1894 F_2 genotypes were screened with 8 SSR in order to identify double recombinants for both the parents in the sorghum chromosome-10 long arm (SBI-10L). The selected $F_{2:4}$ recombinants were GBSed to increase the marker density between flanking markers *Xgap001-Xtxp141* for stay-green QTLs on SBI-10L and a high resolution linkage map was developed using GBS SNPs. Out of 182 only 152 recombinants were replicated thrice in field for stay-green screening for two seasons (Summer 2013 and 2014). Fine mapping of the per cent Green Leaf Area (%GLA) traits identified 33 QTLs and 19QTLs were clustered into 7groups where 8 genes were identified. These were AP2/ERF transcription factor family (Sb10g025053), Ankyrin-repeat protein (Sb10g025310), WD40 repeat protein (Sb10g025320), NBS-LRR Protein (Sb10g025283), Calcium dependant protein kinase (Sb10g030150), LEA2 protein (Sb10g029570), a putative uncharacterized protein (Sb10g024920) and senescence associated protein (Sb10g030520). With this study SBI-10L stay-green genomic regions were delimited from 15Mb to 8 genes co-localized with GWAS MTAs. Further cloning and expression level studies of the identified candidate genes will improve the development of drought tolerant genotypes.

IDT9-092 | Identification and validation of genomic loci associated with Kernel-Fe and Kernel-Zn concentrations in maize

Hindu V[1,3], Palacios-Rojas N[2], Babu R[4], Usha R[3] and Nair SK[1]*

[1]CIMMYT Asia Regional Maize Program, c/o ICRISAT, Patancheru, Telangana, India-502 234.
[2]International Maize and Wheat Improvement Center (CIMMYT), El Batan, Mexico-56130.
[3]Sri Padmavati Mahila Visvavidyalayam, Tirupati, India- 517 502.
[4]Multi-Crop Research Center (MCRC), DuPont Pioneer, Hyderabad, India-500 078.
*E-mail: Sudha.Nair@cgiar.org

Iron (Fe) and zinc (Zn) deficiencies in human diets is a worldwide serious health issue. These deficiencies could overcome through fortification of these micronutrients to staple food crops. One of the global staple food crop, maize is having considerable variation for kernel Fe and Zn concentration. Genome-wide association study (GWAS) was performed to dissect the genomic loci controlling Zn and Fe concentrations in maize kernel using a panel of 923 inbred lines. Based on mixed linear model analysis, corrected for population structure and kinship, 94 significant associations (p<10-4) for Fe (50SNPs), Zn (44SNPs) were detected at the genome-wide level. The identified associations were further validated in three different DH populations by single-marker QTL analysis. The analysis revealed that 5 SNPs (Fe) accounted for 4-27% and 6 SNPs (Zn) accounted for 5-28% of the total phenotypic variation, respectively in DH populations. SNP S7_173181689 on chromosome 7 explained 28% and SNP S8_164741133 on chromosome 8 accounted for 27% phenotypic variation, for Zn and Fe in DH populations. Based on the results from this study, the validated small number of genetic loci could be readily used for germplasm enhancement by marker-assisted selection in breeding for improving Fe and Zn content.

IDT9-093 | The sodium transporter OcHKT1;5 from the halophytic wild rice *Oryza coarctata* Roxb. Tateoka shows distinct transport and structural determinants compared to rice OsHKT15

S. Suji[1], Very A-A[2], Vinekar R.S.[3], Venkataraman G.*[1], Kumaresan K.[4], R. Sowdhamini[3], Parida A[1]

[1]M. S. Swaminathan Research Foundation, Chennai-600113, Tamil Nadu, India
[2]Biochimie & Physiologie Moléculaire des Plantes, Montpellier-34060, France
[3]National Centre for Biological Sciences, (TIFR),Bangalore-560065, Karnataka, India
[4]KrishiVigyanKendra, Tindivanam-604002, Tamil Nadu, India
*E-mail: gayatri@mssrf.res.in

HKT1;5 loci/alleles are contributing determinants of salinity tolerance in wheat and rice. *HKT1*;5 genes encode plasma membrane-localized sodium transporters, retrieving xylem Na^+ into xylem parenchyma cells, thereby reducing shoot Na^+ accumulation. In rice, variation in salt tolerance in specific landraces is linked to allelic variation in *OsHKT1*;5 (*Saltol* locus; *OsHKT1;5-SKC1/OsHKT1;5-Ni*). *Oryza coarctata* is a halophytic wild rice (mangrove associate), growing in fluctuating salinity (20-40 dS m^{-1}) at the seawater-estuarine interface. Reported here are distinct transport characteristics of the salinity stress inducible, plasma membrane localized *O. coarctata* HKT1;5 (OcHKT1;5) vis-à-vis OsHKT1;5. Yeast B31 cells (deficient in sodium extrusion) expressing *OcHKT1,5* are less sensitive to increasing Na^+ in the medium (10-100 mM) than those expressing *OHKT1;5-SKC1*. Transport studies in *Xenopus* oocytes suggest that *OcHKT1,5* is a sodium transporter (consistent with presence of the S-G-G-G motif), and has a has a lower affinity for Na^+ than *OsHKT1;5-Ni*. The K_m given by a Michaelis fit is 32 mM for *OcHKT1,5* and 2 mM for *OsHKT1,5-Ni*. The maximal conductance of OcHKT1;5, on the other hand, is 3.8 fold higher than*OsHKT1;5-Ni* at Na^+ concentrations greater than 3 mM. Homology modeling and simulation (OcHKT1;5 vs OsHKT1;5-Ni) suggests that three key amino acid changes in OcHKT1;5 (in loops present on the extracellular side; E239K, G207R, G214R) change the surface electrostatics at the ion pore, accounting for its lower affinity and/or salt concentration-dependent Na conductance vis-a-vis OsHKT1;5-Ni. Transport characteristics and homology modeling thus suggest OcHKT1;5 could be more efficient than OsHKT1;5-Ni in higher salinity stress conditions.

IDT9-094 | Development of transgenic peanut (*Arachis hypogaea* L.) lines by overexpression of Na^+/H^+ antiporter gene for enhanced salt tolerance

Venkatesh K[1], Amareshwari P[1], Kavi Kishor PB[1] and A. Roja Rani[1]*

[1]Department of Genetics and Biotechnology, Osmania University, Hyderabad-500007, Telangana state, India.
*E-mail: anupallirr@gmail.com

Peanut (Arachis hypogaea L.) is an important oil-yielding cash crop as well as an exportable agricultural commodity of the world. It is a rich source of edible oil, proteins and also plays a vital role in oilseed economy of India. Peanut frequently encounters water-deficit and soil salinity conditions that affect the growth and productivity of peanut crops. The production of groundnut in India needs to be increased from the current production to meet the increasing demand of the oil and confectionery industry. Sodium-proton antiporters could play an important role in plant salt tolerance mechanism. In the present study, SOS1 gene was introduced in peanut variety to enhance salt tolerance. Overall, our result indicates that the overexpression of Na^+/H^+ antiporter gene in groundnut resulted in enhanced tolerance of transgenic plants to salinity stress. Transgenic plants of groundnut with the Na^+/H^+ antiporter gene were developed using Agrobacterium-mediated genetic transformation. Molecular analysis confirmed the presence, stable integration and expression of Na^+/H^+ antiporter gene in the peanut genome. Biochemical analysis of transgenic lines showed higher chlorophyll, K^+ content, proline and lower Na^+ content compared to untransformed controls. Physiological analysis of transgenic lines showed higher biomass and yield compared to untransformed control plants. Genetically engineered salinity tolerant groundnut plants could provide an avenue to the restoration of saline farmlands lost to agriculture and highlighting the potential of Na^+/H^+ antiporter gene for biotechnological applications.

IDT9-095 | Marker assisted selection (MAS) and introgression of quantitative trait loci (QTL) for drought tolerance in rice (*Oryza sativa* L.)

*Prudhvi Raj Vennela[1], S.K. Singh[1], Rajesh Singh[1], Varsha Gayatonde[1], D.K. Singh[1], Y.S. Reddy[1]

[1]Institute of Agricultural Sciences, BHU, Varanasi-221005 U.P. INDIA
*E-mail: vprudhviraj.2@gmail.com

The frequent occurrence of abiotic stresses such as drought has been identified as the key factor for low productivity in the rice rainfed ecosystems. Worldwide, drought affects approximately 23 million ha of rainfed rice. Drought during the cropping season directly affects grain yield (GY), particularly at the reproductive stage (RS), which is the most devastating. Recent studies at IRRI have shown moderate to high heritability of GY under RS stress, suggesting direct selection for GY under RS stress to be a practical approach. Further, the feasibility of combining high yield potential with GY under RS stress has been reported by employing direct selection for GY under RS stress. Marker-assisted selection and the introgression of major-effect QTL(s) for GY under RS stress could be an efficient, fast-track approach for breeding drought-tolerant rice varieties. For drought, most of the quantitative trait loci (QTL(s)) identified in rice and other crops are mostly in the background of non-elite genotypes. If these QTL(s) are transferred into popular rice varieties, the rice yield potential may be improved in rainfed ecosystems. We are reporting in the present study successful evaluation and parental polymorphism among rice genotypes and transfer of major drought QTLs $qDTY_{1.1}$ and $qDTY_{3.2}$ from N_{22} and $qDTY_{12.1}$ from *Vandana* to HUR 105.

IDT9-096 | Development of 50K cotton SNP chip and construction of high density linkage map in *Gossypium hirsutum*

Yadav R[1,5], Salame R V[2], Rai K M[1], Jena S N[1], Singh S K[1], Badole A[2], Mohan P[2], Agarwal R K[3,4], Waghmare V N[2]* and Sawant S V[1,4]*

[1]CSIR-National Botanical Research Institute, Rana Pratap Marg, Lucknow, India.
[2]Central Institute for Cotton Research, Wardha Road, Nagpur, India
[3]CSIR-Centre for Cellular and Molecular Biology, Uppal road, Hyderabad, India.
[4]Academy of Scientific and Innovative Research (AcSIR), New Delhi, India
[5]Lucknow University, Lucknow, India
*E-mail: samirsawant@nbri.res.in, vijayvnw@yahoo.com

Use of genetic modification based applications has grown significantly for crops like cotton, but the classical approach of breeding has been an indispensible method for trait improvements in plants. SNPs are now widely used in molecular assisted breeding and basic studies related to genetics of various crop plants. Here, we report the construction of high density SNP linkage map for allotetraploids cotton *Gossypium hirsutum*. Here, we report the development of SNP chip with 51,347 probes representing 42,377 SNPs using Affymetrix's Axiom technology. The SNP chip was utilized for construction of linkage map of *Gossypium hirsutum* by genotyping F8 RILs. Notably, the SNP call rate for all the genotyped samples was as high as 99.9%. We obtained a total of 2952 high quality polymorphic SNPs among the two parents (used for RILs development) of which we could successfully map 2731 (1867 unique) SNPs on 29 Linkage Groups (LGs). Thus, we also report here a dense intraspecific SNP-linkage map for ***G. hirsutum*** having a total map length of 3576.9 cM and an average intermarker distance of 1.31 cM which is very essential for identification of good QTLs. The SNP-chip will help in providing fast, accurate and cost effective genotyping in genetic linkage studies.

IDT9-097 | Identification of genes and genomic segments for cleistogamy in Pigeonpea (*Cajanus cajan* L.)

Pooja Yadav[1,2], Rachit K Saxena[1,*], VS Kandalkar[2], CV Sameer Kumar[1], Rajeev K Varshney[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Department of Plant breeding and Genetics, Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, Madhya Pradesh, India
*E-mail: r.saxena@cgiar.org

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major grain legume crops of the world predominantly grown in semi-arid tropics and sub-tropical regions. Pigeonpea has open or semi-cleistogamous flowers that promote natural out crossing. However, its open pollination behavior causes genetic deterioration in purity of seeds in varieties. In this direction introgression of cleistogamy or self-pollination behavior in pure line varieties can be a genetic tool to maintain purity of elite lines. In pigeonpea a mutant line ICPL 99050 has been identified as a cleistogamous line. However the cleistogamy has been found to link with shriveled seeds which further hampered the breeding efforts. Therefore, efforts have been initiated to identify the molecular markers/genes/genomic segments associated with cleistogamy and possibly to break its linkage with shriveled seeds. As the first step a recombinant inbred line (RIL) population has been developed from the crossing parents ICPL 99010 (cleisto flowers) and ICP 5529 (open flowers). RILs are being subjected to high density genotyping using 50k SNP array. In parallel RILs are being phenotyped for the cleistogamy and shriveled seeds. Trait phenotyping data together with SNP genotyping data will be used for the identification of genes and genomic segment associated with the target traits. Identified genes/genomic segments for cleistogamy/ shriveled seeds will help in selection of lines with self-pollinating behavior and acceptable seed size.

IDT9-098 | Expression studies of transcription factors under moisture stress in Cotton (*Gossypium hirsutum* L.)

Yadav SA[1,2*], Vamadevaiah HM[3], Katageri IS[2], Assadi NM[3]

[1]CSIR-National Chemical Laboratory, Pune-411008, Maharashtra, India
[2]Institute of Agricultural Biotechnology, UAS, Dharwad-580005, Karnataka, India
[3]Agricultural Research Station, Dharwad farm, UAS, Dharwad-580007, Karnataka, India
*E-mail: sagaryadav04@gmail.com

Cotton (*Gossypium hirsutum* L.) is an important commercial crop playing a significant role in Indian farming and industrial economy. The adverse environmental conditions are the major factors that reduce crop productivity worldwide. The whole process of plant adaptation to the environmental stresses is controlled by orchestration of complex molecular networks. Transcription factors are master-control proteins in all living cells. They often exhibit sequence specific DNA binding and are capable of activating or repressing transcription of multiple target genes. In the present study, six transcription factor genes ***viz.,*** WRKY 19, LIM, NAC, GeBP, WRKY 70 and C_2H_2, showing significant difference of expression on exposure to artificial moisture stress in cotton, were selected. The moisture stress was induced by withholding water from 45 DAS. Expression analyses of transcription factor (TF) genes in 27 cotton genotypes were carried out using qRT-PCR. The relative expression profiles of all the six TF genes revealed that, all the TF genes were significantly up-regulated in genotype 5433 A2 A03 N83 (G_{16}) which is known to be drought tolerant from the survey report of the All India Coordinated Cotton Improvement Project (AICCIP). Present study reports the relevance of selected TF genes in drought tolerance.

IDT9-099 | A new reason for segregation rate distortion in genetic linkage map

Zaynali Nezhad, Khalil

Faculty member, Gorgan University of Agricultural Sciences and Natural Resources
E-mail: khalil1381@yahoo.com

Segregation rate distortion is the first step to check in any genetic linkage map construction. It shows whether the pattern of segregation for each locus is as expected or distorted. In case of distortion, it is recommended to check the reason for distortion. The reason can be applying wrong marker pattern, low quality gel electrophoresis, different survival of individuals, and remind heterozygosity in the parental lines. One other reason for distortion, especially in polyploid species such as bread wheat, can be amplifying more than one locus by each primer pairs but having the same allele sizes. In this situations, while this primer pairs shows only one band on each parent, the pattern on individuals depend on the type of population and the position of the two loci. If the two loci placed on different chromosomes on an F_2 population, number of heterozygotes will increase (much higher than normal F_2), in RILs the number of heterozygotes will be much more then the remind heterozygosity (higher than normal F_2), and in DH heterozygotes individuals will appear which is not expected (similar to normal F_2). If the loci are on the same chromosome, the number of heterozygotes will increase; this increase depends on the distance; the more distance the more heterozygote. If the two loci reach each other, the distortion will be removed because they are not actually as two loci any more. Finally, this kind of distortion can happen if the similarity between alleles occurs even in one of the parents.

IDT9-100 | Characterization of groundnut resistance to bacterial-wilt caused by *Ralstonia solanacearum* by forward and reverse genetics methods

Zhang C[1,2], Zhang N[1,2], Zhuang RR[2], Chen H[1,2], Cai TC [1,2], Gandeka M[1,2], Niaz A[1,2], He GH[3], Rashney RK[4], Zhuang WJ[1,2]*

[1]State key laboratory of ecological pest control for Fujian and Taiwan crops, Fujian Agriculture and Forestry University, Fuzhou, P.R. China
[2]Fujian Key Laboratory of Crop Molecular and Cell Biology, Fujian Agriculture and Forestry University, Fuzhou, P.R. China
[3]Tuskegee University, Tuskegee, AL, USA
[4]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
*E-mail: weijianz@fafu.edu.cn

Bacterial wilt caused by casual agent *Ralstonia solanacearum* (*Rs*) is *a serious disease* in groundnut and great many other plant species. Forward and reverse genetics strategies were adopted in our study. From the view point of forward genetics, the peanut RILs including 300 F_9 progenies derived from Yueyou 92 × Xinhuixiaoli were tested of disease resistance through inoculation with *R.solanacearum* in the field. Resistance to *R.solanacearum* is a quantitative trait. Three QTLs were mapped on an interval 15 cM using a linkage map with SSR and related SNP markers. An Tir-NBS-LRR resistance gene *AhqBW3* was found closely linked with a BW resistance molecular marker *SNP79* which was mapped in a gene locus next to the R gene. *AhqBW3* was showed downregulation under the challenge of Rs inoculation. From the view point of reverse genetics, a novel NBS-LRR resistance gene *AhRRS5*, an LRR-RLK gene *AhRLK1* and an unkown gene *AhRRS22* were upregulated by *Rs* inoculation which were screened from microarray hybridization. They showed resistance phenotypes in transgenic tobacco overexpressing of these three genes. Among of them, Overexpression of *AhRRS5* significantly enhanced the resistance of heterogeneous tobacco to *R. solanacearum*, with diverse resistance levels in different transgenic lines. Several defense-responsive marker genes in hypersensitive response, including HR, SA, JA, and ET signals, were considerably upregulated in the transgenic lines as compared with the wild type in response to *R. solanacearum*. *NPR1* and *NDR1* were also upregulated in response to the pathogen. These results indicate that *AhRRS5* participates in the defense response to *R. solanacearum* through the crosstalk of multiple signaling pathways and the involvement of *NPR1* and R gene signals for its resistance. These studies may guide the resistance enhancement of peanut and other economic crops to bacterial wilt disease.

IDT9-101 | Molecular characterization of pigeon pea rhizobial strains for abiotic stress tolerance from arid and semi-arid zones of Haryana, India

Kuldeep Singh[1]*, Rajesh Gera[1]

[1]Department of Microbiology, CCS Haryana Agricultural University, Hisar, India
*E-mail: kdssc77@gmail.com

Pigeon pea [*Cajanus cajan* (L.) Millspaugh], commonly called as *toor dal* or *arhar dal* in India, is a perennial member of the family *Fabaceae*. It is the only known cultivated food crop of the 32 species that fall under the *Cajaninae* sub-tribe. The crop represents about 5% of world legume production. It is an important legume of rain-fed agriculture in the arid and semiarid tropics. It is an important legume, mainly grown as a hardy and drought-tolerant crop. India is a principal pigeon pea-growing country, contributing nearly 90% of total world's production. Environmental stress is a major component of natural selection in soil ecosystem; the most prominent problematic abiotic factors in the arid regions are drought and high temperature. In the present investigation, a total 196 rhizobial isolates were obtained from 84 soil samples collected from pigeon pea grown fields of South-West Haryana. The different pigeon pea rhizobial isolates were obtained by using trap plant method in pots. On the basis of temperature and drought tolerance, 49 rhizobial isolates were selected for molecular characterization. The genomic DNA of all these rhizobial isolates were isolated by CTAB method and tested for nodC and nifH gene primers and hence authenticated as rhizobia. All the 49 rhizobial isolates of pigeon pea, showed nodC gene amplification, while 35 out of 49 isolates showed nifH gene amplification by using different sets of primers. On the basis of abiotic stress tolerance and molecular characterization, six pigeon pea rhizobial isolates (PPH-8E, PPR-2, PPB-26A, PPM-30A, PPM-33C and PPM-37A) were selected as the most efficient rhizobial isolates, which can be used as a potential biofertilizer to improve yield under high drought and temperature conditions.

List of Participants

S No	Registration ID	Family Name	Name	Affiliation	E-mail
1	P16#ICR000#XSI000022	Abbasi	Nagma	NextGen Life Sciences Pvt. Ltd., New Delhi, India	nagma09@gmail.com
2	P16#ICR000#XXR000157	Abdulmaliki	Rekiya Otuchu	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	rekimalik83@yahoo.com
3	P16#ICR000#XXR000020	Abraha	Mizan Tesfay	University of KwaZulu-Natal (UKZN) and Tigray Agricultural Research Institute (TARI), Axum, Ethiopia	mizantesfay90@gmail.com
4	P16#ICR000#XAR000027	Abubakar	Zainab Adamu	Gombe State University, Gombe, Nigeria	zeepha22@gmail.com
5	P16#ICR000#XXR000167	Adeboye	Kehinde Adewole	The Federal University of Agriculture, Abeokuta (FUNAAB), Abeokuta, Nigeria	kaadeboye@yahoo.com
6	P16#ICR000#XAR000026	Adediran	Olaotan	Federal University of Technology Minna, Minna, Nigeria	o.adediran@futminna.edu.ng
7	P16#ICR000#XXR000170	Adegbehingbe	Felix Taiwo	University of Ibadan, Ibadan, Nigeria	felix_taiwo@yahoo.co.uk
8	P16#ICR000#XXR000027	Adejumobi	Idris Ishola	"Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana"	adejumobiidris@yahoo.com
9	P16#ICR000#TL3000026	Adogoba	Desmond Sunday	CSIR-Savanna Agricultural Research Institute, Tamale, Ghana	adogoba@yahoo.com
10	P16#ICR000#NEF000020	Adu	Gloria Boakyewaa	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	gloriaboakyewaa@yahoo.com
11	P16#ICR000#TL3000024	Aga	Tesfaye Geleta	Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia	tesfayeaga28@yahoo.com
12	P16#ICR000#NEF000041	Agashe	Bhavna	Dupont Pioneer, Hyderabad, India	bhavna.agashe@pioneer.com
13	P16#ICR000#XSI000065	Aggarwal	Ramesh K	CSIR-Centre for Cellular & Molecular Biology (CCMB), Hyderabad, India	rameshka@ccmb.res.in
14	P16#ICR000#XSI000009	Agrawal	Pawan Kumar	ICAR-National Agricultural Science Fund (NASF), New Delhi, India	nationalfund1011@gmail.com
15	P16#FD2511#MER705696	Agudelo	Carlos Berdugo	Bayer, Diegem, Belgium	carlos.berdugo1@bayer.com
16	P16#UD0410#MER695947	Ahmed	Mutez Ali	University of Goettingen, Goettingen, Germany	mahmed@uni-goettingen.de
17	P16#ICR000#TAR000018	Ahmed	Hauwa Oziohu	Ahmadu Bello University (ABU), Zaria, Nigeria	hauwaahmed21@gmail.com
18	P16#ICR000#TL3000033	Ahmed	Benjamin	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	"benujah@yahoo.com ahmedben33@gmail.com"
19	P16#ICR000#NEF000030	Ajay	BC	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	ajaygpb@yahoo.co.in
20	P16#ICR000#TL3000058	Ajeigbe	Hakeem	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria	H.Ajeigbe@cgiar.org
21	P16#ICR000#XAR000032	Ajilogba	Caroline	North-West University, Mafikeng, South Africa	carolfad@yahoo.com
22	P16#ICR000#ICR000078	Akinseye	Folorunso Mathew	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria	f.akinseye@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
23	P16#ICR000#ICR000042	Akpo	Essegbemon	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	e.akpo@cgiar.com
24	P16#UD2510#MER699712	Akuja	Thomas E	South Eastern Kenya University, Kitui, Kenya	akuja05@gmail.com
25	P16#ICR000#ICR000073	Alam	Ashraful	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	a.ashraful@cgiar.org
26	P16#ICR000#ICR000081	Alam	Shamshad	International Rice Research Institute (IRRI), Patancheru, India	s.alam@irri.org
27	P16#ICR000#XXR000190	Albayrak	Onder	Dicle University, Diyarbakir, Turkey	onderalb@hotmail.com
28	P16#ICR000#TL3000045	Alex	Gerald	Naliendele Agricultural Research Institute (NARI), Mtwara, Tanzania	sumbanya@yahoo.com
29	P16#ICR000#XXR000140	Ali	Mohammed Anwar	Acharya N.G. Ranga Agricultural University (ANGRAU), Bapatla, India	anwar.mohammed225@gmail.com
30	P16#ICR000#NEF000011	Ali	Jauhar	International Rice Research Institute (IRRI), Los Banos, The Philippines	J.Ali@irri.org
31	P16#HD2411#MER705560	Aliche	Ernest	Wageningen University & Research, Wageningen, The Netherlands	ernest.aliche@wur.nl
32	P16#ICR000#ICR000006	Alo	Fida	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	F.ALO@CGIAR.ORG
33	P16#ICR000#XXR000014	Al-Shafeay	Amal F	Agricultural Genetic Engineering Research Institute (AGERI), Cairo, Egypt	amal.alshafeay@gmail.com
34	P16#ND1411#MER702927	Alvarez Prado	Santiago	French National Institute for Agricultural Research (INRA), Montpellier, France	santiago.alvarez-prado@inra.fr
35	P16#ICR000#XXR000074	Amareshwari	P	Osmania University, Hyderabad, India	puduthaamareshwari@gmail.com
36	P16#ICR000#TL3000049	Amogoli	Otuba Moses	National Semi Arid Resources Research Institute (NaSARRI), Kampala, Uganda	mozes.otuba@gmail.com
37	P16#ICR000#XXR000191	Amongi	Winnyfred	International Center for Tropical Agriculture (CIAT), Kampala, Uganda	w.amongi@cgiar.org
38	P16#ICR000#SPS000028	Ananda Kumar	BV	Dupont Pioneer, MCRC, Hyderabad, India	Ananda.kumarBV@pioneer.com
39	P16#ICR000#XAR000021	Anaya	Fatima	Cadi Ayyad University, Marrakech, Morocco	anaya.fatima@gmail.com
40	P16#ICR000#ICR000041	Angarawai	Ignatius	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria	I.Angarawai@cgiar.org
41	P16#ICR000#XXR000076	Anjali	N	Jawaharlal Nehru Tropical Botanic Garden and Research Institute (JNTBGRI), Trivandrum, India	anjalinair20@gmail.com
42	P16#ICR000#NEF000014	Anjani	K	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	k.anjani@icar.gov.in

S No	Registration ID	Family Name	Name	Affiliation	E-mail
43	P16#ICR000#XXR000120	Antur	Veeresha B	University of Agricultural Sciences (UAS), Dharwad, India	ambavee@gmail.com
44	P16#MD3110#MER700496	Anumalla	Mahender	ICAR-National Rice Research Institute (NRRI), Cuttack, India	mahenderbio@gmail.com
45	P16#SD1012#MER709169	Anuradha	Ch	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	anu_dna@rediffmail.com
46	P16#ICR000#NEF000043	Aparnna	M	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	aparnna.icrisat@gmail.com
47	P16#ICR000#ICR000092	Are	Ashok Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	a.ashokkumar@cgiar.org
48	P16#ICR000#XXR000145	Arora	Vivek	Bose Institute, Kolkata, India	vikarora.arora@gmail.com
49	P16#ICR000#DAC000006	Arulthambi Luke	Rathna Kumar	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	rathnakumar169@gmail.com
50	P16#GD1512#MER710205	Arya	Mamta	ICAR-Indian Institute of Soybean Research (IISR), Indore, India	mamta.gpb@gmail.com
51	P16#ICR000#TL3000046	Aseete	Paul	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	paseete@gmail.com
52	P16#ICR000#XXR000114	Ashoka	P	University of Agricultural Sciences (UAS), Dharwad, India	ashokapuas@gmail.com
53	P16#ICR000#XAR000025	Askira	Abubakar Bala	Lake Chad Research Institute, Maiduguri, Nigeria	askiralcri@gmail.com
54	P16#ICR000#SGP000006	Atlin	Gary	Bill & Melinda Gates Foundation (BMGF), Seattle, USA	Gary.Atlin@gatesfoundation.org
55	P16#ICR000#XXR000028	Attamah	Patrick	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	attamahpat@yahoo.com
56	P16#ICR000#NEF000058	Audebert	Alain	Cirad UMR AGAP - Equipe PAM/ CERAAS-ISRA, Thiès Senegal, Senegal	alain.audebert@cirad.fr
57	P16#ICR000#SPS000025	Babu	Raman	Dupont Pioneer, MCRC, Hyderabad, India	raman.babu@pioneer.com
58	P16#ICR000#ICR000090	Badolo	Felix	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	f.badolo@cgiar.org
59	P16#MD2811#MER706295	Baig	Khizer	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Nanded, India	khizerbaig1@rediffmail.com
60	P16#ICR000#ICR000016	Bajaj	Prasad	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.bajaj@cgiar.org
61	P16#ICR000#XXR000134	Balasubramanian	P	Tamil Nadu Agricultural University (TNAU), Madurai, India	agribalatnau1991@gmail.com
62	P16#ICR000#XAR000006	Balcha	Lijalem Korbu	Ethiopian Institute of Agricultural Research (EIAR) -Debre Zeit Agricultural Research Center (DZRC), Addis Ababa, Ethiopia	lijupeace@gmail.com
63	P16#ICR000#XHT000003	Balyan	HS	Chaudhary Charan Singh University, Meerut, India	hsbalyan@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
64	P16#ICR000#XSI000008	Bamji	Mahtab S	Dangoria Charitable Trust, Hyderabad, India	"msbamji@gmail.com "
65	P16#ICR000#XXR000061	Baniekal Hiremath	Gangadhar	University of Horticultural Sciences, Bagalkot, India	gangubhm@gmail.com
66	P16#ICR000#XXR000064	Bansal	Ruchi	National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India	Ruchi.Bansal@icar.gov.in
67	P16#ICR000#XSI000018	Bansal	KC	ICAR-National Agricultural Higher Education Project (NAHEP)	kailashbansal@hotmail.com
68	P16#ICR000#NEF000042	Bantte	Kassahun	Jimma University, Jimma, Ethiopia	kassahunb@gmail.com
69	P16#ICR000#NEF000037	Banu	Afsana	University of Agricultural Sciences (UAS), Bangalore, India	afsanabanu.manik@gmail.com
70	P16#ICR000#TL3000016	Barry	Silamana	Institut de l'Environnement et des Recherches Agricoles (INERA), Ouagadougou, Burkina Faso	silabarry@yahoo.fr
71	P16#ICR000#IOC000001	Bartels	Dorothea	University of Bonn, Bonn, Germany	dbartels@uni-bonn.de
72	P16#ND1912#MER710896	Bartsch	Michael	Syngenta Crop Protection AG, Münchwilen, Switzerland	michael.bartsch@syngenta.com
73	P16#ICR000#XXR000141	Barurkar	Praveen Kumar	Agricultural Research Station (ARS), Kalaburagi, India	praveenbarurkar@gmail.com
74	P16#UD1511#MER703318	Barutcular	Celaleddin	Cukurova University, Adana, Turkey	cebar@cu.edu.tr
75	P16#ICR000#HSI000008	Barwale Zehr	Usha	Mahyco, Jalna, India	usha.zehr@mahyco.com
76	P16#ICR000#TAR000030	Basdemir	Fatma	Dicle University, Diyarbakir, Turkey	ftmbsdmr87@hotmail.com
77	P16#ICR000#DAC000004	Bashou	Liao	Oil Crops Research Institute -Chinese Academy of Agricultural Sciences (OCRI-CAAS), Wuhan, China	lboshou@hotmail.com
78	P16#ICR000#MBL000008	Basu	PS	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	psbsu59@gmail.com
79	P16#ICR000#TL3000008	Batieno	Joseph Benoît	Institut de l'Environnement et des Recherches Agricoles (INERA), Ouagadougou, Burkina Faso	batieno52@gmail.com
80	P16#ICR000#NEF000062	Batlang	Utlwang	Botswana University of Agriculture and Natural Resources, Gaborone, Botswana	ubatlang@bca.bw
81	P16#ICR000#SGP000003	Batley	Jacqueline	The University of Western Australia, Perth, Australia	jacqueline.batley@uwa.edu.au
82	P16#ICR000#WAO000009	Batra	Ritu	Chaudhary Charan Singh University, Meerut, India	ritu.biotech24@gmail.com
83	P16#HD2212#MER711639	Baumann	Ute	University of Adelaide, Glen Osmond, Australia	ute.baumann@adelaide.edu.au
84	P16#XD3011#MER707381	Beena	R	Kerala Agricultural University, Thiruvananthapuram, India	beenaajithkumar@gmail.com
85	P16#ICR000#SPS000004	Behera	Srikant	Manyara Biotech Pte. Ltd. , Mumbai, India	srikant@metalhands.in
86	P16#ICR000#ICR000034	Belliappa	Shruthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	shruthibelliappa155@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
87	P16#ICR000#NEF000069	Ben-Hamo	Hilla	NRGene, Ness Ziona, Israel	hila@nrgene.com
88	P16#ICR000#WAO000016	Benitez-Alfonso	Yoselin	University of Leeds, Leeds, UK	Y.Benitez-Alfonso@leeds.ac.uk
89	P16#ICR000#SPS000024	Bennett	Young	Journal of Experimental Botany, Manchester, UK	b.young@lancaster.ac.uk
90	P16#XD3011#MER707230	Bensen	Robert	Syngenta Crop Protection, LLC, Minnesota, USA	robert.bensen@syngenta.com
91	P16#ICR000#CHP000001	Bergvinson	David	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	D.Bergvinson@cgiar.org
92	P16#ICR000#INS000021	Bertram	Robert	US Agency for International Development (USAID), Washington D.C, USA	rbertram@usaid.gov
93	P16#ICR000#XXR000017	Betaw	Hirut Getinut	International Livestock Research Centre (ILRI), Addis Ababa, Ethiopia	H.Getinet@cgiar.org
94	P16#ICR000#TL3000020	Beyene	Meseret	Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia	meseretbbb@yahoo.com
95	P16#TD2911#MER706534	Bharath	CT	University of Agricultural Sciences (UAS), Bangalore, India	bharath7015@gmail.com
96	P16#ICR000#XXR000123	Bharathi	A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	reenmvel@gmail.com
97	P16#ICR000#NEF000035	Bharti	Pooja	University of Agricultural Sciences (UAS), Bangalore, India	poojapb62@gmail.com
98	P16#UD2211#MER705169	Bhat	Muhammad	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Kashmir, India	mashrafbhat@skuastkashmir.ac.in
99	P16#UD2712#MER712385	Bhat	Ramesh	University of Agricultural Sciences (UAS), Dharwad, India	bhatrs@uasd.in
100	P16#ICR000#XGE000005	Bhatnagar	Pooja	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.bhatnagar@cgiar.org
101	P16#GD1711#MER703576	Bheemanahalli	Raju	Kansas State University, Manhattan, USA	rajubr@ksu.edu
102	P16#ICR000#NEF000040	Bhyri	Priyanka	Dupont Pioneer, Hyderabad, India	bhyri.priyanka@pioneer.com
103	P16#ICR000#SPS000015	Bihari	Bipin	AgriGenome Labs Pvt Ltd, New Delhi, India	bipin@aggenome.com
104	P16#HD0311#MER701052	Biju	Sajitha	University of Melbourne, Victoria, Australia	sbiju@student.unimelb.edu.au
105	P16#ICR000#TL3000004	Binagwa	Papias	Selian Agricultural Research Institute (SARI), Arusha, Tanzania	hongera1984@yahoo.com
106	P16#ICR000#ICR000043	Birhanu	Birhanu Zemadim	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	z.birhanu@cgiar.org
107	P16#SD3112#MER713340	Bishi	Sujit Kumar	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	sujitbishi@gmail.com
108	P16#ICR000#TAR000007	Bogale	Tsegaye Getahun	Addis Ababa University (AAU), Addis Ababa, Ethiopia	tseggetahun@yahoo.com
109	P16#ICR000#ICR000013	BoghiReddy	Sailaja	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	B.Sailaja@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
110	P16#ICR000#XXR000082	Bohare	Tinkeshwari	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India	tinabohare@gmail.com
111	P16#ICR000#XXR000108	Bora	Lokesh	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	lokeshbora36099@gmail.com
112	P16#ICR000#XXR000101	Boranayaka	MB	University of Agricultural Sciences (UAS), Raichur, India	mbboranayak@gmail.com
113	P16#ICR000#XXR000149	Borna	Fatemeh	The University of Tehran, Karaj, Iran	fatemehborna@gmail.com
114	P16#ICR000#INS000001	Borrás	Lucas	Universidad Nacional de Rosario, Rosario, Argentina	lborras@unr.edu.ar
115	P16#ICR000#TL3000059	Boukar	Ousmane	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	O.Boukar@cgiar.org
116	P16#ICR000#XXR000188	Breria	Caleb Manamik	World Vegetable Centre and National Pingtung University of Science and Technology (NPUST), Pingtung, Taiwan	caleb.breria@worldveg.org
117	P17#ND0201#MER714134	Brown	Steve	The Peanut Foundation, Tifton, USA	sbrown@peanutsusa.com
118	P16#TD1511#MER703004	Brunel	Nidia	Universidad de Talca, Talca, Chile	nidiabrunel@gmail.com
119	P16#TD1312#MER709798	Buchupalli	Ravindranatha Reddy	Agricultural Research Station (ARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Anantapur, India	b.ravindranathareddy@gmail.com
120	P16#ICR000#NEF000029	Burgueño	Juan Andres	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	J.Burgueno@cgiar.org
121	P16#ICR000#NEF000065	Bustos-Korts	Daniela	Wageningen University & Research, Wageningen, The Netherlands	daniela.bustoskorts@wur.nl
122	P16#FD2511#MER705713	Cabrera-Bosquet	Llorenc	French National Institute for Agricultural Research (INRA), Montpellier, France	llorenc.cabrera-bosquet@inra.fr
123	P16#ICR000#TAR000020	Caguiat	Joanne Domingo	Philippine Rice Research Institute (Philrice), Nueva Ecija, The Philippines	"jm.domingo@philrice.gov.ph "
124	P16#TD0612#AR1580782	Cai	Huanjie	Northwest A&F University, Yangling, China	
125	P16#ICR000#INS000002	Carberry	Peter	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.carberry@cgiar.org
126	P16#ICR000#INS000003	Carminati	Andrea	University of Goettingen, Goettingen, Germany	andrea.carminati@forst.uni-goettingen.de
127	P16#ICR000#XXR000197	Cazenave	Alexandre-Brice	The Samuel Roberts Noble Foundation, Ardmore, USA	abcazenave@noble.org
128	P16#ICR000#ICR000053	Chadalavada	Keerthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	keerthichadalawada@gmail.com
129	P16#ICR000#NEF000006	Chakraborty	Niranjan	National Institute of Plant Genome Research (NIPGR), New Delhi, India	nchakraborty@nipgr.ac.in

S No	Registration ID	Family Name	Name	Affiliation	E-mail
130	P16#WD3011#MER707145	Chakraborty	Koushik	ICAR-National Rice Research Institute (NRRI), Cuttack, India	koushikiari@gmail.com
131	P16#ICR000#ICR000069	Challa	Venkateswarlu	International Rice Research Institute (IRRI), Patancheru, India	c.venkateshwarlu@irri.org
132	P16#XD2812#MER712632	Chamarthi	Sivakumar	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	s.chamarthi@cgiar.org
133	P16#ICR000#XXR000069	Chandrashekara	KN	Upasi Tea Research Institute, Coimbatore, India	knchandu1@gmail.com
134	P16#ICR000#TL3000029	Chaturvedi	Sushil	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	sushilk.chaturvedi@gmail.com
135	P16#WD3011#MER706900	Chaudhari	Gaurav	College of Horticulture, Bangalore, India	CHAUDHARIGAURAV11@gmail.com
136	P16#ICR000#XXR000135	Chaudhary	Saurabh	ICAR-National Research Centre on Plant Biotechnology (NRCPB), New Delhi, India	saurabh.biozone@gmail.com
137	P16#ICR000#XXR000105	Chaudhary	Suman	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	kesarsuman21@gmail.com
138	P16#ND2811#MER706352	Chauhan	Shubhendra	Sam Higginbottom Institute of Agriculture, Technology and Sciences (SHIATS), Allahabad, India	shubhendra.schauhan@shiats.edu.in
139	P16#ICR000#SPS000017	Chaulk-Grace	Christine	Syngenta Seeds, Inc., Waterloo, USA	christine.chaulk-grace@syngenta.com
140	P16#TD2911#MER706506	Chellapilla	Bharadwaj	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	drchbharadwaj@gmail.com
141	P16#MD0711#AR1567503	Chen	Liang	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	cl@sagc.org.cn
142	P16#ICR000#TAR000004	Chen	Hua	Fujian Agriculture and Forestry University (FAFU), Fuzhou, China	hchen2013@163.com
143	P16#ICR000#XSI000045	Cheralu	C	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	cheralu_2006ars@yahoo.co.in
144	P16#ICR000#TL3000002	Chichaybelu	Mekasha	Ethiopian Institute of Agricultural Research (EIAR), DebreZeit, Ethiopia	chichemekasha@gmail.com
145	P16#ICR000#SPT000007	Chidubem	Okeke Paul	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
146	P16#GD0812#MER708825	Chinnaswamy	Appunu	ICAR-Sugarcane Breeding Institute, Coimbatore, India	cappunu@gmail.com
147	P16#ICR000#XGE000009	Chinnusamy	Viswanathan	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	viswanathan@iari.res.in
148	P16#ICR000#SPS000016	Chintamanani	Satya	Syngenta Seeds, Inc.,, Des Moines, USA	satya.chintamanani@syngenta.com
149	P16#ICR000#SPS000001	Chio	Fiona	Illumina, Inc., Hong Kong	wfchio@illumina.com
150	P16#ICR000#ICR000094	Chitaya	Soka	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Lilongwe, Malawi	s.chitaya@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
151	P16#ICR000#ICR000101	Chitikineni	Anu	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	a.chitikineni@cgiar.org
152	P16#ICR000#XXR000038	Choudhary	Sunita	Dupont Pioneer, Wargal, India	sunita963@gmail.com
153	P16#GD1011#MER702129	Christopher	Jack T	The University of Queensland, Toowoomba, Australia	j.christopher@uq.edu.au
154	P16#ICR000#SPT000009	Christopher	Chukwu Chimaobi	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
155	P16#ICR000#XXR000165	Chukwudi	Uchechukwu Paschal	University of Nigeria Nsukka, Nsukka, Nigeria	uchechukwu.chukwudi@unn.edu.ng
156	P16#ICR000#TAR000005	Civava	Rene Mushizi	Université Evangélique en Afrique-UEA, Bukavu, Democratic Republic of the Congo	rene.civava@outlook.com
157	P16#ICR000#INS000004	Cooper	Mark	DuPont Pioneer, Johnston, Iowa, USA	mark.cooper@pioneer.com
158	P16#HD1011#AR1569047	Coupel-Ledru	Aude	French National Institute for Agricultural Research, Montpellier, France	audecoupel.ledru@yahoo.fr
159	P16#ICR000#SPS000029	Cox	Claire	LGC Genomics, Cambridge, UK	
160	P16#ICR000#GWS000001	Crossa	Jose	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	J.CROSSA@CGIAR.ORG
161	P16#ICR000#NEF000060	Dakora	Felix Dapare	Tshwane University of Technology (TUT), Pretoria, South Africa	DakoraFD@tut.ac.za
162	P16#ICR000#XAR000009	Danful	Rukiya	"Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana"	danfulrukiya@ymail.com
163	P16#ICR000#XSI000044	Dangi	Kuldeep Singh	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	deanagri@hotmail.com
164	P16#UD2604#MER664872	Dar	Zahoor	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Kashmir, India	zahoorpbg@gmail.com
165	P16#ICR000#HSI000003	Dar	William	InangLupa Movement Inc, Quezon City, The Philippines	w.dar38@yahoo.com
166	P16#ICR000#NEF000008	Das	Alok	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	alokbio@gmail.com
167	P16#ICR000#ICR000074	Das	Reshmi Rani	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	dasreshmirani@gmail.com
168	P16#ICR000#XXR000126	Dash	Goutam Kumar	ICAR-National Rice Research Institute (NRRI), Cuttack, India	gkdash.bot@gmail.com
169	P16#ICR000#NOC000001	Datta	Swapan K	Visva-Bharati University, Santiniketan, India	swpndatta@yahoo.com
170	P16#ICR000#TAR000028	Datta	Avishek	Asian Institute of Technology, PathumThani, Thailand	datta@ait.asia
171	P16#ICR000#XSI000004	Datta	Karabi	University of Calcutta, Kolkata, India	krbdatta@yahoo.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
172	P16#RD2910#MER700372	DeBruin	Jason	Dupont Pioneer, Illinois, USA	jason.debruin@pioneer.com
173	P16#HD1011#MER702317	del Pozo	Alejandro	Universidad de Talca, Talca, Chile	adelpozo@utalca.cl
174	P16#TD0612#AR1580953	Deng	Xiping	Northwest A&F University, Yangling, China	
175	P16#ICR000#NEF000018	Deosarkar	DB	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	dbdeosarkar@gmail.com
176	P16#ICR000#ICR000046	Deshpande	Santosh	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	s.deshpande@cgiar.org
177	P16#XD3011#MER707192	Deshpande	Sanjeev	University of Agricultural Sciences (UAS), Dharwad, India	sanjeevgpb@gmail.com
178	P16#ICR000#ICR000044	Desmae	Haile	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	h.desmae@cgiar.org
179	P16#ICR000#XXR000124	Devi	Sarita	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	devisaritaa@gmail.com
180	P16#ICR000#XAR000033	Devnarain	Natrisha	University of Pretoria, Pretoria, South Africa	natrisha.devnarain@gmail.com
181	P16#ICR000#WAO000011	Dewanjee	Sujaya	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	sujaya2009@gmail.com
182	P16#ICR000#XXR000200	Dey	Narottam	Visva-Bharati University, Santiniketan, India	narottam.dey@visva-bharati.ac.in
183	P16#ICR000#XXR000025	Dhakarey	Rohit	Karlsruhe Institute of Technology, Karlsruhe, Germany	rohitbiotech@yahoo.co.in
184	P16#ICR000#MBC000009	Dhaliwal	HS	Eternal University, Baru Sahib, India	hsdhaliwal07@gmail.com
185	P16#ICR000#SPS000006	Dhanasekaran	S	Manyara Biotech Pte. Ltd. , Mumbai, India	dhanasekaran@metalhands.in
186	P16#ICR000#XXR000079	Dhanker	Rinku	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	rinku1989d@gmail.com
187	P16#ICR000#XHT000008	Dhankher	Om Parkash	University of Massachusetts Amherst, Amherst, USA	parkash@umass.edu
188	P16#ICR000#XXR000044	Dhanyalakshmi	KH	University of Agricultural Sciences (UAS), Bangalore, India	hemaadhanya@gmail.com
189	P16#ICR000#XXR000088	Dhivyapriya	D	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	dhivyaraj.89@gmail.com
190	P16#ICR000#ICR000107	Dhulipala	Ram	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	r.dhulipala@cgiar.org
191	P16#ICR000#TL3000031	Diakite	Lamissa	Institut d'Economie Rurale (IER), Bamako, Mali	diakite.lamissa@yahoo.fr
192	P16#ICR000#TL3000030	Diallo	Sory	Institut d'Economie Rurale (IER), Segou, Mali	Diallo.sory@yahoo.fr
193	P16#ICR000#ICR000109	Diancoumba	Madina	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	m.diancoumba@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
194	P16#ICR000#XSI000081	Dick	Richard	Ohio State University, Columbus, USA	dick.78@osu.edu
195	P16#ND0512#MER708361	Dippold	Michaela	University of Goettingen, Goettingen, Germany	dippold@gwdg.de
196	P16#ICR000#ICR000096	Divya	K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	divyanu.k@gmail.com
197	P16#ICR000#ICR000065	Dixit	Shilpi	International Rice Research Institute (IRRI), Patancheru, India	shilpi.dixit@irri.org
198	P16#UD1312#MER709868	Dockx	Adrien	UCL - Earth & Life Institute, Louvain-la-Neuve, Belgium	adrien.dockx@uclouvain.be
199	P17#SD2101#MER717679	Dodda	Santosh	Bioseed Research India, Hyderabad, India	santoshkumar.dodda@bioseed.com
200	P16#ICR000#XXR000066	Doddagoudar	Shivanagouda R	University of Agricultural Sciences (UAS), Raichur, India	srdsst@gmail.com
201	P16#ICR000#NEF000057	Dodig	Dejan	Maize Research Institute Zemun Polje, Zemun-Belgrade, Serbia	ddodig@mrizp.rs
202	P16#ICR000#XAR000002	Dossa	Komivi	Oil Crops Research Institute -Chinese Academy of Agricultural Sciences (OCRI-CAAS), Wuhan, China	dossakomivi@gmail.com
203	P16#FD1111#MER702347	Dowla	Mirza Nazim Ud	Murdoch University, Perth, Australia	m.dowla@murdoch.edu.au
204	P16#ICR000#TAR000009	Drabo	Inoussa	West Africa Centre for Crop Improvement (WACCI), University of Ghana, Accra, Ghana	idrabo@wacci.edu.gh
205	P16#ICR000#INS000005	Draye	Xavier	"Universite catholique de Louvain, Louvain-la-Neuve , Belgium"	Xavier.Draye@uclouvain.be
206	P16#ICR000#XXR000051	Dubey	Rama Kant	Banaras Hindu University (BHU), Varanasi, India	ramakant.sls@gmail.com
207	P16#ICR000#XXR000106	Dutta	Debabrata	Bose Institute, Kolkata, India	debabratadutta6@gmail.com
208	P16#ICR000#SPS000022	Dutta	Sharad	Premas Life Sciences Pvt Ltd, New Delhi, India	sharad@premaslifesciences.com
209	P16#ICR000#XXR000089	Dwivedi	Priyanka	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	priyankam28@gmail.com
210	P16#ICR000#TL3000011	Echekwu	Candidus A	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	candyechekwu@gmail.com
211	P16#ICR000#SGP000002	Edwards	Dave	The University of Western Australia, Perth, Australia	dave.edwards@uwa.edu.au
212	P16#ICR000#NEF000007	Eeuwijk	Fred Van	Wageningen University & Research, Wageningen, The Netherlands	fred.vaneeuwijk@wur.nl
213	P16#UD1511#MER703347	Ehlers	Jeffrey	Bill & Melinda Gates Foundation (BMGF), Seattle, USA	Jeff.Ehlers@gatesfoundation.org
214	P16#ICR000#XXR000184	Ekwomadu	Theodora	North-West University, Mmabatho, South Africa	23115394@nwu.ac.za
215	P16#ICR000#TL3000019	Endeshaw	Habte	Ethiopian Institute of Agricultural Research (EIAR), Adama, Ethiopia	endhabte@fastmail.fm
216	P16#ICR000#XXR000023	Eskinder	Gidey Sintayehu	Mekelle University, Mekelle, Ethiopia	eskinder14@yahoo.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
217	P16#ICR000#XXR000168	Etim	NseAbasi NsikakAbasi	Akwa Ibom State University, Uyo, Nigeria	etimbobo@yahoo.com
218	P16#ICR000#INS000006	Ewert	Frank A	University of Bonn, Bonn, Germany	frank.ewert@uni-bonn.de
219	P16#ICR000#ICR000037	Falalou	Hamidou	"International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger"	f.hamidou@cgiar.org
220	P16#ICR000#INS000007	Farquhar	Graham	Australian National University (ANU), Canberra, Australia	Graham.Farquhar@anu.edu.au
221	P16#ICR000#TAR000001	Fellahi	Zine El Abidine	Ferhat Abbas University of Sétif, Sétif, Algeria	zinou.agro@gmail.com
222	P16#MD0711#AR1567470	Feng	Fangjun	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	ffj@sagc.org.cn
223	P16#TD0612#AR1580783	Feng	Hao	Northwest A&F University, Yangling, China	
224	P16#ICR000#TL3000022	Fenta	Berhanu Amsalu	Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia	berhanufenta@gmail.com
225	P16#ICR000#XAR000042	Ferdous	Md Zannatul	Asian Institute of Technology, PathumThani, Thailand	manikbau80@gmail.com
226	P16#ICR000#INS000018	Fereres	Elias	Institute for Sustainable Agriculture-CSIC and University of Cordoba, Cordoba, Spain	ag1fecae@uco.es
227	P16#ICR000#XAR000022	Fghire	Rachid	Cadi Ayyad University, Marrakech, Morocco	r.fghire@gmail.com
228	P16#ICR000#TL3000063	Fikre	Asnake	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Addis Ababa, Ethiopia	Fikreasnake@yahoo.com
229	P17#ID1501#MER716457	Fischer	Tony	CSIRO Agriculture and Food, Canberra, Australia	tony.fischer@csiro.au
230	P16#ICR000#INS000008	Fleury	Delphine	Australian Centre for Plant Functional Genomics (ACPFG), Adelaide, Australia	delphine.fleury@adelaide.edu.au
231	P16#TD2510#MER699615	Flohr	Bonnie	Commonwealth Scientific and Industrial Research Organisation (CSIRO), Canberra, Australia	bonnie.flohr@csiro.au
232	P16#ICR000#WAO000003	Fountain	Jake	"University of Georgia, Tifton, USA"	jfount1@uga.edu
233	P16#ICR000#TAR000029	Fradi	Fajr	National Agricultural Research Institute of Tunisia (INRAT), Tunis, Tunisia	fradifajr@gmail.com
234	P16#ICR000#INS000009	Frederic	Baret	INRA-EMMAH / UMT-CAPTE, Avignon, France	baret@avignon.inra.fr
235	P16#ICR000#SPT000002	Friday	Igwe	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
236	P16#UD1511#MER703259	Fritschi	Felix	University of Missouri, Columbia, USA	fritschif@missouri.edu
237	P16#ED0912#MER709126	Gadri	Yaron	Hebrew University of Jerusalem, Rehovot, Israel	ygadri@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
238	P16#ICR000#XAR000014	Gahlaut	Vijay	Chaudhary Charan Singh University, Meerut, India	zone4vijay@gmail.com
239	P16#ICR000#NEF000061	Gaikwad	Priyanka	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	priyankagaikwad00@gmail.com
240	P16#ICR000#ICR000057	Ganga Rao	NVPR	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	n.gangarao@cgiar.org
241	P16#ICR000#SPS000026	Gangashetti	Mahantesh	DuPont Pioneer, Bangalore Research Center, Bangalore, India	Mahantesh.G@Pioneer.com
242	P16#ICR000#ICR000055	Gangashetty	Prakash	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger	P.Gangashetty@cgiar.org
243	P16#ICR000#ICR000075	Gangurde	Sunil	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	sgangurde40@gmail.com
244	P16#ICR000#ICR000007	Garg	Vanika	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	G.Vanika@cgiar.org
245	P16#ICR000#XXR000075	Garladinne	Mallikarjuna	Agri Biotech Foundation, Hyderabad, India	garladinnemarjun@gmail.com
246	P16#ICR000#ICR000061	Gaur	Pooran	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.gaur@cgiar.org
247	P16#ICR000#XXR000113	Gautam	Tinku	Chaudhary Charan Singh University, Meerut, India	tinkugoutam@gmail.com
248	P16#ICR000#XXR000098	Gayatonde	Varsha Vinayak	Banaras Hindu University (BHU), Varanasi, India	varshapanchu@gmail.com
249	P16#UD2211#MER705171	Gazal	Asima	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Kashmir, India	asimagazal@gmail.com
250	P16#ICR000#TL3000056	Gekanana	Risper	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	G.risper@cgiar.org
251	P16#ICR000#XXR000092	George	Suja	M S Swaminathan Research Foundation (MSSRF), Chennai, India	sujageorge@mssrf.res.in
252	P17#ND3001#MER719022	Ghezzehei	Teamrat	University of California Merced, Merced, USA	taghezzehei@ucmerced.edu
253	P16#ND0512#MER708342	Gho	Carla	Dupont Pioneer, Santiago, Chile	carla.gho@pioneer.com
254	P16#ICR000#ICR000082	Gierend	Albert Johannes	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	a.gierend@cgiar.org
255	P16#ICR000#XHT000002	Gill	Kulvinder	Washington State University, Pullman, USA	ksgill@wsu.edu
256	P16#ICR000#SPS000014	Gillhaußen	Philipp Von	Phenospex, Heerlen, The Netherlands	p.vongillhaussen@phenospex.com
257	P16#ICR000#TL3000023	Girma	Nigusie	Ethiopian Institute of Agricultural Research (EIAR), Debrezeit, Ethiopia	girmanigusie@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
258	P16#ICR000#TL3000021	Girsil	Tigist Shiferaw	Ethiopian Institute of Agricultural Research (EIAR), Adama, Ethiopia	tshiferaw2006@gmail.com
259	P16#ICR000#SPS000020	Glazov	Evgeny	South Asia Pacific, Illumina, Brisbane, Australia	eglazov@illumina.com
260	P16#UD2911#MER706844	Gobu	R	Banaras Hindu University (BHU), Varanasi, India	gobu.agri@gmail.com
261	P16#ICR000#TL3000064	Good	Lauren	Bill & Melinda Gates Foundation (BMGF), Seattle, USA	Lauren.good@gatesfoundation.org
262	P16#ICR000#XXR000043	Gopala Krishnan	S	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	gopal_icar@yahoo.co.in
263	P16#ICR000#XXR000005	Gorim	Linda	University of Saskatchewan, Saskatoon, Canada	linda.gorim@usask.ca
264	P17#HD1201#MER716030	Govindan	Velu	International Maize and Wheat Improvement Center (CIMMYT), New Delhi, India	velu@cgiar.org
265	P16#ICR000#XXR000099	Govindaraj	Venkatesh Prasath	Annamalai University, Chidambaram, India	gvprasath91@gmail.com
266	P16#ICR000#ICR000077	Govindaraj	M	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	m.govindaraj@cgiar.org
267	P16#ICR000#NEF000001	Govindasamy	V	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	" govindasamy@iari.res.in"
268	P16#ICR000#NEF000073	Gowda	Manje	International Maize and Wheat Improvement Center (CIMMYT), Nairobi, Kenya	M.Gowda@cgiar.org
269	P17#XD1101#MER715828	Grieu	Philippe	Université de Toulouse/INP-ENSAT, Castanet Tolosan, France	grieu@ensat.fr
270	P16#ICR000#XGE000001	Grover	Anil	University of Delhi-South Campus, New Delhi, India	anil.anilgrover@gmail.com
271	P16#HD1108#MER687639	Guo	Baozhu	USDA-Agricultural Research Service, Tifton, USA	baozhu.guo@ars.usda.gov
272	P16#ICR000#XSI000001	Guo	Peiguo	Guangzhou University, Guangzhou, China	guopg@gzhu.edu.cn
273	P16#ICR000#NOC000002	Gupta	HS	Borlaug Institute of South Asia (BISA), New Delhi, India	hsgupta@lycos.com
274	P16#ICR000#XHT000001	Gupta	PK	Chaudhary Charan Singh University, Meerut, India	pkgupta36@gmail.com
275	P16#ICR000#ICR000050	Gupta	Rajeev	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	g.rajeev@cgiar.org
276	P16#ICR000#XXR000042	Gupta	Saurabh	Indian Institute of Information Technology (IIIT), Allahabad, India	rs159@iiita.ac.in
277	P16#ICR000#ICR000045	Gupta	SK	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	s.gupta@cgiar.org
278	P16#ICR000#SPS000002	Gupta	Praveen	Premas Life Sciences, New Delhi, India	praveen@premaslifesciences.com
279	P16#ICR000#XXR000142	Gurikar	Chennappa	University of Mysore, Mysore, India	chinnagurikar@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
280	P16#ICR000#ICR000088	H Rao	Bindumadhava	AVRDC - The World Vegetable Center South Asia, Hyderabad, India	bindu.madhava@worldveg.org
281	P16#UD1511#MER703324	Habben	Jeff	Dupont Pioneer, Iowa, USA	sally.thompson@pioneer.com
282	P16#ICR000#XXR000148	Haddadi	Shaghayegh H	University of Tehran, Tehran, Iran	sh_haddadi@ut.ac.ir
283	P16#ICR000#XXR000146	Hake	Anil Arjun	University of Agricultural Sciences (UAS), Dharwad, India	anilhake30@gmail.com
284	P16#ICR000#IOC000002	Hammer	Graeme	The University of Queensland, Brisbane, Australia	g.hammer@uq.edu.au
285	P16#ICR000#XXR000132	Hanumanthu	Nagaraja	University of Mysore, Mysore, India	nagarajh82@gmail.com
286	P16#SD0511#MER701216	Hasanuzzaman	Md	University of Tasmania, Tasmania, Australia	md.hasanuzzaman@utas.edu.au
287	P16#ICR000#XAR000029	Hassan	Lateefat Bolanle	Ahmadu Bello University (ABU), Zaria, Nigeria	lbhassan@abu.edu.ng
288	P16#ICR000#XXR000037	Hegde	Shridhar	Pioneer Hi-Bred Private Limited, Chikkaballapur, India	shridhar.hegde@pioneer.com
289	P16#ICR000#TL3000006	Hella	Joseph P	Sokoine University of Agriculture, Morogoro, Tanzania	jp_hella@yahoo.co.uk
290	P16#ICR000#NEF000003	Henry	Amelia	International Rice Research Institute (IRRI), Los Banos, The Philippines	a.henry@irri.org
291	P16#ICR000#ICR000033	Hingane	Anupama	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	H.Anupama@cgiar.org
292	P16#ND2111#MER704839	Holbrook	C Corley	USDA-Agricultural Research Service, Tifton, USA	corley.holbrook@ars.usda.gov
293	P16#WD3011#MER706982	Holla	Sumantha	University of Agricultural Sciences (UAS), Bangalore, India	sumanthaholla@gmail.com
294	P17#ND0901#MER715461	Holz	Maire	University of Goettingen, Goettingen, Germany	maire.holz@forst.uni-goettingen.de
295	P16#ICR000#WAO000012	Hossain	Md. Amir	Bangladesh Agricultural University (BAU), Mymensingh, Bangladesh	amir04@gmail.com
296	P16#ICR000#XXR000152	Hotti	Avinalappa	University of Milan, Lodi, Italy	avihotti@gmail.com
297	P16#ICR000#SPS000023	Hummel	Gregoire	Phenospex, Heerlen, The Netherlands	g.hummel@phensopex.com
298	P16#ICR000#XXR000178	Hussain	Muhammad Mubashar	University of Sargodha, Sargodha, Pakistan	mubashar_uca@yahoo.com
299	P16#ICR000#XAR000023	Ibitoye	Dorcus Olubunmi	National Horticultural Research Institute (NIHORT), Ibadan, Nigeria	bunmiajisafe@yahoo.com
300	P16#ICR000#XAR000008	Ige	Adenike Damilola	"Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana"	niccollo4real@yahoo.com
301	P16#ICR000#TAR000012	Indriatama	Wijaya Murti	Center for Isotope and Radiation Application, Jakarta, Indonesia	wijaya@batan.go.id

S No	Registration ID	Family Name	Name	Affiliation	E-mail
302	P16#ICR000#XXR000033	Issa Zakari	Mahaman Mourtala	"Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana"	issazakarym@yahoo.fr
303	P16#ICR000#TAR000016	Issaharou Matchi	Issiaka	University of Diffa, Diffa, Niger	issakissaharou@gmail.com
304	P16#ICR000#XXR000159	Iwuala	Emmanuel Nkmakolam	University of Lagos, Lagos, Nigeria	iwuala097@gmail.com
305	P16#ICR000#XXR000199	Jabborova	Dilfuza	Institute of Genetics and Plant Experimental Biology, Тошкент, Uzbekistan	dilfuzajabborova@yahoo.com
306	P16#ICR000#SPT000006	Jacob	Anthony Unoke	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
307	P16#ICR000#ICR000024	Jain	Ankit	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	A.Jain@cgiar.org
308	P16#ICR000#ICR000086	Jain	Abhinav	International Rice Research Institute (IRRI), Hyderabad, India	a.jain@irri.org
309	P16#ICR000#WAO000014	Jaiswal	Vandana	CSIR-National Botanical Research Institute (NBRI), Lucknow, India	vandana.jaiswal2009@gmail.com
310	P16#ICR000#XXR000086	Jangra	Sumit	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	sumit.jangra712@gmail.com
311	P16#MD1912#MER710828	Jat	Ram	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	rajatagron@gmail.com
312	P16#WD3011#MER707154	Jatan	Ram	CSIR-National Botanical Research Institute (NBRI), Lucknow, India	ramjatanraj@gmail.com
313	P16#ICR000#XXR000151	Javid	Majid Ghorbani	University of Tehran, Tehran, Iran	mjavid@ut.ac.ir
314	P16#ICR000#WAO000015	Jha	Uday Chand	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	u9811981@gmail.com
315	P16#FD2810#MER700192	Jhang	Tripta	CSIR-Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow, India	t.jhang@cimap.res.in
316	P16#GD1310#MER697154	Jiang	Dong	Nanjing Agricultural University, Nanjing, China	jiangd@njau.edu.cn
317	P16#ICR000#TL3000025	Jinbaani	Alhassan Nuhu	CSIR-Savanna Agricultural Research Institute, Tamale, Ghana	jinbaani@yahoo.com
318	P16#ICR000#MBC000007	Jing	Ruilian	Chinese Academy of Agricultural Sciences (CAAS), Beijing, China	jingruilian@caas.cn
319	P16#ICR000#NEF000053	Jiru	Sheleme Beyene	Hawassa University, Awassa, Ethiopia	shelemeb@gmail.com
320	P16#ICR000#INS000011	Jobbagy	Esteban	Universidad Nacional de San Luis, San Luis, Argentina	jobbagy@gmail.com
321	P16#ND1411#MER702895	Jogloy	Sanun	Khon Kaen University, Khon Kaen, Thailand	sjogloy@gmail.com
322	P16#ICR000#NEF000009	Johnston	Amal	Heidelberg University, Heidelberg, Germany	amal.johnston@cos.uni-heidelberg.de
323	P16#ICR000#XHT000004	Joshi	AK	Borlaug Institute of South Asia (BISA), New Delhi, India	a.k.joshi@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
324	P16#ICR000#XXR000078	Jukanti	Aravind Kumar	ICAR-Central Arid Zone Research Institute (CAZRI), Jodhpur, India	aravindjukanti@gmail.com
325	P16#ICR000#TAR000022	Ka	Sambalaha	Senegalese Institute of Agricultural Research, Kolda, Senegal	kasam74@gmail.com
326	P16#TD2911#MER706501	Kadam	Sandeep	College of Horticulture, Bagalkot, India	sandeepkadam15@gmail.com
327	P16#WD1412#MER709938	Kailappan	Amudha	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	amudha_pbg@yahoo.com
328	P16#MD2111#MER704699	Kakkera	Aparna	Jawaharlal Nehru Technological University (JNTU), Hyderabad, India	aparna_jgd@rediffmail.com
329	P16#ICR000#ICR000030	Kale	Sandip	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	S.Kale@cgiar.org
330	P16#ICR000#ICR000039	Kaliamoorthy	Sivasakthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	sakthibiotechbdu@gmail.com
331	P16#ICR000#NEF000017	Kalpande	Hirakant V	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	hvkalpande@rediffmail.com
332	P16#WD1412#MER709922	Kamalnath Reddy	KR	ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, India	kamalnath.reddy@gmail.com
333	P16#ICR000#NEF000024	Kambalimath	Sumanth Kumar	Ankur Seeds, Nagpur, India	sumanthkumark@ankurseeds.com
334	P16#ICR000#XSI000003	Kamma	Krishnappa	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	K.KAMMA@cgiar.org
335	P16#XD3011#MER707333	Kamoshita	Akihiko	University of Tokyo, Tokyo, Japan	akamoshita@anesc.u-tokyo.ac.jp
336	P16#WD1412#MER709994	Kandula	Naga Madhuri	Regional Agricultural Research Station (RARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Tirupati, India	nagamadhurikv@gmail.com
337	P16#ICR000#XXR000195	Kang	Yun	The Samuel Roberts Noble Foundation, Ardmore, USA	ykang@noble.org
338	P16#ND2811#MER706364	Kanubothula	Sitaramireddy	University of Hyderabad, Hyderabad, India	krsitaram1@gmail.com
339	P16#ICR000#TAR000026	Kaoneka	Seleman	Agricultural Research Institute-Ilonga, Morogoro, Tanzania	s_kaoneka@yahoo.com
340	P16#ICR000#TL3000017	Karidiataou	"Gnankambary Traore "	Institut de l'Environnement et des Recherches Agricoles (INERA), Ouagadougou, Burkina Faso	inera.direction@fasonet.bf
341	P16#ICR000#NEF000075	Karthika	G	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	karthi.tnau07@gmail.com
342	P16#ND2811#MER706425	Kaur	Navneet	IIT Roorkee, Roorkee, India	navneetkaursekhon88@gmail.com
343	P16#ICR000#NEF000078	Kaur	Jagmeet	Punjab Agricultural University (PAU), Ludhiana, India	jagskaur@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
344	P16#ICR000#XSI000013	Kavi Kishor	PB	Osmania University, Hyderabad, India	pbkavi@yahoo.com
345	P16#SD1911#MER704129	Kavya	HP	University of Agricultural Sciences (UAS), Bangalore, India	kavya.horantur@gmail.com
346	P16#ICR000#TL3000047	Kesiime	Eunice	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	eunicekesiime@gmail.com
347	P16#ICR000#ICR000017	Khan	Aamir	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	A.Khan@cgiar.org
348	P16#ICR000#TAR000019	Khan	Nadia	University of Karachi, Karachi, Pakistan	nadiakhan@uok.edu.pk
349	P16#ICR000#XXR000077	Khan	Mohd Shahanbaj	B.S.Abdur Rahman University, Chennai, India	shahnawazkhandrr@gmail.com
350	P16#TD1511#MER703113	Khan	Jameel	University of Agricultural Sciences (UAS), Bangalore, India	jameelbiotec@gmail.com
351	P16#ICR000#XSI000059	Khan	MJ	Agriculture Today, New Delhi, India	mjkhan.agriculture@gmail.com
352	P16#ICR000#NEF000048	Khera	Pawan	Mahindra Agri Solutions Ltd, Hyderabad, India	khera.pawan@mahindra.com
353	P16#ICR000#INS000012	Kholova	Jana	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	J.Kholova@cgiar.org
354	P16#ICR000#XAR000020	Kiboi	Milka	Embu University College, Embu, Kenya	milka.kiboi@gmail.com
355	P16#ICR000#TL3000038	Kilango	Michael	Agricultural Research Institute-Uyole (ARI-U), Mbeya, Tanzania	michaelkilango@yahoo.com
356	P16#ICR000#SPS000011	Kim	Bellbull	TheragenEtex Bio Institute, Yeongtong-gu, Korea	bellbull@theragenetex.com
357	P16#ICR000#TAR000027	Kimaro	Didas	University of KwaZulu-Natal (UKZN) and Agro-Scientific Research Centre-Chollima, Morogoro, Tanzania	didaskelei@yahoo.com
358	P16#ICR000#XSI000020	Kimothi	Shiv Prasad	Indian Council of Agricultural Research (ICAR), New Delhi, India	adgcoordination@ gmail.com
359	P16#ICR000#XSI000010	Kimurto	Paul K	Egerton University, Egerton, Kenya	kimurtopk@gmail.com
360	P16#ICR000#TL3000055	Kioko	Amos	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	a.kioko@cgiar.org
361	P16#ICR000#NEF000010	Kirioukhova	Olga	Heidelberg University, Heidelberg, Germany	olga.kirioukhova@cos.uni-heidelberg.de
362	P16#ICR000#NEF000052	Kishore	Sandhya	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	kishoregene@gmail.com
363	P16#ND2410#MER699580	Koehl	Karin	Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany	koehl@mpimp-golm.mpg.de

S No	Registration ID	Family Name	Name	Affiliation	E-mail
364	P16#TD2211#MER704846	Kohli	Ajay	International Rice Research Institute (IRRI), Los Banos, The Philippines	a.kohli@irri.org
365	P16#SD3112#MER713339	Kokkanti	Rekha	Sri Padmavati Mahila Visvavidyalayam, Tirupati, India	kokknatirekha@gmail.com
366	P16#ICR000#TAR000008	Kolawole	Adesike Oladoyin	West Africa Centre for Crop Improvement (WACCI), University of Ghana, Accra, Ghana	adesike@yahoo.com
367	P16#ICR000#TAR000013	Kosgei	Alice	Machakos University College, Machakos, Kenya	songj.aliz@gmail.com
368	P16#ICR000#XSI000011	Kothari	SL	Amity University of Biotechnology, Jaipur, India	slkothari28@gmail.com
369	P16#GD1512#MER710254	Kotyal	Kavita	University of Agricultural Sciences (UAS), Bangalore, India	kavitakotyal@gmail.com
370	P16#ICR000#TL3000032	Kouyate	Zoumana	Institut d'Economie Rurale (IER), Segou, Mali	zkouyate@yahoo.fr
371	P16#ICR000#XXR000083	Kovi	Basavaraj	University of Agricultural Sciences (UAS), Raichur, India	basurajk7@gmail.com
372	P16#ICR000#NEF000049	Krishna	V Sudershan	Mahindra Agri Solutions Ltd, Hyderabad, India	KRISHNA.VALLABHANENI@mahindra.com
373	P16#ICR000#ICR000056	Krishnamurthy	L	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	LKM1949@gmail.com
374	P16#ICR000#ICR000014	Kudapa	Himabindu	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	k.himabindu@cgiar.org
375	P16#ICR000#NEF000070	Kulkarni	VN	JK Seeds, Hyderabad, India	vnkulkarni@jkseeds.net
376	P16#ICR000#TAR000011	Kulwal	Pawan	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India	pawankulwal@gmail.com
377	P16#ICR000#MBC000003	Kumar	Arvind	International Rice Research Institute (IRRI), Los Banos, The Philippines	a.kumar@irri.org
378	P16#ICR000#TAR000010	Kumar	Ashish	Jawaharlal Nehru Agricultural University (JNKVV), Rewa, India	ashishashish2612@gmail.com
379	P16#ICR000#XXR000072	Kumar	Deepak	Central University of Jammu, Jammu, India	deepakinjnu@gmail.com
380	P16#ICR000#XXR000080	Kumar	MV Nagesh	Regional Agricultural Research Station (RARS), Professor Jayashankar Telangana State Agricultural University (PJTSAU), Palem, India	psoilseeds@gmail.com
381	P16#XD2809#MER695065	Kumar	Rahul	DAV university, Jalandhar, India	rahulihbt@gmail.com
382	P16#UD1511#MER703267	Kumar	Sudhir	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	sudhirnpf@gmail.com
383	P16#MD2811#MER706253	Kumar	GD Satish	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	gd.satishkumar@icar.gov.in
384	P16#UD2911#MER706798	Kumar	Sumit	University of Hyderabad, Hyderabad, India	sumit.gre@gmail.com
385	P16#ICR000#SPS000013	Kumar	Anand	DSS Takara, Hyderabad, India	anand_kumar@dsstakarabio.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
386	P16#SD1712#MER710569	Kumar	Narendra	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	narendrapb09@gmail.com
387	P16#UD2712#MER712333	Kumar	Reetesh	Panjab University, Chandigarh, India	SRIV.REETESH@GMAIL.COM
388	P16#ICR000#WAO000013	Kumar	Sourabh	Chaudhary Charan Singh University, Meerut, India	sourabhkumar7669@gmail.com
389	P16#ICR000#NEF000039	Kumria	Ratna	Dupont Pioneer, Hyderabad, India	kumria.ratna@pioneer.com
390	P16#ICR000#NEF000044	Kundapura	V Ravishankar	ICAR-Indian Institute of Horticultural Research (IIHR), Bangalore, India	kv_ravishankar@yahoo.co.in
391	P16#WD0911#MER702023	Kwon	TR	National Institute of Agricultural Sciences, Jeonju, Korea	trkwon@korea.kr
392	P16#XD1611#MER703573	Lake	Lachlan	University of Adelaide, Adelaide, Australia	lachlan.lake@sa.gov.au
393	P16#MD2111#MER704672	Lakshmanan	Prakash	Sugar Research Australia (SRA), Brisbane, Australia	plakshmanan@sugarresearch.com.au
394	P16#ICR000#NEF000080	Lambrides	Christopher	The University of Queensland, Brisbane, Australia	chris.lambrides@uq.edu.au
395	P16#ICR000#WAO000002	Lestari	Puji	Indonesian Center for Agricultural Biotechnology and Genetic Reseources Research and Development-Indonesian Agency for Agricultural Research and Development(ICABIOGRAD-IAARD), Bogor, Indonesia	lestari_71@yahoo.com
396	P16#ICR000#MBC000004	Li	Zhikang	Chinese Academy of Agricultural Sciences (CAAS), Beijing, China	lizhikang@caas.cn
397	P16#ICR000#SPS000009	Li	Chuanying	BGI Research, Beijing, China	lichuanying@genomics.cn
398	P16#ND1411#MER702969	Linden	Gerard	Wageningen University & Research, Wageningen, The Netherlands	gerard.vanderlinden@wur.nl
399	P16#ICR000#SPS000007	Liu	Xin	BGI Research, Beijing, China	liuxin@genomics.cn
400	P16#TD1511#MER703021	Lokhande	Prakash	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri, India	pklokhande@gmail.com
401	P16#MD0711#AR1567506	Lou	Qiaojun	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	lqj@sagc.org.cn
402	P16#ICR000#SPS000008	Lu	Shankang	BGI Research, Beijing, China	lushankang@genomics.cn
403	P16#ICR000#INS000013	Luo	Lijun	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	lijun@sagc.org.cn
404	P16#ICR000#XXR000013	Lutonadio	Genie Spirou	University of Kinshasa, Kinshasa, Democratic Republic of the Congo	geniespiroulutonadio01@gmail.com
405	P16#ICR000#TAR000014	Macharia	Joseph Maina	Kenyatta University, Nairobi, Kenya	machariamjoseph@gmail.com
406	P16#ICR000#XXR000021	Madebo	Miilion Paulos	Dilla University, Dilla, Ethiopia	millionpa12@gmail.com
407	P16#MD1212#MER709477	Madireddi	Sai Kiran	University of Hyderabad, Hyderabad, India	saimadireddi@gmail.com
408	P16#ICR000#ICR000051	Madugula	Praveen	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	pravi313@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
409	P16#ICR000#XXR000194	Magangi	Wilfred Abincha	Makerere University, Kampala, Uganda	wilabin@yahoo.com
410	P16#ICR000#NEF000026	Mahale	Barku	Ankur Seeds, Nagpur, India	
411	P16#GD2912#MER712705	Mahatma	Mahesh	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	maheshmahatma@gmail.com
412	P16#ICR000#XAR000024	Mala	Kachalla Kyari	Lake Chad Research Institute, Maiduguri, Nigeria	kkmala506@yahoo.com
413	P16#ICR000#XXR000056	Malamasuri	Kadasiddappa	University of Agricultural Sciences (UAS), Dharwad, India	kadasiddappa.m@gmail.com
414	P16#ICR000#XAR000017	Mallana Gowdra	Mallikarjuna	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	mg.mallikarjuna@icar.gov.in
415	P16#ICR000#ICR000015	Mallikarjuna	BP	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	B.Mallikarjuna@cgiar.org
416	P16#ICR000#WAO000006	Mamidala	Praveen	Telangana University, Nizamabad, India	pmamidala@gmail.com
417	P16#SD3112#MER713315	Manasa	R	University of Agricultural Sciences (UAS), Bangalore, India	manasaraju23@gmail.com
418	P16#ICR000#ICR000048	Manasa	KG	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	g.manasa@cgiar.org
419	P16#ICR000#ICR000010	Manchikatla	Praveen Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	praveen1211987@gmail.com
420	P16#UD2211#MER705141	Mangrauthia	Satendra	ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, India	skmdrr@gmail.com
421	P16#ICR000#NEF000031	Mani	Elangovan	UniPhosphorous Ltd, Hyderabad, India	Elangovan.M@advantaseeds.com
422	P16#ICR000#XXR000102	Mani	BR	University of Agricultural Sciences (UAS), Dharwad, India	mbreddys8102014@gmail.com
423	P16#ICR000#NEF000059	Manimekalai	R	Sugarcane Breeding Institute, Coimbatore, India	rmanimekalaiicar@gmail.com
424	P16#ICR000#XSI000037	Manohar Rao	D	Osmania University, Hyderabad, India	dmanoharrao@yahoo.com
425	P16#ICR000#XAR000015	Manonmani	V	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	vmano_2004@yahoo.com
426	P16#TD2911#MER706609	Manuka	Rakesh	BITS PILANI K K Birla Goa campus, Goa, India	rakesh_manuka@yahoo.com
427	P16#ICR000#ICR000083	Manyasa	Eric	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	e.manyasa@cgiar.org
428	P16#TD2911#MER706621	Marriboina	Sureshbabu	University of Hyderabad, Hyderabad, India	msuresh.biochem@gmail.com
429	P16#ICR000#TAR000034	Masuka	Benhidah Pamhidzai	University of Zimbabwe, Marondera, Zimbabwe	trimasuka@gmail.com
430	P16#ICR000#WAO000005	Mathews	Cherian	Tshwane University of Technology (TUT), Pretoria, South Africa	cherianm47@gmail.com
431	P16#ICR000#XAR000041	Matina	Grace	Agricultural Research Institute-Ilonga, Morogoro, Tanzania	gmgramadee37@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
432	P16#ICR000#TL3000053	Mazaengo	Karantin D	Ministry of Agriculture Training Institute - Uyole, Mbeya, Tanzania	mkarantin@yahoo.co.uk
433	P17#XD0401#MER714778	McLean	Gregory Berry	Queensland Alliance for Agriculture and Food Innovation (QAAFI) & The University of Queensland, Brisbane, Australia	greg.mclean@daf.qld.gov.au
434	P16#ICR000#NEF000072	Mehtre	Shivaji P	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	shivaji_pmehtre@rediffmail.com
435	P16#MD0711#AR1567499	Mei	Hanwei	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	hmei@sagc.org.cn
436	P16#ICR000#SPT000003	Mercy	Osagie Itohan	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
437	P16#TD1312#MER709832	Meshram	Jayant	ICAR-Central Institute for Cotton Research, Nagpur, India	j.h.meshram@gmail.com
438	P16#JD2512#MER711986	Messina	Carlos	DuPont Pioneer, Johnston, Iowa, USA	charlie.messina@pioneer.com
439	P16#ICR000#XSI000080	Mies	David	Global Plant Breeding Consultant, Mahomet, USA	dwmies@gmail.com
440	P17#TD0301#MER714354	Millet	Emilie	French National Institute for Agricultural Research (INRA), Montpellier, France	emilie.millet@inra.fr
441	P16#ICR000#TL3000001	Miningou	Amos	Institut de l'Environnement et des Recherches Agricoles (INERA), Ouagadougou, Burkina Faso	miningou_amos@yahoo.fr
442	P16#ICR000#TL3000044	Minja	Athanas	Naliendele Agricultural Research Institute (NARI), Mtwara, Tanzania	athasta@yahoo.com
443	P16#ICR000#ICR000064	Minnuru	Nagamallika Devi	International Rice Research Institute (IRRI), Patancheru, India	m.nagamallikadevi@irri.org
444	P16#ICR000#HSI000009	Mishra	PK	Govt. of India, New Delhi, India	
445	P16#ICR000#ICR000057	Mishra	Nilesh	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	m.nilesh@cgiar.org
446	P16#MD2811#MER706260	Mittal	Shikha	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	shikhamittal259@gmail.com
447	P16#ICR000#HSI000010	Moephuli	Shadrack	Agricultural Research Council, Pretoria, South Africa	MoephuliS@arc.agric.za
448	P16#ICR000#XAR000036	Mofokeng	Maletsema Alina	ARC-Grain Crops Institute, Potchefstroom, South Africa	MofokengA@arc.agric.za
449	P16#ICR000#TL3000036	Mohammad	Sanusi Gaya	Centre for Dryland Agriculture-Bayero University Kano, Kano, Nigeria	sgmohammed@yahoo.com
450	P16#ICR000#TL3000009	Mohammed	Haruna	Savanna Agricultural Research Institute (SARI)/Tshwane University of Technology (TUT), Tamale, Ghana	Haruna_mohammed67@yahoo.com
451	P16#ICR000#XXR000116	Mohan	Nidhi	Banaras Hindu University (BHU), Varanasi, India	nidhimohan91@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
452	P16#ICR000#XSI000042	Mohan Rao	Ch	Telangana Academy of Sciences (TAS) & CSIR-Centre for Cellular & Molecular Biology (CCMB), Hyderabad, India	mohan@ccmb.res.in
453	P16#ICR000#NEF000023	Mohanraj	K	ICAR-Sugarcane Breeding Institute, Coimbatore, India	mohangene@yahoo.com
454	P16#ICR000#XCP000001	Mohapatra	Trilochan	ICAR & Secretary DARE, New Delhi, India	dg.icar@nic.in
455	P17#XD0102#AR1602035	Mohr	Knut	LGC Genomics, Alexandria, USA	Knut.Mohr@lgcgenomics.com
456	P16#ICR000#TL3000051	Monyo	Emmanuel	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	e.monyo@cgiar.org
457	P16#GD1512#MER710247	More	Ambika	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Parbhani, India	ambikamore@rediffmail.com
458	P16#ICR000#TL3000050	Motagi	Babu	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria	B.N.Motagi@cgiar.org
459	P16#ICR000#TAR000017	Moukoumbi	Yonnelle Dea	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	Y.Moukoumbi@cgiar.org
460	P16#ICR000#TL3000013	Mponda	Omari	Naliendele Agricultural Research Institute (NARI), Mtwara, Tanzania	kalanjekanduru@gmail.com
461	P16#ICR000#SPS000019	Mrkusich	Eli	South Asia Pacific, Illumina, Melbourne, Australia	emrkusich@illumina.com
462	P16#ICR000#XAR000045	Mubuka	Amina Subira	Makerere University, Kampala, Uganda	asmubuka@gmail.com
463	P16#WD3011#MER707106	Mudalkar	Shalini	University of Hyderabad, Hyderabad, India	mudalkar.shalini@gmail.com
464	P16#XD2311#MER705307	Muddarsu	Venkata Ramana	Sikkim University, Gangtok, India	venkat.muddarsu@gmail.com
465	P16#WD3011#MER707140	Mudigonda	Pooja	University of Agricultural Sciences (UAS), Bangalore, India	pooj.smiley@gmail.com
466	P16#ICR000#TL3000007	Mugisha	Johnny	Makerere University, Kampala, Uganda	jomugisha@agric.mak.ac.ug
467	P16#ICR000#MBL000007	Mukankusi	Clare	International Center for Tropical Agriculture (CIAT), Kampala, Uganda	c.mukankusi@cgiar.org
468	P16#WD2109#MER694168	Muktadir	MD Abdul	University of Sydney, Narrabri, Australia	md.muktadir@sydney.edu.au
469	P16#HD1512#MER710275	Muktha	J	University of Agricultural Sciences (UAS), Bangalore, India	muktha.j@gmail.com
470	P16#ICR000#XAR000048	Muniswamy	S	Agricultural Research Station (ARS), Gulbarga, India	muniswamygpb@gmail.com
471	P16#ICR000#ICR000038	Murugesan	Tharanya	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	m.tharanya@gmail.com
472	P16#ICR000#XXR000100	Murugesan	Ashok Kumar	M S Swaminathan Research Foundation (MSSRF), Chennai, India	ashokkumar.mb@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
473	P16#ICR000#XHT000008	Muthurajan	Raveendran	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	raveendrantnau@gmail.com
474	P16#ICR000#XXR000049	Muthuramu	S	Tamil Nadu Agricultural University (TNAU), Paramakudi, India	smuthuramu@gmail.com
475	P16#ICR000#TL3000043	Mwakimata	Romanus	Sokoine University of Agriculture, Morogoro, Tanzania	mwakimata@gmail.com
476	P16#ICR000#XAR000038	Mwenda	Emmanuel Thomas	Agricultural Research Institute-Ilonga, Morogoro, Tanzania	emmamwenda@yahoo.com
477	P16#ICR000#XXR000202	Nabateregga	Mabel	Makerere University, Kampala, Uganda	mnabateregga@gmail.com
478	P16#ICR000#ICR000062	Nachimuthu	Vishnu Varthini	International Rice Research Institute (IRRI), Patancheru, India	v.varthini@irri.org
479	P16#ICR000#NEF000038	Naga	Supreetha	University of Agricultural Sciences (UAS), Bangalore, India	supreetasharaff@gmail.com
480	P16#ICR000#ICR000063	Naik	Shilpa Mahadeva	International Rice Research Institute (IRRI), Patancheru, India	s.naik@irri.org
481	P16#ICR000#XXR000063	Nalina	M	Upasi Tea Research Institute, Coimbatore, India	nalinam08@gmail.com
482	P16#ICR000#TAR000032	Namugga	Prossy	University of KwaZulu-Natal (UKZN) and National Agricultural Research Organisation (NARO), Kabale, Uganda	namuggak@gmail.com
483	P16#ICR000#XXR000150	Nasirzadeh	Leila	Seed and Plant Improvement Institute (SPII), Karaj, Iran	l.nasirzadeh@gmail.com
484	P16#ND1411#MER702988	Natarajan	Sijesh	The University of Queensland, Queensland, Australia	s.natarajan@uq.edu.au
485	P16#TD2211#MER704908	Natarajan	Kumari	Maize Reasearch Station TNAU, Palani, India	soundhini@yahoo.co.in
486	P16#ICR000#ICR000012	Nayak	Spurthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	S.Nayak@cgiar.org
487	P16#ICR000#XHT000009	Nayyar	Harsh	Panjab University, Chandigarh, India	harshnayyar@hotmail.com
488	P16#ICR000#TL3000037	Ndunguru	Agnes	Ministry of Agriculture Food Security and Cooperatives Agriculture Reseach Insititute - Uyole, Mbeya, Tanzania	agnessndunguru@yahoo.com
489	P16#ICR000#ICR000098	Nebie	Baloua	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	B.Nebie@cgiar.org
490	P16#UD1511#MER703256	Neog	Prasanta	Assam agricultural University, Jorhat, India	neogprasanta@rediffmail.com
491	P16#ICR000#TL3000040	Nestory	Shida Mahenge	Selian Agricultural Research Institute (SARI), Arusha, Tanzania	nemahenge@yahoo.com
492	P16#ICR000#NEF000021	Neumann	Kerstin	Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany	neumannk@ipk-gatersleben.de
493	P16#ICR000#ICR000023	NG	Eng Hwa	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	n.enghwa@cgiar.org
494	P16#ICR000#MBL000001	Nguyen	Henry	University of Missouri, Columbia, USA	nguyenhenry@missouri.edu

S No	Registration ID	Family Name	Name	Affiliation	E-mail
495	P16#ICR000#NEF000022	Nichols	Shirley	AgResearch, Hamilton, New Zealand	shirley.nichols@agresearch.co.nz
496	P16#ICR000#NEF000025	Nikam	Sachin	Ankur Seeds, Nagpur, India	sachinnikam@ankurseeds.com
497	P16#ICR000#NEF000032	Nisarga	KN	University of Agricultural Sciences (UAS), Bangalore, India	nishukgowda@gmail.com
498	P16#ICR000#ICR000089	Njuguna-Mungai	Esther	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	E.njuguna@cgiar.org
499	P16#ICR000#TL3000003	Nkalubo	Stanley T	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	tamusange@yahoo.com
500	P16#ICR000#SPT000005	Nnaemeka	Okafor Henry	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
501	P16#ICR000#SPT000004	Nnamdi	Ofuonye Jude	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
502	P16#ND2811#MER706428	Noble	Tom	Queensland University of Technology (QUT), Brisbane, Australia	tj.noble@hdr.qut.edu.au
503	P16#ICR000#TL3000060	Nouhoun	Belko	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	N.Belko@cgiar.org
504	P16#ICR000#SPS000003	Nwosu	Victor	Mars Chocolate North America, Hackettstown, USA	victor.nwosu@effem.com
505	P16#ICR000#TL3000042	Nyanana	Flora	Sokoine University of Agriculture, Morogoro, Tanzania	fnyanana2002@yahoo.com
506	P16#ICR000#ICR000054	Nzungize	John	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	j.nzungize@cgiar.org
507	P16#ICR000#TAR000024	Obala	Jimmy	University of KwaZulu-Natal (UKZN), Pietermaritzburg, South Africa	jimmyobala@gmail.com
508	P16#ICR000#XAR000028	Ogunkanmi	Adebayo	University of Lagos, Lagos, Nigeria	logunkanmi@unilag.edu.ng
509	P16#ICR000#TL3000015	Ojiewo	Chris	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Addis Ababa, Ethiopia	C.Ojiewo@cgiar.org
510	P16#ICR000#ICR000040	Ojulong	Henry	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	H.Ojulong@CGIAR.ORG
511	P16#ICR000#TL3000014	Okello	David Kalule	National Semi Arid Resources Research Institute (NaSARRI), Soroti, Uganda	kod143@gmail.com
512	P16#ICR000#ICR000100	Okori	Patrick	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Lilongwe, Malawi	P.Okori@cgiar.org
513	P16#ICR000#XXR000177	Oloyede	Funmilayo Mary	Osun State University (UNIOSUN), Osogbo, Nigeria	funmilayooloyede@yahoo.co.uk
514	P16#ICR000#TL3000012	Olufajo	Olusoji	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	sojiolufajo@yahoo.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
515	P16#ICR000#XXR000193	Omari	Mikidadi Abubakar	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	mikisb2340@yahoo.com
516	P16#ICR000#TL3000061	Omoigui	Lucky	International Institute of Tropical Agriculture (IITA), Kano, Nigeria	Lomoigui@cgiar.org
517	P16#ICR000#TAR000031	Onzima	Benard	Makerere University, Kampala, Uganda	benardonzima@yahoo.com
518	P16#ICR000#TL3000005	Oteng-Frimpong	Richard	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	kotengfrimpong@gmail.com
519	P16#ICR000#ICR000095	Ouedraogo	Ouindyam Colette	University of Ouagadougou/ International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	c.ouedraogo@icrisatml.org
520	P16#ICR000#XXR000035	Owusu	Emmanuel Yaw	Savanna Agricultural Research Institute (SARI), Tamale, Ghana	owusuemmagh@yahoo.com
521	P16#UD1511#MER703291	Ozias-Akins	Peggy	University of Georgia, Tifton, USA	pozias@uga.edu
522	P16#ICR000#XSI000082	Padhee	Arabinda K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), New Delhi, India	a.padhee@cgiar.org
523	P16#UD2911#AR1577731	Padma Latha	Y	Agricultural Research Station (ARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Reddipalli, India	sahadevardd@gmail.com
524	P16#TD1511#MER703155	Pal	Kamal	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	kkpal9426476749@gmail.com
525	P16#ICR000#NEF000079	Pal	Bijendra	Bioseed Research India, Hyderabad, India	bijendra.pal@bioseed.com
526	P16#ICR000#ICR000085	Palakolanu	Sudhakar Reddy	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.sudhakarreddy@cgiar.org
527	P16#ICR000#XXR000073	Palavalasa	Hima Kumari	Osmania University, Hyderabad, India	phimakumari@gmail.com
528	P16#MD0711#MER701486	Palta	Jairo	The University of Western Australia, Perth, Australia	jario.palta@uwa.edu.au
529	P16#JD2711#MER706102	Palve	Adinath	Anand Agricultural University, Anand, India	adinath.palve@gmail.com
530	P16#MD2811#MER706288	Pandagale	Arvind	Vasantrao Naik Marathwada Krishi Vidyapeeth (VNMKV), Nanded, India	arvindpandagale@yahoo.co.in
531	P16#ICR000#ICR000001	Pandey	Manish	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	m.pandey@cgiar.org
532	P16#ICR000#ICR000019	Pandey	Arun Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	P.Arunkumar@cgiar.org
533	P16#ICR000#ICR000087	Parankusam	Santisree	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	S.Parankusam@cgiar.org
534	P16#ICR000#XGE000002	Pareek	Ashwani	Jawaharlal Nehru University (JNU), New Delhi, India	ashwanipareek@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
535	P16#ICR000#INS000014	Parent	Boris	French National Institute for Agricultural Research (INRA), Montpellier, France	boris.parent@supagro.inra.fr
536	P16#ICR000#GWS000004	Parida	Swarup	National Institute of Plant Genome Research (NIPGR), New Delhi, India	swarup@nipgr.ac.in
537	P16#ICR000#XSI000084	Parida	Ajay	Institute of Life Sciences (ILS), Bhubaneswar, India	director@ils.res.in
538	P16#ICR000#HSI000001	Paroda	RS	Indian Council of Agricultural Research (ICAR), New Delhi, India	taasiari@gmail.com
539	P16#ICR000#ICR000005	Parupalli	Swathi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	P.Swathi@cgiar.org
540	P16#SD2611#MER705840	Parvathaneni	Lakshmamma	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	lakshmiparvathaneni@rediffmail.com
541	P16#ICR000#XXR000053	Parveda	Maheshwari	Osmania University, Hyderabad, India	maheshwariraop@gmail.com
542	P16#ICR000#XXR000054	Pasala	Ratna Kumar	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	ratna.pasala@icar.gov.in
543	P16#GD1512#MER710177	Passot	Sixtine	Universite catholique de Louvain, Louvain-la-Neuve, Belgium	sixtine.passot@uclouvain.be
544	P16#ICR000#ICR000035	Pasupuleti	Janila	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.janila@cgiar.org
545	P16#ICR000#ICR000004	Patel	Kishan	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	kishan.btech@gmail.com
546	P16#ICR000#XSI000083	Pathak	Himanshu	ICAR-National Rice Research Institute (NRRI), Cuttack, India	director.nrri@icar.gov.in
547	P16#ICR000#NEF000047	Patil	Virupaxagouda	Mahindra Agri Solutions Ltd, Hyderabad, India	PATIL.VIRUPAXAGOUDA@mahindra.com
548	P16#TD2211#MER705039	Patil	Sucheta	CSIR-National Chemical Laboratory (NCL), Pune, India	suchetap001@gmail.com
549	P16#WD3011#MER707048	Patil	Malagouda	University of Agricultural Sciences (UAS), Dharwad, India	patilmalagouda@gmail.com
550	P16#ICR000#NEF000054	Patil	BC	University of Agricultural Sciences (UAS), Dharwad, India	patilbc10195@uasd.in
551	P16#ICR000#HSI000007	Pattanayak	Shobhana K	Govt. of India, New Delhi, India	secy-agri@nic.in
552	P16#ICR000#SPS000030	Paul	Alan	LGC Genomics, Bangalore, India	
553	P16#ICR000#XSI000039	Pawar	Smita C	Osmania University, Hyderabad, India	smita.prof@gmail.com
554	P16#ICR000#ICR000027	Pazhamala	Lekha	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	L.Pazhamala@cgiar.org
555	P16#ICR000#SPS000018	Pegadaraju	Venki	Agrigenomics, Illumina, Minnesota, USA	vpegadaraju@illumina.com
556	P16#ICR000#NEF000045	Peleg	Zvi	Hebrew University of Jerusalem, Rehovot, Israel	zvi.peleg@mail.huji.ac.il
557	P16#ICR000#XGE000006	Pereira	Andy	University of Arkansas, Fayetteville, USA	apereira@uark.edu

S No	Registration ID	Family Name	Name	Affiliation	E-mail
558	P16#XD3011#MER707417	Person	Taylor	Colorado State University, Colorado, USA	tperson47@gmail.com
559	P16#ICR000#ICR000068	Perumalla	Janaki Ramayya	International Rice Research Institute (IRRI), Patancheru, India	p.ramayya@irri.org
560	P16#ICR000#TAR000002	Pervin	Salma	Bangladesh Agricultural University (BAU), Mymensingh/ Bangladesh Rice Research Institute (BRRI), Gazipur, Bangladesh	pervinsalma@yahoo.com
561	P16#ICR000#ICR000067	Pettam	Mamatha	International Rice Research Institute (IRRI), Patancheru, India	pettemmamatha23@gmail.com
562	P16#ICR000#XXR000057	Phuke	Rahul Madhavarao	ICAR-Indian Agricultural Research Institute (IARI), Indore, India	rahulphuke18@gmail.com
563	P16#ICR000#NEF000063	Phukon	Munmi	University of Aberdeen, Aberdeen, UK	munmiphukan@gmail.com
564	P16#ICR000#IPP000001	Pieruschka	Roland	"Institute of Bio- and Geosciences Plant Sciences (IBG-2), Jülich, Germany"	r.pieruschka@fz-juelich.de
565	P16#ICR000#XSI000030	Podile	Appa Rao	University of Hyderabad, Hyderabad, India	podilerao@gmail.com
566	P16#ICR000#TAR000015	Pokharel	Bhanu Bhakta	Agriculture and Forestry University, Bharatpur, Nepal	bhanu.pokharel@gmail.com
567	P16#GD1512#MER710230	Ponnuswamy	Revathi	ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, India	revathi.ponnusamy@gmail.com
568	P16#ICR000#XAR000011	Pothula	Srivalli	University of Agricultural Sciences (UAS), Dharwad, India	srivalli.pothula@gmail.com
569	P16#ICR000#XXR000117	Pradeep	CM	University of Agricultural Sciences (UAS), Raichur, India	pradeep0393@gmail.com
570	P16#ICR000#XXR000103	Praharaj	Subhashisa	G B Pant University of Agriculture and Technology, Pantnagar, India	praharaj93@gmail.com
571	P16#ICR000#ICR000093	Pranesh	K Jayadevappa	International Rice Research Institute (IRRI), Patancheru, India	praneshkj@gmail.com
572	P16#ICR000#MBC000010	Prasad	Manoj	National Institute of Plant Genome Research (NIPGR), New Delhi, India	manoj_prasad@nipgr.ac.in
573	P16#TD2911#MER706466	Prayaga	Lakshmi	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	lprayaga@rediffmail.com
574	P16#ICR000#NEF000033	Preethi	NV	University of Agricultural Sciences (UAS), Bangalore, India	reddypreethi.reddy@gmail.com
575	P16#ICR000#MBC000002	Price	Adam	University of Aberdeen, Aberdeen, UK	a.price@abdn.ac.uk
576	P16#ICR000#ICR000066	Priyadarshi	Rahul	International Rice Research Institute (IRRI), Patancheru, India	r.priyadarshi@irri.org
577	P16#ICR000#WAO000008	Punna	Jayamma	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	jayapunna@gmail.com
578	P16#UD0103#MER656008	Puppala	Naveen	New Mexico State University, Clovis, USA	npuppala@nmsu.edu

S No	Registration ID	Family Name	Name	Affiliation	E-mail
579	P16#ICR000#ICR000058	Purushothaman	R	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	purushothmurthy@gmail.com
580	P16#GD1512#MER710228	Pushpa	BN	University of Agricultural Sciences (UAS), Bangalore, India	pushpalatha0001@gmail.com
581	P16#ID1112#MER709295	Putta	Latha	Regional Agricultural Research Station (RARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Tirupati, India	latha_damu@yahoo.com
582	P16#ND2811#MER706359	Rachapudi	Sreeharsha	University of Hyderabad, Hyderabad, India	rvsreeharsha@gmail.com
583	P17#SD1401#MER716214	Rachaputi	C N Rao	The University of Queensland, Gatton, Australia	rao.rachaputi@uq.edu.au
584	P16#TD0410#MER695866	Radhajeyalakshmi	Raju	Tamil Nadu Agricultural University (TNAU), Vagarai, India	radhajeyalakshmi@hotmail.com
585	P16#ICR000#NOC000004	Radhakrishnan	T	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	radhakrishnan.nrcg@gmail.com
586	P16#ICR000#NEF000056	Rafique	Suphia	Department of Biotechnology/ Jamia Hamdard University, New Delhi, India	suphia123@gmail.com
587	P16#ICR000#XCP000002	Raghavan	Vijay	Department of Biotechnology (DBT), New Delhi, India	vijay.dbt@nic.in
588	P16#ICR000#XXR000052	Raghavendra	T	Acharya N.G. Ranga Agricultural University (ANGRAU), Nandyal, India	raghavendraagrico@gmail.com
589	P16#WD0712#MER708664	Ragimasalawada	Madhusudhana	Indian Institute of Millets Research (IIMR), Hyderabad, India	madhu@millets.res.in
590	P16#ICR000#XXR000091	Rahman	Hifzur	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	rahman.biotech@gmail.com
591	P16#ICR000#XXR000004	Rahman	Shah Moinur	Hajee Mohammad Danesh Science & Technology University, Dinajpur, Bangladesh	nurhstu@gmail.com
592	P16#MD1411#MER702809	Rahman	A K M Mahbub	Bangladesh Agricultural University (BAU), Gazipur, Bangladesh	kbdbabu@gmail.com
593	P16#ICR000#XXR000128	Rai	Pooja	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	poojarai140@gmail.com
594	P16#ICR000#WAO000010	Rajasheker	G	Osmania University, Hyderabad, India	grajashekharou@gmail.com
595	P16#ICR000#NEF000051	Rajesh	A	Mahindra Agri Solutions Ltd, Hyderabad, India	ADILAPU.RAJESH@mahindra.com
596	P16#UD1511#MER703268	Raju	Dhandapani	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	dandyman2k3@yahoo.co.in
597	P16#ICR000#XXR000095	Rajurkar	Ashish Balkrishna	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	ashu.raj123@gmail.com
598	P16#ICR000#XAR000047	Rakhmanov	Bakhtiyor	Center of Genomics and Bioinformatics, Tashkent, Uzbekistan	bakhtiyor.rakhmanov@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
599	P16#MD1212#MER709480	Rakshitha	HC	University of Agricultural Sciences (UAS), Bangalore, India	rakshithahc42.rr@gmail.com
600	P17#TD1001#MER715611	Ramalingam	Poornima	Tamil Nadu Agricultural University (TNAU), Sivagangai, India	poornimabio18@yahoo.com
601	P16#ICR000#XXR000131	Ramchander	S	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	rubulochander_009@yahoo.co.in
602	P16#ICR000#NEF000071	Ramchandran	E	JK Seeds, Hyderabad, India	ramchandran@jkseeds.net
603	P16#ICR000#XXR000143	Ramsankar	C	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	cramsankar007@gmail.com
604	P16#ICR000#XXR000071	Rana	Maneet	ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi, India	rana.maneet@gmail.com
605	P16#MD2811#MER706268	Rana	Vijay	CSK Himachal Pradesh Agricultural University, Palampur, India	vijayrana_2005@rediffmail.com
606	P16#ND1411#MER702906	Rana	Jyoti	Murdoch University, Murdoch, Australia	rana.om.jyoti@gmail.com
607	P16#UD2211#MER705160	Rane	Jagadish	ICAR-National Institute of Abiotic Stress Management (NIASM), Pune, India	jagrane@hotmail.com
608	P16#UD1511#MER703271	Ranganathan	Chandrababu	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	chandrarc2000@yahoo.com
609	P16#HD1512#MER710332	Rangappa	Krishnappa	ICAR, Research Complex for NEH region, Umiam, India	Krishphysiology@gmail.com
610	P16#SD1308#MER687971	Ranu	Rajinder	Colorado State University, Fort Collins, USA	rranu@colostate.edu
611	P16#ICR000#XXR000130	Rao	Poornachandra	University of Mysore, Mysore, India	pckrao.06@gmail.com
612	P16#TD1511#MER703077	Rao	SS	Indian Institute of Millets Research (IIMR), Hyderabad, India	ssrao@millets.res.in
613	P16#ICR000#XSI000058	Rao	Vivek	Jagran-Meerut, Meerut, India	mjvivekrao@yahoo.com
614	P16#ICR000#SGP000004	Rapp	Ryan	Illumina, Inc., San Diego, USA	rrapp@illumina.com
615	P16#GD1512#MER710232	Rashmi	K	University of Agricultural Sciences (UAS), Bangalore, India	rashmipalb1190@gmail.com
616	P16#ICR000#XXR000136	Rasool	Souliha	Punjab Agriculture University (PAU), Ludhiana, India	souliha.rasool@gmail.com
617	P16#ICR000#TAR000025	Rathnathunga	Elpitiya Udari Uvindhya	University of Ruhuna, Matara, Srilanka	uvindhyaru@gmail.com
618	P16#ICR000#LOC000003	Rathore	Abhishek	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	a.rathore@cgiar.org
619	P16#GD1512#MER710204	Ratnaparkhe	Milind	ICAR-Indian Institute of Soybean Research (IISR), Indore, India	milind.ratnaparkhe@gmail.com
620	P16#ICR000#NEF000050	Ravindra	JV	Mahindra Agri Solutions Ltd, Hyderabad, India	jayanti.venkataravindra@mahindra.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
621	P16#WD2812#MER712424	Reddy	Bethi	Regional Agricultural Research Station (RARS), Acharya N.G. Ranga Agricultural University (ANGRAU), Nandyal, India	bgreddy1955@gmail.com
622	P16#ICR000#XSI000031	Reddy	Arjula Ramachandra	University of Hyderabad, Hyderabad, India	arjulsl@yahoo.com
623	P16#ICR000#XSI000038	Reddy	V Dashavantha	Osmania University, Hyderabad, India	vdreddycpmb@yahoo.com
624	P16#ICR000#XSI000041	Reddy	A Vishnuvardhan	ICAR-Indian Institute of Oilseeds Research (IIOR), Hyderabad, India	director.iior@icar.gov.in
625	P17#ID2901#MER718665	Reddy	Umesh	West Virginia state university, West Virginia, USA	ureddy@wvstateu.edu
626	P16#ICR000#XAR000043	Ressaissi	Yosra	National Agricultural Research Institute of Tunisia (INRAT), Tunis, Tunisia	yos.re@hotmail.fr
627	P16#ED1811#MER704086	Rohila	Jai	USDA-Agricultural Research Service, Stuttgart, USA	jai.rohila@ars.usda.gov
628	P16#ICR000#ICR000052	Romana	Kirandeep K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	k.romana@cgiar.org
629	P16#ICR000#ICR000022	Roorkiwal	Manish	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	m.roorkiwal@cgiar.org
630	P16#ICR000#XXR000121	Roy	Anirban	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	anirbanneelroy@gmail.com
631	P16#ICR000#NEF000055	Roy	Durlave	Northern Agro Services Ltd, Dhaka, Bangladesh	rnd@northernfertilizer.org
632	P16#ICR000#TL3000062	Rubyogo	Jean Claude	International Center for Tropical Agriculture (CIAT), Arusha, Tanzania	j.c.rubyogo@cgiar.org
633	P16#ICR000#ICR000108	Rupavatharam	Srikanth	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	r.srikanth@cgiar.org
634	P16#ICR000#XXR000087	Ruperao	Pradeep	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	p.ruperao@uq.edu.au
635	P16#ICR000#INS000015	Sadras	Victor	South Australian Research and Development Institute (SARDI), Adelaide, Australia	Victor.Sadras@sa.gov.au
636	P16#ND1411#MER702954	Saeed	Bushra	University of Delhi-South Campus, New Delhi, India	bushra.saeed1@gmail.com
637	P16#ICR000#XXR000060	Saha	Saurav	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	sauravs.saha@gmail.com
638	P16#ICR000#SPS000021	Saha	Debjani	Premas Life Sciences Pvt Ltd, New Delhi, India	debjani@premaslifesciences.com
639	P16#UD2911#AR1577703	Sahadeva Reddy	B	Agricultural Research Station (ARS), Acharya N.G. Ranga Agriciultural University (ANGRAU), Anantapur, India	sahadevardd@gmail.com
640	P16#ICR000#TL3000010	Sako	Dramane	Institut d'Economie Rurale (IER), Kayes, Mali	dramanesako@yahoo.fr

S No	Registration ID	Family Name	Name	Affiliation	E-mail
641	P16#ICR000#XXR000111	Salam	Shaheen A	Regional Agricultural Research Station (RARS), Pattambi, India	shaheensalam121@gmail.com
642	P16#ICR000#XAR000004	Sallam	Ahmad	Assiut University, Assiut, Egypt	amsallam@aun.edu.eg
643	P16#TD0504#MER661506	Samaila	Jeremiah	Harper Adams University, England, UK	jsamaila@harper-adams.ac.uk
644	P16#ICR000#NOC000005	Sambasiva Rao	KRS	Acharya Nagarjuna University, Nagarjuna Nagar, India	krssrao@gmail.com
645	P16#ICR000#ICR000032	Sameer Kumar	CV	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	C.Sameerkumar@cgiar.org
646	P16#ICR000#XXR000127	Sampangi-Ramaiah	Megha H	ICAR-Indian Institute of Horticultural Research (IIHR), Bangalore, India	megha.hs28@gmail.com
647	P16#ICR000#NEF000036	Sanasam	Debina	University of Agricultural Sciences (UAS), Bangalore, India	debina01@gmail.com
648	P16#ICR000#IDC000002	Sandhu	JS	Indian Council of Agricultural Research (ICAR), New Delhi, India	ddgcs.icar@nic.in
649	P16#ICR000#TAR000035	Sangwan	Pooja	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	choudhary.shweta737@gmail.com
650	P16#ICR000#XXR000055	Sanka	Thippeswamy	Syngenta Seeds, Inc., Hyderabad, India	thippeswamys@gmail.com
651	P16#ICR000#XXR000107	Sankaranarayanan	Kavitha	Anna University K B Chandrashekar Research Centre (AU-KBC), Chennai, India	skavitham@yahoo.com
652	P16#ND1411#MER702983	Saranga	Yehoshua	Hebrew University of Jerusalem, Rehovot, Israel	shuki.saranga@mail.huji.ac.il
653	P16#TD1312#MER709808	Sarsu	Fatma	International Atomic Energy Agency (IAEA), Vienna, Austria	F.sarsu@iaea.org
654	P16#ICR000#XXR000133	Sathishraj	Rajendran	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	r.sathishrajbiotech@gmail.com
655	P16#HD1512#MER710299	Satpute	Gyanesh	ICAR-Indian Institute of Soybean Research (IISR), Indore, India	gksatpute@yahoo.co.in
656	P16#UD0908#MER686918	Satturu	Vanisri	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	vanisree_dhar@yahoo.com
657	P16#ICR000#NEF000068	Satyadev	V	UniPhosphorous Ltd, Hyderabad, India	satyadev@advantaseeds.com
658	P16#ND1411#MER702930	Savin	Roxana	University of Lleida, Lleida, Spain	savin@pvcf.udl.cat
659	P16#ICR000#ICR000002	Saxena	Rachit	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	r.saxena@cgiar.org
660	P16#ICR000#INS000016	Schroeder	Julian	University of California, San Diego, USA	jischroeder@ucsd.edu
661	P17#GD0501#MER714855	Schwartz	Nimrod	Hebrew University of Jerusalem, Rehovot, Israel	nimrod.schwartz@mail.huji.ac.il

S No	Registration ID	Family Name	Name	Affiliation	E-mail
662	P16#ICR000#XXR000104	Sebastian	Anil	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	sebastiananil.151@gmail.com
663	P16#ICR000#TL3000052	Sebatta	Christopher	Makerere University, Kampala, Uganda	sebattac@gmail.com
664	P16#ICR000#ICR000072	Seetharam	K	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	k.seetharam@cgiar.org
665	P16#TD2911#MER706528	Sekhar	Kalva M	University of Hyderabad, Hyderabad, India	madhansekhar@gmail.com
666	P16#ICR000#XXR000084	Sellamuthu	Reena	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	reenasen23@gmail.com
667	P17#GD0202#MER719692	Selvaraj	Gopalan	National Research Council of Canada, Saskatoon, Canada	gopalan.selvaraj@nrc-cnrc.gc.ca
668	P16#ICR000#XAR000013	Sen	Poulomi	Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India	poulomisen6121991@gmail.com
669	P16#WD3011#MER706903	Sengupta	Debashree	University of Hyderabad, Hyderabad, India	debashreehcu@gmail.com
670	P16#ICR000#TAR000006	Seta	Shimelis Alemayehu	Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia	shimitiwarc2012@gmail.com
671	P16#ICR000#XXR000115	Shah	Asif Ashraf	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Jammu, India	ashu.ashraf@gmail.com
672	P16#ICR000#WAO000017	Shahbazi	Maryam	Agriculture Biotechnology Research Institute of Iran (ABRII), Karaj, Iran	MShahbazi@abrii.ac.ir
673	P16#ICR000#NEF000046	Shahpur	Shambuling	Mahindra Agri Solutions Ltd, Hyderabad, India	SHAHAPUR.SHAMBULING@mahindra.com
674	P16#ICR000#XSI000021	Shahzad	Anwar	Aligarh Muslim University, Aligarh, India	ashahzad.bt@amu.ac.in
675	P16#ICR000#XAR000031	Shandu	Siphiwokuhle	ARC-Grain Crops Institute, Potchefstroom, South Africa	ShanduS@arc.agric.za
676	P16#ICR000#NEF000013	Shanker	Arun K	ICAR-Central Research Institute for Dryland Agriculture (CRIDA), Hyderabad, India	arunshank@gmail.com
677	P16#ICR000#LOC000002	Sharma	Shivali	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	shivali.sharma@cgiar.org
678	P16#ICR000#XXR000201	Sharma	Seema	KSKV Kachchh University, Bhuj, India	seemabhargavsharma@gmail.com
679	P16#WD3011#MER707102	Sharma	Ram	CSIR-Institute of Himalayan Bioresource Technology (IHBT), Palampur, India	rksharma.ihbt@gmail.com
680	P16#ICR000#SPS000010	Sharma	Naveen	Syngenta Seeds, Inc., Hyderabad, India	naveen.sharma@syngenta.com
681	P16#ICR000#XSI000006	Sharma	RP	ICAR-National Research Centre on Plant Biotechnology (NRCPB), New Delhi, India	rpsnrcpb@yahoo.co.in
682	P16#ICR000#XSI000055	Sharma	Sushma	Chaudhary Charan Singh University, Meerut, India	sushma_sharma130@yahoo.co.in

S No	Registration ID	Family Name	Name	Affiliation	E-mail
683	P16#ICR000#XSI000032	Sharma	Rameshwar Prasad	University of Hyderabad, Hyderabad, India	rpssl@uohyd.ernet.in
684	P16#ICR000#XSI000007	Sharma	PC	Guru Gobind Singh Indraprastha University, New Delhi, India	prof.pcsharma@gmail.com
685	P16#ICR000#XSI000012	Sharma	PK	Chaudhary Charan Singh University, Meerut, India	Pks264@rediffmail.com
686	P16#ICR000#NEF000066	Sharma	Ambika	Eternal University, Baru Sahib, India	pritesh2010@gmail.com
687	P16#ICR000#INS000017	Sharp	Robert	University of Missouri, Columbia, USA	SharpR@missouri.edu
688	P16#GD1512#MER710236	Shashibhushan	NB	University of Agricultural Sciences (UAS), Bangalore, India	shashibhushannb@gmail.com
689	P16#ICR000#INS000010	Shashidhar	HE	University of Agricultural Sciences (UAS), Bangalore, India	heshashidhar@gmail.com
690	P16#ICR000#XXR000065	Shashidhara	N	Pandit Jawaharlal Nehru College of Agriculture and Research Institute (PAJANCOA) & RI, Karaikal, India	shashidhara.gpb@gmail.com
691	P16#ICR000#XXR000112	Sheeba	A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	sheebateddy@gmail.com
692	P16#XD0712#MER708736	Shekoofa	Avat	University of Tennessee, Knoxville, USA	ashekoof@utk.edu
693	P16#TD0612#AR1580949	Shen	Yufang	Northwest A&F University, Yangling, China	
694	P16#ICR000#NEF000012	Shetty	Arun	MARS Chocolate, Gurgaon, India	Arun.Shetty@effem.com
695	P16#ICR000#TAR000023	Shimelis	Hussien	University of KwaZulu-Natal (UKZN), Pietermaritzburg, South Africa	Shimelish@ukzn.ac.za
696	P16#WD3011#MER707148	Shivhare	Radha	CSIR-National Botanical Research Institute (NBRI), Lucknow, India	radha.shivhare09@gmail.com
697	P16#ICR000#XSI000014	Siddiq	EA	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	easiddiq@gmail.com
698	P16#TD1907#MER682414	Siddique	Kadambot	The University of Western Australia, Perth, Australia	kadambot.siddique@uwa.edu.au
699	P16#ICR000#XXR000138	Silambarasan	M	Agricultural College and Research Institute, Madurai, India	silambutnau@gmail.com
700	P16#ICR000#XXR000097	Singaram	Ambika	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	ambikasingaram@gmail.com
701	P16#ICR000#NOC000010	Singh	NP	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	npsingh1960@rediffmail.com
702	P16#ICR000#XHT000005	Singh	Rakesh	ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India	rsingh@nbpgr.ernet.in
703	P16#ICR000#XAR000010	Singh	Jang Bahadur	ICAR-Indian Agricultural Research Institute (IARI), Indore, India	jangbsingh@gmail.com
704	P16#ICR000#XXR000144	Singh	Chandrakant	Junagadh Agricultural University, Junagadh, India	chandrakant.singh07@gmail.com
705	P16#JD1311#MER702716	Singh	Vijaya	The University of Queensland, Brisbane, Australia	v.singh@uq.edu.au

S No	Registration ID	Family Name	Name	Affiliation	E-mail
706	P16#ICR000#XXR000050	Singh	Naresh Pratap	Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, India	naresh.singh55@yahoo.com
707	P16#UD1511#MER703265	Singh	Amrit Lal	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	alsingh16@gmail.com
708	P16#TD1511#MER702995	Singh	Sukhwinder	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	Suk.Singh@cgiar.org
709	P16#ICR000#XXR000110	Singh	Sadhana	Defence Institute of Bio-Energy Research, Nainital, India	sadhnasingh1986@gmail.com
710	P16#ICR000#ICR000080	Singh	Uma Maheshwar	International Rice Research Institute (IRRI), Patancheru, India	uma.singh@irri.org
711	P16#ICR000#ICR000026	Singh	Vikas Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Vikas.Singh@cgiar.org
712	P16#ICR000#XXR000118	Singh	Rakshita	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	singhrakshita19@gmail.com
713	P16#MD1912#MER710799	Singh	Anil	ICAR-Indian Institute of Agricultural Biotechnology (IIAB), Palampur, India	anils13@gmail.com
714	P16#SD3112#MER713327	Singh	Arun	ICAR-Indian Institute of Rice Research (IIRR), Hyderabad, India	aksgene2010@gmail.com
715	P16#ICR000#XSI000017	Singh	Kuldeep	ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India	kuldeep.singh4@icar.gov.in
716	P16#ICR000#XSI000075	Singh	Gurbachan	Agricultural Scientists Recruitment Board (ASRB), New Delhi, India	"gurbachansingh@icar.org.in "
717	P16#ICR000#XXR000041	Singh	Kuldeep	Chaudhary Charan Singh Haryana Agricultural University (CCS HAU), Hisar, India	kdssc77@gmail.com
718	P16#ICR000#NEF000081	Singh	Mandeep	Bioseed Research India, Hyderabad, India	mandeep.b@bioseed.com
719	P16#ICR000#NEF000077	Singh	Sarvjeet	Punjab Agricultural University (PAU), Ludhiana, India	sarvjeetm@rediffmail.com
720	P16#ICR000#XGE000003	Singla-Pareek	Sneh Latha	International Centre for Genetic Engineering and Biotechnology (ICGEB), New Delhi, India	snehicgeb.res.in
721	P16#TD1810#MER698341	Sinha	Ragini	ICAR-Indian Institute of Agricultural Biotechnology (IIAB), Jharkhand, India	ragini150983@gmail.com
722	P16#ICR000#ICR000025	Sinha	Pallavi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	P.Sinha@cgiar.org
723	P16#ICR000#NOC000006	Sivasankar	Shoba	CRP GL and CRP DC, Patancheru, India	s.sivasankar@cgiar.org
724	P16#ND1411#MER702957	Slafer	Gustavo	University of Lleida & ICREA, Lleida, Spain	slafer@pvcf.udl.cat
725	P16#ICR000#NEF000034	Smitha Rani	JA	University of Agricultural Sciences (UAS), Bangalore, India	smirja.arakesh@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
726	P16#ICR000#XXR000039	Somanaboina	Anil Kumar	Osmania University, Hyderabad, India	anilkumarou@gmail.com
727	P16#ICR000#SPS000012	Son	John	TheragenEtex Bio Institute, Yeongtong-gu, Korea	bongjun.son@therabio.kr
728	P16#ICR000#ICR000021	Soni	Pooja	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	poojasoni.sps@gmail.com
729	P16#WD3011#MER707112	Sood	Priyanka	National Institute of Plant Genome Research (NIPGR), New Delhi, India	priyankasood03@gmail.com
730	P16#HD2411#MER705584	Soolanayakanahally	Raju	Agriculture and Agri-Food Canada, Saskatoon, Canada	rajusy@gmail.com
731	P16#ICR000#XXR000068	Soregaon	Chandrakant D	College of Agriculture, Vijayapur, India	soregaoncd@uasd.in
732	P16#XD3011#MER707325	Soren	Khela	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	sorenars@gmail.com
733	P16#WD3011#MER707123	Sowjanya	MS	University of Agricultural Sciences (UAS), Bangalore, India	ms.sowjanya89@gmail.com
734	P16#ICR000#XXR000067	Sowmya	HC	University of Agricultural Sciences (UAS), Raichur, India	hc.sowmya@gmail.com
735	P16#ICR000#XXR000085	Sowmya	HR	University of Agricultural Sciences (UAS), Bangalore, India	sowmyahreddy@yahoo.co.in
736	P16#UD1511#MER703337	Sreeman	Sheshshayee	University of Agricultural Sciences (UAS), Bangalore, India	msshesh1@uasbangalore.edu.in
737	P16#ICR000#XXR000090	Sridevi	R	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	agrirose.28@gmail.com
738	P16#ICR000#NOC000007	Srinivasa Rao	Ch	ICAR-Central Research Institute for Dryland Agriculture (CRIDA), Hyderabad, India	cherukumalli2011@gmail.com
739	P16#ICR000#ICR000031	Srivastava	Rakesh K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	r.k.srivastava@cgiar.org
740	P16#ICR000#XXR000192	Sserumaga	Julius Pyton	National Crops Resources Research Institute (NaCRRI), Kampala, Uganda	j.serumaga@gmail.com
741	P16#XD3011#MER707403	Stephen	Roy	Kerala Agricultural University, Thiruvananthapuram, India	roykau@gmail.com
742	P16#ICR000#ICR000099	Sudini	Hari Kishan	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	h.sudini@cgiar.org
743	P16#ICR000#XXR000003	Sultana	Razia	Bangladesh Agricultural University (BAU), Mymensingh, Bangladesh	dipabdau@gmail.com
744	P16#ICR000#SPT000008	Sunday	Onu Bathlomew	Ebonyi State Institute of Agriculture Research, Abakaliki, Nigeria	
745	P16#FD1111#MER702427	Sunkalikar	Laxman	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Jagtial, India	

S No	Registration ID	Family Name	Name	Affiliation	E-mail
746	P16#ICR000#XXR000058	Suresh	R	Tamil Nadu Rice Research Institute, Aduthurai, India	sureshpbg@gmail.com
747	P16#ND1411#MER702971	Suvarna	Praneeth	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	suvarnapraneeth@gmail.com
748	P16#TD1511#MER703056	Swain	Sabyasachi	IIT Bombay, Mumbai, India	sabyasachiswain16@gmail.com
749	P16#ICR000#CHP000002	Swaminathan	MS	M S Swaminathan Research Foundation (MSSRF), Chennai, India	founder@mssrf.res.in
750	P16#ICR000#XXR000139	Swarnalakshmi	K	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	swarna_bga@yahoo.com
751	P16#FD0212#MER707785	Talwar	Harvinder	Indian Institute of Millets Research (IIMR), Hyderabad, India	talwar@millets.res.in
752	P16#ICR000#HSI000004	Taneja	NK	Chaudhary Charan Singh University, Meerut, India	vc@ccsuniversity.ac.in
753	P16#ICR000#ICR000102	Tapsoba	Hamado	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali	h.tapsoba@cgiar.org
754	P16#ICR000#IDC000001	Tardieu	Francois	French National Institute for Agricultural Research (INRA), Montpellier, France	francois.tardieu@supagro.inra.fr
755	P16#ICR000#ICR000084	Tathineni	Revathi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	revathi.biotech87@gmail.com
756	P16#ICR000#ICR000029	Teggi	Ashwini	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	ashwini.teggi93@gmail.com
757	P16#ICR000#INS000019	Teme	Niaba	L'Institutd'économierurale-Centre régional de recherche agricole (IER-CRRA), Bamako, Mali	niabateme@gmail.com
758	P16#HD1512#MER710321	Tengli	Srikant	University of Agricultural Sciences (UAS), Bangalore, India	srikanttengli@gmail.com
759	P16#ICR000#XXR000109	Thakur	Padma	Banaras Hindu University (BHU), Varanasi, India	padma.13291@gmail.com
760	P16#XD2311#MER705352	Thakur	Vidisha	Banasthali Vidyapith, Jaipur, India	vidisha.thakur30@gmail.com
761	P16#MD2811#MER706227	Thangthong	Nuengsap	Khon Kaen University, Khon Kaen, Thailand	nuengsap.th@gmail.com
762	P16#ND1411#MER702950	Thatikunta	Ramesh	Professor Jayashankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	thatikuntaramesh@gmail.com
763	P16#FD0411#MER701132	Thirunavukkarasu	Nepolean	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	tnepolean@gmail.com
764	P17#ED0601#MER715078	Thompson	Andrew	Cranfield Soil and AgriFood Institute, England, UK	a.j.thompson@cranfield.ac.uk
765	P16#ICR000#ICR000003	Thudi	Mahendar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	t.mahendar@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
766	P16#WD3011#MER707141	Tiwari	Shalini	CSIR-National Botanical Research Institute (NBRI), Lucknow, India	shalini8apr@gmail.com
767	P16#ICR000#NOC000008	Tonapi	Vilas	Indian Institute of Millets Research (IIMR), Hyderabad, India	tonapi@millets.res.in
768	P16#ICR000#NEF000004	Torres	Rolando	International Rice Research Institute (IRRI), Los Banos, The Philippines	r.torres@irri.org
769	P16#ICR000#TAR000033	Tram	Nguyen Thi Hoai	Hue University, Hue, Vietnam	hoaitramnt@gmail.com
770	P16#ICR000#XXR000046	Tripathi	Pramila	ICAR-Indian Institute of Sugarcane Research (IISR), Lucknow, India	pramila.t.21@gmail.com
771	P16#ICR000#XSI000036	Trivedy	Kanika	Central Sericultural Research and Training Institute, Berhampore, India	kanikatrivedy@gmail.com
772	P16#ICR000#IDC000003	Tuberosa	Roberto	University of Bologna, Bologna, Italy	roberto.tuberosa@unibo.it
773	P16#ICR000#XXR000002	Tura	Habtamu	University of Adelaide, Adelaide, Australia	habtamu.tura@acpfg.com.au
774	P16#MD0407#MER680016	Turner	Neil	The University of Western Australia, Perth, Australia	neil.turner@uwa.edu.au
775	P16#ICR000#WAO000007	Tyagi	Jaagriti	Amity University, Noida, India	jaagriti.tyagi13@gmail.com
776	P16#ICR000#INS000020	Tyerman	Stephen	University of Adelaide, Adelaide, Australia	steve.tyerman@adelaide.edu.au
777	P16#ICR000#XXR000172	Uba	Charles Uwazuruike	University of Nigeria Nsukka, Nsukka, Nigeria	Charlesuba192@gmail.com
778	P17#WD1101#MER715699	Uga	Yusaku	National Agriculture and Food Research Organization (NARO), Tsukuba, Japan	yuga@affrc.go.jp
779	P16#ICR000#TL3000034	Umar	Muhammad Lawan	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	mahammadlawan@yahoo.com
780	P16#ICR000#LOC000001	Upadhyaya	Hari	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	h.upadhyaya@cgiar.org
781	P16#ICR000#XXR000094	Usha Kiranmayee	KNS	Osmania University, Hyderabad, India	knskira@gmail.com
782	P16#ICR000#TL3000035	Usman	Alhassan	Institute for Agricultural Research (IAR) Samaru-ABU, Zaria, Nigeria	almuh2013@yahoo.com
783	P16#ICR000#IOC000005	Vadez	Vincent	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	V.VADEZ@CGIAR.ORG
784	P16#ICR000#SPS000027	Vaid	Bhupesh	DuPont Pioneer, Udaipur, India	Bhupesh.Vaid@pioneer.com
785	P16#ICR000#XXR000047	Vaithiyalingan	M	Tamil Nadu Agricultural University (TNAU), Tindivanam, India	mvaithiyalingan@gmail.com
786	P16#ICR000#WAO000004	Valliyodan	Babu	University of Missouri, Columbia, USA	valliyodanb@missouri.edu
787	P16#ICR000#ICR000009	Valluri	Vinod Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	v.vinodkumar@cgiar.org

S No	Registration ID	Family Name	Name	Affiliation	E-mail
788	P16#FD1111#MER702320	van Oosterom	Erik J	The University of Queensland, Brisbane, Australia	erik.van.oosterom@uq.edu.au
789	P16#WD3011#MER706997	Vanishri	BR	University of Agricultural Sciences (UAS), Bangalore, India	vanishribr41@gmail.com
790	P16#ICR000#XXR000119	Vanitha	A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	ajjanvanitha@gmail.com
791	P16#ICR000#XHT000006	Vara Prasad	PV	Kansas State University, Manhattan, USA	vara@ksu.edu
792	P16#ICR000#ICR000036	Variath	Murali	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	v.murali@cgiar.org
793	P16#ICR000#COC000001	Varshney	Rajeev	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	r.k.varshney@cgiar.org
794	P16#MD2811#MER706281	Vasi	Ashvathama	University of Agricultural Sciences (UAS), Dharwad, India	ashvathamavh@uasd.in
795	P16#ICR000#ICR000028	Vechalapu	Suryanarayana	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	surya_biotech06@yahoo.co.in
796	P16#ICR000#XAR000012	Veera	Jayalakshmi	Regional Agicultural Research Station (RARS), Nandyal, India	veera.jayalakshmi@gmail.com
797	P16#MD2612#MER712018	Vemuri	Hindu	Sri Padmavati Mahila Visvavidyalayam, Tirupati, India	hinduvemuri@gmail.com
798	P16#MD0711#MER701512	Venkataraman	Gayatri	M S Swaminathan Research Foundation (MSSRF), Chennai, India	gayatri@mssrf.res.in
799	P16#ICR000#XXR000040	Venkatesh	K	Osmania University, Hyderabad, India	kvenkatesh111@gmail.com
800	P17#UD2401#MER718116	Venkateshgowda	Prakash	Bioseed Research India, Hyderabad, India	prakash.v@bioseed.com
801	P16#ICR000#XXR000096	Vennela	Prudhvi Raj	Banaras Hindu University (BHU), Varanasi, India	v.prudhviraj2@gmail.com
802	P16#ICR000#NEF000019	VenuPrasad	R	Africa Rice Centre (AfricaRice), Ibadan, Nigeria	R.Venuprasad@cgiar.org
803	P16#ICR000#ICR000047	Vijay Kumar	KV	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	k.vijaya@cgiar.org
804	P16#ICR000#XXR000048	Vijaya Prabhakar	A	Tamil Nadu Agricultural University (TNAU), Coimbatore, India	a.vijayp@ymail.com
805	P16#TD1511#MER702996	Vikram	Prashant	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	p.vikram@cgiar.org
806	P16#ICR000#ICR000071	Vinayan	MT	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	m.vinayan@cgiar.org
807	P16#TD2911#MER706525	Vinutha	DN	University of Agricultural Sciences (UAS), Bangalore, India	vinuthagpb@gmail.com
808	P16#ICR000#ICR000049	Vinutha	KS	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	vinuthaks.mysore@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
809	P16#ICR000#ICR000070	Vipparla	Abhilash Kumar	International Rice Research Institute (IRRI), Patancheru, India	abhilash.kumar@irri.org
810	P16#ICR000#ICR000011	Vishwakarma	Manish Kumar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	M.Vishwakarma@cgiar.org
811	P16#TD1511#MER703025	Voothuluru	Priya	University of Missouri, Columbia, USA	voothulurup@missouri.edu
812	P16#ICR000#NEF000076	Vyas	Pritesh	Eternal University, Baru Sahib, India	pritesh2010@gmail.com
813	P17#XD0102#AR1602033	Vyas	Darshna	LGC Genomics, Alexandria, USA	darshna.vyas@lgcgenomics.com
814	P16#ICR000#TL3000018	Wakesa	Temesgen	Ethiopian Institute of Agricultural Research (EIAR), Addis Ababa, Ethiopia	tsena2009@gmail.com
815	P16#XD3011#MER707415	Walia	Harkamal	University of Nebraska, Lincoln, USA	hwalia2@unl.edu
816	P16#ND0711#MER701678	Wallach	Rony	Hebrew University of Jerusalem, Rehovot, Israel	rony.wallach@mail.huji.ac.il
817	P16#TD0612#AR1580952	Wang	Shiwen	Northwest A&F University, Yangling, China	shiwenwang@nwsuaf.edu.cn
818	P16#MD0711#AR1567513	Wang	Feiming	Shanghai Agrobiological Gene Centre (SAGC), Shanghai, China	wfm@sagc.org.cn
819	P16#ICR000#XXR000011	Wang	Xiao	Nanjing Agricultural University, Nanjing, China	wangxiao209@126.com
820	P16#ICR000#ICR000106	Wani	Suhas P	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	S.Wani@cgiar.org
821	P17#HD1201#MER716031	Warner	David	DuPont Pioneer, Iowa, USA	dave.warner@pioneer.com
822	P16#ICR000#ICR000097	Wasudeo	Narkhede Gopal	VN Marathwada Krishi Vidyapeeth, Parbhani, India	gopnarkhede@gmail.com
823	P16#ICR000#NEF000002	Wehner	Gwendolin	Julius Kühn-Institut (JKI), Quedlinburg, Germany	gwendolin.wehner@julius-kuehn.de
824	P16#ICR000#XXR000153	Wekha	Nelson Wafula	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	nelwaf@gmail.com
825	P16#HD1011#MER702303	Welcker	Claude	French National Institute for Agricultural Research (INRA), Montpellier, France	claude.welcker@supagro.inra.fr
826	P16#MD2111#MER704750	Wen	Ruoyu	MARS Chocolate, Beijing, China	ruoyu.wen@effem.com
827	P16#ICR000#ICR000091	Whitbread	Anthony M	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	a.whitbread@cgiar.org
828	P16#ICR000#TL3000039	Williams	Magdalena	Maruku Agricultural Research Institute (MARI), Bukoba, Tanzania	mmagere@yahoo.com
829	P16#TD0612#AR1580775	Wu	Pute	Northwest A&F University, Yangling, China	

S No	Registration ID	Family Name	Name	Affiliation	E-mail
830	P16#ICR000#NEF000005	Xie	Xiaobing	International Rice Research Institute (IRRI), Los Banos, The Philippines	X.Xiaobing@irri.org
831	P16#ICR000#IOC000006	Xiong	Lizhong	Huazhong Agricultural University, Wuhan, China	lizhongx@mail.hzau.edu.cn
832	P16#TD2012#MER711037	Xu	Jianlong	Agricultural Genomics Institute/ Chinese Academy of Agricultural Sciences (CAAS), Shenzhen, China	xujlcaas@126.com
833	P16#ICR000#ICR000018	Yadala	Ramakrishna	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	ram.innove@gmail.com
834	P16#ICR000#NOC000009	Yadav	OP	ICAR-Central Arid Zone Research Institute (CAZRI), Jodhpur, India	"opyadav21@yahoo.com "
835	P16#ICR000#XXR000070	Yadav	Vijay	ICAR-Indian Grassland and Fodder Research Institute (IGFRI), Jhansi, India	vijayyadav777@gmail.com
836	P16#TD1511#MER703002	Yadav	Arun	Australian National University (ANU), Canberra, Australia	arun.yadav@anu.edu.au
837	P16#MD2811#MER706180	Yadav	Vinod	Bisco Bio Sciences Pvt Ltd, Hyderabad, India	vinod.yadav@limagrain.in
838	P16#WD3011#MER707109	Yadav	Chandra	National Institute of Plant Genome Research (NIPGR), New Delhi, India	cbyadav17@gmail.com
839	P16#ICR000#XXR000093	Yadav	Richa	Lucknow University, Lucknow, India	richayadav.biotech@gmail.com
840	P16#ICR000#ICR000076	Yadav	Pooja	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	iampoojayadav@gmail.com
841	P16#UD2911#MER706732	Yadav	Sagar	CSIR-National Chemical Laboratory (NCL), Pune, India	sagaryadav04@gmail.com
842	P16#ICR000#ICR000020	Yaduru	Shashidhar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	shasidhar.y@gmail.com
843	P16#ICR000#XAR000049	Yamanura	M	University of Agricultural Sciences (UAS), Dharwad, India	yaman_gpb4357@rediffmail.com
844	P16#ICR000#ICR000103	Yang	Tao	Chinese Academy of Agricultural Sciences (CAAS)/International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Beijing, China	yangtao02@caas.cn
845	P16#ICR000#XAR000035	Yattara Inamoud Ibny	Fadimata	Tshwane University of Technology (TUT), Pretoria, South Africa	fad_yatt2007@yahoo.fr
846	P16#ICR000#XXR000189	Yildirim	Mehmet	Dicle University, Diyarbakir, Turkey	mehmety@dicle.edu.tr
847	P16#ICR000#TL3000027	Yirzagla	Julius	CSIR-Savanna Agricultural Research Institute, Tamale, Ghana	yirzagla@yahoo.com
848	P16#TD0612#AR1580947	Yue	Shanchao	Northwest A&F University, Yangling, China	yueshanchao@nwafu.edu.cn
849	P16#ICR000#XXR000029	Yussif	Kassim Baba	"Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana"	babayussifk@gmail.com

S No	Registration ID	Family Name	Name	Affiliation	E-mail
850	P16#ICR000#ICR000079	Zaidi	Pervez Haider	International Maize and Wheat Improvement Center (CIMMYT), Patancheru, India	phzaidi@cgiar.org
851	P16#ICR000#TL3000041	Zakayo	Eunice Matari	Selian Agricultural Research Institute (SARI), Arusha, Tanzania	eunicereuben@yahoo.com
852	P16#ICR000#XAR000016	Zargar	Sajad Majeed	Sher-e-Kashmir University of Agricultural Sciences and Technology (SKUAST), Srinagar, India	smzargar@gmail.com
853	P16#ICR000#XAR000018	Zaynali Nezhad	Khalil	Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran	khalil1381@yahoo.com
854	P16#WD2311#MER705240	Zhang	Xia	Biotechnology Research Institute (BRI), CAAS, Beijing, China	zhangxia@caas.cn
855	P16#FD0912#MER709064	Zhang	Fucang	Northwest A&F University, Yangling, China	matthew1222@163.com
856	P16#ICR000#XXR000009	Zhang	Chong	Fujian Agriculture and Forestry University (FAFU), Fuzhou, China	chongzhang2015@163.com
857	P16#TD0612#AR1580784	Zhao	Xining	Northwest A&F University, Yangling, China	
858	P16#ICR000#GWS000003	Zhao	Yusheng	Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany	zhao@ipk-gatersleben.de
859	P16#MD2811#MER706291	Zhao	Jun	Biotechnology Research Institute (BRI), CAAS, Beijing, China	zhaojun01@caas.cn
860	P16#ICR000#SPS000005	Zhong	Bryan	Manyara Biotech Pvt. Ltd. , Singapore	b.zhong@manyarabio.com
861	P16#JD2011#MER704551	Zhou	Sam	MARS Chocolate, Beijing, China	sam.zhou@effem.com
862	P16#TD0612#AR1580773	Zou	Yufeng	Northwest A&F University, Yangling, China	zouyufeng1222@163.com

Notes

Notes

Notes

Notes

Notes

Notes

Sponsors

illumina AUTHORIZED CHANNEL PARTNER

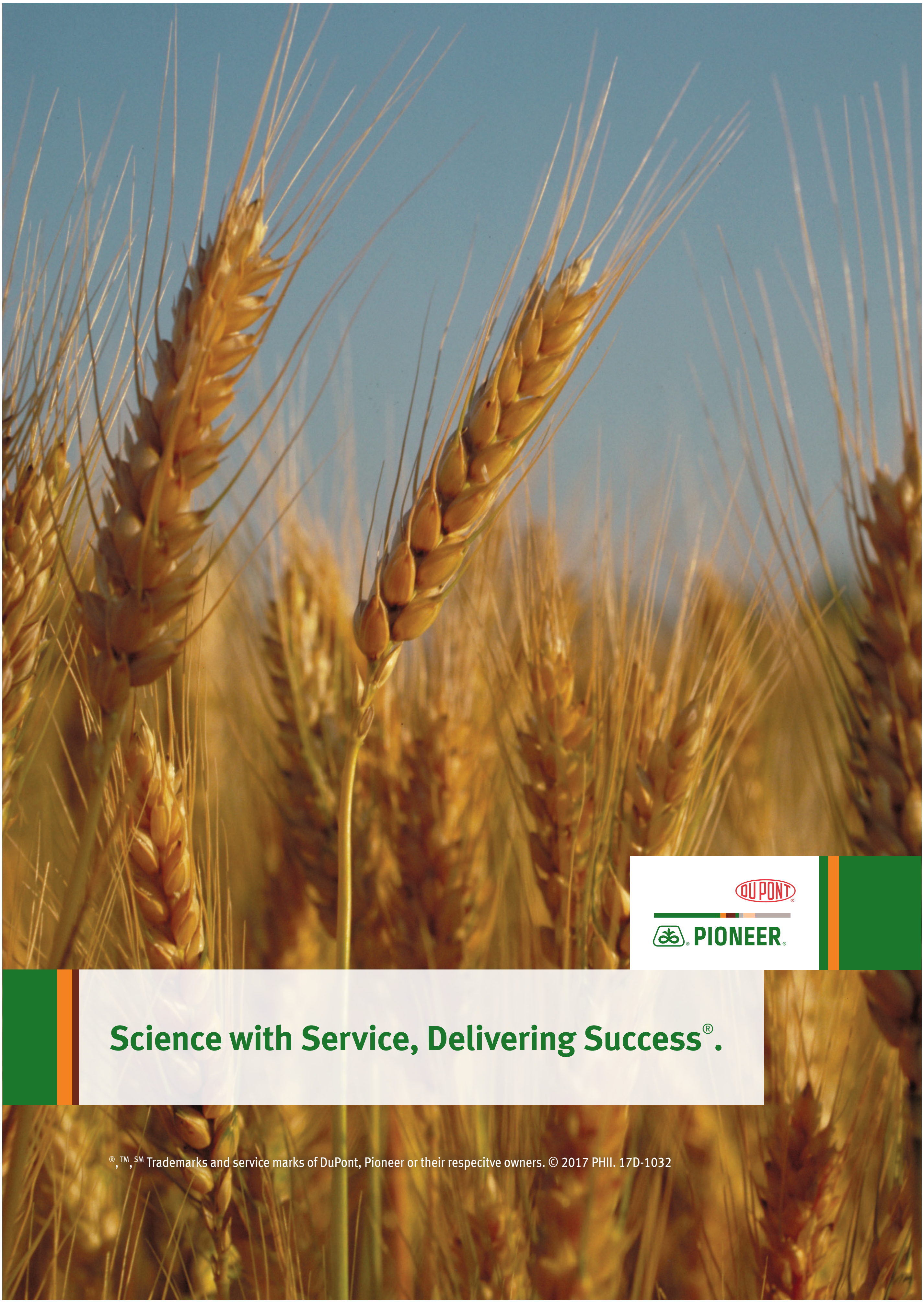
premas life sciences

Accelerating plant and animal genomic breakthroughs

A history of progress. A future of promise.

Visit our booth to learn more about the new GBS solution - TruSeq® Genotype Ne as well as a comprehensive range of genomic solutions.

Be sure to attend the Sequencing and Genotyping Workshop on Thursday 23rd February to hear Illumina Director of Agrigenomics, Dr Ryan Rapp present on the topic:
“Using Genomics to Breed for the Future: Sequencing and Genotyping Platforms”.


DUPONT
PIONEER
Science with Service, Delivering Success®.

syngenta

the
good
growth
plan

Agriculture already uses 70% of the world's fresh water. And many countries are facing severe shortages. A rising global population and changing rainfall patterns mean we must make the most of this precious resource. As one of the world's leading agricultural companies, Syngenta is helping farmers to grow more while also conserving water. As part of The Good Growth Plan, we are committed to improving the average productivity of the world's major crops by 20% without using more water, land or inputs. And we are ready to work with growers, governments, NGOs and all who share this agenda. Please follow our progress at www.goodgrowthplan.com

Company Introduction

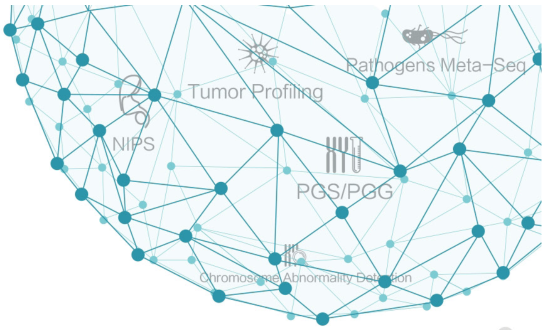
About Us

Manyara Biotech Pte Ltd is a Singapore based Biotech company. It provides a wide range of products, services and consultancy for Agriculture, Biotech and Pharmaceutical companies, hospitals, government research Institutes and universities. Manyara provide lab and field automation products, Bio-banking and sample collection and semiautomatic and fully automatic storage systems. Manyara also provides products and services for Genotyping and Sequencing. With many year experiences, Manyara Biotech would help customer to achieve their research or production needs with limit budget by providing one stop solutions.

Special Production for Agriculture

Pollen Analyzer	Leaf Sampler	Seed Germination Pouch	Fast PCR Setup
Ampha Z30	AK – EP100	AK - CYG	Mantis
			

Contact Info: sales@manyarabio.com, www.manyarabio.com



华大基因 BGI | MGI 华大智造

Reinforce your NGS the BGI Sequencers

BGISEQ-500

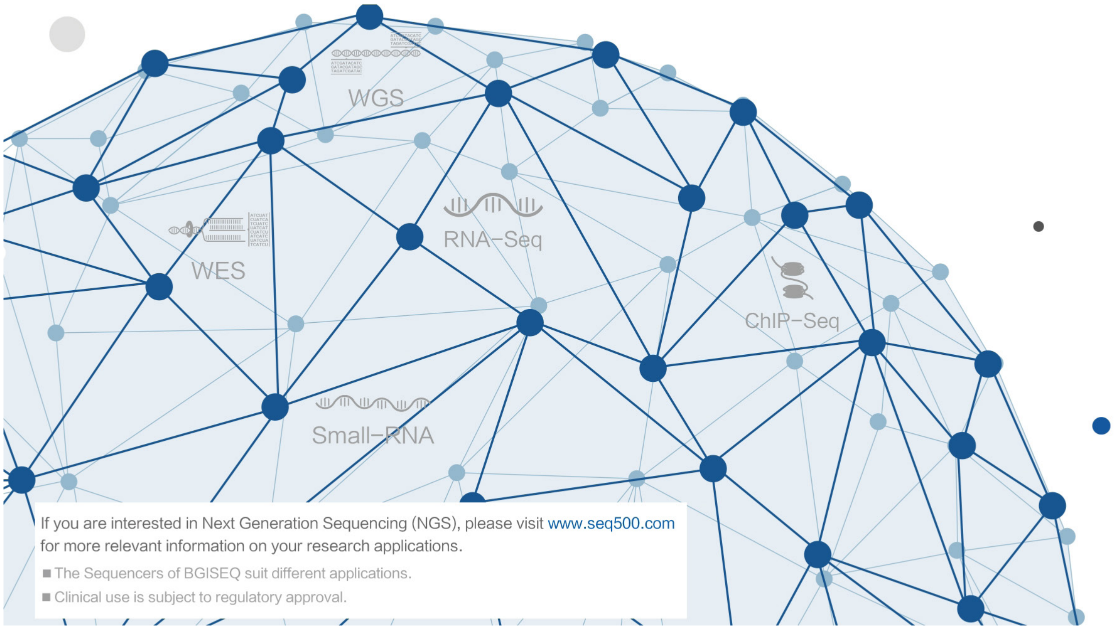
Accuracy Simplicity Speed Flexibility Affordable

BGISEQ-50

Sharp
Superior application performance based on DNB and cPAS technologies

Dedicated
Customized desktop sequencer for dedicated and flexible applications

Smart
One-touch sequencing with unattended mode support



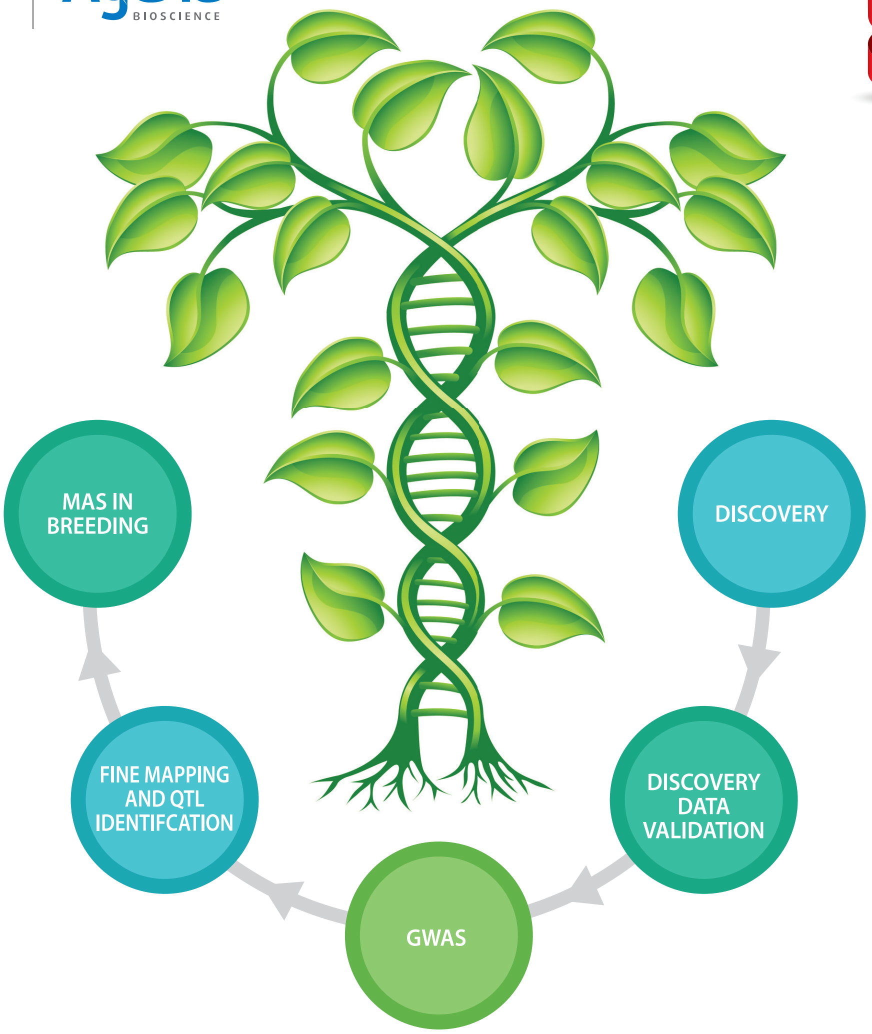
If you are interested in Next Generation Sequencing (NGS), please visit www.seq500.com for more relevant information on your research applications.

- The Sequencers of BGISEQ suit different applications.
- Clinical use is subject to regulatory approval.

affymetrix
Biology for a better world

Agena
BIOSCIENCE

iLS®
YOUR PARTNER IN LIFE



SNP DISCOVERY TO BREEDING PROGRAMS

Explore and Exploit DNA variation in Agrigenomics using the most Advanced tool for Rapid cost effective and High throughput Genetic Screening

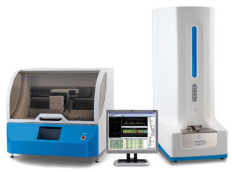
Lab to Field (feed the growing population)

Axiom Automated Genotyping solution from affymetrix offers :-

- Cost-effetive customization never possible before
- No beads, No dropouts, No problems
- Multi-species design on a single array
- Automated clustering for haploid, diploid and polyploid crops 100s to million of SNPs on 16-24-96-384 on well format Scalable throughput upto 3000 samples/week
- 15 custom genotyping array for various crops with India sepcific content is completed successfully

Mass ARRY value for targeted Genotyping :-

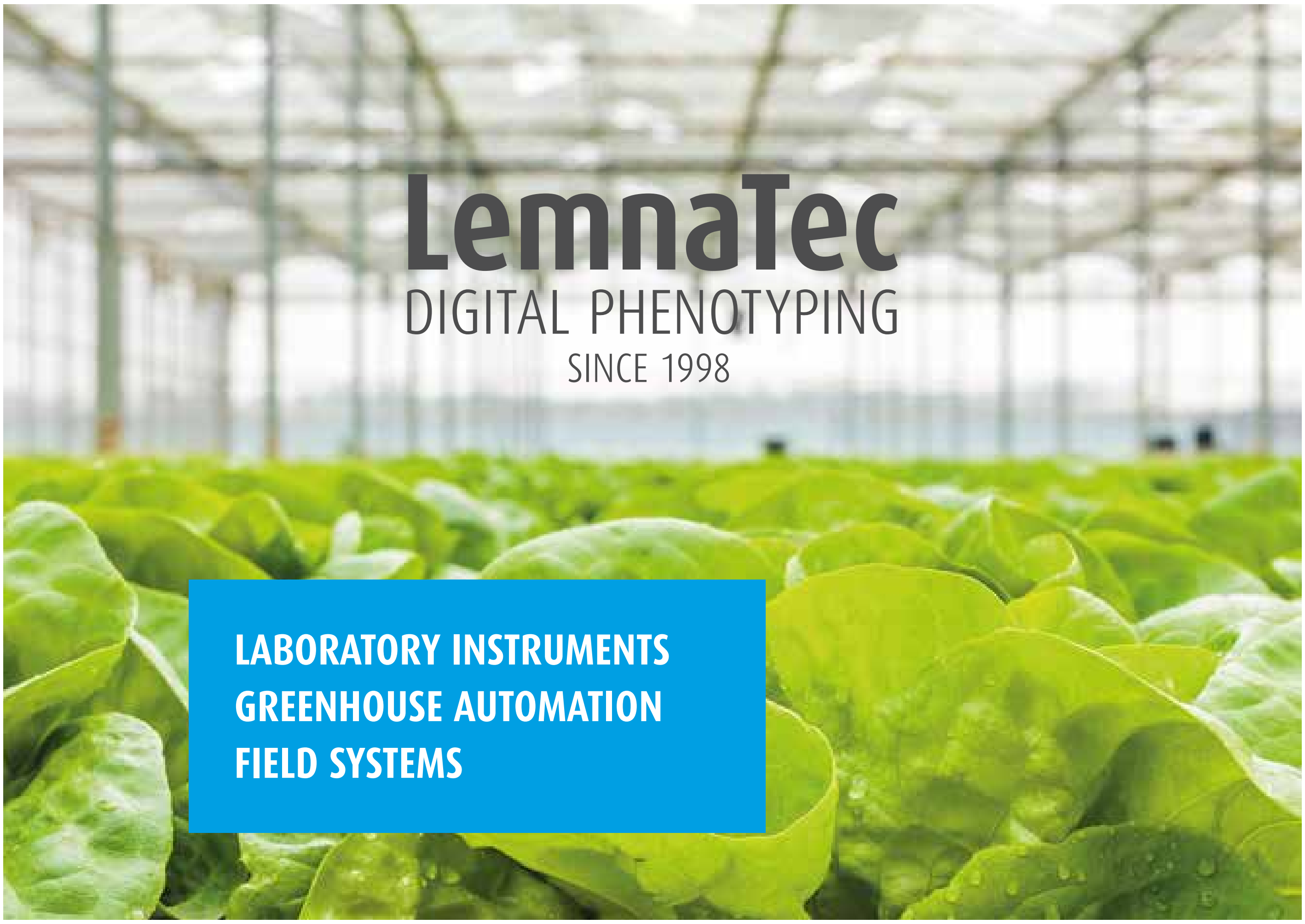
- Translating validating SNPs into robust, cost effective commercial implementation
- Dye free technology exploits the intrinsic property of DNA for analysis
- Multiplexing of 2-60 SNPs/well
- Cost effective and very highthroughput as required by agricultural sector
- Application supported as genotyping, GX, Methylation, Microbial Detection, sampl Id etc



LIST OF CATALOG AND CUSTOM ARRAY - **RICE, PIGEON PEA, COTTON, CHICK PEA, GROUND NUT, WHEAT, BRINJAL, CUCUMBER, SOYBEAN, SORGHUM, BRASSICA, CABBAGE, WATERMELON, PEPPER, LETTUCE, APPLE ETC. AND UNDER MYDESIGN CUSTOM DESIGN ARRAY FOR ANY OF THE SPECIES**

To know more, call us @ **+ 91 124 455 9 800 - 99**, e mail us @ **info@imperialls.com**

Imperial Life Sciences Pvt.Ltd. : 463 Pace City II, Sector - 37, Gurgaon - 122 001, Haryana, India F : 0124 - 455 9801 www.imperialls.com



LEMNATEC

SInce 1998, LemnaTec has pioneered the development of machines and software to automate the process of digital phenotyping. Now, with its Scanalyzer family of systems for laboratory, greenhouse and field applications, LemnaTec provides the most complete range of plant phenotyping solutions to scientists across the world.

LABORATORY

In the coming months, LemnaTec will launch a new range of affordable laboratory instruments to complement the high-throughput Scanalyzers. The first of these is the PhenoBox, an entry level imaging cabinet for fruit and small plants. Designed to be low-cost, transportable and easy-to-use, the PhenoBox will be popular in organisations where budgets are limited.

GREENHOUSE

LemnaTec's Moving Field concept provides standardized growing conditions to enable scientists to monitor the development of plants in large numbers. Advanced imaging techniques deliver comprehensive data sets relating to parameters including growth, colour, water distribution, surface heat emission and photosynthesis.

FIELD

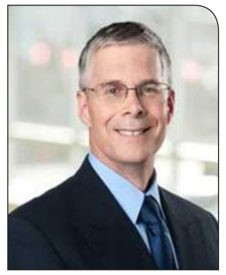
The Field Scanalyzer monitors a large field plot 24x7, 365 days of the year. Automated routines deliver data from a wide range of sensors providing detailed information about crops in real time, throughout the lifetime of plants. This technique has revolutionised the way agricultural research is conducted.

LemnaTec

WWW.LEMNATEC.COM


Worldwide No.1
WINTERSTEIGER
in field research equipment.

Chief Patrons


David Bergvinson

Director General
International Crops Research Institute for
the Semi-Arid Tropics (ICRISAT)
India


M S Swaminathan

Founder & Mentor
M S Swaminathan Research Foundation
(MSSRF)
India

Co-patrons

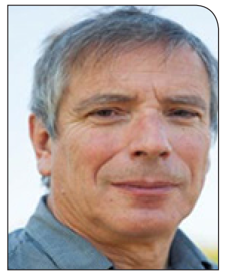

T Mohapatra

Director General, ICAR &
Secretary, DARE
Government of India
India


K VijayRaghavan

Secretary
Department of Biotechnology (DBT)
Government of India
India

InterDrought Chair


Francois Tardieu

Research Director
National Institute of Agronomic Research
(INRA)
France

InterDrought Vice-Chair


J S Sandhu

Deputy Director General,
Crop Sciences
Indian Council of Agricultural Research
(ICAR)
India

InterDrought Past Chair


Roberto Tuberosa

Professor
University of Bologna
Italy

Conference Organization Chair


Rajeev Varshney

Research Program Director,
Genetic Gains
International Crops Research Institute
for the Semi-Arid Tropics (ICRISAT)
India

Team ID-V @ ICRISAT


Anu Chitikineni

Senior Manager
Center of Excellence in
Genomics


Manjula B

Administrative Officer
Center of Excellence in
Genomics


Poornima B

Senior Administrative
Associate
Center of Excellence in
Genomics


Sriswathi M

Senior Scientific Officer
Center of Excellence in
Genomics


Ankit Jain

Visiting Scientist
Center of Excellence in
Genomics


Nilesh Mishra

Senior Scientific Officer
Center of Excellence in
Genomics

Local Committee @ ICRISAT


Hari Upadhyaya

Head
Genebank


Rajeev Gupta

Theme Leader
Genomics & Trait
Discovery


Pooja Bhatnagar Mathur

Theme Leader
Cell, Molecular Biology &
Genetic
Engineering


Shivali Sharma

Theme Leader
Pre-breeding


Abhishek Rathore

Theme Leader
Biometrics


Eng Hwa NG

Theme Leader
Forward Breeding


Pooran M Gaur

Theme Leader
Crop Improvement


Manish Roorkiwal

Scientist
Genomics & Molecular
Breeding


Himabindu Kudapa

Scientist
Genomics & Molecular
Breeding


Manish K Pandey

Scientist
Groundnut Genomics,
Genomics & Trait Discovery


Mahendar Thudi

Senior Scientist
Chickpea Genomics,
Genomics & Trait
Discovery


Rachit K Saxena

Senior Scientist
Applied Genomics,
Genomics & Trait
Discovery


Rakesh K Srivastava

Principal Scientist
Molecular Breeding
Genomics & Trait
Discovery


Santosh P Deshpande

Senior Scientist
Molecular Breeding
Genomics & Trait Discovery


Lekha Pazhamala

WoS Scientist
Genomics & Trait Discovery