CFA-Molecular Breeding

NGGIBCI-2014

4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement

February 19 – 21, 2014
ICRISAT, Patancheru, India

Programme & Abstract Book

Organized by

ICRISAT
Science with a human face

In collaboration with:

Generation

DBT, India

In partnership with:

CGIAR RESEARCH PROGRAM ON Grain Legumes

CGIAR RESEARCH PROGRAM ON Dryland Cereals

Message from the Director General

It is a pleasure to welcome you to the 4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI-2014) organized by ICRISAT in collaboration with CGIAR Generation Challenge Programme (GCP) and Department of Biotechnology (DBT), Government of India, and in partnership with CGIAR Research Program (CRP) on Grain Legumes and CGIAR Research Program (CRP) on Dryland Cereals. This workshop is in continuation of the earlier three workshops on NGS data analysis organized by ICRISAT in 2003, 2010 and 2012. Indeed, it has been a wonderful experience for ICRISAT to work with GCP and DBT to organize this important workshop in Hyderabad, the happening city of India which hosts ICRISAT, an international agricultural research institute of the CGIAR, and several national agricultural research institutes.

Next generation genomics has been projected as the seventh most important disruptive innovation technology in the context of potential economic impact in 2025 as per a recent survey of McKinsey Global Institute. The most important areas benefitted from this technology include human health and agriculture. I am pleased to mention that ICRISAT is in the forefront of deploying these technologies in integrated breeding to develop resilient crop varieties with increased yield and quality in order to sustain and elevate the livelihood and health of millions of resource-poor farmers of the world.

I believe that to make the best use of next generation genomics in improving agricultural crops, it is important to bring genomics, phenomics and breeding informatics together in the same ecosystem. We at ICRISAT have started to work in this direction.

With the participation of renowned global scientists, the NGGIBCI 2014 should serve as an important venue for inspiring new ideas, presenting cutting-edge research studies, and encouraging collaboration between/among researchers for application of next generation genomics for crop improvement. This is the crying need of developing countries of sub-Saharan Africa, Asia and South America.

I would like to congratulate the workshop organizers, Rajeev Varshney and his team, as a part of ICRISAT's Critical Focus Areas (CFA)-Molecular Breeding, for gathering in this meeting a galaxy of eminent scientists and leading luminaries of their respective areas.

I welcome you to an inspiring, educational and enjoyable workshop and a memorable stay in Hyderabad!

William D. Dar
Director General

15 February 2014

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Welcome, logistics, and thanking note…

It is my great pleasure and honor to welcome you to the 4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI) in Hyderabad, India. The 4th NGGIBCI is being organized by ICRISAT as its activities of Critical Focus Area (CFA)-Molecular Breeding in collaboration with CGIAR Generation Challenge Programme (GCP), Department of Biotechnology (DBT), Government of India in partnership with CGIAR Research Program on Grain Legumes (CRP-GL) and CGIAR Research Program on Dryland Cereals (CRP-DC). This workshop is expected to help us in understanding and discussing modern genomics and integrated breeding methodologies for crop improvement.

This workshop is in the series of earlier three workshops organized by us in 2009, 2010 and 2012. The major emphasis of earlier workshops has been on next generation sequencing (NGS) data analysis but now this 4th NGGIBCI is moving ahead by discussing NGS and high throughput genotyping technologies in modern breeding approaches. We are pleased to share that this NGGIBCI workshop is the largest meeting in the series with >150 delegates from 20 countries. The scientific programme is very rich in high quality science with enormous impact on crop breeding.

We are thankful to all participants especially speakers, co-chairs, special invitees for accepting our request and agreeing to participate in the meeting. The workshop at this scale could be organized because of support from ICRISAT including Research Program-Grain Legumes (RP-GL), Research Program-Dryland Cereals (RP-DC), CRP-GL, CRP-DC; GCP and DBT in various ways. We also appreciate generous support from sponsors (please see last pages of Abstract Book).

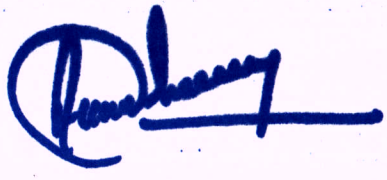
I would like to thank the senior management of ICRISAT, especially Dr William D. Dar, Director General for his guidance and support in organizing this meeting. I am also thankful to Dr CLL Gowda, Deputy Director General-Research and Dr Stefania Grando, Director, RP-DC for their help and suggestions. I would also like to thank my colleagues from the Center of Excellence in Genomics (CEG) mainly Anu Chitikineni, B Manjula, B Poornima Reddy, B Anjaiah, Himabindu Kudapa, Manish Roorkiwal, Vikas Singh, Manish Pandey, Rachit Saxena and Preethi Kholay. Sincere thanks are also due to colleagues from different divisions/units of ICRISAT such as Human Resources and Operations; Farm, Engineering and Transport Services; Housing and Food Services; Purchase, Supplies and Disposal Services; Financial Services and Strategic Marketing and Communication Office for their innumerable help in arranging different things to make this meeting a grand success. I would also like to thank my several other colleagues from CEG, RP-GL and RP-DC.

In summary, I strongly believe that the 4th NGGIBCI workshop is expected to provide an outstanding forum to stimulate ideas and to initiate intense discussions about feature innovative findings in the area of genomics research and modern breeding technologies for crop improvement.

We are doing our best to make your participation in the workshop and stay in Hyderabad fruitful and enjoyable. Please do not hesitate to contact me or my colleagues from the team in case we can be of any help during your stay.

Hope the meeting would be scientifically rewarding as well as enjoyable for all of you.

Have a happy stay in Hyderabad, India!



February 16, 2014

(Rajeev Varshney)
Chair, 4th NGGIBCI

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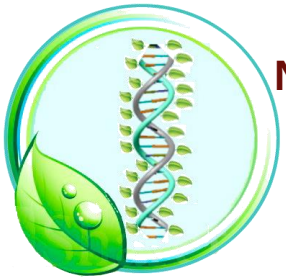

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(Ralph W Cummings Auditorium)

ICRISAT Science with a human face

Generation

Department of Biotechnology
Ministry of Science and Technology
Government of India

Technical Programme

Wednesday, February 19, 2014

08:00 – 08:30	Registration	
08:30 – 11:00	**Inaugural Session**	
08.30 – 08.:50	Welcome and remarks	**Rajeev Varshney** *Chair, 4th NGGIBCI, ICRISAT* India
08:50 – 09:00	Remarks about Integrated Breeding	**P K Gupta** *Chair, Accelerated Crop Improvement Programme, Department of Biotechnology* India
09:00 – 09:10	Remarks about Modern Genomics	**Swapan K Datta** *Deputy Director General (Crop Science), ICAR* India
09:10 – 09:25	Inaugural Address	**William D Dar** *Director General, ICRISAT* India
09:25 – 09:30	Introduction of speaker	**Rajeev Varshney** *ICRISAT* India
09:30 – 10:15	Inaugural lecture: **Digital revolution of agriculture – omics-based agricultural development**	**Wang Jun** *Executive Director* *BGI-Shenzhen* China
10:15 – 11:00	*Group Photo/High Tea*	

11:00 – 12:30	**Session I: Next Generation Genomics** **Co-Chairs: KK Narayanan & Manoj Prasad**	
11:00 – 11:30	Validating, improving and applying genome assemblies using NGS	**Dave Edwards** *University of Queensland* Australia
11:30 – 12:00	Applications of genotyping-by-sequencing for wheat breeding and genetics	**Jesse Poland** *Kansas State University* USA
12:00 – 12:30	Integration of DArT and DArTseq genome profiling platforms with KDDart IT support for breeding and pre-breeding applications	**Andrzej Kilian** *Diversity Arrays Technology Pty Ltd (DArT)* Australia
12:30 – 13:30	*Lunch*	
13:30 – 15:30	**Session II: Novel Mapping Approaches and QTLs** **Co-Chairs: Noel Ellis & Hari Upadhyaya**	
13:30 – 14:00	High density genotyping and phenotyping data: challenges of leveraging novel technologies for the valorization of PGRs	**Andreas Graner** *IPK-Gatersleben* Germany
14:00 – 14:30	Dissection of complex traits in wheat using MAGIC	**Colin Cavanagh** *CSIRO* Australia
14:30 – 15:00	Functional mechanisms of drought tolerance identified in subtropical maize (*Zea mays* L.) using genome-wide association mapping and transcriptome approaches	**T Nepolean** *IARI* India
15:00 – 15:30	Genome sequence and QTL identification for major agronomic traits of mungbean (*Vigna radiata*)	**Suk-Ha Lee** *Seoul National University* Korea
15:30 – 16:00	*Tea & Coffee*	
16.00 - 17.30	**Session III: Sequence to Phenotype** **Co-Chairs: Kadambot HM Siddique & Philippe Ellul**	
16:00 – 16:30	Whole genome re-sequencing reveals agronomically important loci in rice using MutMap and QTL-seq	**Ryohei Terauchi** *Iwate Biotechnology Research Center* Japan
16:30 – 17:00	Large-scale application of GbS in the Seeds of Discovery (SeeD) project: 'Rightsizing' of methods and initial results	**Peter Wenzl** *CIMMYT* Mexico
17:00 – 17:30	3000 rice genomes – Update and plans	**Kenneth McNally** *IRRI* The Philippines
18:30 onwards	*Welcome Dinner @ Mary Cummings Park, ICRISAT*	

Thursday, February 20, 2014

08:30 – 10:00	**Session IV: Genomics-Assisted Breeding Co-Chairs: Stefania Grando & Ramesh Aggarwal**	
08:30 – 09:00	Possibilities and limitations of plant genome sequences for plant sciences	**Richard Visser** *Wageningen University* The Netherlands
09:00 – 09:30	Genomics based marker development and breeding for resistance in barley	**Frank Ordon** *JKI-Institute for Resistance Research and Stress Tolerance* Germany
09:30 – 10:00	Whole genome strategies for marker-assisted plant breeding	**Yunbi Xu** *CIMMYT-China* China
10:00 – 10:30	*Tea & Coffee*	
10:30 – 12:30	**Session V: Integrated Breeding I Co-Chairs: EA Siddiq & JS Sandhu**	
10:30 – 11:00	The opportunity to improve wheat performance in low-yielding environment	**Peter Langridge** *Australian Centre for Plant Functional Genomics(ACPFG)* Australia
11:00 – 11:30	Integrated breeding in dryland cereals at ICRISAT: present status and future opportunities	**Stefania Grando** *ICRISAT* India
11:30 – 12:00	Identification of QTL controlling grain protein content, zinc and iron content in rice	**Shailaja Hittalmani** *UAS - Bangalore* India
12:00 – 12:30	Development and use of mutants induced by EMS in the background of upland variety Nagina22 for rice functional genomics	**T Mohapatra** *CRRI* India
12:30 – 13:30	*Lunch*	
13:30 – 15:30	**Session VI: Integrated Breeding Co-Chairs: RP Sharma & Shoba Sivasankar**	
13:30 – 14:00	Hybrid breeding in wheat	**Jochen Reif** *IPK-Gatersleben* Germany
14:00 – 14:30	Integrated breeding in grain legumes: some examples in chickpea, pigeonpea and groundnut	**Rajeev Varshney** *ICRISAT* India
14:30 – 15:00	The ten years (2004 to 2014): progress in peanut genetics and genomics	**Baozhu Guo** *USDA-ARS/University of Georgia* USA
15:00 – 15:30	Genomics based tools for omega-3 fatty acid rich oil seed crop, Linseed	**Vidya Gupta** *NCL-Pune* India
15:30 – 16:00	*Tea & Coffee*	

16.00-17.30	**Session VII: Breeding for Target Environments** **Co-Chairs: HS Balyan & Narendra Tuteja**	
16:00 – 16:30	Genomics approaches to enhance durum wheat production	**Roberto Tuberosa** *University of Bologna* Italy
16:30 – 17:00	Stress resilient and nutritionally enriched maize for the tropics - product development to seed delivery	**BM Prasanna** *CIMMYT-Kenya* Kenya
17:00 – 17:30	Adaptation to high soil in wheat Determined by allelic variation and gene duplication	**Tim Sutton** *Australian Centre for Plant Functional Genomics (ACPFG)* Australia
18:30 onwards	*Gala Dinner @ Anniversary Lawns (205 Bldg), ICRISAT*	

Friday, February 21, 2014

08:30 – 10:00	**Session VIII: Genomic Selection** **Co-Chairs: Jeff Ehelrs & Pooran Gaur**	
08:30 – 09:00	What do we need to do to bring genomics tools into routine use in cultivar development?	**Gary Atlin** *BMGF* USA
09:00 – 09:30	Genomic prediction incorporating genotype x environment with pedigree, markers and environmental covariate	**Jose Crossa** *CIMMYT* Mexico
09:30 – 10:00	LPmerge: an R package for merging genetic maps by linear programming	**Jeffrey Endelman** *University of Wisconsin* USA
10:00 – 10:30	*Tea & Coffee*	
10:30 – 12:30	**Session IX: Decision Support Platforms for Breeding** **Co-Chairs: Graham McLaren & Eric Y Danquah**	
10:30 – 11:00	Modelling GxE interaction prior to genomic prediction	**Fred van Eeuwijk** *Wageningen University* The Netherlands
11:00 – 11:30	Next generation genetic improvement	**John Hickey** *University of Edinburgh* UK
11:30 – 12:00	The effect of genetic relationships and other factors on genomic prediction accuracy in public plant breeding programs	**Aaron Lorenz** *University of Nebraska* USA
12:00 – 12:30	An open platform approach for management and analysis of next-generation genotyping data by breeders and geneticists	**Ramil Mauleon** *IRRI* The Philippines
12:30 – 13:30	*Lunch*	

13:30 – 15:00	**Session X: New Horizons for Crop Improvement** **Co-Chairs: Jacqueline Batley & MV Rajam**	
13:30 – 14:00	Taking a walk on the wild side: prospecting for traits in the wild progenitor species of cultivated chickpea	**Doug Cook** *UC-Davis* USA
14:00 – 14:30	Functional genomics in common bean and soybean	**Scott Jackson** *University of Georgia* USA
14:30 – 15:00	Drought grain yield QTLs in rice	**Arvind Kumar** *IRRI-India* India
15:00 – 15:30	*Tea & Coffee*	
15.30 -17.00	**Concluding Session**	
15:30 – 15:35	Introduction of speaker	**Rajeev Varshney** *ICRISAT* India
15:35 – 16:20	Concluding lecture**: Adoption of modern breeding tools in developing countries: Challenges and opportunities**	**Jean-Marcel Ribaut** *Director, Generation Challenge Programme* Mexico
16:20 – 16:35	Future perspectives on genomics	**Asis Datta** *NIPGR* India
16:35 – 16:50	Future perspectives on breeding	**CLL Gowda** *Deputy Director General- Research, ICRISAT* India
16:50 – 17:00	Vote of thanks	**Rajeev Varshney** *ICRISAT* India
18:30 onwards	*Dinner @ IMOD Plaza, ICRISAT*	

Abstracts

Inaugural lecture

Digital revolution of agriculture – omics-based agricultural development

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With advances in technologies, large scale omic-based studies have become available. Data generated for genomes, transcriptomes, methylomes would provide unique opportunities for better understanding and application of biology, which would bring about the digital revolution of agricultural development. Furthermore, understanding and application of the omic data can be basically categorized into three steps including ‘read’ to generate the omic and phenotypic data, ‘understand’ to predict the phenotype from omic data, and ‘use’ to design the desired crops. BGI has been working on those different stages, trying to push this digital agricultural development forward. In order to generate omic data and phenotypic data, we developed different platforms to effectively collect comprehensive omic data and different methods to analyze these data sets. For predicting phenotypes from the omic data, we tried different strategies to analyze the genetic mechanisms for different traits from omic data. Finally these obtained data and information are applied for the breeding of those crops, and we have set up cases in which the omic data was applied successfully to aid the breeding of crops.

Notes

Session I:

Next Generation Genomics

Validating, improving and applying genome assemblies using NGS

Edwards D

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Abstract

Next generation DNA sequencing has revolutionised biology. However, the low cost and relative ease in generating draft genome assemblies has led to the production of many genome sequences of questionable quality or applicability. Methods are urgently required to validate and improve these draft assemblies. We have developed several approaches to assess the quality of draft genome assemblies, identify regions of misassembly and correct assemblies. These approaches can be applied to a broad range of genomes which have either been completed or are undergoing development. In addition, we have developed methods for high resolution SNP discovery for the assessment of genome evolution and trait association in complex crop genomes.

Notes

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Applications of genotyping-by-sequencing for wheat breeding and genetics

Poland JA

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Abstract

The rapid advancements in next-generation sequencing have enable use of direct sequencing for genotyping plant and animal populations. Capitalizing on this, we have developed a reduced representation sequencing approach, genotyping-by-sequencing, to produce low-cost genome-wide markers for breeding and genetics studies. For genomic selection in wheat, GBS has now been applied to a number of breeding programs and populations and found to be a robust and flexible marker platform for inexpensive genomic profiling and selection. Presented here are a number of applications and evaluations of genomic selection using GBS in wheat. To further enable the utility of GBS, we developed a targeted amplicon approach for tagging and selection of single loci of large effect. Using a different set of barcodes, targeted amplicons are 'spiked' into GBS libraries enabling very low-cost genotyping of known targets. Overall, the low-cost and flexibility of GBS have enabled a new generation of molecular breeding in wheat providing the framework for genomic selection on a scale not previously possible.

Integration of DArT and DArTseq genome profiling platforms with KDDart IT support for breeding and pre-breeding applications

Kilian A*, Carling J, Heller-Uszynska K, Jaccoud D, Hopper C, Xia L, Caig V, Detering F, Uszynski G

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Abstract

Diversity Arrays Technology (DArT™) was developed over 15 years ago as the first affordable whole genome profiling technology to enable more efficient crop research and improvement. At the moment DArT and its new implementation, DArTseq, has been developed for over 150 organisms, including all significant cereal crops and their relatives. In the last four years we have launched a new service using DArT complexity reduction methods combined with Next Generation Sequencing platforms. This new (DArTseq™) platform has been already applied to over 250,000 DNA samples, predominantly crop plants, but also microorganism and many animal systems. The technology scans between 100,000- 200,000 loci for DNA variation targeting primarily genic regions through the application of “methyl filtration”-based complexity reduction method. DArTseq platform can be easily adjusted to different applications by matching marker densities with the real needs of specific deployment of genome profiling in research or breeding. DArTseq delivers both silico-DArT markers (based on SNPs, Indels and methylation variation) and “traditional” SNP markers discovered by DArT PL’s analytical pipeline within the fragments detected in genomic representations. We will present a number of examples of application of DArT and DArTseq to crop breeding and genetics as well as in product purity/genetic ID testing as well as integration of DArTseq markers with genomics resources in several organisms. We will describe our platforms for efficient genome profile data production (DArTdb and DArTsoft). We will also present our new IT platform (KDDart) for storing marker, phenotypes and environmental data as well as integration of analytical pipelines with data storage.

Notes

Session II:

Novel Mapping Approaches and QTLS

High density genotyping and phenotyping data: challenges of leveraging novel technologies for the valorization of PGR

Graner A[1,*], Stein N[1], Kilian B[1], Neumann K[1], Kuon J[1], Keilwagen J[2], Scholz U[1], Mascher M[1], Klukas C[1]

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Abstract

Conventional crop plant breeding essentially rests on repeated cycles of crossing and selection. This approach has warranted the development of superior cultivars over the past decades. However, it is only sustainable, if the genetic diversity that is lost in the process of selection is adequately replenished by introducing novel diversity into the genepool. *Ex-situ* conservation of plant genetic resources represents the major backbone to maintain the intraspecific diversity of many important crop plant species. At present about 7 million seed samples are stored in far more than 1000 *ex-situ* collections worldwide. However, the vast diversity resting on the shelves of genebanks has been tapped into only marginally.

Hence, genebanks are increasingly expected to provide informed access to their genetic resources. At the highest level of resolution, this means that each genebank accession is tagged with information on individual alleles along with their phenotypic effects. Progress will be reviewed regarding the utilization of PGR of barley (*Hordeum vulgare*) regarding (i) sequence analysis and trait mapping as well as (ii) phenotypic cataloging of accessions using automated imaging. While the application of novel technology in both areas opens up a wealth of entry points for genetic analyses, it also generates and amasses humongous streams of data. Therefore, data management will need serious consideration when aiming at the phenotypic and genotypic characterization of comprehensive genebank collections.

Notes

Notes

Dissection of complex traits in wheat using MAGIC

Cavanagh C[1,*], Boden S[1], Cullis B[2], Stephen S[1], Wang P[1], Taylor J[1], Rebetzke G[1], Verbyla A[1], Verbyla K[1], Morell M[1], Swain S[1]

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Abstract

Complex traits are a major challenge to researchers in many crops and model organisms. In addition to the number of loci that may be contributing to the genetic variance within a crop there are many additional factors that contribute to the challenge of understanding the underlying genetic perturbations that control these traits. We will describe our research approach in wheat, an allohexaploid, to understand two complex traits of importance to wheat production; the first, critical for sound establishment and providing an opportunity for greater sowing depths under dry conditions is coleoptile length. The second trait, “paired spikelets” is driven by a complex interaction of environmental and genetic cues. While the coleoptile length data is normally distributed and can be analysed via conventional means the low penetrance trait of paired spikelets requires an alternative approach for analysis. We will provide an update on our progress in understanding the underlying genetics for these two traits.

Notes

Functional mechanisms of drought tolerance identified in subtropical maize (*Zea mays* L.) using genome-wide association mapping and transcriptome approaches

Nepolean T[1,*], Hossain F[1], Shiriga K[1], Sharma R[1], Kanika A[1], Nidhi S[1], Mohan S[1], Mittal S[1], Rathore A[2], Shah T[2], Gupta HS[1]

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Abstract

Genome-wide association mapping using a subtropical maize population revealed that SNPs are significantly associated with agronomic traits under drought stress. Two models from GenABEL and two from GAPIT identified 64 strong SNP associations for drought stress that constituted 17 false discovery rate (FDR) corrected associations among traits and locations. More than 30 associations were identified throughout the genome for anthesis-silking interval and kernel row number across all data sets. FDR-corrected SNPs PZE-105073274 and PZE-105073275 were mapped on chromosome 5 and were associated with several agronomic traits including grain yield. SNP-Trait associations showed that cumulative effect of stomatal closure, root development, ROS, and ion homeostasis increased water use efficiency under drought stress. Further, two contrasting genotypes (HKI1532-drought tolerant and PC3-drought sensitive) from the AM panel were subjected to genome-wide transcriptome assay. Transcriptomes revealed that phosphoprotein cascades genes and transcription factors related to ABA-dependant stomatal closure to signalling work in concert to overcome reduced photosynthesis. Under stress, the genes involved in osmotic adjustments and transporter proteins were found to be co-expressed to maintain the water balance, and those involved in cell wall modifications and protein and lipid metabolism to maintain the metabolic functions under stress. The SNPs and the transcriptomes associated with molecular functions helped in understanding the complex regulation of genes under drought stress.

Notes

Genome sequence and QTL identification for major agronomic traits of mungbean (*Vigna radiata*)

Kang YJ[1], Hwang WJ[1], Shim S[1], Jackson JA[2], Schafleitner R[3], Srinives P[4], Varshney RK[5], Lee SH[1,*]

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[2]Institute for Plant Breeding, Genetics and Genomics, University of Georgia, 111 Riverbend Rd, Athens, GA 30602, USA
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Abstract

Mungbean [*Vigna radiata* (L.) Wilczek], a self-pollinated diploid plant with 2n = 22 chromosomes, is an important legume crop that is primarily cultivated in Asia. We constructed a draft genome sequence of mungbean to facilitate genome research into the subgenus *Ceratotropis* and to enable a better understanding of the evolution and crop improvement of Vigna species. The draft genome sequence covers 80% of the estimated genome, of which 50.1% consists of repetitive sequences. In total, 22,427 high confidence protein-coding genes were predicted. Based on the *de novo* assembly of additional wild mungbean species, the divergence of what was eventually domesticated and the sampled wild mungbean species appears to have predated domestication. Moreover, the *de novo* assembly of a tetraploid *Vigna* species (*Vigna reflexo-pilosa*) provided genomic evidence of a recent allopolyploid event. Also, we constructed a mungbean genetic map from an F_6 population of 190 recombinant inbred lines generated by single-seed descent from a cross between VC1973A and the Korean landrace V2984 (*V. radiata* var. *radiata*) through genotyping by sequencing (GBS). Of 1,993 single nucleotide polymorphisms (SNPs), 1,321 (covering 11 linkage groups) were successfully mapped onto the genetic map. Several QTLs for major agronomic traits including flowering will be presented. The present assembly of *V. radiata* will facilitate genome research and accelerate molecular breeding of the subgenus *Ceratotropis.*

Session III:

Sequence to Phenotype

Notes

Whole genome resequencing reveals agronomically important loci in rice using MutMap and QTL-seq

Terauchi R*, Abe A, Takagi H, Natsume S, Yaegashi H, Fekih R, Tamiru M

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Abstract

Due to recent development of next-generation sequencing (NGS) technologies, whole genome sequencing (WGS) of crops became routine. Taking advantage of WGS, we developed MutMap (Abe et al. 2010, Nature Biotechnol. 30:174) and QTL-seq (Takagi et al. 2013 Plant J. 74:174) methodologies to rapidly identify the mutated genes and QTL, respectively, and applied them to identify agronomically important loci in rice. In this presentation, I introduce these methods and show the examples of applications as well as latest improvement of the methods.

Notes

Large-scale application of GbS in the *Seeds of Discovery* (SeeD) project: 'Rightsizing' of methods and initial results

Hearne H[1], Romero A[2], Li H[1], Sansaloni C[1], Petroli C[1], Sierra A[1], Galvez H[1], Martinez M[1], Singh S[1], Ellis M[1], Soca G[1], Kilian A[3], Buckler E[2], Wenzl P[1*]

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Abstract

The *Seeds of Discovery* (SeeD) project (http://seedsofdiscovery.org) strives to take advantage of next-gen DNA-sequencing technologies to mobilize novel genetic variation from genebanks into maize and wheat-breeding programs. We are in the process of genome-profiling approximately 120,000 accessions of CIMMYT's wheat genebank and 35,000 maize-landrace accessions (populations) from the genebanks at CIMMYT, INIFAP and other institutions, in order to link molecular data to field-performance data. Genotyping-by-sequencing (GBS) is our method of choice because it minimizes ascertainment bias, a key feature when characterizing underexplored genepools. We use two complementary GbS 'flavors' targeted at different applications. The systematic genebank-diversity surveys are conducted using the DArTseq approach, developed by Diversity Arrays Technology P/L, which surveys *Pst*I-based restriction enzyme fragments. In this approach, a limited number of fragments are sequenced at sufficient depth to make imputation largely unnecessary, allow calling of heterozygotes, and classify presence-absence variation (PAV) polymorphisms. In the case of maize, we are applying the DArTseq approach to DNA pools representing 30 genetically heterogeneous individuals per landrace accession to simultaneously estimate allele frequencies within, and genetic distances among accessions. For association-mapping experiments in maize, however, we use the ApeKI-based GbS approach developed at Cornell University to maximize the number of loci surveyed, while imputing missing data using a large reference dataset. We will present an overview of the various components of the SeeD project and then outline our work on maize-DNA pools and a comprehensive association study using a panel of 4,000 maize landraces.

3000 rice genomes – update and plans

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Abstract

IRRI, the Chinese Academy of Agricultural Sciences (CAAS) and BGI-Shenzhen have undertaken re-sequencing of an extensive collection of rice genetic resources to uncover allelic variation. Three thousand types of rice coming from the International Rice Gene Bank (IRG), the China National Crop Gene Bank and CAAS working collections were sequenced at an average depth of 13X (ranging from about 5X to over 60X depth). Reference-based alignment to the japonica Nipponbare genome has identified variants at ~19M loci by stringent criteria. Variant calling using other reference genomes for rice is currently underway with other partners. Seed from the sequenced entries is being made available through the IRG and CAAS so that detailed phenotyping for high priority traits for breeding can be accomplished. This phenotyping data will enable genome-wide association studies as well as genetic, physiological and biochemical studies.

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Session IV:

Genomics-Assisted Breeding

Notes

Possibilities and limitations of plant genome sequences for plant sciences.

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Abstract

More and more genome sequences of many important crops become available. The promises of using this type of information to improve and speed up breeding processes are numerous. Major challenges in different crop plants, especially the cross-fertilising polyploïd ones, are genome assembly and haplotype discrimination. Having different genomic tools available (like SNPs) makes every crop potentially amenable to MAS. However, the question which is important to address at this stage is how all the ~omics knowledge can be linked best to breeding programmes. Having sequence data as such is not the solution to all problems. Knowing which genes play a role in particular processes but even more important which alleles are contributing the largest effect to the trait and which combinations of alleles can be best combined to obtain the desired amount of improvement in a trait are key. Knowing where to find and how to combine the different alleles and traits in crossing programmes is a challenge but slowly becoming available. For this good databases with extensive information about many phenotypes and genotypes is important. Likewise the availability of (software) tools to query all these kinds of databases and be able to extract the essential information is a major challenge. At Wageningen we have experience with running projects (like eg the Virtual Lab of Plant Breeding) which try to deliver tools and concepts to make the best use of all kinds of available ~omics datasets and increase the time and efficiency of current breeding programmes.

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Genomics based marker development and breeding for resistance in barley

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Abstract

Barley is hit by many pathogens and breeding for resistance is of prime importance to minimise yield losses. With the advent of molecular techniques in the 1990s, markers for many resistance genes in barley have been developed facilitating efficient marker based selection procedures and an enhanced incorporation of these genes in high yielding cultivars. While this was time consuming and laborious in the past, today genomic resources like the 9k iSelect chip, physical and two sequence based maps of the barley genome, next generation sequencing techniques, e.g. genotyping by sequencing (GBS) or exome capture, and the availability of the GenomeZipper, comprising a virtual linear order of genes of different monocot species, facilitate efficient marker development and marker saturation for genes and QTL of interest in barley. This on the one hand allows the marker based incorporation of resistance genes or QTL derived from un-adapted germplasm or wild relatives with a minimal linkage drag and on the other hand considerably enhances marker saturation, which is a prerequisite for gene isolation via map based cloning. Using these genomic resources resulted recently in the isolation of the BaMMV/BaYMV resistance gene *rym11* and is at present applied to several major genes and QTL encoding resistance to viral (BaMMV/BaYMV, BYDV) and fungal pathogens (*Puccinia hordei*, *Blumeria graminis*). The isolation of genes involved in resistance will transfer resistance breeding in the future to the allele level facilitating the sequenced based identification of novel alleles in large gene bank collections and their direct use in barley breeding.

Whole genome strategies for marker-assisted plant breeding

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Abstract

We present an update on the whole genome strategies that were proposed by Xu et al 2012 (Molecular Breeding 29:833–854), which was defined to represent a set of molecular marker-assisted breeding procedures that utilize full genome sequencing and genome-wide molecular markers to effectively address various genomic and environmental factors through a representative or complete set of genetic resources and breeding materials. These strategies are now increasingly based on understanding of specific genomic regions, genes/alleles, haplotypes, linkage disequilibrium (LD) block(s), gene networks and their contribution to specific phenotypes. Large-scale and high density genotyping, high throughput and precision phenotyping and global profile e-typing (environmental assay) are three key components of these strategies. One of the current major constrains is the ascertainment bias associated with single reference genomes that have been widely used but only sample a part of the genetic variation existing in a crop species. Such bias can be minimized or eliminated through development of chips, arrays and GBS strategies to reveal genetic variation hidden in diverse ecotypes of the same crop. Development of markers with better representativeness can be achieved through resequencing of three 1000X genomes, mapping with bi-parental populations that have been genotyped with high density through genotyping-by-sequencing, and established reads- contigs and scaffolds through deep resequencing. Significant components that contribute to the improvement of genetic gain in marker-assisted plant breeding, including unlocking genetic variance, improving heritability estimation, increasing selection intensity and shortening breeding cycle time, will be discussed.

Notes

Session V:

Integrated Breeding I

The opportunity to improve wheat performance in low-yielded environments

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Abstract

Agriculture has an excellent record of productivity growth over the last fifty years. However, the rate of productivity growth has slowed dramatically in the past decade. This presentation will focus on strategies to improve the performance of wheat and barley, two of the most important global crops, in low yielding environments.

Low-yielding environments are characterised by a wide range abiotic stresses such as extreme temperature, low water availability, high light intensity, high salt, and mineral deficiencies or toxicities that can severely reduce crop plant productivity. In many cases, several types of abiotic stress challenge crop plants simultaneously. Higher plants have evolved multiple, interconnected strategies that enable them to survive unpredictable environmental fluctuations. However, these strategies are not always well developed in the cereal cultivars and most of the strategies are focused on plant survival at the expense of yield.

Wheat and barley have the advantages of extensive monitoring and archiving of genotypes and associated phenotypic data and the availability of unique populations adapted to specific environments and end-uses. These advantages are becoming increasing significant as analytic tools improve. However, application of genomics research still faces a number of serious issues. In particular, many of the key traits influencing yield are poorly understood at the physiological and genetic levels and hard to reliably phenotype. A broad approach to using new resources and techniques to tackle abiotic tress tolerance in wheat will be presented with some specific examples of how these results can influence practical crop improvement.

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Integrated Breeding in Dryland Cereals at ICRISAT: Present status and future opportunities

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Sorghum and millets are grown by more than 33 million smallholder households in the drylands of Africa and Asia. The production and productivity of sorghum, pearl millet and finger millet are constrained by several biotic and abiotic stresses. At ICRISAT, in partnership with national and international institutions, we are using modern approaches of integrating advanced genomics, phenomics, biometrics and bio-informatics to enhance genetic gains to improve productivity of dryland cereals.

ICRISAT-led initiative to sequence pearl millet genome and plan for developing finger millet genomic resources in near future will lead to accelerated utilization of genomic information in breeding programs. In collaboration with Cornell University, the successful implementation of genotyping-by-sequencing data analysis pipeline for dryland cereals, especially sorghum, has changed the landscape of application of molecular marker technology from specific genomic regions to whole genome scans. Recent efforts in establishing a state-of-art high-throughput phenotyping platform at ICRISAT to dissect complex traits such as drought and its integration in modelling work will lead to a paradigm shift on how we further our efforts for ideotype breeding for each target agro-ecological zones. The recent surge in generation of 'BIG DATA' from *omics* has reiterated the importance of biometrics and bio-informatics, not only to handle the data but also to analyze and help interpret the same by developing user-friendly platforms/tools. Towards this end, ICRISAT is actively participating in development and utilization of platforms/initiatives such as Breeding Management System, plant breeding program management tools. While dryland cereals research is at an exciting stage of utilizing the recent advances in the *omics* fields, integration of all these tools and techniques into the crop improvement activities remains a major challenge.

Identification of QTL controlling grain protein content, zinc and iron content in rice

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Notes

Abstract

Protein content in rice in existing varieties rice varies from 6–9 per cent and are low in micronutrients. Most rice consuming population suffers from protein deficiency because of low protein and nutrients. However, in local varieties and land races they vary and present in higher proportions. In this study a local rice cultivar with 13-14 per cent grain protein, with 13-18 ppm Iron and 29 ppm of Zn in grain was identified and transferred into high yielding variety and mapped on rice chromosome. A mapping population of 700 RIL's was developed and QTL for grain protein, Fe and Zn were mapped on rice chromosome on 1, 3, 6, 8, 9, 10 and 11 rice chromosomes. QTL with 5-18 percent of phenotypic variation for protein content was observed. Three major QTL for Zn and five for Fe content were identified. An SSR marker tightly linked to grain protein was identified and mapped. Three seed storage genes were identified by expression analysis. High protein content was transferred to BPT – 5204. Five promising RIL's containing13-15 per cent protein were mass multiplied and popularized. One of them is proposed for release and is in the second year of trial. Genotypes with 58 ppm Zn and 26 PPM of Fe are identified and being tested for development of new variety. The others are being tested and seeking for commercialization. Lines with 15-18 percent of lysine and methione increase have been identified as compared to existing rice varieties.

Notes

Development and use of mutants induced by EMS in the background of upland variety Nagina22 for rice functional genomics

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Abstract

Rice (*Oryza sativa*) is the staple food of more than half of the world's population. The International Rice Genome Sequencing Project (IRGSP) generated very high quality sequences that were used to predict the number and type of genes, and the non-genic regions containing repeats and mobile genetic elements. Concerted efforts are required to understand the function of individual genes, and their interactions among themselves as well as with environment in relation to variation in traits for a directed genetic manipulation of this important crop for the benefit of the mankind. One of the approaches to determine functions of genes employs natural mutants available in the germplasm or those induced by physical, chemical or biological agents. Mutants facilitate unveiling the causal relationships between coding/regulatory sequences and plant performance, and also cloning of the corresponding genes. Therefore a number of international efforts are underway for generation, collection and characterization of mutants for providing technological platform for functional genomics. In an indigenous effort funded by the Department of Biotechnology (DBT), Government of India, a set of 22, 292 EMS mutagenised lines have been generated in the background of an upland rice variety Nagina-22. EMS was chosen since it gives high point mutation densities by base substitution either in the transcribed regions or in the regulatory elements of a gene that might alter gene function leading to creation of a series of alleles of a gene. The uniqueness of this national effort is phenotyping for a range of traits. Elaborate phenotyping by different partner institutions has led to identification of mutants for plant growth and architecture, flowering, maturity, grain number, shape and size, yield, resistance to blast and bacterial leaf blight diseases, phosphorus use efficiency, and tolerance to herbicide, drought and salinity. Inheritance of selected mutants has been carried out using F_2 populations developed from the cross of the mutants with wild type Nagina22. Mutant loci for seed size and plant height have been mapped using SSR markers on chromosomes 5 and 4, respectively. Transcriptome profiling using rice microarrays has revealed altered expression of only a limited set of genes in these mutants. In contrast, hundreds of genes were found differentially regulated in a gain-of-function mutant having higher level of tolerance to moisture deficit stress. This mutant also showed longer roots and more of partially closed stomata under stress. Two of the mutants, one for plant height and the other for seed size were characterized in detail. The dwarf mutant showed proportionate reduction in each of the internodes as compared to wild type. The gene, identified through positional candidate approach and verified by co-segregation analysis, was found to encode Carotenoid Cleavage Dioxygenase7 (CCD7) and identified as an allele of *htd1.* The mutant carried substitution of two nucleotides CC to AA in the sixth exon of the gene that resulted in substitution of serine by a stop codon in the mutant. The short grain mutant had shorter, narrower, and lesser cells in as compared to the wild type. The candidate gene region on the short arm of chromosome 5 includes *srs3,* which was already reported to control grain size in rice. It encodes kinesin 13 family proteins with a major role in mediation of microtubule organisation during mitosis. Sequencing of 11kb *srs3* gene region revealed a substitution of C to T in the coding region of the mutant leading to creation of a stop codon. Sequencing of the kinesin motor domain region of the gene did not reveal presence of this mutation in 96 germplasm lines having significant grain size variation. Results suggested utility of the mutant resource in rice functional genomics including discovery of new genes for traits agronomic importance and allele mining.

Session VI:

Integrated Breeding II

Hybrid breeding in wheat

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Abstract

Hybrid breeding is a remarkable success story in several allogamous species. The main advantages of hybrid *versus* line varieties are increased trait values due to the exploitation of heterosis, larger yield stability especially in marginal environments, and the ease of stacking dominant major genes. We examined 1.604 single-cross wheat hybrids and their 135 parental lines in field trials for grain yield, plant height, flowering time, biotic stress resistances, frost tolerance, as well as quality traits**.** We observed that hybrids were for most traits superior to the mean of their parents. Furthermore, we found that hybrids outperformed their parents with respect to their yield stability. This clearly underlines the potential to improve stress resistance switching from line to hybrid breeding. One important challenge in hybrid wheat breeding is the development of accurate methods to predict hybrid performance before evaluating crosses in intensive field trials. We developed association mapping, ridge regression best linear unbiased prediction (RR-BLUP), Bayes-A, Bayes-B, Bayes-C, and Bayes-Cπ approaches to predict hybrid wheat performance. Moreover, we bridged the gap between marker-assisted and genomic selection implementing weighted RR-BLUP. The accuracy of the developed prediction approaches were studied using the phenotypic data in combination with 9k and 90k SNP array data. The high cross validated accuracies clearly underlines the potential of genomics based prediction of hybrid performance in wheat.

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Integrated breeding in grain legumes: some examples in chickpea, pigeonpea and groundnut

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Abstract

Grain legumes serve as vital sources of protein, micronutrients such as iron to meet the nutritional requirement in vegetarian diets and therefore also referred as 'poor people's meat'. In recent past, ICRISAT and its partners have developed large scale genomic resources including molecular markers, BAC-end sequences (BESs), transcript reads, and comprehensive transcriptome assemblies in chickpea, pigeonpea and groundnut, the three major semi-arid tropics (SAT) legumes. Recently, draft genome sequences of pigeonpea (48,680 genes) and chickpea (28,269 genes) have been reported, representing 73% and 74% of the respective genomes. In addition ninety chickpea genomes have also been re-sequenced, revealing 4.4 million vari¬ants (SNPs and INDELs). Efforts to sequence groundnut genome are underway. Based on genomic resources, dense genetic maps, QTL maps as well as physical maps for these legume species have also been developed. Analysis of phenotyping data together with genotyping data has provided candidate/associated markers for drought-tolerance-related root traits, resistance to *Fusarium wilt* (FW) & *Ascochyta blight* (AB) in chickpea; resistance to foliar diseases in groundnut; sterility mosaic disease (SMD) and fertility restoration in pigeonpea. For accelerated product development molecular breeding approaches have been initiated for developing cultivars with enhanced drought tolerance in chickpea and disease resistance in chickpea and groundnut. Advances in genomics and molecular breeding in grain legumes will be presented.

The ten years (2004 to 2014): progress in peanut genetics and genomics

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Abstract

Plant breeding, genetics, and genomics play a critical role in sustainable agriculture specifically in improving crop productivity, quality, and resistance to pests and diseases. The germplasm collections have been treasures of crop genetic resources. Utilization of the collections of wild peanut species has been slow because of the limited breeding and genetic tools available to assist breeders in interspecific introgression of desirable traits into cultivated peanut although a few successful cases were documented such as 'NemaTAM' and 'Tifguard' with nematode resistance, 'GPBD 4' with rust and late leaf spot resistances, and 'Bailey' with multiple disease resistances. Peanut molecular genetics and genomics also have demonstrated the potential for transforming peanut breeding and cultivar development through increased integration of marker-assisted breeding. During the past 10 years, since the U.S. Peanut Genome Initiative was launched in 2004 in Atlanta and expanded to global efforts in 2006 in Guangzhou, China, the international peanut community has been working together through coordination of efforts in genome research beginning with molecular marker development, improvement of map resolution and coverage, and development of mapping populations. The peanut genome sequencing project was launched in 2012 by the Peanut Genome Consortium to sequence both wild ancestors and cultivated peanuts. The collaborative and coordinated efforts since 2004 have contributed to development of large-scale genomic resources and tools in order to effectively tap into germplasm collections. The reference genome sequence and the high density maps will serve well into the future for peanut cultivar development and research. The International peanut conference of AAGB-2014 will be held in Savannah, GA, in November 2014.

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Genomics based tools for omega-3 fatty acid rich oil seed crop, linseed

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Abstract

Linseed/ Flax (*Linum usitatissimum* L.) is one of the earliest domesticated crops with the highest contents of the essential ω-3 fatty acid (FA), alpha-linolenic acid (ALA); and bioactive phenolic compounds such as lignans, predominantly secoisolariciresinol diglucoside (SDG), phenolic acids and flavonoids. However, there are scanty genomic resources available in linseed. We initiated studies to develop DNA markers wherein three microsatellite enrichment methods coupled with the next generation sequencing was utilised to develop 290 SSR markers. Computational approach such as EST database mining was exploited to develop 927 genic SSR markers. We further mined the linseed genome for glycosyltransferases where 137 genes belonging to 14 phylogenetically distinct groups were identified. Among the ten genes selected for transcript profiling, the LuUGT74S1 gene showed the highest expression in developmental seed stages indicating it's putative *in planta* function as Secoisolariciresinol glycosyltransferase. We also mined linseed genome to identify miRNA, as they are known to play an important role in plant growth and development and NBS-LRR genes, the largest class of disease-resistance genes. This lead to identification of 116 conserved miRNAs and 147 NBS-LRR genes in linseed genome. India has a large collection of linseed germplasm (2239 accessions). To analyse the Indian linseed diversity we developed the core collection of Indian linseed (222 lines) using 12 morphological characters. GBS analysis of a subset of this population leads to identification of QTLs for yield in linseed. The developed core collection represents the diverse linseed accessions and can be utilised for wide applications in breeding.

Session VII:

Breeding for Target Environments

Genomics approaches to enhance durum wheat production

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Abstract

Durum wheat is widely grown in Mediterranean countries where is staple to hundreds of millions. The main limitations to durum wheat production are the constraints caused by biotic and abiotic stress. Linkage and association mapping applied to elite materials have allowed us to map QTLs that influence (i) yield *per se* (i.e. unrelated to flowering time) under a broad range of water regimes and (ii) resistance to fungal and virus diseases. In some cases, codominant markers suitable for high-throughput screening have been derived and are being deployed for marker-assisted selection. Association mapping has allowed us to identify 12 QTLs that consistently affect the adult resistance to UG99 and other highly virulent races of stem rust. Fine mapping is underway in order to positionally clone the relevant loci for three major QTLs that affect yield *per se* (chromosome 3BS), leaf rust resistance (chromosome 7BL) and virus resistance (chromosome 1B). For the grain yield QTL on chromosome 3B, the fine mapping has been facilitated by the availability of the annotated genome sequence from bread wheat. However, a limitation in using a hexaploid wheat template is due to the presence of rearrangements (e.g. PAV) that may prevent the identification of all the ORFs present in the target region in durum wheat. The sequencing of the durum wheat genome would further facilitate positional cloning while providing a more precise avenue to a genotype-by-sequencing approach. Exome-capture enabling platforms are being deployed to capture locus-specific polymorphism that provide clues for identifying candidate genes and additional polymorphisms.

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Stress resilient and nutritionally enriched maize for the tropics – product development to seed delivery

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Abstract

Accelerated development and delivery of high-yielding, climate resilient and nutritionally enriched tropical/subtropical maize cultivars that contribute to enhanced food security and sustainable intensification of maize-based systems is the focus of CIMMYT's Global Maize Program. Besides continued and successful efforts in developing drought tolerant tropical/subtropical maize germplasm, emphasis is on accelerated development and deployment of heat stress resilient germplasm in South Asia and sub-Saharan Africa. Strong partnership with the seed industry in Africa, Latin America and Asia is a key factor for successful deployment of CIMMYT-derived climate resilient tropical maize germplasm. Molecular marker-assisted breeding for provitamin A enrichment implemented by CIMMYT under HarvestPlus Program, including identification, validation and utilization of production markers, is perhaps one of the finest examples of allele mining work leading to improved varieties. The first-generation provitamin A-enriched maize varieties have been released in Zambia in September 2012, and the next-generation provitamin A lines (with >15 ug/g provitamin A) have been recently developed. Enhancing genetic gains and breeding efficiency using doubled haploidy, high throughput and precision phenotyping, high-density genotyping, MAS for key traits with less complex inheritance, and rapid-cycle genomic selection for improving complex traits, is critical for improved maize productivity in the tropics. There is also a distinct need to establish global phenotyping network for comprehensive characterization of genetic resources and breeding materials for an array of target traits. This would significantly accelerate genomics-assisted breeding, diversification of the genetic base of elite breeding materials, and effectively countering the effects of global climate changes.

Adaptation to high soil in wheat determined by allelic variation and gene duplication

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Abstract

Boron deficiency and toxicity severely limit crop production worldwide. In Southern Australia where high soil boron is the problem for cereal growers, genetic approaches to utilise plant adaptation to boron have been a long term priority for cereal breeding programs. The major tolerance locus in wheat, *Bo1*, is located on 7BL while four QTL for tolerance have been mapped in the barley genome. In barley and wheat the major loci have now been cloned, illustrating processes that breeders can utilise to identify and deploy variation for this trait. In selecting for performance, early farmers around the Mediterranean, through the Middle East and into India and China developed wheat landraces with varying levels of tolerance. A similar process was occurring in barley but the results were very different. Our data reveals divergent evolution of boron tolerance in wheat compared to barley. While in both species transcriptional regulation of boron transporter genes is a common mechanism, tissue specificity differs and, in barley, tolerance is achieved by tandem gene duplication. In wheat, gene duplication was also combined with the generation of allelic diversity. It is curious that the genetic basis for tolerance has developed so differently for these two closely related species and the relative success of breeding for boron tolerant wheat versus barley may lie in the narrow allelic variation seen in barley compared to wheat. Allele screening in a panel of bread and durum wheats originating from diverse agro-ecological zones shows that matching functionally different boron tolerance alleles to the level of boron in the environment appears to be critical.

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Session VIII:

Genomic Selection

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What do we need to do to bring genomics tools into routine use in cultivar development?

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Abstract

Low-cost, high density genotyping is revolutionizing plant breeding in highly commercialized crops. Multi-national seed companies (MNSCs) have linked industrial-scale genotyping with integrated phenotypic, pedigree, and marker databases to shorten breeding cycles, improve prediction accuracy, and increase selection intensity. This has required large investments in breeding informatics. Large MSNCs have integrated breeding databases that allow breeders to trace haplotypes back to program ancestors, estimate their phenotypic effects in a wide range of germplasm and environments, and detect them in segregating populations. These genotypes are being used both to determine the probability that an individual or line will carry a particular disease or pest resistance or quality trait, and to predict complex polygenic traits. Both genotypic information and phenotypic predictions are provided to MNSC breeders in easily understood formats that facilitate selection. In the smaller public and private sector breeding programs serving smallholders in the developing world, high-density genotypic information is being exploited mainly for gene discovery, in a piecemeal fashion that is poorly integrated with cultivar development. To truly harness the power of genomics to increase rates of genetic gain, breeding programs must develop integrated breeding informatics databases that can be easily linked to breeder-friendly genomic prediction pipelines. To date, few CGIAR or national breeding programs have even implemented the relatively simple pre-requisites for exploiting genomics prediction, which include integrated pedigree and phenotypic databases, quality control genotyping, and mixed-model effect estimation. A large-scale, integrated, and concerted effort is needed to bring the promise of genomics to bear on increasing rates of genetic gain in the fields of smallholder farmers. The Gates Foundation is eager to support creative and collaborative partnerships to exploit the potential of the genomics revolution in cultivar development.

Notes	

Genomic prediction incorporating genotype x environment with pedigree, markers and environmental covariate

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Abstract

Modern genotyping technologies can characterize genomes in great detail using a large number of markers, and modern information systems can generate large volumes of environmental data. Potentially, these two sources of information can be used to describe genotype x environment interaction (GE), that is, how environmental conditions modulate genes' effects on traits. In principle, GE can account for by fitting interactions between markers and environmental covariates (ECs). However, when genotypic and environmental information are highly dimensional, modeling all possible interactions explicitly becomes infeasible. We have developed models for simultaneously modeling the main effects of markers and/or pedigree and interaction effects of large numbers of genetic markers and of large numbers of ECs using co-variance functions. The proposed approach is a random effects model on all the markers, all the ECs and all interactions between markers and ECs and is similar to previous norm of reaction models used in animal and plant breeding. In this study we assessed the propose models in several data sets comprising different crops evaluated under different environmental conditions. We show how incorporating GE with pedigree, marker and EC into the genomic model can improve prediction accuracy to a different degree depending on the type of plant population under studied.

Notes

LPmerge: an R package for merging genetic maps by linear programming

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Abstract

Consensus genetic maps based on multiple biparental families are an important resource for genetics research, including genome-wide association analysis and genome sequence assembly. Because different markers are segregating in each family, constructing one linkage map across all families is often slower and more error-prone than a two-step approach in which separate linkage maps are constructed for each family and then merged. A new R package for merging linkage maps, called LPmerge, has been developed and published on CRAN. The LPmerge software uses linear programming (LP) to efficiently minimize the mean absolute error between the consensus map and the component linkage maps. This minimization is performed subject to linear inequality constraints that ensure the ordering of the markers in the linkage maps is preserved. When marker order is inconsistent between linkage maps, a minimum set of ordinal constraints is removed to resolve the conflicts. In a comparison with other leading software on a real barley dataset, the error between the consensus map and four linkage maps was consistently smaller with LPmerge.

Session IX:
Decision Support Platforms for Breeding

Modelling GxE interactions prior to genomic prediction

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Abstract

In relatively little time, genomic prediction has become a major tool in selection strategies. The aim of genomic prediction can be defined as the prediction of phenotypes from full marker profiles, without an intermediate QTL detection step. In the context of more traditional QTL linkage and association mapping it is also possible to predict phenotypes from marker profiles, but then the markers are selected based on the strength of their association with QTLs. An important question is how to use genomic prediction for multiple environments containing genotype by environment interaction. A popular suggestion to generalize genomic prediction to multiple environments is by defining a structure matrix on the environmental dimension of the random genotype by environment effects. This structure matrix on the environmental side complements a structure matrix on the genotype side of the same effects. This latter genotype structure matrix is commonly known as the kinship matrix and is typically based on the full set of molecular markers. We will discuss various options of structuring the environmental side of the genotype by environment effects and relate those options to patterns of genotype by environment interactions.

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Next generation genetic improvement

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Abstract

Genomic selection (GS) is now routine in most major commercial livestock breeding programs. Highly accurate breeding values for Mendelian sampling terms can be obtained with modest marker densities, using simple statistical models, if GS training populations comprise sufficient numbers of (e.g. 10) of close relatives. In practice genotyping is the major additional cost for breeding programs that implement GS. Breeding programs where GS is now routine combine standard low-density marker platforms and genotype imputation algorithms to minimize genotyping costs without compromising accuracy. Given these successes we should now think about we could further increase the rates of genetic progress.

Because GS gives accuracy for breeding values for Mendelian sampling terms that are close to the asymptote, routes to further rates of genetic progress need to go beyond the pursuit of accuracy. In this paper we will use simulation to demonstrate the potential of two other approaches, namely increasing the rate of recombination and the use of genome editing.

Because recombination is relatively rare much of the standing genetic variation (or mutational variance) cannot be utilized for selection. Recombination can be modified through genetic selection or through environmental factors. If recombination rate were inflated more genetic variance would be available for selection upon. Genome editing is a new technology that allows individual nucleotides to be “edited”. This could enable parents to be fixed for undesirable alleles or to have new variation be created in a targeted way.

Our simulations showed that both inflated recombination rate and of genome editing have great potential to increase the rates of genetic improvement.

Notes

The effect of genetic relationships and other factors on genomic prediction accuracy in public plant breeding programs

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Abstract

Genomic selection is a powerful approach to applying markers for selection for complex traits in plant breeding programs. Several factors affect the prediction accuracy of genomic selection models, including marker imputation, training population composition, and heritability of trait evaluations. We have found that genotyping-by-sequencing works well for genomic prediction despite high levels of missing data. Using all marker data and imputing missing data generally works better than filtering markers based in missing data frequency. The relationship between training population and selection candidates also affects prediction accuracy. We show that adding unrelated individuals to the training population can actually reduce prediction accuracy. Methods based on shared linkage phase between training population candidates and selection candidates hold potential for designing better training populations.

Notes

An open platform approach for management and analysis of next-generation genotyping data by breeders and geneticists

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Abstract

The advent of various affordable nucleotide sequencing technologies caused the shift to use these technologies to generate molecular markers for plant breeding and genetic studies. With thousands to millions of SNP marker data being generated by each assay run, the data deluge has been overwhelming for plant breeders and geneticists. Handling huge amount of datasets have been a struggle, and often bioinformaticians are being engaged to deal with the data and its subsequent analyses. At IRRI, we have adopted user-friendly bioinformatics analyses tools that are publicly available and in prevalent use by the medical and human genetic community to address the data and analyses issues that beset non-bioinformatics-savvy scientists. A customized GALAXY is deployed, which currently hosts tools for SNP calling from various genotyping technologies (e.g. Illumina Beadstudio and infinium, Fluidigm, Genotype-by-sequencing, NGS-resequencing) and downstream data manipulation for use by analysis tools that breeders are already familiar with. Analysis tools are being integrated such as TASSEL and R-based GWAS packages. Infrastructure development for systematic data storage is currently being addressed by the Genotyping Data Management System developed under the Generation Challenge Program (GCP), and in the future, by systems developed by the International Rice Informatics Consortium (IRIC). These tools will enable breeders and geneticists to directly analyze their data and quickly make decisions from the results.

Session X:

New Horizons for Crop Improvement

Taking a walk on the wild side: prospecting for traits in the wild progenitor species of cultivated chickpea

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Abstract

All domesticated species are impacted in unintended, often negative ways during domestication and breeding. Their narrow genetic status derives from random demographic processes and from changes in the nature of selection during breeding and cultivation. Loss of adaptive alleles, fixation of deleterious alleles, and low genetic diversity in cultivated species necessarily constrains our ability to expand the cultivation of domesticated species into environments beyond those under which domestication occurred, e.g., into more extreme climates, marginal soils, or with reduced agricultural inputs. We are addressing this need in chickpea, the world's second most important pulse legume, by harnessing the capacity of wild relatives to survive in harsh environments. Chickpea is a global commodity of critical importance to food security in low income, food deficit countries, but also in developed countries. Effective use of wild germplasm in chickpea improvement requires new and systematic surveys of genotypes from natural environments, identification of adaptive alleles to environmental extremes, and incorporation of the diversity of wild alleles into purpose driven populations for trait analysis and breeding. We focus on climate resilience, nitrogen fixation and seed nutrient density, with the goal of more sustainable and stable production systems. We combine upstream ecology and genomics to assemble and characterize wild germplam and to identify and characterize high value genes; population development to remove barriers to use of wild alleles for trait assessment and breeding; and phenotyping and modeling of trait-gene associations to enhance the precision and rate with which wild alleles are applied to crop improvement.

Notes

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Functional genomics in common bean and soybean

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Abstract

Using a variety of genomic and informatics approaches, we are exploring functional aspects of legume genomes with a focus on soybean and common bean. These two species diverged ~20 MYA and share a whole genome duplication (WGD) that is basal to the Papilionoid group of legumes. After their divergence, soybean underwent another WGD ~8 MYA. Thus, these genomes have duplicated genes that derived either from the basal WGD, both soybean and common bean, or from just the most recent WGD, soybean. Using RNA-seq to measure gene transcriptin and methyl seq to measure DNA methylation, we have explored the functional consequences of the WGDs and compared and contrasted the events in the two lineages. One of the first steps was to re-annotate the genomes as many gene predictions are, in fact, transposable elements, or fragments thereof, and complicate functional analyses due to extensive methylation. Results on annotation and the interaction of DNA methylation on gene transcriptional activity and WGDs will be presented and discussed.

Notes

Drought grain yield QTLs in rice

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Abstract

Drought is the most severe constraint reducing rice yield in rainfed environments. The increased occurrence and severity of drought stress have led to a high yield decline in rice in recent years in drought-affected areas. Drought research in rice over the past decade has shifted from improving secondary traits based on selection of root traits, osmotic potential, transpiration efficiency and others and have concentrated on direct selection for grain yield under drought. This approach has led to the successful development and release of 17 drought-tolerant rice varieties in South Asia, Southeast Asia and Africa. These newly developed varieties combined high yield potential and good yield under drought, breaking the myth that drought-tolerant varieties always possess low yield potential. Using grain yield as a selection criterion, 14 QTLs showing a large effect against high-yielding drought-susceptible popular varieties were identified. Six of these (*$qDTY_{1.1}$, $qDTY_{2.2}$, $qDTY_{3.1}$, $qDTY_{3.2}$, $qDTY_{6.1}$, $qDTY_{12.1}$*) showed an effect against two or more high-yielding genetic backgrounds in both the lowland and upland ecosystem, indicating their usefulness in increasing the grain yield of rice under drought. In breeding for drought tolerance, use of identified QTLs through marker assisted approach and standardized managed drought phenotyping of larger introgression BC_2/BC_3 populations allowed selection of lines combining positive interactions between different QTLs as well as between QTLs and background thereby obtaining higher yield under drought. The yield of popular rice varieties IR64 and Vandana has been successfully improved through a well-planned marker-assisted backcross breeding approach and QTL introgression in several backgrounds is in progress. The identification of large-effect QTLs for grain yield under drought and the higher yield increase under drought obtained through the use of these QTLs that has not been reported in other cereals indicate that rice, because of its continuous cultivation in two diverse ecosystems (upland, drought tolerant, and lowland, drought susceptible), has benefited from the existence of larger genetic variability than in other cereals that can be successfully exploited using marker-assisted breeding.

Concluding Lecture

Adoption of modern breeding tools in developing countries: challenges and opportunities

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Abstract

A major challenge facing international agriculture and development is combating hunger by increasing agricultural productivity through using modern technologies to improve crops for harsh environments. With the emergence of crop information systems and related analytical pipelines, the increasing availability of online genotyping services and data analysis, and the boost in global communication with access to web servers and cell phones, some of the technical limitations to adopting modern breeding in developing countries have been overcome. However, it is fair to say that providing access to the technology is only part of the equation, the easiest part I am tempted to say, as there is no adoption without skilled people on the ground and strong support services. Critical factors for sustainable adoption include providing adequate support for potential users to learn how to use the tools, providing an enabling learning and collaborative environment. Such services must include a local component through regional hubs, for example, and one should not underestimate the effort required to change how people operate, even if the benefits of adopting new approaches are quite obvious. Having a clear buy-in from the leadership of target breeding institutions, with clear means to enforce adoption, is also key for effective change in mind-set and behavior.

Some of these challenges and opportunities will be presented and discussed in the practical context of the Integrated Breeding Platform initiative. As we come to understand more about the complex issues inherent to the transfer and application of new plant biotechnologies to developing countries, we recognise that many solutions can be found only through true and innovative partnerships.

Notes

Posters

List of Posters

S No	Title	Authors*
1	Center of Excellence in Genomics (CEG) @ ICRISAT for enhancing adoption of molecular breeding in developing countries	Varshney RK, Thudi M, Chitikineni A, Rathore A, Senthilvel S, Shah T, Grabdo S
2	Bioinformatics resources @ ICRISAT for Integrated breeding – A sorghum case study	Shah T, Ramu P, Deshpande S, AshokKumar A, Prakash AB, Reddy P, Sawkins M, McLaren G, Hash CT, Varshney RK, Ware D, Grando S
3	Biometrics resources @ ICRISAT for delivering statistically sound research design and data analysis for quality science	AnilKumar V, Das RR, Maraboina R, Reddy TM, Dasari R, Rondedla A, Rathore A
4	Genetic resources conservation and strategies for enhanced utilization in crop improvement	Upadhyaya HD, Sharma S, Dwivedi SL, Singh S, Varshney RK, Vetriventhan M, Pattanashetti SK, Lalitha N
5	Next generation genomics for chickpea (*Cicer arietinum* L.) improvement	Varshney RK, Kudapa H, Roorkiwal M, Thudi M, Chitikineni A, Odeny DA, Sabbavarapu MM, Jaganathan D, Singh MK, Katta KM, Agarwal G, Khan AW, Ganga Rao NVPR, Gaur PM, Upadhyaya HD, Rathore A, Krishnamurthy L, Shah TM, Sharma M, Samineni S, Siambi M, Waliyar F
6	Present status of integrated breeding in chickpea	Gaur PM, Srinivasan S, Thudi M, Sabbavarapu MM, Roorkiwal M, Jaganathan D, Singh MK, Krishnamurthy L, Chitikineni A, Gangarao NVPR, Kudapa H, Kimurto P, Fikre A, Jayalakshmi V, Mannur DM, Vijayakumar AG, Varshney RK
7	Advances in genomics for pigeonpea improvement	Varshney RK, Saxena RK, Singh VK, Kumar V, Patel K, Obala J, Parupalli S, Kaoneka SR, Saxena KB, SameerKumar CV, Chanda V, Upadhyaya HD, Sharma M, Rathore A, Ghanta A, Dharmaraj PS, Yamini KN, Muniswamy S, Tongoona P, Shimelis HA

8	Infusing genomics in hybrid breeding program of pigeonpea (*Cajanus cajan*)	Saxena RK, Sameerkumar CV, Saxena KB, Lekha PT, Sinha P, Singh VK, Katta MAVSK, Kumar V, Hingane A, Srikanth S, Kulshreshtha A, Krishnamurthy L and Varshney RK.
9	Development and deployment of genomic resources for groundnut improvement	Varshney RK, Pandey MK, Janila P, Khera P, Sriswathi M, Shasidhar Y, Upadhyaya HD, Rathore A, Sudini H, Nayak S, Vishwakarma MK
10	Introgression of *FAD* (*Fatty Acid Desaturase*) mutant alleles for enhanced oil quality in groundnut using marker-assisted backcrossing	Janila P, Pandey MK, Upadhyaya HD, Murali TV, Manohar SS, Sriswathi M, Khera P, Radhakrishnan T, Ganesamurthy K, Manivannan N, Vasanthi R, Dobariya KL, Bera SK, Misra JB, Nigam SN, Varshney RK
11	Translating genomics and molecular breeding advances to farmer preferred cultivars in pearl millet	Srivastava RK, Hash CT, Varshney RK, Vadez V, Blümmel M, Yadav R, Yadav OP, Nepolean T, Rajaram V, Sharma R, Gupta SK, Rai KN, Bhattacharjee R, Senthilvel S, Supriya, Kumar S, Narasu ML, Yadav RC, Singh G, Boubacar AK, Haussmann BIG
12	Pearl millet improvement: research strategy and Impact	Pearl millet Improvement team at ICRISAT and Partners (by Gupta SK)
13	Genomics application for sorghum improvement	Deshpande S, Ramu P, Weltzein-Rattunde E, Rattunde F, AshokKumar A, SrinivasaRao P, Varshney RK, Grando S
14	*In silico* identification of candidate genes involved for grain Fe and Zn concentration in sorghum using reported cereals gene homologs	Anuradha K, Prakash B, Deshpande S, Ramu P, Shah T, AshokKumar A, Grando S
15	The CGIAR Research Program on Grain Legumes	Ellis N, Nagaraji S, Beebe S, Ghanem M, Okori P, Chaturvedi SK, Tamo M, Agrawal SK, Gaur P, Gopalakrishnan S, Kumar CVS and Varshney RK
16	The CGIAR Research Program on Dryland Cereals	Sivasankar S, Nagaraji S, Cisse N, Hash CT, Grando S, Ojulong H, Verma R, Gupta SK and Kumar A

*Present authoring is underlined

Center of Excellence in Genomics (CEG) @ ICRISAT for enhancing adoption of molecular breeding in developing countries

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Abstract

Molecular breeding is being successfully deployed at several advanced research institutes (ARIs) and/or private sectors in developed countries or by some CGIAR centres in developing countries. Although adequate genomic information is available in almost all crop species, NARS partners in developing countries are yet to adopt molecular breeding due to mainly lack of physical infrastructure and limited expertise in molecular breeding. The Center of Excellence in Genomics (CEG, http://www.icrisat.org/ceg) at ICRISAT, therefore, is engaged to address above mentioned issues by offering marker genotyping services on cost-to-cost basis as well as conducting training courses in modern breeding. With state-of-art marker genotyping platforms like ABI 3730 DNA Genetic analyzer (SSR genotyping), diversity arrays technology (DArT) platform (DArT genotyping), Illumina BeadXpress (SNP genotyping), Illumina MiSeq (genotyping-by-sequencing; Illumina HiSeq 2500 will be installed in coming months), CEG-ICRISAT has provided genotyping services to a range of partners including NARS, ARIs, small and medium enterprises (SMEs) and CGIAR centers in many countries. Similarly after organizing 10 training courses using a range of tools from Integrated Breeding Platform (IBP) and other Open Access programmes, 257 scientists from several countries of sub-Saharan Africa and South Asia have been trained. Such efforts of CEG-ICRISAT are expected to enhance adoption of molecular breeding in developing countries.

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Bioinformatics resources @ ICRISAT for integrated breeding – A sorghum case study

Shah T[1*], Ramu P[1], Deshpande S[1], AshokKumar A[1], Prakash AB[1], Reddy P[1], Sawkins M[3], McLaren G[3], Hash CT[2], Varshney RK[1], Ware D[4], Grando S[1]

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Abstract

The critical component of any molecular breeding program is the effective management and utilization of germplasm and phenotyping data with its associated marker information and genotyping data. The Integrated Breeding Platform (IBP) provides a customizable workflow based system (IBWS) for the sorghum community to collate, manage, analyze and share data. Electronic data capture systems, use of ontologies, a curated database and decision support systems for molecular breeding programs are some of the salient features of the IBWS.

The Genotyping Data Management System (GDMS) which is an integral part of the IBWS, focuses on handling the low to high throughput genotyping data from different marker systems and platforms (SSRs, DArTs and SNPs). In addition to the marker, genotyping and fingerprinting information, the system also handles maps, QTLs and allows for exchange of data with the analytical tools.

Genome browser and comparative map viewer from GMOD consortium are integrated together to access ultra-high throughput data generated through the Next Generation Sequencing (NGS) such as the genotyping by sequencing (GBS), RAD (Restriction site Associated DNA) Sequencing, etc. This allows the scientists to use the genome sequence information and anchor all the marker, QTL, gene annotations and expression data to increase their breeding efficiency.

As the volume of data generated increases significantly, prototypes are being developed for the analysis tools (genome-wide association studies (GWAS) and genomic selection (GS)) and underlying databases that will use the iPlant Cyberinfrastructure and the architecture of comparative genomics databases such as Gramene.

Notes

Biometrics resources @ ICRISAT delivering statistically sound research design and data analysis for quality science

AnilKumar V, Das RR, Maraboina R, Reddy TM, Dasari R, Rondedla A, Varshney RK, Rathore A*

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Abstract

Biometrics deals with the application and development of statistical tools for efficient and appropriate research design and data analysis in biological and allied sciences. Biometrics Unit, ICRISAT provides biometric inputs to help ICRISAT researchers to achieve quality, credibility and cost-effectiveness in their scientific research. Biometrics Unit is a central research and analysis support facility for all ICRISAT locations. We also provide research and analysis support to partnering NARS institutes.

Biometrics Unit assists research programs by providing inputs in terms of experiment planning, data management, data analysis, publication writing and project proposal development. We help researchers by delivering timely and appropriate data analysis for proper reporting, interpretations and publishing. We also ensure accountability for data quality and statistical soundness in publications. Some of the analysis offered are Single and Multi-Site GxE Analysis, Multivariate Analysis, Spatial Analysis, On-Farm Trial Analysis, Molecular Marker Analysis, Molecular Diversity Analysis, Genetic Linkage Map, QTL/Linkage Mapping, Genome Wide Association Studies (GWAS), Genomic Selection (GS) and etc.

Strong Data Management support is also a key activity of Biometrics Unit. Data management support includes data compilation, cleaning, curation, breeding data management, online sharing and making inferences through several open sources and propriety software such as Dataverse and aWhere platforms.

Biometrics Unit in heavily involved in capacity building activities of ICRISAT, partnering scientist and students. We conducts regular training each year across the globe with special emphasis on ASIA, ESA and WCA. Biometrics Unit has conducted 16 trainings programs in last 5 years. Biometrics Unit develops appropriate statistical methods and bio-computing procedures and programs where needed but not available. In collobration with genomics scientists we are developing several molecular breeding tools including ISMU2.0, ISMU1.0 and iMAS2.0.

Notes

Genetic resources conservation and strategies for enhanced utilization in crop improvement

Upadhyaya HD*, Sharma S, Dwivedi SL, Singh S, Varshney RK, Vetriventhan M, Pattanashetti SK, Lalitha N

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Abstract

Global food production will need to double to feed ~9 billion people by 2050. There is urgent need to increase food production, requiring development of better adapted, higher yielding, and resource-use-efficient crop cultivars. To this end, effective utilization of plant genetic resources in breeding is the most sustainable way to conserve biodiversity and increase food production. ICRISAT has 120,454 accessions of its mandate crops and six small millets preserved in its genebank, of which 104,000 unique accessions submitted as safety duplicate for conservation to Svalbard Global Seed Vault, Norway. Managing and utilizing such large diversity is the greatest challenge to germplasm curators and crop breeders. Promoting use of germplasm in crop improvement programs is a major concern as the breeders are reluctant to use germplasm largely either due to lack of reliable information on economic traits besides linkage drag or due to breakdown of co-adapted gene complexes. The reduced subsets, representing diversity in the germplasm collection of a given species preserved in genebank, in the form of core or mini core collections are the ideal genetic resources for discovering new sources of variations for use in crop improvement programs. Two decades of research at ICRISAT has led to the establishment of core and mini core collections or genotype-based reference sets and their subsequent evaluations has resulted several new sources of variations for resistance to abiotic and biotic stresses, some with specific adaptation and/or nutritionally seed-dense types. The advances in genomics on these crops are now assisting researchers dissect population structure, diversity, and marker-trait associations for agronomically beneficial traits using association genetics, i.e., SNPs and candidate genes associated with many agronomically beneficial traits detected in sorghum, with similar studies in progress in chickpea and groundnut. Wild relatives harbor genes for resistance to diseases and insect pests. Pre-breeding research has been initiated to enrich cultigens genepool. Resistance to pod borer in chickpea and pigeonpea or to late leaf spot in groundnut has been successfully introgressed. Synthetics in groundnut are recycled to further enrich genepool for enhanced productivity. Over 1.4 m seed samples provided to researchers in 147 countries have led to the release of 75 germplasm lines as cultivars in 39 countries.

Notes

Next generation genomics for chickpea (*Cicer arietinum* L.) improvement

Varshney RK[*,1], Kudapa H[1], Roorkiwal M[1], Thudi M[1], Chitikineni A[1], Odeny DA[2], Sabbavarapu MM[1], Jaganathan D[1], Singh MK[1], Katta KM[1], Agarwal G[1], Khan AW[1], Ganga Rao NVPR[2], Gaur PM[1], Upadhyaya HD[1], Rathore A[1], Krishnamurthy L[1], Shah TM[1], Sharma M[1], Samineni S[1], Siambi M[2], Waliyar F[3]

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Abstract

Large scale genomic resources including draft genome sequence, re-sequencing of 90 lines, comprehensive transcriptome assembly and high density genetic maps have been developed for chickpea. Linkage mapping and genome wide association studies (GWAS) are being used for trait mapping. One genomic region ("QTL-hotspot") harboring QTLs for several drought tolerance traits has been identified and genotyping-by-sequencing (GBS) approach is being used to fine-map this region. Introgression of this region in to elite chickpea lines have shown yield improvement under irrigated as well as rainfed conditions. Similarly QTLs controlling important biotic stresses like *Fusarium wilt* (FW) and *Ascochyta blight* (AB) have been mapped and used for introgression. In parallel, association mapping approaches using genotyping data for 1882 markers and sequence data for 10 genes together with phenotyping data for 24 drought tolerance traits on the reference set comprising 300 genotypes provided 335 significant marker-trait associations (MTAs). In addition, 5X- 10X coverage whole genome re-sequencing data have been generated on the reference set that is being used for GWAS analysis. In order to deploy genomic selection (GS), a training population of 320 elite breeding lines was phenotyped at two locations for yield related traits. Generated genome-wide marker profiling data (total >3000 markers) along with phenotyping data was used with a range of regression and bayesian based statistical methods to predict genomic estimated breeding values. Furthermore, several transcriptomics and functional genomics approaches such as RNA-seq, Massive Analysis of cDNA Ends (MACE) with parental genotypes of mapping populations as well NILs have provided some candidate genes for biotic and abiotic stress response that are being validated through quantitative real time PCR (qRT-PCR) and TILLING approaches. Genetic mapping of these candidate genes may provide perfect markers for use in chickpea molecular breeding.

Present status of integrated breeding in chickpea

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Abstract

The large scale genomic resources developed during recent years have made it possible to integrate modern breeding approaches in chickpea improvement. A genomic region controlling root traits and several other traits related to drought tolerance contributing >30% phenotypic variation has been introgressed into three popular chickpea varieties, JG 11 and KAK 2 from India and Chefe from Ethiopia, using marker-assisted backcrossing (MABC). A set of 20 BC_3F_4 introgression lines of JG 11 was evaluated at 3 locations in India (Patancheru, Nandyal, Gulbarga) and one each in Kenya (Koibatek) and Ethiopia (Debre Zeit) during 2011-12. Another set of 20 BC_3F_4 introgression lines of JG 11 lines was evaluated at 4 locations in India (Patancheru, Nandyal, Gulbarga, Dharwad) during 2012-13. Several progenies with significantly higher yield than JG 11 were identified at each location and in each growing condition (rainfed/irrigated). In addition, pyramiding of resistance to fusarium wilt and ascochyta is being carried out using MABC. A marker-assisted recurrent selection (MARS) program is also in progress in two crosses (JG 11 × ICCV 04112 and JG 130 × ICCV 05107) involving four elite desi genotypes. To pyramid superior alleles of the favorable QTLs identified based on F_3 genotyping data and F_5 phenotyping data, a set of eight lines were selected and two cycles of intercrossing completed. A multi-parent advanced generation inter-cross (MAGIC) population has been used to develop over 1100 lines at ICRISAT. Twenty-eight two-way, 14 four-way and 7 eight-way crosses were made to develop this MAGIC population from 8 parents which include cultivars and elite breeding lines from India and Africa. The MAGIC lines constitute a valuable genetic resource for trait mapping and gene discovery. In addition, these are being used directly in breeding programs. ICRISAT has shared F_4 seed from 4-way and 8-way crosses with several institutes in South Asia and sub-Saharan Africa. We expect that the use of integrated breeding approaches will continue to increase in chickpea improvement for accelerating the breeding process and genetic gain.

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Notes	Advances in genomics for pigeonpea improvement

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Abstract

Pigeonpea is the sixth most important legume crop in the world with a total production area of 4.75 M ha. Pigeonpea crop productivity is challenged by several biotic (*Fusarium* wilt (FW) and sterility mosaic disease (SMD)) and abiotic (water logging and soil salinity) stresses. In past, molecular breeding could not be deployed in pigeonpea breeding due to non-availability of molecular markers associated with trait, partly because of non-availability of genomic resources and low level of polymorphism. Therefore, in recent past, ICRISAT and its partners have developed large-scale genomic resources such as genome sequence, simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) based markers, high quality consensus genetic map, quantitative trait loci (QTL) maps and transcriptomic resources. In order to identify the genomic regions responsible for the trait of interest (FW and/or SMD resistance), three bi-parental mapping populations each consisted of 188 lines have developed. Further, to develop high resolution mapping population we are developing one nested association mapping (NAM) population of 2,000 lines derived from 10 elite crossing combinations. Additionally, multi-parent advanced generation inter-cross (MAGIC) population with 500 lines derived from 8 elite and diverse founder parents and two introgression libraries (ILs) or advanced back-cross quantitative trait loci (AB-QTL) mapping population of 149 and 183 lines derived from C. acutifolius and C. cajanifolius, respectively are being developed for enhancing genetic diversity in cultivated gene pool from landraces and wild species respectively. Reference set of 300 lines representing global diversity of *Cajanus* germplasm is also being utilized for genome-wide association study (GWAS) for mapping economically important traits. Multi-location phenotyping for targeted traits is being conducted under field conditions. Detailed analysis of both genotyping and phenotyping data will provide useful information on marker(s)/ gene(s)/ haplotype(s)- trait association that can be used in future genomic-assisted breeding programs.

Infusing genomics in hybrid breeding program of pigeonpea (*Cajanus cajan*)

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Abstract

Pigeonpea is an important pulse crop, well-suited for rainfed and semi-arid cropping system. The released draft genome sequence and commercial cytoplasmic nuclear male sterility (CMS)-based hybrids has been the significant contributions of ICRISAT. The pigeonpea hybrids ICPH 2671, ICPH 2740 and ICPH 3762 have become popular by outperforming the local varieties with 30-40% higher yield in Asia under rainfed ecosystem. Breeding heterotic hybrids conventionally for different niches is a herculean task. Genomic approaches have been initiated to accelerate the hybrid breeding programs. With the large scale commercial hybrid seed production, ensuring the quality of F_1 seed is of utmost importance. Towards this, marker based hybrid purity assessment kit has been developed for ICPH 2671. Identification of potential restorers, marker based purity assessment for hybrids, CMS (A-) and their maintainer (B-) lines derived from A4 systems are being carried out. In this regard, mitochondrial genomes of wild species (C. *cajanifolius*), the source of CMS, hybrid, A- and B-line have been sequenced and candidate genes (*nad4l* and *nad7a*) identified. In addition, a heterotic pool is also being generated using whole genome re-sequencing of parental lines of hybrids which will assist the existing hybrid breeding efforts. The advantage of two line hybrid breeding system has encouraged the evaluation and characterization of a temperature-sensitive male sterile line for its potential use. Various studies are being carried out at the molecular and cellular level to identify putative candidate genes that will help elucidate the underlying molecular mechanism. These efforts promise accelerated hybrid breeding program in Asia and other regions of the semi arid tropics

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Development and deployment of genomic resources for groundnut improvement

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With an objective to increase breeding efficiency for accelerated development of superior genotypes, ICRISAT and its partners have developed and deployed thousands of genetic markers such as SSRs (>6000), DArTs (>15,000 features) and SNPs (90 KASP assays) in several genetic applications. ICRISAT is also participating in the global efforts for genome sequencing of diploid and tetraploid groundnut. The above efforts resulted in development of many genetic maps (82-198 loci), consensus maps (>3600 loci) and identification of QTLs for drought tolerance related traits (153 QTLs) and foliar disease resistance (143 QTLs). Efforts are underway to conduct genetic and QTL mapping for oil content, oil/nutritional quality, seed dormancy, nodulation, disease resistance, drought tolerance and pod yield. Association mapping conducted using large scale genotyping (4597 DArT features and 154 SSRs) and multiple season phenotyping data (51 traits) identified a total of 524 highly significant marker-trait associations (MTAs). Further efforts are in progress to identify MTAs at high genetic resolution through comprehensive genome-wide association studies (GWAS) in diverse groundnut global germplasm sets (ICRISAT reference set, minicore collections of USA and China). Three elite cultivars (TAG 24, JL 24 and ICGV 91114) were improved through MABC approach by introgressing a major QTL for rust resistance. The introgression lines showed high rust resistance (disease score of 2.0 on 1.0-9.0 scale) along with significant increase in pod yield (56-96%). MABC efforts to develop lines with high oleate trait individually as well as pyramiding with genes/QTLs for two foliar diseases (LLS and rust) are underway. In addition, efforts have been initiated to deploy genomic selection for improvement of complex traits such as yield under drought stress.

Introgression of FAD (*Fatty Acid Desaturase*) mutant alleles for enhanced oil quality in groundnut using marker-assisted backcrossing

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Abstract

Peanut (*Arachis hypogaea* L.) kernels contain 48-50% oil, and oleic (O) and linoleic (L) fatty acids constitute about 80% of the oil. High O/L (oleic to linoleic acid) ratio has benefits to consumer's health as well as food processing industry. In general, the O/L ratio in normal peanut is about 2.0, however, in case of genotypes with FAD (*Fatty Acid Desaturase*) gene mutants it can go as high as >20.0. Allele specific and cleaved amplified polymorphic sequence (CAPS) markers specific to FADA and FADB mutant alleles were validated in a set of genotypes and were deployed to increase O/L ratio through marker-assisted backcrossing (MABC). ICRISAT along with four other national centers in India initiated MABC efforts to enhance O/L ratio in six elite genotypes that have >50% of seed oil content. Allele-specific markers for FADA and FADB mutant alleles differentiated the genotypes possessing mutations in A and B genomes, respectively. These markers were used for confirmation of F_1 plants as well as for selection of heterozygotes among backcrossed BC_1F_1, BC_2F_1 and BC_3F_1 plants. Since allele specific markers were unable to differentiate heterozygous and homozygous individuals because of their dominant nature, the co-dominant CAPS markers were deployed to select the homozygous alleles of the high O/L ratio parent in BC_2F_2 populations. A three step-strategy has been proposed to identify homozygotes in $BC_1/_2/_3F_2$ populations for optimization of the resources.

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Translating genomics and molecular breeding advances to farmer preferred cultivars in pearl millet

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Abstract

Pearl millet is a hardy cereal capable of growing in the hottest, driest and harshest climatic conditions. With investment of relatively limited resources, significant progress has been made towards generation of genomic resources and molecular breeding. Genomic resources like EST libraries from well-characterized drought-tolerant and -sensitive mapping population parents have been developed. EST-SSR, in-del, and SNP sequence polymorphisms between have been established. New EST-SSR primer pairs with the prefix name IPES =ICRISAT Pearl millet EST Stress), detecting >100 mapped loci with the prefix name Xipes have been developed. A total of 5,800 putative SNPs were identified. More than 20,000 SNPs using GBS and RAD sequencing strategies have been mined. Mapping populations like chromosome segment substitution lines (CSSLs), pearl millet inbred germplasm association panel (PMiGAP), and bi-parental RIL populations have been developed. Pearl millet genome is being sequenced. The first draft assembly of the world reference genotype Tift23D2B1-P5, and generation of sequence data on PMiGAP and hybrid parental lines is in progress. Genetic linkage maps and trait mapping have been done for downy mildew, blast, and rust resistance, drought tolerance and its components, flowering time, stover quality, yield components and grain Zn and Fe density. Mapping for flowering stage heat tolerance, striga resistance, low P tolerance, and heterotic gene pool formation is in progress. QTLs introgression lines and their improved test-cross hybrids for downy mildew (GHB 538, HHB 67 second cycle improvement) and blast (HHB 146) resistance is under advance stages of multilocation testing under national testing system in India.

Pearl Millet improvement: research strategy and impact

Pearl millet Improvement team at ICRISAT and Partners

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is a major warm-season cereal grown on about 30 million ha worldwide, largely in the arid and semi-arid tropical regions of Africa (18 million ha) and Asia (11 million ha) with India accounting for largest area (>9 million ha). Pearl millet in these regions is primarily grown for grain production to serve as a major source of dietary energy and nutrition, although stover is also being increasingly valued as an important fodder resource. Open-pollinated varieties (OPVs) and hybrids are two broad cultivar options in pearl millet with hybrids having 25-30% grain yield advantage over OPVs. Therefore, the major emphasis in India has been on hybrid development, with grain yield as the highest priority trait. The diversification of cultivar base with mostly dual-purpose hybrids has led to 24 kg/ha/year of grain yield increase during the last 15 years as compared to only 5.2 kg/ha/year of yield increase during the pre-hybrid phase of 1950-1965.

The strategy in India is to develop and disseminate diverse range of improved breeding lines and hybrid parents and their extensive use both by the public and private sector research organizations in hybrid development, breeding for resistance to downy mildew [Sclerospora graminicola (Sacc. Schroet.] has been an integral part of pearl millet improvement in India. Diversified parental lines with downy mildew (DM) resistance have kept at bay the periodic DM epidemics witnessed in 1960s and 1970s. Recently, leaf blast (Pyricularia grisea (Cooke) Sacc.) has emerged as serious a problem as DM in India. Pathogenic variability for this disease has been characterized, effective screening techniques have been developed, resistance sources have been identified, and resistance breeding has been initiated. There are other diseases of sporadic occurrence and minor importance for which screening techniques have been developed and resistance sources have been identified, but no substantial resistance breeding efforts have been made. In the African regions, major emphasis has been on OPV development. Considering the limited gains from OPV development, hybrid breeding work has now been initiated for Africa also. Hybrid cultivars in these regions will face the same biotic problems of DM and blast as in India. Further, there are greater problems of Striga and insect-pests such as head miner (Heliocheilus albipunctella de Joannis) and stem borer (Coniesta ignefusalis Hampson), which will pose greater challenges in pest resistant hybrid development as it has been in case of pest resistant OPV development, especially in the Western and Central African region. While pearl millet improvement for the relatively better endowed environments will continue to be of the highest priority in SA hybrid program, relatively greater emphasis than in the past is now being placed to develop parental lines and hybrids adapted to arid zone which still has unpredictable seed market, and there is not as well developed research infrastructure and germplasm base.

Climate change and associated problems of rising temperatures, water shortages, recurrent droughts, and soil salinity are increasingly becoming more serious problems to agricultural production. Pearl millet is especially endowed with climate-change resilient attributes. For instance, among the major cereals, it is most drought tolerant, and also most salinity tolerant, next only to barley. It is also most tolerant to high air temperatures. Pearl millet is grown as a summer season crop in parts of Gujarat, Rajasthan and Uttar Pradesh states of India where air temperatures during flowering often exceed 42oC. Majority of the hybrids have very poor seed set under such environments. However, some hybrids with excellent seed set have been identified and become commercial. These give 4-5 t/ha grain yield under high management conditions as compared to the national average of just about a ton under rainfed conditions in the normal rainy season. Genetic variability for reproductive-stage heat tolerance in germplasm, and in improved populations and elite breeding lines has been identified, paving the way for heat tolerance breeding. These materials have potential uses in breeding heat tolerant cultivars in other parts of the world facing similar environmental challenges. Genetic variability for tolerance to salinity and terminal drought that has the most detrimental effect on grain yield has also been identified. No efforts so far have been made in breeding for salinity tolerance. Conventional breeding efforts in breeding for terminal drought tolerance have met with little success. Taking recourse to biotechnological intervention, QTL for panicle harvest index, a measure of terminal drought tolerance, have been identified. These need to be validated for their effects in different genetic backgrounds and in the target drought-prone environments to set the stage for their systematic deployment in the parental lines of hybrids. Revolution in genomics technology may further accelerate the process of identification of the genomic regions associated with terminal drought tolerance and their cost-effective and rapid deployment.

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Genomics application for sorghum improvement

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Abstract

Sorghum, 'camel of cereals' is livelihoods for several million farm-families in semi-arid regions of Africa and Asia. Recent advances in genomics including re-sequencing, transcriptome and utilizing New Generation Sequences (NGS) tools for genotyping-by-sequencing (GBS) has changed the landscape of moleculr marker application from specific loci/genomic regions to whole genome scale. The recent success in development and release of striga resistance cultivars with introgression of 2 to 3 striga resistance QTLs in Sudan has served as catalyst. Efforts for global germplasm collection characterization using GBS has helped in improved understanding of the genetic diversity and helped to close the genomic region window (harboring several genes) governing several agronomic traits. With availability of more than 100 sorghum genomes and 40 transcriptomes (through re-sequencing approach) will further help us to identify candidate genes for these traits. Utilizing TILLING and Eco-TILLLING population further efforts would be made to pin down the function of these gens and possibly identify better alleles for the traits. Current progress in developing new BCNAM population, introgression of staygreen QTLs , shoot fly resistance QTLs, bmr genes and their further pyramiding along with additional re-sequencing/transcriptomic studies would help address some of important production constraints for sorghum. The development of breeder-friendly marker systems for NARS partners would for major research output from this research.

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In silico identification of candidate genes involved for grain Fe and Zn concentration in sorghum using reported cereals gene homologs

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Abstract

Sorghum is among the top 10 crops that feed the world. It is a good source of energy, protein, carbohydrate, vitamins and minerals including the trace elements. It is one of the cheapest and sustainable options to combat the micronutrient malnutrition, particularly Fe and Zn in predominantly sorghum eating populations. Identification of genes governing grain Fe and Zn concentration in sorghum is of interest. Earlier studies on other cereals showed role of number of genes for grain Fe Zn homeostasis and uptake, transport and loading but so far no reports available on genomic regions/ QTLs and candidate genes governing sorghum grain Fe and Zn concentration.

A homology (*In-silico*) search of 91 candidate genes involved in governing grain Fe and Zn concentration in cereals (Rice, wheat, maize and barley) was performed on sorghum genome. Blast was performed against the sorghum genome database and downloaded Fe and Zn gene sequences as query. Total 77 hits were found on sorghum genomic regions, which are involved in Fe and Zn homeostasis. Highest number of genes found on chromosome 1 (24 blast hits) and least on chromosome 8. Genes associated with grain Fe and Zn concentration from maize and wheat showed 100 percent homology on sorghum genome. On sorghum genome, highest number of hits were identified on chr 1 and 6, from all the 4 crops. Out of 24 hits on chromosome 1, 10 hits (from genes of wheat, barley, rice, maize) pertaining to Nicotianamine synthase (NAS) gene were in same general genomic region around 61Mbp on sorghum chromosome 1. Blast hits on sorghum chromosomes from genes of wheat, barley, rice, maize pertaining to Nicotianamine synthase (NAS), Zip (Zn transporter protein) and YSL (yellow stripe like) gene were shown higher percent homology. These could be putatively associated with Fe and Zn grain concentration in sorghum. Candidate genes (Homologs) identified in this study can be used for the development of functional markers for improving grain Fe and Zn concentration in sorghum.

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The CGIAR Research Program on Grain Legumes

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Abstract

Grain legumes are protein-rich foods that balance cereal-based diets and are the least resource demanding option to improve the nutrition of people with few resources. This dietary benefit is complemented by micronutrients and other bioactive compounds in legume seeds. Grain legumes supply up to 60% of daily protein intake for the poor in parts of sub-Saharan Africa, but only 13% for hundreds of millions of poor in South Asia. Grain legumes can take their nitrogen from the air in place of fertilizer, contributing enormously to sustainable intensification and raising food production. Legumes can be sold at a good price yet tend to be farmed on the least productive land (which they enrich) thus they can benefit resource poor farmers.

The CGIAR Research Program on Grain Legumes gathers researchers working on the major legume crops of the developing world who can benefit from the common biology and shared market systems. The Research Program on Grain Legumes coordinates the activities of four CGIAR Centers ICRISAT, CIAT, ICARDA and IITA linking these with research partners in many countries, notably the Ethiopian Institute of Agricultural Research, the Indian Council of Agricultural Research, the Turkish General Directorate of Agricultural Research, and EMBRAPA the Brazilian Agricultural Research Organization, all of whom are represented in the management of the research program.

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The CGIAR Research Program on Dryland Cereals

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The CGIAR Research Program on Dryland Cereals operates in the dryland regions of Africa and Asia with the goal of improving food security, income, nutrition and health of the smallholder farmers in these regions. The target crops of the program, barley, finger millet, pearl millet and sorghum are climate-hardy, resilient, micronutrient-rich cereals. Sorghum and millets are also gluten-free. Although grown for a variety of end uses in a number of countries across the world, their resilience to extremes of drought and heat, and to poor and degraded soils, make them “insurance crops” in areas where poor agricultural conditions prevail, as in the drylands of sub-Saharan Africa and Asia.

Dryland Cereals is a partnership between two members of the CGIAR Consortium – ICRISAT as lead center, and ICARDA, along with a number of public and private institutes and organizations, governments, and farmers globally.

Notes

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4th International Workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement

February 19-21, 2014

ICRISAT, Patancheru, India

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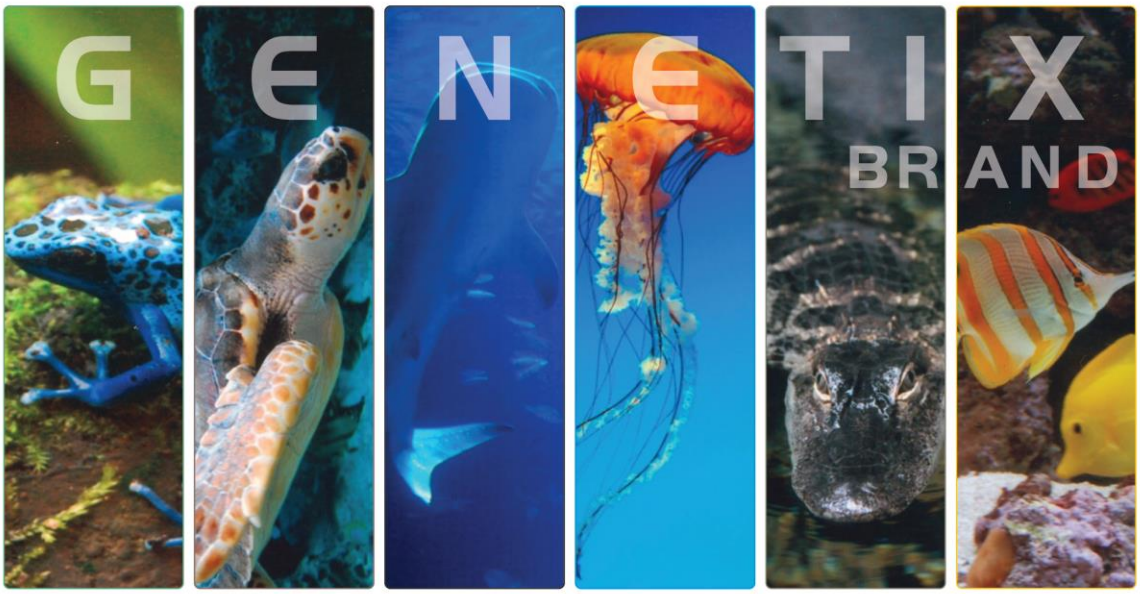

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Genomics

Genome sequences

- Pigeonpea - 72.7% coverage *(Nature Biotech 2012, 30:83-89)*
- Chickpea - 73.8% coverage *(Nature Biotech 2013, 31:240-246)*
- Sorghum - 94.5% coverage (available through US-led team)
- Pearl millet (in progress)
- Groundnut (in progress)
- Mitochondrial genomes of A-, B- and R-lines of pigeonpea

Marker resources

- >10,000 SSRs across mandate crops
- >10,000 SNPs across mandate crops
- High density DArT arrays in all mandate crops
- KASPar, Illumina GoldenGate and VeraCode assays for chickpea, pigeonpea and groundnut

Molecular breeding

- Chickpea - advanced lines for drought tolerance and resistance to *Fusarium* wilt and *Aschochyta* blight
- Groundnut - advanced lines for resistance to rust
- Sorghum - advanced lines for drought tolerance and resistance to shoot fly and *Striga*
- Pearl millet - HHB67 Improved line for downy mildew resistance

Decision support tools

- iMAS for trait mapping
- ISMAB for molecular breeding
- GDMS for data management
- ISMU for mining SNPs based on NGS
- Open data

Genotyping

Crops

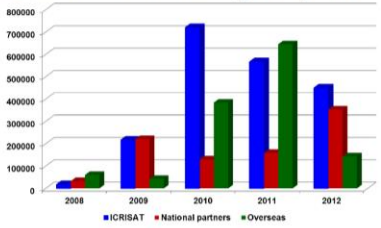
- Rice
- Wheat
- Maize
- Barley
- Sorghum
- Pearl millet
- Finger millet
- Oats
- Chickpea
- Groundnut
- Pigeonpea
- Sweet potato
- Tomato
- Potato
- Onion
- Garlic
- Cassava
- Tobacco
- Cotton
- Mango
- Banana
- Guava
- Litchi
- Mulberry

Projects

- Fingerprinting of cultivars
- Genetic diversity analysis
- Linkage mapping
- Association mapping
- QTL mapping
- Marker-assisted selection
- Genomic selection

Beneficiaries

- Researchers from national agricultural research systems in Africa, Asia, Europe and Latin America
- Agricultural research institutes
- Research foundations
- Universities
- Small-scale breeding companies

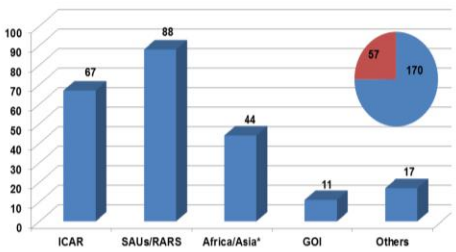


Overview on data generated for SSR and DArT markers

Capacity building

Students from sub-Saharan Africa and South Asia

Participants in training courses



227 scientists (57 women) trained

ICRISAT
Science with a human face

International Crops Research Institute for the Semi-Arid Tropics

Inclusive Market-Oriented Development (IMOD) – our approach to bringing prosperity in the drylands.

ICRISAT is a member of the CGIAR Consortium.

May 2013

About **ICRISAT**

ICRISAT
Science with a human face

International Crops Research Institute for the Semi-Arid Tropics

CGIAR

ICRISAT is a member of the CGIAR Consortium

The **International Crops Research Institute for the Semi-Arid Tropics** (ICRISAT) is a non-profit, non-political organization that conducts agricultural research for development in Asia and sub-Saharan Africa with a wide array of partners throughout the world. Covering 6.5 million square kilometers of land in 55 countries, the semi-arid tropics have over 2 billion people, of whom 644 million are the poorest of the poor. ICRISAT innovations help the dryland poor move from poverty to prosperity by harnessing markets while managing risks – a strategy called Inclusive Market-Oriented Development (IMOD).

ICRISAT is headquartered in Patancheru near Hyderabad, Andhra Pradesh, India, with two regional hubs and five country offices in sub-Saharan Africa. It is a member of the CGIAR Consortium. CGIAR is a global research partnership for a food secure future.

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