OSMANIA UNIVERSITY
100 YEARS
Centenary Celebrations
1917-2017

CELEBRATING 50 yrs
DEPARTMENT OF GENETICS

ज्ञान-विज्ञान विमुक्तये

National Conference on

MOLECULAR INSIGHTS IN GENETICS AND BIOTECHNOLOGY

- EMERGING TRENDS AND FUTURE PROSPECTS

27 and 28th February 2017

ABSTRACTS & SOUVENIR

DEPARTMENT OF GENETICS
& BIOTECHNOLOGY
Osmania University
Hyderabad - 500007,
Telangana State, INDIA

SCIENTIFIC PROGRAMME

Venue	:	**Mekaster Auditorium,** Osmania University, Hyderabad-500 007
Registration	:	8.30 A.M. to 10.00 A.M.
Inaugural Session	:	9.30 A.M. to 11.00 A.M.
Tea Break	:	11.00 A.M. to 11.15 A.M.
Plenary talk	:	11. 15 A.M. to 11.45 P.M.
Speaker	:	Prof. Arjula Ramachandra Reddy, Emeritus Professor, University of Hyderabad, Hyderabad.

Keynote Addresses: 27-02-2017

Session I	:	Gene Mining and Structural Investigation (11.45 A.M.to 1:30 P.M.)
Chairpersons	:	**Prof. Pratibha Nallari,** Dept. of Genetics, OU
Rapporteur	:	**Dr. H. Surekha Rani,** Dept. of Genetics, OU
Speaker	:	1. Dr. László Szabados, Hungary.
Speaker	:	2. Dr. S. Gourinath, Professor, JNU, New Delhi.
Speaker	:	3. Dr. Sangita Mukhopadhyay, CDFD, Hyd.
Speaker	:	4. Dr. Satish Kumar, CCMB, Hyd.
Lunch	:	**1.30 P.M.to 2.15 P.M.**

LEAD LECTURES

Session II	:	Stem cell & regulatory proteins (2.15 P.M.to 3.30 P.M.)
Chairpersons	:	**Prof. T. Padma (Retd.),** Dept. of Genetics, OU.
Rapporteur	:	**Dr. G. Sumanlatha**, Dept. of Genetics, OU.
Speakers	:	1. Dr. Vijayalakshmi Venkatesan, NIN, Hyderabad 2. Dr. Lakshmi Kiran Chelluri, Global hospitals, Hyderabad. 3. Dr. Santisree Parankusam, ICRISAT, Hyderabad 4. Dr. Gopala Krishnan S, ICAR-IARI, New Delhi
Tea Break	:	**3.30 P.M.to 3. 45 P.M.**
Session III	:	Molecular modeling & proteomics (3.45 P.M. to 5.30 P.M.)
Chairpersons	:	**Prof. K. Ulaganathan,** CPMB, OU
Rapporteur	:	**Dr. K. Ramakrishna,** CPMB, OU
Speakers	:	1. Dr. Rathnavel, IIT, Hyderabad 2. Dr. Burra V L S Prasad, Amity University, UP. 3. Dr. Vijay Raina, Nektar Pharmaceuticals, Hyderabad 4. Dr. Pasupuleti Sreenivasa Rao, Narayana Medical College and Hospitals

Followed by cultural programme 6 :00 to 8 :30 P.M.

The leaf proteome signatures provide molecular insights into the abiotic stress tolerance in chickpea: A priming and proteomics approach

Parankusam Santisree*, Pooja Bhatnagar-Mathur and Kiran K. Sharma

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad-502324, Telangana, India
E-mail: S.Parankusam@cgiar.org/ santhikinnu@gmail.com

Understanding the proteomic differences under stress conditions is a promising approach for global food security by providing useful insights into the stress tolerance mechanisms in plants. In our study we focused on developing the leaf proteome signatures associated with major abiotic stresses in chickpea (*Cicer arietinum* L.) such as drought, heat, salt were compared to the control using comparative label-free quantitative proteomics. The proteomic analysis identified a total of 590, 248 & 797 differentially regulated proteins by drought, heat and salt stress respectively. Several crucial stress induced and repressed proteins were identified and categorized based on ontology and pathway analysis. The proteins which are essentially related to the electron transport chain in photosynthesis, aminoacid biosynthesis, ribosome synthesis and secondary metabolite synthesis may play key roles in inducing heat and drought tolerance in chickpea. On the other hand, priming with exogenous application of certain plant protecting compounds has become increasingly popular technique in plant stress biology. Despite its relevance as a plant growth and stress regulator, the current knowledge about the mechanism of nitric oxide (NO) action is still limited. Our study provided evidence that the foliar application of NO donor can enhance stress tolerance by modulating a number of proteins in chickpea. Proteomic studies on priming in the context of abiotic stress identified key protein targets and signaling pathways that are being involved in the stress alleviation. Understanding the active metabolic adjustments in tolerant genotype under stress and inducing the stress tolerance in sensitive genotype by exogenous NO application offers a comprehensive and systematic approach to tackle abiotic stress in chickpea. This study offer valuable insights on the mechanisms of stress tolerance that help plant biologists to develop designer crops to withstand a wider range of climatic variability under the current scenario of climate change.