NGGIBCI-V

ICRISAT
Science with a human face

5th International Conference
on

Next Generation Genomics & Integrated Breeding for Crop Improvement

February 18-20, 2015

ICRISAT, Patancheru, India

natureINDIA

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CEG's Vision is to make it possible for agricultural breeding & research programs to fully utilize modern genomics tools in developing countries.

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- CFA - Molecular Breeding
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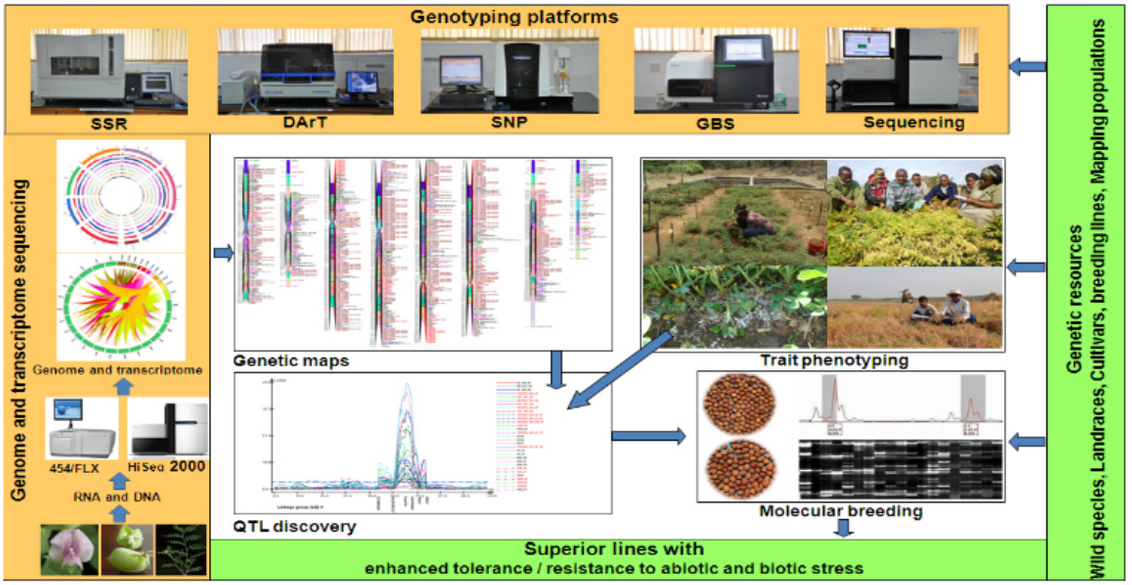
Workshops / Conferences

- InterDrought-V
- 5th NGGIBCI - 2015
- 4th NGGIBCI - 2014
- VI ICLGG - 2012
- 3 NGS Workshop - 2012
- 2 NGS Workshop - 2010
- 1 NGS Workshop- 2009
- 2 MAS Workshop- 2010
- AAGB - 2008

About the CEG

Efficient plant breeding requires high-throughput allele determination at low cost for better prediction of an individual's phenotype from its genotype. This is the primary reason for the establishment of ICRISAT's Center of Excellence in Genomics (CEG). To cater the needs of molecular breeding community, the CEG has three main components i.e. applied genomics research and sequencing, high quality marker genotyping services and capacity building in modern genomics and molecular breeding.

Integrated genomics and breeding activities



http://ceg.icrisat.org

ICRISAT
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International Crops Research Institute for the Semi-Arid Tropics

Message from the Director General

Hunger and malnutrition are preventing hundreds of millions of children from realizing their full potential that will have long-term implications on society and economic development. Over 800 million people are estimated to be chronically undernourished. The vast majority, over 790 million, live in developing countries (FAO, The State of Food Insecurity in the World 2014). It is essential to adopt an inclusive and demand-driven approach to innovation to ensure the outputs of science-based development are focused on addressing the issue of nutritional security in the developing world in an equitable and sustainable manner. The genomics revolution is one of the powerful digital platforms that can dramatically increase our capacity to utilize genetic diversity and develop robust and nutritious crop varieties faster and cheaper than crop improvement practices used during the first Green Revolution.

Next-generation sequencing (NGS) is projected to be the seventh most important disruptive technology towards increased economic impact by 2025 (McKinsey Global Institute, 2014). In the last decade, NGS not only accelerated the genomics and genetics research-based solutions in humans, but has also dramatically impacted agriculture research.

Through partnerships, ICRISAT has contributed to the genomics revolution through the sequencing of two of its mandate crops – chickpea and pigeonpea. We are now applying this information to accelerate the development of climate change-resilient varieties for sorghum, millets, chickpea, pigeonpea and groundnut. ICRISAT has always valued its partnership with national and international research programs and private sector partners towards modernizing breeding programs to develop farmer-preferred varieties better, faster and cheaper.

It gives me great pleasure to welcome you to the 5th International Conference on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI-2015) organized by ICRISAT in collaboration with Bill & Melinda Gates Foundation and the CGIAR

Generation Challenge Programme (GCP). This conference builds on the success of the past four conferences on NGS data analysis (2003, 2010, 2012 and 2014) and we are grateful for the opportunity to host these important international gatherings to exchange ideas, identify best practices and build strong, international partnerships to harness the power of modern tools to better serve the needs of smallholder farmers in the developing world.

NGGIBCI-V 2015 brings together over 300 participants from over 30 countries who are leaders in their respective fields of crop improvement and provides a platform where new ideas and cutting-edge science related to the modernization of crop improvement will be presented and discussed and new partnerships formed to apply next generation genomics to accelerate genetic gains in food crops – both for yield and improved nutritional quality – to improve the lives of smallholder farmers and address malnutrition for both urban and rural consumers in the developing world.

I wish you a productive meeting as you learn and map out the next steps to advance our utilization of genetic resources to address malnutrition and climate change, and to develop input use efficiency and market-oriented varieties that will empower smallholder farmers to lift their families out of poverty and into prosperity.

A warm welcome to ICRISAT.

David Bergvinson

M. S. SWAMINATHAN RESEARCH FOUNDATION

M. S. Swaminathan
Founder Chairman

Message

Making hunger-free and malnutrion-free society is the ultimate goal of every agricultural scientist and other stakeholders. However, it is sad to note that even today about 30 percent of the world's population suffer from malnutrition. Human being suffering with hunger and malnutrion face huge challenge in sustaining a healthy and active lives. For example, the vitamin and mineral deficiencies in children lead to several abnormalities such as stunted growth, blindness and incomplete brain development. The hunger and malnutrition not only has affected the poor, but the unbalanced life style and food habits of wealthy section of the society are the main cause of health problems due to less food intake (undernourishment) or overeating (overnourishment).

The green revolution has played key role in bringing self-sufficiency in food in several developed and developing countries. However, this self-sufficiency has not solved the problem of malnutrion and hence, it is important to diversify the food basket of the societies to ensure the availability of all the nutritional component in their dining plate irrespective of their economic classes. There is an urgent need to spread awareness in the societies about the balanced food/nutrition intake for developing a healthy and prosperous society globally. To achieve above mentioned goal, it is imperative to deploy modern technologies to accelerate the ongoing process. In this context, next-generation genomics (NGG) has shown a great promise in facilitating the trait-genetics and trait improvement more precisely and in less time. This gives me immense pleasure that ICRISAT is organizing the 5th International Conference on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI-V) in Hyderabad, India. This is a great platform which provides an opportunity to all the participants to share their views and ideas with the experts coming across the world. I am very hopeful that this conference will be a great success in achieving its target in understanding and discussing modern genomics and integrated breeding methodologies for crop improvement.

It is a well-known fact that the biological resources and diversity are vital to humankind's economic and social development. The NGG backed by strong technological advancements will facilitate agriculture-based innovations such as the development of nutrient-rich crops to eradicate hunger. In addition, the ICRISAT mandate crops have a bigger role in diversifying the current food availability leading to achieving the zero hunger challenge. In addition to the development of new crop varieties, the other modern technologies will also be a driving force for the dissemination and adoption in large scale impacting the livelihoods of marginalized rural communities. In summary, the science-based innovation for solving the agricultural problems and modern knowledge transfer technologies need more attention of all the stakeholders.

Every effort should be made to help in developing a hunger-free and nutrition-rich society. In this direction, NGG has a great role to play. I thank the organizers of NGGIBCI-V, especially Rajeev Varshney, for bringing the experts across the world and proving a venue for sharing knowledge and ideas.

I wish a great success to this conference in achieving its mission leading to prosperity in the livelihoods of farmers and ending hunger and malnutrition

17 February 2015

M S Swaminathan

3rd Cross Street, Taramani Institutional Area, Chennai (Madras) 600 113, INDIA
Phone: +91-44-2254 2790, 2254 2698 Fax: +91 -44-2254 1319
Email: founder@mssrf.res.in; swami@mssrf.res.in

डा. एस. अय्यप्पन
सचिव एवं महानिदेशक
Dr. S. AYYAPPAN
SECRETARY & DIRECTOR GENERAL

भारत सरकार
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GOVERNMENT OF INDIA
DEPARTMENT OF AGRICULTURAL RESEARCH & EDUCATION
AND
INDIAN COUNCIL OF AGRICULTURAL RESEARCH
MINISTRY OF AGRICULTURE, KRISHI BHAVAN, NEW DELHI 110 001
Tel.: 23382629; 23386711 Fax: 91-11-23384773
E-mail: dg.icar@nic.in

MESSAGE

With current exponential growth rate, world population of 7.3 billion today is expected to cross 9.6 billion by 2050 which may further reach to 10.9 billion by 2100. Biggest future challenge is going to be ensuring food security for this ever-growing population which means availability of enough food for today with surplus to store food that can provide enough in future as well. UN world Food Program has reported that more than 900 million people in the world do not get right/nutritious food to eat. To achieve this goal of surplus food, there is need to increase food production at least 50%. Crop production has witnessed significant yield loss in recent years due to increasing water scarcity and climate change. With Indian prospective, agriculture sector accounts for over 14% of the gross domestic product (GDP) and 12% of country's exports, providing employment to over 50% of the work force. Agriculture in India is one of the most important sector striving towards food security as well as inclusive growth and development. In such scenario, crop productivity is directly related with hunger, poverty and sustainability. Therefore, improvements in crop productivity with a focus on small-scale farmers can serve the purpose of food security. To achieve global food security, the development of crop varieties that produce high yields in harsh climatic conditions will be a key strategy. In addition, world has been witnessing surge of food price volatility, limiting both access to and availability of food, especially staple items upon which much of the world's poor depend.

During past decade next generation sequencing (NGS) technology have gained tremendous popularity and are believed to play a significant role in crop improvement. Scientist have different opinion about the role of NGS technology in improving crop productivity to feed the world, and maintain the environment under the apparent climate changing scenario. In general, NGS technologies are considered to enhance global food production by increasing crop yields and reduce production costs. These modern technologies help the poor and small-hold farmers by developing stress-tolerant and disease-resistant crops and by enriching staple foods, such as addition of essential vitamins. By developing improved and adapted agricultural crops, NGS can contribute on reducing poverty and can help increase food security for a growing global population.

I hope that conference will serve as suitable platform for students, scientists and policymakers to share their view point about the necessary efforts to provide food security for vastly increasing population. I understand scientists can share their experience on using latest next generation genomics/sequencing tools for increasing crop production and ensuring sustainable food security for all.

(S. Ayyappan)

Dated the 6th February, 2015
New Delhi

ICRISAT
Science with a human face

International Crops Research Institute for the Semi-Arid Tropics

Welcome message from the Chair, NGGIBCI!

It gives me immense pleasure to welcome you all to the 5th International Conference on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI- V) at ICRISAT, Patancheru, India. This conference is being organized as part of the Critical Focus Area (CFA)-Molecular Breeding in continuation to the earlier series of workshop/conference on the role of next generation genomics and high throughput genotyping technologies in modern breeding approaches. NGGIBCI-V is being organized by ICRISAT in collaboration with Bill & Melinda Gates Foundation and CGIAR Generation Challenge Programme (GCP).

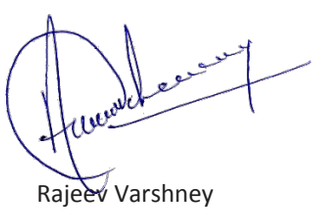
Although earlier series of workshop/conference were restricted to selected participants, based on the overwhelming response and request from several researchers in previous years, this year we opened the conference for interested researchers. We are pleased to share that this NGGIBCI conference has become the largest meeting in the series with over 300 delegates from more than 30 countries. The conference is being organized in 10 sessions covering 40 presentations by eminent speakers. In addition, we have also included one dedicated session for poster presentations for young researchers to get an opportunity to present their work and interact with eminent scientists. We are thankful to all the participants especially speakers, co-chairs, special invitees for accepting our request and agreeing to participate in the conference that has made the programme scientifically rich.

I would like to extend my sincere thanks to the senior management of ICRISAT for their guidance and support in organizing this conference. I would also like to thank my colleagues from the Center of Excellence in Genomics (CEG) especially Anu Chitikineni, B Manjula, M Sriswathi, B Poornima Reddy, Ankit Jain, Manish Roorkiwal, Himabindu Kudapa, Pawan Khera, B Anjaiah, Rachit Saxena, Manish Pandey, Mahendar Thudi and Abhishek Rathore. Sincere thanks are also extended 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, Knowledge Sharing & Innovation, and Strategic Marketing and Communication for their innumerable help in arranging different things to make this conference a grand success. I would also like to thank several other colleagues from CEG, Research Program-Grain Legumes and Research Program-Dryland Cereals. We would like to thank our media partner, Nature India for their support. We also appreciate the generous support from all our sponsors (please see last pages of the book).

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

In summary, I strongly believe that the NGGIBCI-V conference is expected to provide a suitable platform for researchers to share their ideas/experience and have intense discussions about the role of next generation genomics for crop improvement.

Have a happy stay in Hyderabad, India!



February 17, 2015 Rajeev Varshney

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natureINDIA
www.nature.com/natureindia

3A, 5th Floor, DLF Corporate Park, M G Road Phase-3
Gurgaon 122002, Haryana, India
Ph: +91 124 3079600/+91-124-3079657

EDITORIAL

Editor: Subhra Priyadarshini

Copy Editor: T. V. Padma

Art and design: Ajay Kumar Bhatt

ADVERTISING & SPONSORSHIP

Product Manager, Nature jobs and Advertising:
Sonia Sharma, M: +91 9650969959
sonia.sharma@nature.com

SUBSCRIPTIONS & REPRINTS

Sonia Sharma: +91-124-3079657, M: +91 9650969959,
naturejobs.india@nature.com

Project Coordinator: Sana Mohsin

+91-124-3079657, M: +91 7042147383

NATURE JOURNAL QUERIES

Manager, Sales Support, NPG: Jacob Thomas
+91-124-3079646, M: +91 9818171996
jacob.thomas@nature.com

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From the Genomes to the Fields

The developing country perspective of food security is anything but lavish. It has always been about reaching subsistence nutrition to the teeming millions – for instance, the thought behind most of India's food policies is "let's ensure that the poorest of the poor get basic carbohydrates and proteins to survive".

Scientists in developing countries, therefore, are faced with a bigger challenge of not just making newer crops to counter changing climate or shrinking resources, but also to make crops that can produce huge volumes. Given the odds, it seems pertinent that Next Generation Sequencing (NGS) is being heralded as the new uncrowned king of technologies that could do the trick for developing countries.

This brings us to the question of resources available to scientists in developing countries to participate in this global shift towards genomics and integrated breeding. Or, for that matter, their access to global databases that can then be used to meet local needs. In January 2015, *Nature Genetics* endorsed the need to support an international initiative that makes plant genome data across the world's seed banks accessible to plant breeders and researchers[1]. The journal will work with authors to ensure that researchers get access to phenotype data that is linked to published genetic data.

Maintaining the 11 international gene bank collections alone costs about 18 million US dollars every year. Scientists have increasingly advocated mining this biodiversity for food security and creating an internationally accessible informatics infrastructure to catalogue the diversity of the world's seed collections[2]. After mining the superior alleles, it is imperative to use them in the breeding programs and the approach has been referred as integrated breeding approach.

In the light of new genomic interventions in several crops such as rice, maize, barley, wheat, legumes, sorghum, millets, chickpea, pigeon pea and groundnut – crops that the developing

world immensely benefits from – ICRISAT's 5th International Conference on Next Generation Genomics and Integrated Breeding for Crop Improvement will be an interesting meet to watch.

Nature India, a showcase of India's science, is proud to be associated with the conference as its media partner. We hope that the conference, with a star-studded international speakers' list, will identify novel native varieties that can make their way from genebanks to the fields, discuss trends in high-throughput SNP genotyping, as also take a significant first step in giving to the world some new climate smart varieties.

1. Growing access to phenotype data. Nat. Genet. 47, 99 (2015)
2. Agriculture: Feeding the future. Nature 499, 23-24 (2013)

Subhra Priyadarshini
Editor
natureINDIA

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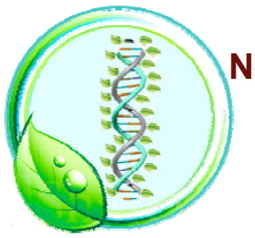


NGGIBCI-V

5th International Conference on Next Generation Genomics and Integrated Breeding for Crop Improvement

February 18-20, 2015

ICRISAT, Patancheru, India
(Ralph W Cummings Auditorium)

Technical Programme

Wednesday, February 18, 2015		
08:30 onwards	Registration	
08:45 – 10:00	**Inaugural Session**	
08:45 – 09:00	Welcome	**Rajeev Varshney** *Chair, NGGIBCI-V, ICRISAT,* India
09:00 – 09:10	Opening remarks	**Peter Carberry** *Deputy Director General (Research), ICRISAT,* India
09:10 – 09:20	Inaugural address	**Asis Datta** *Founder & Former Director, National Institute of Plant Genome Research,* New Delhi, India
09:20 – 09:30	Inspirational message	**Surinder Vasal** *World Food Prize Laureate*
09:30 – 10:00	Inaugural lecture: **Genomics interventions to ensure food and nutritional security in developing countries**	**Howard Yana-Shapiro** *MARS Inc,* USA
10:00 – 10:30	***Group Photo/High Tea***	
10:30 – 12:30	**Session I: Next Generation Genomics Co-Chairs: PK Gupta and HS Gupta**	
10:30 – 11:00	Next generation barley genomics	**Nils Stein** *IPK- Gatersleben,* Germany
11:00 – 11:30	Chromosome sequencing and assembling: Close encounters in wheat	**Andrew Sharpe** *National Research Council of Canada,* Canada
11:30 – 12:00	From the genome to the field: The role of the French Plant Genomic Center	**Helene Berges** *INRA-CNRGV,* France
12:00 – 12:30	Next generation genomics and integrated breeding in legumes	**Rajeev Varshney** *ICRISAT,* India
12:30 – 13:30	***Lunch***	
13:30 – 15:30	**Session II: Genome Sequencing and Germplasm Re-sequencing Co-Chairs: Jeff Ehlers and Hari Upadhyaya**	
13:30 – 14:00	From genebank to field- leveraging genomics to identify and bring novel native variation to breeding pools	**Sarah Hearne** *CIMMYT,* Mexico
14:00 – 14:30	Comparative genome sequence between *Vigna radiata* and *Vigna angularis*	**Suk-Ha Lee** *Seoul National Uni,* South Korea
14:30 – 15:00	High-throughput SNP genotyping for rice improvement	**Michael Thomson** *IRRI,* The Philippines
15:00 – 15:30	NGS and plant variant discovery and exploitation in plants: some lessons	**David Marshall** *The James Hutton Inst*, Scotland
15:30 – 16:00	***Tea & Coffee***	
16:00 – 17:40	**Session III: Genomics Platforms Co-Chairs: Eric Danquah and Shoba Sivasankar**	

16:00 – 16:20	The BecA-ILRI Hub and its contribution to African agricultural biotechnology and crop improvement	**Appolinaire Djikeng** *BecA-ILRI Hub,* Kenya
16:20 – 16:40	Sequencing and arrays with Illumina	**Cindy Lawley** *Illumina Inc.*, USA
16:40 – 17:00	Douglas Scientific Array Tape™ platform and its application in genomics assisted breeding	**Venkatramana Pegadaraju** *Douglas Scientific,* USA
17:00 – 17:20	To in-source or outsource: Challenges and considerations for developing a genetic marker program in 2015 and beyond……	**Steve Asquith** *LGC Genomics,* USA
17:20 – 17:40	New era for molecular breeding with cost effective SNP genotyping solutions	**Bhaswar Maity** *Affymetrix ILS*, India
17:40 – 18:30	**Poster Session**	
18:30 onwards	***Welcome Dinner @ IMOD Plaza, ICRISAT***	
Thursday, February 19, 2015		
08:30 – 10:00	**Session IV: Trait Mapping Co-Chairs: Ramesh Aggarwal and Baozhu Guo**	
08:30 – 09:00	Development and use of a sorghum backcross nested association mapping population for trait dissection	**David Jordan** *Uni Queensland,* Australia
09:00 – 09:30	Challenges and advantages of MAGIC genetic map construction	**Emma Huang** *CSIRO,* Australia
09:30 – 10:00	Applying high-throughput genomics to crops for the developing world	**Jason Wallace** *Cornell University,* USA
10:00 – 10:30	***Tea & Coffee***	
10:30 – 12:30	**Session V: Genome Dynamics and Systems Biology Co-Chairs: Noel Ellis and Naveen Puppala**	
10:30 – 11:00	Advances and prospects in forage systems biology and molecular breeding	**German Spangenberg** *DEPI, La Trobe Uni,* Australia
11:00 – 11:30	Improving genome assemblies and capturing genome variation data for applied crop improvement	**Dave Edwards** *Uni Western Australia,* Australia
11:30 – 12:00	Prospecting for gene function in complex natural and agricultural systems	**Douglas Cook** *University of California-Davis* USA
12:00 – 12:30	Genome sequencing to support germplasm analysis and utilization	**Robert Henry** *Uni Queensland,* Australia
12:30 – 13:30	***Lunch***	
13:30 – 15:30	**Session VI: Genomics-Assisted Breeding - I Co-Chairs: HS Dhaliwal and Chittranjan Bhatia**	
13:30 – 14:00	Trait-associated SNPs provide insights into heterosis in maize	**Patrik Schnable** *Iowa state University,* USA
14:00 – 14:30	Practice of whole genome molecular marker assisted breeding in BGI	**Gengyun Zhang** *BGI-Shenzhen,* China
14:30 – 15:00	Genomics based breeding research for improving resistance to biotic and abiotic stress in cereals	**Frank Ordon** *JKI- Federal Research Centre for Cultivated Plants,* Germany
15:00 – 15:30	DArT PL's support for agricultural research and practice: delivery model and technology package	**Andrzej Kilian** *DArT Pty Ltd,* Australia
15:30 – 16:00	***Tea & Coffee***	
16.00-17.30	**Session VII: Genomics-Assisted Breeding - II Co-Chairs: Tim Sutton and Bharat Chattoo**	
16:00 – 16:30	Accomplishments in soybean molecular breeding and future perspectives	**Henry Nguyen** *University of Missouri,* USA
16:30 – 17:00	Genome-wide association of SNPs in stress responsive genes with salinity tolerance in rice	**Trilochan Mohapatra** *Central Rice Res Inst,* India
17:00 – 17:30	Establishment of wild pea *Pisum fulvum* chromosome segment substitution lines in cultivated *P. sativum* genetic background, as a tool to study domestication and to broaden genetic diversity	**Petr Smykal** *Palacký Uni Olomouc,* Czech Republic

17:30 – 19:00	**Poster Session**	
19:00 onwards	***Gala Dinner @ Anniversary Lawns (205 Bldg), ICRISAT***	
Friday, February 20, 2015		
08:30 – 10:00	**Session VIII: Climate Resilience Genomics and Breeding Co-Chairs: Kadambot Siddique and Ajay Parida**	
08:30 – 09:00	Climate-resilient maize development and delivery in the tropics through public-private partnerships: CIMMYT's experiences and perspective	**BM Prasanna** *CIMMYT,* Kenya
09:00 – 09:30	Advent of climate smart rice varieties through genomics-assisted breeding	**Jauhar Ali** *IRRI,* The Philippines
09:30 – 10:00	Adaptation to water limitation and climate change: From trait dissection to yield	**Vincent Vadez** *ICRISAT,* India
10:00 – 10:30	***Tea & Coffee***	
10:30 – 12:30	**Session IX: Novel Breeding Approaches Co-Chairs: EA Siddiq and Pooran Gaur**	
10:30 – 11:00	Genomic selection in plants: a new tool for crop improvement	**Mark Sorrells** *Cornell University* USA
11:00 – 11:30	New developments in genomic-enabled prediction models	**Jose Crossa** *CIMMYT,* Mexico
11:30 – 12:00	Potential of promotion of alleles by genome editing for improving quantitative traits in livestock breeding programs	**John Hickey** *University of Edinburgh,* UK
12:00 – 12:30	Integration of physiological breeding and genomic selection for wheat improvement	**Jesse Poland** *Kansas State University,* USA
12:30 – 13:30	***Lunch***	
13:30 – 15:00	**Session X: New Horizons for Crop Improvement Co-Chairs: Swapan Datta and KC Bansal**	
13:30 – 14:00	Bringing genomic data into routine use in cultivar development: reducing costs and improving the tools for breeders	**Gary Atlin** *Bill & Melinda Gates Foundation,* USA
14:00 – 14:30	Cassava genomics - applying genomic technologies to benefit smallholder farmers in Africa	**Steve Rounsley** *Dow Agrosciences,* USA
14:30 – 15:00	Diversity Seek (DivSeek): A community-driven effort to harness the genetic potential of the world's genebanks	**Peter Wenzl** *Global Crop Diversity Trust,* Germany
15:00 – 15:30	Trends in agricultural genomics and Nature journal standards	**Myles Axton** *Nature Genetics,* USA
15:30 – 16:00	***Tea & Coffee***	
16:00 – 17.45	**Concluding Session**	
16:00 – 16:30	Next generation genomics and the zero hunger challenge	**MS Swaminathan** *Emeritus Chairman and Chief Mentor, M S Swaminathan Research Foundation,* India
16:30 – 17:00	Concluding lecture**: Translating biology: The Generation Challenge Programme- a successful case study**	**Jean-Marcel Ribaut** *Director, Generation Challenge Programme,* Mexico
17:00 – 17:15	Inspirational message	**JS Sandhu** *Deputy Director General (Crop Science), ICAR,* India
17:15 – 17:30	Concluding remarks	**David Bergvinson** *Director General, ICRISAT,* India
17:30 onwards	Wrap-up	**Rajeev Varshney** *Chair, NGGIBCI-V, ICRISAT*
18:00 onwards	***Closing Dinner @ Mary Cummings Park, ICRISAT***	

Inaugural Lecture

Dr Howard-Yana Shapiro

Chief Agricultural Officer
The First Mars Advanced Research Institute Fellow
Mars Incorporated
University of California-Davis
Davis, USA
howard.shapiro@effem.com

Howard has been involved with sustainable agricultural and agroforestry systems, pattern recognition, plant breeding, molecular biology and genetics for over 40 years releasing hundreds of cultivars into the public domain. He has worked with indigenous communities, NGO's, governmental agencies and the private sector around the world. A former university professor for 15 years, Fulbright Scholar, Ford Foundation Fellow, National Endowment for the Humanities Fellowship in 2007 Howard was made a Fellow of the World Agroforestry Centre and authored the IAASTD chapter on Biotechnology and Biodiversity. He is founding Chairperson of the External Advisory Board of the Agriculture Sustainability Institute at UC Davis. In 2009 he was named recipient of The Award of Distinction from The College of Agriculture and Environmental Sciences, UC Davis. He led the global effort sequencing, assembling and annotating the Theobroma cacao genome and is part of the leadership team for the Arachis genome global effort. In 2010 he was named a Senior Fellow, Plant Sciences, the University of California, Davis. September 2011, he announced the formation of the African Orphan Crops Consortium, set up to sequence, assemble and annotate 101 of the key African food crops in order to breed more nutritious plants. He as well set up the African Plant Breeding Academy with UC Davis at the World Agroforestry Centre in Nairobi which opened the 3rd of December 2013. He has served on both for profit and NGO boards.

He has been interviewed and published extensively in print, on the radio and television many times: BBC, CCTV, New York Times, Financial Times, NPR, Washington Post, The Wall Street Journal, The Guardian, Fortune, The Economist, ABC, Scientific American and Frankfurt Allemange Zeitung, Der Speigel, International Finance Corporation amongst many.

Genomics Interventions to Ensure Food and Nutritional Security in Developing Countries

Howard-Yana Shapiro

MARS Incorporated, USA
E-mail: howard.shapiro@effem.com

Stunting caused by Chronic hunger and malnutrition will not be ended through food supplementation. With more than 35% of the children in rural Africa stunted, a global effort on the fundamental food crops of those populations must be initiated to deliver the nutritional needs to end this plague. This effort is unprecedented in plant science. It is not a single crop but a large portfolio of diverse crops being worked on simultaneously that will allow the world to radically reduce the incidence of stunting. This effort is underway with the African Orphan Crops Consortium. Using state of the art genomics, 101 key food crops of Africa will be breed for nutritional enhancement, increased yields, climatic resilience, water and nutrient use efficiency and pest and disease resistance. Each crop will be resequenced 100 times. This is the first step in a new improved nutritional food security system. How this will reach translation and scale is the critical issue.

Abstracts

(*and biography of invited Speakers*)

Session I

Next Generation Genomics

Co-chairs

Prof PK Gupta

Emeritus Professor
Ch Charan Singh University
Meerut
India

Dr. HS Gupta

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

Dr. Nils Stein

Group Leader
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben
Germany
stein@ipk-gatersleben.de

Dr. Nils Stein, Dr. rer.nat., researcher and leader of the research group Genome Diversity at Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany.

Nils Stein earned his PhD in genetics at University of Hohenheim (Stuttgart, Germany) in 1997. He worked as a post-doc (1998-2001) at Zurich University, Switzerland, where he isolated a leaf rust resistance gene from hexaploid wheat via positional cloning in a closely related diploid wheat species. He moved to IPK, Gatersleben, in 2001. Since 2007 he is leading the group 'Genome Diversity' of the Genebank department. The main focus of his research is structural and comparative genome analysis in Triticeae species such as barley, wheat and rye, with emphasis on barley. Nils is co-coordinator of the European Triticeae Genomics Initiative (ETGI), and since 2008 he is chairing the International Barley Genome Sequencing Consortium (IBSC). He is the chair of the Scientific Coordinating Committee (SCC) of the Research Program Plant2030 of Germany's ministry of education and research, and is one of the two national representatives of the research committee of the international Wheat Initiative (http://www.wheatinitiative.org/). Nils Stein serves as associate editor for the journals Molecular Plant, BMC Plant Biology, Functional & Integrative Genomics and Japanese Journal of Breeding Science. In 2010 he was awarded the *Günter und Anna Wricke Forschungspreis* in applied Genetics and Breeding Research for his contributions in cereal genome analysis.

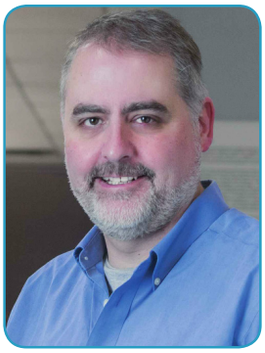
Next Generation Barley Genomics

Nils Stein

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466 Stadt Seeland, OT Gatersleben, Germany
Email: stein@ipk-gatersleben.de

Barley is one of the most important cereal crop species. It is a close relative to wheat and rye. Its haploid genome size exceeds 5 Gigabases (Gbp), almost twice the size of any fully sequenced organism or crop species. Recently, the International Barley Sequencing Consortium (IBSC) succeeded in establishing access to a gene-centric view of the barley genome: a physical map densely integrated with the genetic map and substantiated by ~400 megabases of assembled whole genome shotgun sequences containing more than 20,000 transcriptionally active genes. This resource is under constant improvement and up to now more than 60% of the assembled genomic sequence information (1.2 Gbp) could be integrated into a genetic frame. IBSC is furthermore heading for a complete genome sequence, and a minimal tiling path (MTP) of overlapping BAC clones provided by the physical map is being processed for hierarchical map-based sequencing. Raw sequencing data of all seven barley chromosomes will be accumulated in early 2014.

This step-changing resource of genomic sequence information is enabling true genome scale analysis in barley and lays the foundation for genomics based breeding, crop improvement and comparative/evolutionary analyses within the genus *Hordeum* and between Triticeae species. State-of-the-art examples of barley genomic research and applications exploiting the potential of the new resource will be presented.



Dr Andrew Glenn Sharpe

Research Officer
National Research Centre Canada
Saskatoon
Canada
Andrew.Sharpe@nrc-cnrc.gc.ca

Dr. Andrew Sharpe is a Research Officer at the National Research Council Canada (NRC) in Saskatoon. Dr. Sharpe obtained his B.Sc in biological sciences at the University of Leicester in 1988, and gained Ph.D in plant genetics from the University of East Anglia in 1997 while working in the Cambridge Laboratory at the John Innes Centre, Norwich, UK. This contribution led to the elucidation of the genome structure of amphidiploid *Brassica napus* (oilseed rape / canola). The focus on *Brassica* crop research continued when Dr. Sharpe moved to the Agriculture and Agri-Food Canada, Saskatoon Research Centre in late 1997. He was involved in coordinating the development of genetics and genomics resources for all the *Brassica* crop species until 2008 when he moved to the NRC facility to lead the DNA Technologies Laboratory. This position led to the establishment of next-generation sequencing and bioinformatics platforms at NRC, which have subsequently been used in a range of collaborative genome sequencing efforts in *Brassica*, pulse and cereal crops. Most recently, Dr. Sharpe has been engaged in sequencing bread wheat chromosome 1A as part of the International Wheat Genome Sequencing Consortium effort and, separately, whole chromosome sequencing of related grass species.

Chromosome Sequencing and Assembling: Close Encounters in Wheat

Andrew Sharpe

National Research Council Canada
Email: Andrew.Sharpe@nrc-cnrc.gc.ca

Recent advances in sequencing technologies and bioinformatics are now enabling practical access to the large grass genomes at the sequence level, and as a consequence, expediting genetics and breeding research in the important cereal crops. While the profound utility of complete reference genomes for bread and durum wheat are still not fully realized, significant resources have been delivered in the form of a reference sequence for one chromosome, a 'survey sequence' for each individual half chromosome, and whole genome assemblies of the ancestral diploid genomes. Wheat genetics research has long benefitted from the availability of a rich collection of cytogenetic material and these resources have played a key role in the development of the new sequence repositories described above. The ability of wheat to host additional chromosomes in a stable fashion extends not just to wheat genetic material, but also chromosomes from related or 'alien' grass species. Indeed, this ability has enabled the introgression of valuable genetics, not available in wheat, to address important agronomic issues such as enhanced tolerance to disease. This presentation will profile the technological advances that have enabled the recent progress in wheat chromosome sequencing, the current state of the art, and the direction and impact of future technological advances.

Dr Helene Berges

Director
INRA-French Plant Genomic Resource Center (CNRGV)
Toulouse
France
helene.berges@toulouse.inra.fr

Dr. Hélène Bergès is Managing Director of the French Plant Genomic Resources Center at the French National Institute for Agricultural Research (INRA), Toulouse, France.

Helene Bergès earned her PhD in genetics and molecular biology at the University Paul Sabatier (Toulouse, France) in 1995. She worked as a post-doc in the Laboratory of Plant-Microbe Interactions (LIPM), on projects aiming at better understanding of the mechanisms underlying the molecular dialogue between *Medicagotruncatula* and its symbiotic bacterium *Sinorhizobiummeliloti*. Since 2003, she is the Managing Director of the Plant Genomic Centre (CNRGV) located in France. Dedicated to plant genome research, the CNRGV holds more than 15 million unique samples from plant models (*Arabidopsis thaliana*, *Medicagotruncatula*) and crop plants (wheat, maize, pea, sunflower, barley, rapeseed, radish, etc.). The CNRGV is actively involved in plant genomic efforts by producing new resources as well as developing innovative molecular tools for the international scientific community.Hélène Bergès is member of various international consortia (International Wheat Genome Sequencing Consortium (IWGSC), International Barley Genome Sequencing Consortium (IBSC), Sugarcane Genome Sequencing Initiative (SUGESI)…). She's also member of the scientific committee of the Parliamentary Office for the Evaluation of Scientific and Technological Choices (http://www.senat.fr/opecst/eng/index.html) in France.

From the Genome to the Field: The Role of the French Plant Genomic Center

Beydon G, Marande W, Rodde N, Prat E, Fourment J, Courtial A, Gautier N, Arnal N, Cauet S, Vautrin S, Bellec A, Bergès H*

INRA/CNRGV - Chemin de Borde Rouge - 31326 - Castanet-Tolosan - France
*Email: hberges@toulouse.inra.fr

Agricultural research must deal with major issues on various scales, in the light of the changing climatic and demographic context, where energy resources are limited. In this context of plant improvement and adaptation, genome exploration is one of the strategic approaches of choice. Indeed, for species of interest, genomics defines gene content, their organization, biological function and also their variability between different samples. This knowledge facilitates the identification of interesting plant genes, which can play a role in pathogenic resistance, or in the quality process, and in agronomic performance. In terms of biodiversity, which exists among all genotypes of the same species and their related wild forms, genomics helps deepen our knowledge of the main metabolic pathways and to rationalize the selection of new varieties. To manage this challenge, genomic research can take advantage of the extraordinary growth observed since the 90s. This revolution combined with specialized biological resources is the key to the successful management of genomic research projects. Genomic resources are mainly represented by libraries of large DNA inserts that are essential for the exploration of complex plant genomes, which may vary in size from a few million nucleotides to several billion. Dedicated to plant genome research, the French Plant Genomic Center (CNRGV) holds more than 15 million unique samples, including plant models (*Arabidopsis thaliana*, *Medicagotruncatula*) and crop plants (wheat, maize, pea, sunflower, barley, rapeseed, radish, etc.). The CNRGV is actively involved in the plant genomic effort by producing new resources as well as developing innovative molecular tools for the international scientific community. We have developed innovative approaches involving BAC libraries to study plant genomes, in order to efficiently focus on genomic region of interest. We'll present various scientific projects in order to illustrate the importance of this strategy in order to decipher plant genome complexity.

Dr. Rajeev K Varshney

Principal Scientist-Applied Genomics
Research Program Director - Grain Legumes
Director-Center of Excellence in Genomics
Winthrop Research Professor-The University of Western Australia
International Crops Research Institute for the Semi-Arid Tropics
Patancheru
India
r.k.varshney@cgiar.org

Dr. Rajeev Varshney, an Indian national and Principal Scientist is serving ICRISAT as a Research Program Director, Grain Legumes and Director - Center of Excellence in Genomics. In addition to serving ICRISAT, Rajeev, in his dual appointment earlier served CGIAR Generation Challenge Program based in Mexico as Theme Leader for six years. Before joining ICRISAT, he worked at Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany, for five years.

Rajeev has a basic background in molecular genetics and possess more than 15 years research experience in international agriculture. The primary contribution of Rajeev Varshney includes genome sequencing of pigeonpea, chickpea, peanut, pearl millet, sesame, mung bean and azukibean and the first generation of molecular breeding products in chickpea and groundnut, in addition to large-scale genomic resources such as molecular markers, transcriptome assemblies, high density genetic maps and QTLs for a range of traits in legumes. Rajeev has a prolific publication record with >200 publications in leading journals of international reputes including Nature, Nature Biotechnology, Nature Communications, PNAS etc., 10 edited books and special issues (as Guest Editor) for several journals to his credit. He has been a frequent invited speaker in several national/ international conferences including G-8 Conference on "Open Data for Agriculture", FAO conference on "Application of Biotechnologies in Developing Countries" and brainstorming session on digital agriculture chaired by Mr Bill Gates. Rajeev has won several awards/fellowships including Elected Fellow of Indian National Science Academy (INSA), National Academy of Agricultural Sciences (NAAS), India; Crop Science Young Scientist Award (Crop Science Society of America); INSA Young Scientist Medal; Associate NAAS Fellow; NASI Young Scientist Platinum Jubilee Award, and The Greater Good Initiative Award of Illumina.

Next Generation Genomics and Integrated Breeding in Legumes

Rajeev K Varshney

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru -502324, Hyderabad, India
School of Plant Biology and Institute of Agriculture, The University of Western Australia, Australia
Email: r.k.varshney@cgiar.org

Food security is a major global concern as still >800 million people are suffering from starvation and malnutrition in Sub-Saharan Africa (SSA) and Asia. Legume crops such as chickpea, pigeonpea and groundnut play important role to ensure food and nutritional security in developing countries. For developing climate change-ready legume varieties with enhanced yield and nutritional quality, next generation genomics and integrated breeding approaches are being used. In this context, large-scale genomic resources including draft genome sequences, germplasm re-sequencing, transcriptome assemblies, molecular markers, high density genetic maps and cost-effective genotyping platforms have been developed in these legume crops. In parallel, specialized genetic stocks such as reference set, RIL, MAGIC and NAM population have been developed. These germplasm resources are being genotyped using high-density genotyping/re-sequencing and phenotyped in different agro-climatic conditions. Analysis of these massive genotyping and phenotyping data is providing markers/genes associated with traits of interest using linkage mapping and genome wide association studies (GWAS). Efforts have also been initiated to deploy genomics-assisted breeding (GAB) approaches and superior lines with enhanced drought tolerance in chickpea and disease resistance in chickpea and groundnut have been developed. However, it is essential to empower NARS partners for sustainable deployment of GAB to feed ever-growing population in developing countries of SSA and Asia.

Session II

Genome Sequencing and Germplasm Re-sequencing

Co-chairs

Dr. Jeffery Ehlers

Program Officer
Bill & Melinda Gates Foundation
Seattle
USA

Dr HD Upadhyaya

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

Dr Sarah Jane Hearne

Seed Maize Lead/Senior Scientist
International Maize and Wheat Improvement Center (CIMMYT)
Texcoco
Mexico
s.hearne@cgiar.org

Dr. Sarah Hearne: Born and educated in the UK, Sarah grew up with farming and rural business. She specialized in plant science early in her career, graduating with a first class honours degree in applied plant science from the University of Manchester, followed by a PhD from the University of Sheffield in molecular genetics and physiology. She went to work as a post-doctoral fellow at CIMMYT in 2001, focusing on molecular evaluation of maize germplasm with resistance to *Striga*. She moved to Kenya to take up positions as postdoctoral fellow and scientist with IITA She has worked on diversity analysis and marker discovery in genebank collections of cowpea, cassava and maize; and drought breeding in maize, cowpea and cassava, employing molecular tools to accelerate and target gain. After seven years in Africa, Sarah returned to Mexico to join CIMMYT to take up the post of senior scientist and leader of the SeeD maize theme. During the exciting time at CIMMYT she has worked with a range of excellent partners and colleagues to develop and employ new genotypic characterisation approaches, and completing the genotyping of CIMMYTs gene bank maize collection. She has coordinated the use and analysis of the broadest GWAS panel for maize, identifying high value alleles novel to modern breeding pools, and has simulated and defined breeding strategies for maize to capture novel alleles for mono-, oligo- and polygenic traits. She is a member of the Society for Experimental Biology and is an honorary research fellow at the University of Sheffield in the UK.

From Genebank to Field- Leveraging Genomics to Identify and Bring Novel Native Variation to Breeding Pools

Sarah Hearne

CIMMYT, Mexico
Email: S.Hearne@cgiar.org

Seeds of Discovery (SeeD) is an ambitious multi-partner 10-year project seeking to unlock the hidden diversity present in maize and wheat genebank holdings of the CGIAR, and make useful diversity available to breeders. The delivery to breeders of information and high value germplasm containing novel native alleles is achieved through the interlinked objectives of 1) genotypic characterisation of genebank holdings, 2) allele discovery achieved through targeted phenotyping of sub-sets of genebank collections and use of GWAS and bi-parental populations, 3) pre-breeding to develop bridging germplasm and 4) the use and development of enabling tools such as software, analytical methods and training. The project has been running for three years, funded predominantly by the Mexican Ministry of Agriculture (SAGARPA). We present an overview of the work on maize, highlighting knowledge developed on; the use and adaptation of NGS technologies for genotyping in open pollinated heterogeneous materials, the application of GWAS in maize genebank holdings, integrative approaches to selection of germplasm for targeted phenotyping, and pre-breeding strategies employing tools from MABC to genomic selection combining discovery with product development.

Prof. Suk-Ha Lee
Department of Plant Science
College of Agriculture and Life Sciences
Seoul National University
Seoul
Korea
sukhalee@snu.ac.kr

Dr. Suk-Ha Lee, a professor and soybean breeder, has joined the Department of Plant Science at Seoul National University in the Republic of Korea since 1998. Prior to his current role, Lee spent 12 years in the soybean breeding program at the National Institute of Crop Science, Rural Development Administration, in Korea. Lee received his Ph.D. in Agronomy from the University of Georgia in 1990 and earned his Master's (1985) and Bachelor's degrees (1980) in Crop Sciences from Seoul National University. Lee was selected as President of the International Crop Science Society (April 2008 to August 2012), and served as the President of Korean Society of Crop Science in 2011. He is the member of Korean Academy of Science and Technology.

Lee's laboratory group sequenced a *G. soja* genotype, the wild relative of *G. max*. More recently, his group completed the genome sequencing of mungbean (*Vigna radiata*) and adzuki bean (*Vigna angularis*).

Comparative Genome Sequence between *Vigna radiata* and *Vigna angularis*

Kang YJ[1], Satyawanra D[1], Shim S[1], Lee T[1], Lee J[1], Hwang WJ[1], Kim S[1], Lestari P[2], Laosatit K[3], Kim KH[4], Ha TJ[5], Chitikineni A[6], Kim MY[1], Ko JM[7], Gwag JG[8], Moon JK[4], Lee YH[1], Park BS[9], Varshney RK[6*], Lee SH[1,10*]

[1]Department of Plant Science and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea
[2]Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD-IAARD), Jalan Tentara Pelajar No. 3A Bogor 16111, Indonesia
[3]Program in Plant Breeding, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University, Kamphaeng Saen, Nakhon Pathom 73140, Thailand
[4]National Institute of Crop Science, Rural Development Administration, Suwon, 441-857, Korea
[5]Research Policy Bureau, R&D Performance Evaluation & Management Division, Nongsaengmyeong-ro 300, Wansan-gu, Junju, 560-500, Korea
[6]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[7]Soybean Research Team, Legume & Oil Crop Research Division, Jeompiljae-ro 20, Miryang, Gyeongnamdo, 627-803, Korea
[8]National Agrobiodiversity Center of NAAS, RDA, Suwon 441-707, Korea
[9]The Agricultural Genome Center, National Academy of Agricultural Science, Rural Development Administration, Suwon, 441-707, Korea
[10]Plant Genomics and Breeding Institute, Seoul National University, Seoul, 151-921, Korea

*Email: sukhalee@snu.ac.kr, r.k.varshney@cgiar.org

Mungbean (*Vigna radiata* var. *radiata*) is a fast-growing, warm-season legume crop that is primarily cultivated in Asia, and Adzuki bean (*Vigna angularis* var. *angularis*) is a dietary legume crop in East Asia. Here, we report a draft genome sequence of mungbean and adzuki bean to facilitate genome research into the subgenus *Ceratotropis* which includes several important dietary legumes in Asia, and to enable a better understanding of the evolution of leguminous species. The genome assembly of mungbean covered 431 Mb, corresponding to 80% of the total assembled sequences, while that of adzuki bean covers 75% of the estimated genome. Gene prediction revealed 22,427 and 26,893 high confidence protein-coding genes in mungbean and adzuki bean, respectively, which was evidenced by RNAseq of different tissues. Based on the *de novo* assembly of additional wild mungbean and adzuki bean species, the divergence of what was eventually domesticated and the sampled wild mungbean and adzuki bean species appears to have predated domestication. Comparative genome sequence will be highlighted for speciation and domestication of legume species in this paper.

Dr Michael Thomson

Senior Scientist & Head of the Genotyping Services
International Rice Research Institute (IRRI)
Los Banos
The Philippines
m.thomson@irri.org

Dr. Michael Thomson is currently Senior Scientist and Head of the Genotyping Services Lab at the International Rice Research Institute (IRRI), Los Baños, Philippines. He is working to optimize high-throughput SNP genotyping to increase the rate of genetic gain in rice. He received his PhD in plant breeding from Cornell University in 2002, working with Dr. Susan McCouch to map yield-enhancing QTLs from wild rice. He was an International Research Fellow in Indonesia for two years, and then joined IRRI in 2005 mapping QTLs for salinity tolerance with Dr. Abdelbagi Ismail. In 2009 he was promoted to lead IRRI's research on SNP marker development and validation for breeding applications in rice.

High-Throughput SNP Genotyping for Rice Improvement

Thomson MJ[1], Reveche MY[1], Dilla-Ermita CJ[1], Castaneda NV[1], Malitic- Layaoen G[1], Sanchez G[1], Dwiyanti MS[1], Juanillas V[1], Mauleon RP[1], Chin JH[1], Collard B[1], McCouch S[2] , Nissila E[1]

[1]International Rice Research Institute, Metro Manila, Philippines
[2]Cornell University, Ithaca, NY
Email: m.thomson@irri.org

The Genotyping Services Laboratory (GSL) has been established at IRRI to provide rapid and cost-effective marker services for rice research and breeding programs (http://gsl.irri.org). To increase our sample throughput we have implemented the Brooks PlantTrakHx handheld leaf punching system for rapid barcoded sampling of leaf tissue from the greenhouse and field. Lyophilized leaf tissue in 96-well plates then proceeds to automated DNA extraction using an LGC oKtopure system with magnetic bead-based sbeadex kits. Sample tracking, inventories, and request/workflow management will be handled by the OcimumBiotracker LIMS recently configured for GSL. Sets of 24 SNPs on a Fluidigm EP1 system are being used for rapid genotyping of markers targeted to specific QTLs and genes controlling traits of interest, including top GWAS hits and gene-based SNPs. Diversity analysis, SNP fingerprinting and QTL mapping currently use an IlluminaInfinium 6K SNP chip developed at Cornell University.

At the same time, genotyping by sequencing (GBS) approaches with 96 and 384 barcoded samples per sequence lane are being evaluated for high-resolution genome scans at a low cost per sample. Whole genome sequence data from the 3,000 rice genomes project and resequenced breeding lines will also facilitate more precise imputation of GBS data, with the database infrastructure and analysis enabled by the Genomic and Open-Source Breeding Informatics Initiative (GOBII) led by Cornell University. Future efforts will focus on large-scale deployment of GBS across breeding materials to enable QC genotyping, tracking of donor introgressions, and integration of genome-wide prediction into the variety development pipelines.

Dr. David Marshall

Information and Computational Sciences Group Leader
The James Hutton Institute
Dundee
Scotland
United Kingdom
david.marshall@hutton.ac.uk

Dr. David Marshall currently is Head of Information and Computational Sciences at the James Hutton Institute in Scotland. He current leads a team of over 50 scientists and students who work on a range of computational aspects of plant and environmental sciences at scales ranging from the analysis of microRNAs and alternative splicing to modelling the social and environmental impact of climate change models. His background is in plant population genetics and he has worked for over 30 years on the development and exploitation of molecular markers in plant biodiversity and plant breeding applications. More recently, he has led a team which is developing series of visualisation tools to aid in the understanding of patterns of molecular diversity derived from high throughput sequencing data sets.

NGS and Plant Variant Discovery and Exploitation in Plants: Some Lessons

Bayer M[1], Ribeiro A[1,2], Milne L[1], Flavell A[2], Marshall D[1],*

[1]The James Hutton Institute
[2]Division of Plant Sciences, the University of Dundee
*Email: David.Marshall@hutton.ac.uk

The development of NGS technologies has revolutionised the discovery and exploitation of DNA polymorphism in plant genetics and breeding. However, a combination of relatively poor reference genome sequences on which to map NGS reads and anchoring, rather than ordering, of the genome sequences of many important crop plants mean that it is important to be aware of many of the resulting complications when interpreting experimental results. In this talk I will give some examples of the problems that can arise and highlight some approaches that at least shed light on the problems using example data from a number of crops.

Session III

Genomics Platforms

Co-chairs

Dr EY Danquah

Professor & Director
West Africa Centre for Crop Improvement
University of Ghana
Legon
Ghana

Dr S Sivasankar

Director, CRP-Dryland Cereals
International Crops Research Institute for
the Semi-Arid Tropics (ICRISAT)
Patancheru
India

Dr. Appolinaire Djikeng

Director - Biosciences Eastern and Central Africa (BecA) Hub
ILRI
Nairobi
Kenya
a.djikeng@cgiar.org

Dr. Appolinaire Djikeng was appointed Director of BecA Hub in June 2013. In his current role, Appolinaire leads the BecA Hub team and ensures delivery on the core activity areas (that include research, capacity building, technology platforms development and research related services, networking, product development and delivery from research outputs) focused on improving the livelihoods of smallholder farmers and other vulnerable communities in Africa. Appolinaire is a genomics scientist and joined BecA Hub in September 2009 as Senior Scientist and Technology Manager. Since joining the BecA-ILRI Hub and before his appointment as Director, Appolinaire led various teams focusing on 1) the acquisition and management of biosciences technologies, 2) the provision of research related services, and 3) integrating research and capacity building activities for agricultural development. Prior to joining BecA-ILRI Hub, Appolinaire spent over 15 years of active research at academic and not-for-profit research institutions (University of Yaoundé I – Cameroon; Yale University – USA; the Institute for Genome Research – TIGR, USA; and the J Craig Venter Institute – JCVI, USA). Over the years, Appolinaire's research has focused on the regulation of gene expression, genomics, metagenomics and technology development focusing on: a) developing better control tools for emerging infectious diseases, b) improving human health and c) improving agricultural productivity. Appolinaire is a proponent of capacity building in Africa using a bioscience knowledge base for agricultural development, public health and food security.

Appolinaire graduated with BSc and MSc from the University of Yaoundé I (Cameroon) and completed a PhD in Biochemistry at Brunel University (London, UK).

The Beca-ILRI Hub and its Contribution to African Agricultural Biotechnology and Crop Improvement

Appolinaire Djikeng*, Nasser Yao

BecA-ILRI Hub, International Livestock Research Institute (ILRI),
P.O. Box 30709, Nairobi, Kenya
*Email: a.djikeng@cgiar.org

The Biosciences eastern and central Africa (BecA)-ILRI Hub is a co-creation of the African Union's New Partnership for Africa's Development (AU/NEPAD) and the International Livestock Research Institute (ILRI). The mission of the BecA-ILRI Hub is to mobilize bioscience for Africa's development. It is delivered by providing a centre of excellence in agricultural biosciences to empower African scientists and institutions to generate and harness innovations for regional impact through improved agricultural productivity. The BecA-ILRI Hub leads and supports research; designs and implements capacity building activities in support of African NARS scientists; operates state-of-the-art facilities; and acquires the latest technologies and promotes their applications to accelerate the generation and utilization of research and capacity building innovations/outputs. Key technology platforms established and in operation at the BecA-ILRI Hub include genomics, bioinformatics, diagnostics, nutritional analysis, molecular breeding and transformation. These platforms operate individually and in integration to ensure that the BecA-ILRI Hub is fully integrated to address challenges related to African farming and agro-industrial systems, and is specifically used to enhance crop and livestock productivity, improve food safety and nutrition, and develop a variety of bio-based products and services. The breeding platform (with integration of genomics, bioinformatics capabilities), and leveraging of its operations as one of the IBP Hubs, aims at enhancing breeding and the overall variety development using modern breeding approaches. The platform is built around key components: the Breeding Management System (BMS) which is a suite of comprehensive tools, embedded in a single place, and commonly used by breeders for their day-to-day activities; the Genomics platform; the Bioinformatics platform; and the Integrated Genotyping Support and Service (IGSS).

The major areas addressed through the platform include, training of breeders for efficient use of modern tools for variety development, complete genome profiling of parental lines and target breeding populations, data integration and management, data analysis and interpretation of results for decision support. Key innovations emerging from activities conducted by the BecA-ILRI Hub and multiple partners have marked its first decade. Other aspects of the BecA-ILRI Hub's critical role and increasing relevance in African agricultural transformation will be discussed.

Dr Cindy Taylor Lawley

Sr. Manager
Market Development
Illumina, Inc.
San Francisco
USA
clawley@illumina.com

Dr. Cindy Lawley currently works as a senior manager at Illumina where she coordinates market development through strategic and collaborative efforts with academic and industry partners. Cindy completed her PhD through Scripps Institution of Oceanography in 2004 where she used genetic methods as tools to study marine fish populations among the Channel Islands off Southern California. In addition, she holds a Single Subject Teaching Credential and English as a second language teaching certification; and has taught in public high school before completing her graduate work. Her mission is to facilitate implementation of scalable sequencing and genotyping tools into medical research, fisheries, agriculture and education.

Sequencing and Arrays with Illumina

Cindy Lawley

Illumina, Inc., San Francisco, CA, USA
Email: clawley@illumina.com

Low cost, high sequencing quality and long reads are important aspects of implementing genomic tools for new uses and markets. Scientists of all disciplines are using genomic tools to answer questions that were previously not possible within budgets of most labs. The revolution in use of genomic tools requires a careful discussion around goals and methods in any given project. We highlight examples of innovative methods that can be leveraged for any species and any project. We also emphasize the questions to consider when choosing an approach using sequencing and genotyping methods.

Dr Venkatramana Pegadaraju

Douglas Scientific
Minneapolis
USA
venki.pegadaraju@douglasscientific.com

Dr. Venkatramana Pegadaraju (Venki) is Director of Agrigenomics business unit at Douglas Scientific. Venki's current roles involves interfacing with the global agricultural communities to advance genomics-based technology solutions for crop improvement programs. Prior to joining Douglas Scientific, Venki held multiple roles in both public and private sector crop improvement programs. In his previous role at BioDiagnostics, Inc., Venki established and expanded the molecular breeding and genomics technology services to offer reliable and cost effective DNA based testing services in a wide range of crops to support small- and medium-scale seed industry partners in various countries

Venki's research expertise spans across multiple areas, including functional genomics, crop transformation, genomics assisted breeding and molecular genetics. During his tenure at Monsanto, Venki concept validated several genes for their role in yield and stress response and identified key genes for Monsanto's trait development pipeline. His work on characterizing the mode of action for drought-tolerant genes supported the development of the first generation commercial drought-tolerant transgenic corn for Monsanto. In addition to servicing the commercial seed industry, Venki was associated with various CGIAR and ICAR institutes during the early phase of his research career.

Venki was awarded his Ph.D. degree in molecular, cellular and developmental biology from Kansas State University for dissecting novel defense signaling pathways against phloem feeding insects. During the course of his research career, Venki authored many scientific articles, received several awards, and has been invited for talks at various academic institutions as well at the annual conferences of professional societies. Venki serves as a research expert for Society of Commercial Seed Technologists, and is on the board of the US-Technical Advisory Group of the American Oil Chemist Society.

Douglas Scientific Array Tape™ Platform and its Application in Genomics Assisted Breeding

Venkatramana Pegadaraju, Venki Pegadaraju*

Douglas Scientific, 3600 Minnesota Street, Alexandria, MN, 56308
*Email: venki.pegadaraju@douglasscientific.com

Advancements in high throughput array and sequencing based genotyping methods have significantly impacted the field of agricultural genomics. Particularly, in the area of crop breeding, breeders have access to several millions of SNP markers in a range of crops to assess the genetic variation, map and characterize QTL's for several agronomic traits with high resolution. A wide range of these SNP detection platforms are available for breeding applications and is essential to identifying the most optimal genotyping platform to maximize efficiency and save costs in a breeding program. In general the demands for high density SNP genotyping is reduced in breeding schemes subsequent to the discovery phase and breeders screening large population with a panel of low to medium density markers. Douglas Scientific Array Tape platform offers flexible and cost-effective genotyping solutions for a range of breeding and QA/QC projects. We will discuss the throughput and automation capabilities of Douglas Scientific Array Tape platform and demonstrate its application in various marker assisted selection schemes.

Dr Steven Asquith

Director-Technical Services
LGC Genomics
Herts
UK
steven.asquith@LGCGroup.com

Dr. Steve Asquith: As a genetics graduate, Steve has worked at LGC Genomics/KBioscience for in excess of 12 years. Prior to this he worked in the pharmaceutical industry at GlaxoSmithKline, developing and working in their high throughput genotyping facility. Steve's background is in genotyping chemistry optimisation and adaption onto high throughput platforms. Having run the LGC Genomics Service facility for approximately eight years, he is now in the position of Technical Services Director, working on new technologies and determining customer needs in the industry.

Out-Sourcing vs In-Sourcing Considerations for Lab Services

Steven Asquith

LGC Genomics, UK
Email: Steven.Asquith@LGCGroup.com

The use of genetic mapping and marker assisted selection in plant breeding has been revolutionised by the advance of technologies available in molecular biology and the availability of laboratory automation platforms which can generate vast amounts of genetic data to interrogate a genome. As the use of these tools and the automation systems which enable their wide spread use has become more important, plant geneticists across the globe are faced with investment decisions to decide which technologies to access within their own laboratories and where to use a service provider to ensure access to the right data and the platforms required to generate it. In this presentation we examine the key variables to assess when evaluating options for the outsourcing partnership approach or the development of in-house capacity and the requirements to ensure a flexible programme capable of delivering the "right" data and the technologies which drive them. Key elements of the presentation include:

What bioinformatics is required?

- When to invest in a particular technology as it develops and where should it deliver advantages to a research programme.
- Control of commercially sensitive data – is this a real consideration?
- The challenges of collaborating with different groups around the globe.
- Case studies on successful insourcing and outsourcing programmes.

Invited Speaker Bio

Dr Bhaswar Maity

National Sales Manager-Genomics
Imperial Life Sciences/Affymetrix
Gurgaon
India
bhaswar.maity@imperialls.com

Dr. Bhaswar Maity is National Sales Manager, Genomics, at Imperial Life Sciences, Gurgaon. He was formerly the Regional Accounts Manager with illumina Inc from 2010-2013, managing and establishing high-end genomics technology solutions in India and neighbouring countries. He received his doctoral degree from Jadavpur University as a forensic geneticist at the Central Forensic Science Laboratory, Kolkata, West Bengal. He served as Project Manager at TCGA from 2005-2007, prior to joining Labindia as a Field Application Support Manager for applied biosystem genomics tools from 2007-2008. He has played a key role in marketing illumina technologies in India as Product Manager with Premas Biotech during 2009-2010. He has extensive work experience with cutting-edge genomics technologies and has published 10 research papers in international peer-reviewed journals during his doctoral work. His research spans genetic marker development and screening in human populations, with a focus on forensic genetics and genetic markers to decipher ethnicity of population with controversial origin.

New Era for Molecular Breeding with Cost Effective SNP Genotyping Solutions

Bhaswar Maity

Imperial Life Sciences/Affymetrix, Gurgaon, India
Email: bhaswar.maity@imperialls.com

In recent years, tremendous advancements have been made in the area of plant genomics, leading to a dramatic increase in the number of genomic tools and technologies for almost every crop species. Importantly, this progress has been driven by next generation sequencing- (NGS-) based technologies and high-throughput marker genotyping systems that have truly revolutionized plant genomics. NGS Technologies from Pacific Bioscience offers unprecedented sequencing read length to assemble a complex genome successfully and can generate a reference map with variations even for polyploid plant species.

The availability of reference sequence data does not always guarantee that the discovered SNP can be converted into a valid marker; it has to be validated in the population. Since SNPs are most abundant and informative, the availability of high throughput SNP genotyping platforms and chemistry provides an opportunity to simultaneously screen hundreds to thousands of markers per individual. Low cost and high throughput assay makes it possible to implement genotyping strategy in large populations and shorten the time for the development of new varieties in diverse crop types. Axiom technology from Affymetrix with readily available arrays and customized genotyping options offers a tool for genome-wide association, replication, fine mapping and candidate gene studies. Agena Bioscience offers Mass Spectrometry based technology for downstream marker validation and large-scale screening. The superior accuracy and sensitivity of the MassARRAY has enabled development of novel targeted assays and panels whilst maintaining low cost structures and high throughput as required by the agricultural community.

Session IV

Trait Mapping

Co-chairs

Dr RK Aggarwal

Chief Scientist (Director Grade) &
Professor (Biological Sciences), AcSIR
Centre for Cellular and Molecular Biology
Hyderabad
India

Dr Baozhu Guo

Research Plant Pathologist
United States Department of Agriculture-
Research Service
Tifton, USA
Baozhu.Guo@ars.usda.gov

Dr David Jordan

Professor Research Fellow in Genetics and Plant Breeding
Sorghum Team Leader
Queensland Alliance for Agriculture and Food Innovation
University of Queensland
Brisbane
Australia
david.jordan@uq.edu.au

Dr. David Jordan is a Professor of plant breeding and genetics at the University of Queensland. He has 23 years of experience as a sorghum breeder geneticist in both the public and private sectors, and has led the public sorghum pre-breeding program in Australia for the last decade. This is a long-running and successful program with a reputation for integrating across disciplines and linking research from the strategic to the applied. Breeding lines from this program are widely used in Australia and internationally, with 100% of the commercial hybrid sold in Australia having genetics from the program. David has a diverse research portfolio with active projects funded by the Bill and Melinda Gates Foundation, The Grains Research and Development Corporation, The Australian Research Council, Australian Centre for International Agricultural Research and private sector seed companies. The main themes of his research are exploiting genetic diversity to increase productivity, genetic dissection of complex traits that contribute to yield in water-limited environments and the development and optimization of new breeding strategies through the integration of new technologies.

Development and Use of a Sorghum Backcross Nested Association Mapping Population for Trait Dissection

Jordan DR[1], Hunt C[1,2], Cruickshank A[2], Mace ES[1,2]

[1]University of Queensland Queensland Alliance for Agriculture and Food Innovation,
[2]Hermitage Research Facility, Warwick, QLD Australia
Email: david.jordan@uq.edu.au

The nested association mapping (NAM) strategy (Yu et al. 2008) provides a way of combining the high resolution provided by association mapping with the power of conventional QTL mapping in RIL populations. The method involves creating an integrated set of RIL-based mapping populations from a set of diverse parent lines. Individual lines are genotyped at low to medium density and the parents are re-sequenced or screened using high density genotyping systems and the data used to impute progeny scores. Typical NAM designs involve crossing a reference parent to a range of exotic lines. We developed a variant of this method which employed a backcross design with selection for height and maturity to ensure that the resulting inbred lines could be evaluated for performance in Australian environments. Our BCNAM population forms part of an ongoing breeding and diversification activity which has continued for 10 years and consists of more than 80 exotic lines crossed to an elite adapted recurrent parent. Each subpopulation consists of 30-100 lines to give a total populations size of >4000 individuals. This is an ongoing program which has been active for more than 10 years and has more than 100K data points for a range of important traits. In addition to this, more than 300 lines from the NAM have been licensed to private industry for use in breeding. In this paper we report on the value of this resource to elucidate the genetic architecture of a range of traits in sorghum and other cereals.

Dr Emma Huang

Statistical Geneticist and Senior Research Scientist
CSIRO
Brisbane
Australia
emma.huang@csiro.au

Dr. Emma Huang is a statistical geneticist and senior research scientist with CSIRO Digital Productivity and Agriculture Flagships. She received her doctorate in biostatistics from the University of North Carolina in 2007, developing methods to map the association between genes and disease in humans. Since moving to Brisbane in 2007, her research has focused on modernizing genetic analysis in crop plants such as sugarcane and wheat. Dr Huang has received numerous awards in her career, including the Reynolds and Fryer Fellowships during her Ph.D. research; the Gertrude Cox Scholarship from the American Statistical Association; and an International Science Linkages Grant from the Australian Academy of Sciences. In 2011 she was awarded the Julius Career Award from CSIRO and a Discovery Early Career Researcher Award from the Australian Research Council to address the need for statistical methods to help produce wheat varieties that will contribute to Australian food security.

Challenges and Advantages of MAGIC Genetic Map Construction

Huang BE[1],[*] Shah R[1,2], Ahfock D[1,2], Wood I[2], Stephen S[3], Cavanagh CR[3]

[1]CSIRO Digital Productivity and Agriculture Flagships, Dutton Park, QLD, Australia
[2]School of Mathematics and Physics, University of Queensland, St Lucia QLD, Australia
[3]CSIRO Agriculture Flagship, Acton, ACT, Australia
*Email: emma.huang@csiro.au

Multiparent Advanced Generation InterCrosses (MAGIC) have become increasingly popular as genetic resource panels due to the resolution and power they bring to questions of unraveling genomic structure and gene-trait associations. The basis for many of these analyses is the genetic map, the construction of which we have thoroughly investigated in two bread wheat MAGIC populations. We present here a summary of the challenges and advantages of map construction in MAGIC, including novel advances in correcting for segregation distortion and characterizing uncertainty in high-density maps. The increased recombination and genetic diversity relative to biparental populations ensure the importance of MAGIC maps both in downstream analyses and in anchoring physical maps.

Further, our ability to include distorted regions which may have biological significance, and to estimate the uncertainty associated with mapped regions, provides us with a comprehensive pipeline for analysis of genetic structure. We demonstrate our mapping framework, implemented in a publically available R package (mpMap), on simulated data and that from four-way and eight-way MAGIC populations.

Dr Jason Wallace

Postdoctoral Associate
Institute of Biotechnology
Cornell University
Ithaca
USA
jgw87@cornell.edu

Jason Wallace is interested in applying modern genomic methods to address global food security. He earned his B.S. in integrative biology from Brigham Young University (Utah, USA) and Ph.D in molecular, cellular, and developmental biology from Yale University (Connecticut, USA). He is now finishing a post-doc with Dr. Edward S. Buckler (Cornell University, New York, USA), where he applies genomic and bioinformatic tools to improve crops. His work focuses on using genome-wide marker sets to determine patterns of genetic diversity, develop mapping tools, and identify regions underlying agronomic traits.

He has ongoing collaborations with both the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and the International Maize and Wheat Improvement Center (CIMMYT) to develop tools for crops in the developing world.

Applying High-Throughput Genomics to Crops for the Developing World

Jason Wallace

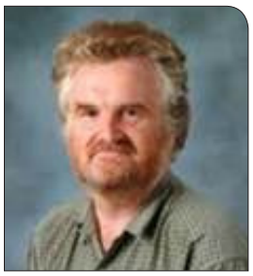
Institute of Biotechnology
Cornell University, Ithaca
USA
Email: jgw87@cornell.edu

Modern high-throughput sequencing opens the way for cutting-edge genomics in a wide variety of crops, including the so-called "orphan crops" with few or no genetic resources. For example, using high-throughput genotyping protocols (such as genotyping-by-sequencing) enable us to create large marker sets for almost any crop. We can then use these datasets to analyze patterns of genetic diversity, create suites of molecular tools, and identify genetic loci underlying agronomic traits. I present here several case studies of such work in pearl millet (Pennisetum glaucum), barnyard millet (Echinochloa spp.), and maize (Zea mays). Since genetic data are now easy to obtain, the breeding bottleneck has shifted from genotyping to phenotyping. We now need to develop ways to quickly and accurately measure crop phenotypes and apply these to breeding programs to continue to accelerate crop development and achieve global food security.

Session V

Genome Dynamics and Systems Biology

Co-chairs



Dr Noel Ellis

Director, CRP-Grain Legumes
International Crops Research Institute for the
Semi-Arid Tropics (ICRISAT)
Patancheru
India

Dr Naveen Puppala

College Associate Professor
Peanut Breeder
New Mexico State University
Clovis
USA

Dr German C Spangenberg

Executive Director-Biosciences Research Division
DEPI Victoria
Professor-School of Applied Systems Biology
La Trobe University
Melbourne
Australia

Dr. German Spangenberg, FTSE: After completing MSc (Agricultural Sciences) at the University of Uruguay, Uruguay, and PhD from the University of Heidelberg and Max-Planck-Institute of Cell Biology in Heidelberg, Germany, Professor Spangenberg undertook postdoctoral studies at the Max-Planck-Institute of Cell Biology and the Institute of Plant Sciences at the Swiss Federal Institute of Technology (ETH), Zuerich, Switzerland.

Professor Spangenberg held positions as Assistant Professor and Associate Professor at the ETH Zuerich where he obtained his DSc in agribiotechnology, before joining the Department of Environment and Primary Industries (DEPI), Victoria, where he held positions as Director, Plant Biotechnology Centre and Research Director, Plant Genetics & Genomics.

Professor Spangenberg is Executive Director of the Biosciences Research Division of DEPI Victoria; Professor (Plant Genetics & Genomics) and Head of School of Applied Systems Biology with La Trobe University; and Director AgriBio (DEPI), the Centre for AgriBioscience. He is also Chief Scientist of the Dairy Futures Cooperative Research Centre; and Director and Chief Scientific Officer of the agricultural biotechnology company Phytogene Pty Ltd.

He was elected Fellow of the Australian Academy of Technological Sciences and Engineering in 2007 and was the recipient of the Australian Thinker of Year 2006 Award.

Professor Spangenberg is recent past President of the International Association for Plant Biotechnology.

Advances and Prospects in Forage Systems Biology and Molecular Breeding

German C Spangenberg

AgriBio, Centre for AgriBioscience, La Trobe University, Victoria 3083, Australia
Email: german.spangenberg@ecodev.vic.gov.au

Recent advances in forage systems biology and applications of high-throughput methodologies, from genome to phenome analyses, in key forages, their endosymbionts and associated microbiomes will be described. These have enabled new approaches in the development and application of an integrated suite of technologies and capabilities in molecular breeding of forages. Selected examples of these approaches in 'forage symbiomes' will be presented.

Dr Dave Edwards

Professor
University of Western Australia
Perth
Australia
dave.edwards@uq.edu.au

Dr. David Edwards is a Professor in the School of Plant Biology at the University of Western Australia. He was formerly a Professor at the School of Agriculture and Food Science at the University of Queensland. He received his PhD from the University of Queensland and has previously held positions within academia (University of Adelaide, Australia; University of Cambridge, UK; McGill University, Canada; and the University of Queensland), government (Long Ashton Research Centre, UK, Department of Primary Industries, Victoria, Australia) and industry (ICI seeds, UK). His training is in genomics, but over the last 15 years he has moved into bioinformatics and currently all his team members are computationally based. His research interests include the structure and expression of plant genomes; the discovery and application of genome variation; and applied bioinformatics; with a focus on crop plants and accelerating crop improvement in the face of climate change.

Improving Genome Assemblies and Capturing Genome Variation Data for Applied Crop Improvement

Dave Edwards

University of Western Australia, Perth, Australia
Email: dave.edwards@uwa.edu.au

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 and identify regions of misassembly to correct assemblies. These approaches can be applied to a broad range of genomes which have either been completed or are undergoing development.

While the production of draft genome assemblies is a valuable first step in understanding a species at the genome level, knowledge of genome variation between individuals allows the association of genome variation with important traits. We have developed several tools for the characterisation of genome variation at the single nucleotide, gene and chromosome level as well as systems for the management and interrogation of this variation data. The application of these systems can assist in the acceleration of genomics based crop improvement.

Invited Speaker Bio

Dr Doug Cook

Professor
Department of Plant Pathology
University of California - Davis
USA
drcook@ucdavis.edu

Dr. Douglas R. Cook is a Professor in the Department of Plant Pathology at the University of California-Davis. He was formerly the Director of the College of Agriculture and Environmental Sciences Genomics Facility at UC Davis, and is currently Director of the Feed the Future Innovation Lab for Climate Resilient Chickpea. He received his doctoral degree from the University of Wisconsin-Madison as a bacterial geneticist in the Department of Plant Pathology, and conducted postdoctoral research at the Carnegie Institution of Washington's Department of Embryology at the Johns Hopkins University on maize transposable elements. He served on the faculty of Texas A&M University from 1992-2000, prior to joining UC Davis, and as an adjunct Professor of International Graduate School in Bioinformatics and Genome Research at the Universitat Bielefeld in Germany from 2002-2008. He was among a small group of colleagues who together pioneered the use of *Medicago truncatula* as a model genetic and genomic system for investigation of legume biology. For the past decade he has been a leading advocate for the application of basic legume science towards pressing agricultural needs in the developing world. His current research spans model and crop legume systems, with a dual focus on (1) forward genetics, biochemistry and cell biology to characterize genes governing symbiotic development in *M. truncatula*, and (2) ecological genomics and association genetics to understand gene function in complex natural and agricultural legume systems.

Prospecting for Gene Function in Complex Natural and Agricultural Systems

Penmetsa RV[1], Greenspan A[1],Chang P[1,2],Carrasquilla-Garcia N[1],Mamo B[1], Vance L[1], Mir R[1], Moenga S[1],Siler EA[3], Rose JL[4], Fikre A[5],Tar an B[6], Friesen M[3],Alford B[1], Kim DH[7], Nuzhdin S[2], Bukun B[8], Aydogan A[9],Varshney RK[7], Berger JD[10], Kahraman A[11], von WettbergE[4], Douglas R Cook[1*]

[1]University of California - Davis, CA 95616, USA.
[2]University of Southern California, Los Angeles, California 90089, USA; [3]Michigan State University, East Landing, Michigan 48824, USA; [4]Florida International University, Miami, Florida 33199, USA; [5]Ethiopian Institute for Agricultural Research, Addis Ababa, Ethiopia; [6]University of Saskatchewan, Saskatoon S7N 5A8, Canada; [7]International Crops Research Institute for the Semi-Arid Tropics, Patancheru 502324, India; [8]Dicle University, Diyarbakir 21280, Turkey; [9]Turkish Agricultural Research System, Ankara 06170, Turkey; [10]CSRIO Plant Industry, Perth, Western Australia 6913, Australia;
[11]Harran University, Sanliurfa 63300, Turkey.
*Email: drcook@ucdavis.edu.

We are characterizing the potential of chickpea's wild relatives for crop improvement. 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 germplasm; population development to remove barriers to use of wild alleles; phenotyping and modeling of trait-gene associations to enhance the precision and rate with which wild alleles are applied. We have completed ecological characterization and genetic resource collection for ~2,000 wild accessions, used genotyping by sequencing to deduce population genetic parameters, initiated whole genome re-sequencing of 1,100 accessions, collected co-occurring bacterial symbionts, surveyed seed and flowering phenotypes, and initiated development of nested association mapping and backcross introgression panels. In parallel to the analysis of plant populations, we have initiated genomics and community ecology of legume-associate microbes from both wild species at their center of origin and their domesticated counterparts globally. Sequencing the genome of ~400 Mesorhizobium genomes reveals a history of horizontal gene transfer of symbiotic genes from the natural symbiont of Cicer spp to atypical genomic backgrounds, presumably to balance adaptation to agricultural situations with the requirement for symbiotic competency. We have also initiated culture-independent metagenomic studies of rhizosphere and phylosphere microbial communities throughout the plant species' center of origin, to investigate the biogeography of plant-associate microbes. We are testing the hypothesis of plant-microbiome coevolution in a range-wide study system, as well as characterizing the population genetics of key crop pathogens in wild systems.

Professor Robert J Henry

Director
Queensland Alliance for Agriculture and Food Innovation
(QAAFI)
University of Queensland
Brisbane
Australia
robert.henry@uq.edu.au

Dr. Robert James Henry is Professor of Innovation in Agriculture and Director, Queensland Alliance for Agriculture and Food Innovation, University of Queensland.

Professor Henry is one of the most highly cited scientists in agriculture internationally, specializing in research on the development of new products from plants. He is Professor of Innovation in Agriculture, and Foundation Director of the Queensland Alliance for Agriculture and Food Innovation, an Institute of the University of Queensland. He was previously Director of the Centre for Plant Conservation Genetics at Southern Cross University and Research Program Leader in the Queensland Agricultural Biotechnology Centre. He has been involved in establishing several Cooperative Research Centres in Australia and has contributed to the management of research funding by Rural Research and Development Corporations. He was awarded a higher doctorate (D Sc) by the University of Queensland for his work on variation in plants, is a Fellow of the Royal Australian Chemical Institute, recipient of the Guthrie Medal for his contributions to cereal chemistry and a Fellow of the Australian Academy of Technological Sciences and Engineering.

Genome Sequencing to Support Germplasm Analysis and Utilization

Robert Henry

Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, 4072,QLD, Australia
Email: robert.henry@uq.edu.au

Next generation sequencing is a tool for the characterization of variation available in germpalsm for use in crop improvement. Analysis of the whole genome of wild crop relatives can identify new and novel gene pools, new options for interspecific hybridization, and support discovery of new alleles at key loci. Sequencing of wild rice populations in Australia has uncovered possible new taxa for use in breeding. These populations are divergent from Asian and domesticated rice but part of the primary gene pool. They display genetic diversity in parts of the genome with low variation within the domesticated gene pool. This germplasm is a valuable source of useful variation in breeding for disease resistance and quality. Analysis of Eucalypt genomes has demonstrated widespread reticulate evolution and hybridization between species in this important forest group. Domesticated gene pools can also be evaluated by sequence based methods. Analysis of diverse wheat germplasm has identified novel alleles of differentially expressed genes associated with bread quality. Coffee sequencing is characterizing important quality genes and germplasm sources. Comparison of fruit, nut and forest tree genomes has defined relationships between species and identified genes associated with key traits for transformational genetic improvement. Genome sequencing in sugarcane and related species underpins their re-invention as energy crops. Improving methods and strategies for whole genome sequence capture and analysis will enable accelerated discovery and utilization of novel genetic variation in crop improvement.

Session VI

Genomics-Assisted Breeding-I

Co-chairs

Dr H S Dhaliwal

Vice-Chancellor
Eternal University
Baru Sahib, H.P.
India

Dr C R Bhatia

Former Secretary
Department of Biotechnology
New Delhi
India

Dr Patrick Schnable

Director-Plant Science Institute &
Center for Plant Genomics
Department of Plant Science
Iowa state University
Ames
USA
schnable@iastate.edu

Dr. Patrick Schnable is a distinguished professor at Iowa State University where he holds an endowed chair and directs the Plant Sciences Institute. He is also a ChangJiang Scholar Professor at China Agriculture University. Schnable received his BS from Cornell University and his PhD from Iowa State University; he conducted post-doctoral research at the Max Planck Institute in Köln, Germany.

Schnable's wide-ranging investigations of the maize genome have resulted in >120 peer-reviewed publications and an h-index of 56. Schnable is a fellow of the American Association for the Advancement of Science, serves as an associate editor for PLoS Genetics (Impact Factor 8.7), and is the chair of the American Society of Plant Biology's Science Policy Committee. He is a past chair and current member of the Maize Genetics Executive Committee.

Schnable is also the managing partner for Data2Bio LLC, which designs, conducts, analyzes and interprets Next Generation Sequencing projects.

Trait-Associated SNPs Provide Insights into Heterosis in Maize

Patrick S. Schnable

Iowa State University, Iowa, USA
Email: schnable@iastate.edu

The phenomenon of heterosis has been observed for more than a century, but the underlying genetic mechanisms remain elusive. To better understand these genetic mechanisms, seven yield-related traits with varying levels of heterosis were subjected to GWAS using four related populations composed of 6,230 lines for which genotypes were available at ~13M sites. Multi-variant GWAS approaches that considered only additive effects explained ~40-70% of the heritability of the seven traits. The percentage of phenotypic variation explained by these genome-wide markers was negatively correlated with the level of heterosis. A GWAS model that included both additive and dominant gene action increased the proportion of the narrow sense heritability explained by 15-45 percentage points. The amount of heterosis per trait was positively correlated with the number of trait-associated variants identified via GWAS that exhibited positive dominant gene action and the magnitudes of their effects. Hence, these findings provide strong support for the view that positive dominant gene action contributes to heterosis.

Dr Gengyun Zhang

Deputy Director
BGI Tech Solutions Co., Ltd.
Shenzhen
China
zhanggengyun@genomics.org.cn

Dr. Gengyun Zhang is combining molecular and conventional plant breeding techniques to cccelerate the development of new cultivars, especially focusing on whole genome based molecular marker assisted selection systems for different crops, based on high throughput sequencing and data analysis capacities in BGI-SZ.

Dr Zhang obtained his Ph.D. in turfgrass breeding in 2003 from Rutgers University's Department of Plant Biology and Pathology; New Brunswick; a Master of Science in biochemistry in 1990 from the Graduate School of Beijing Agricultural University; Beijing, and a Bachelor of Science in genetics & cell biology in **1986 from Peking** University.

He has been **Deputy Director of BGI on Agriculture; General Manager, Life Science Division, U**niversity of Washington, Seattle; Research Associate, College of Forest Resources at Rutgers University, New Brunswic; Research Associate, Department of Plant Biology and Pathology, Postdoctoral Fellow; a Visiting Scholar at the Chinese Academy of Sciences, Beijing, and Research Associate, Institute of Genetics.

Practice of Whole Genome Molecular Marker Assisted Breeding in BGI

Gengyun Zhang

BGI-Shenzhen
Email: zhanggengyun@genomics.cn

The quick advances of sequencing technology, based on NGS, make it easier to elucidate whole genome sequence of a species, even for neglected species. The genotyping (genome diversity) of different individuals could be obtained economically through a sequencing based procedure. The desired individual in a segregating population could be easily picked out. The breakthrough of genome sequencing technology dramatically improved our capacity to recognize and exploit biodiversity in germplasms. These dramatically improved the efficiency of our selection. Supported by the largest high throughput sequencing and bioinformatics platforms established in BGI, series breeding projects have been finished. Our successes indicated that there are no further technical obstacles for applying whole genome molecular marker assisted selection, for plant or animal species. Whole genome marker assisted selection system can dramatically increase our genetic gains in breeding procedure. The technical platforms established in BGI could provide practical and economic support for global breeding efforts.

Dr Frank Ordon

JKI-Federal Research Centre for Cultivated Plants
Institute for Resistance Research and Stress Tolerance
Quedlinburg
Germany
frank.ordon@jki.bund.de

Dr. Frank Ordon is head of the Institute for Resistance Research and Stress Tolerance of the Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants, Germany, and honorary professor for 'molecular resistance breeding' at the Martin-Luther-University, Halle-Wittenberg, Germany. He studied agricultural science at the Justus Liebig University in Giessen, Germany, where he also got his PhD and state doctorate. He is the editor in chief of *Plant Breeding* and is a member of several editorial boards, e.g. *Theoretical and Applied Genetics*, and *Journal of Applied Genetics*, and of scientific advisory boards, e.g. of the IPK Gatersleben. He is chair of the Research Committee of the Wheat Initiative. Frank has a basic background in classical and molecular plant breeding, with special emphasis on breeding for resistance against viral and fungal pathogens in barley and wheat.

His primary contributions include genetic analyses of resistance, and the development of molecular markers for major resistance genes and QTL, especially against virus diseases, up to gene isolation. Besides this, he is working on improving tolerance to abiotic stress in several crop species. Frank has published the results of his studies in more than 100 papers in peer-reviewed journals.

Genomics Based Breeding Research for Improving Resistance to Biotic and Abiotic Stress in Cereals

Perovic D[1], Serfling A[1],Perner K[1], Mitterbauer E[1], Knöchel N[1], Fettköther T[1], Wehner G[1], Lehnert H[1], Silvar C[3], Krämer I[1], Habekuss A[1], Kopahnke D[1], Graner A[2], Stein N[2], Ordon F[1*]

[1]Julius Kühn-Institute (JKI), Institute for Resistance Research and Stress Tolerance,
Erwin-Baur-Str. 27, 06484 Quedlinburg, Germany
[2]Leibniz Institute for Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466 Gatersleben, Germany
[3]Department of Ecology, Plant and Animal Biology, University of Coruña, Campus da Zapateira s/n, 15071A Coruña, Spain
*Email: frank.ordon@jki.bund.de

Feeding the earth´s growing population against the background of climate change is one of the major future challenges. In this respect wheat and barley are of special importance. However, both are hit by many fungal and viral pathogens causing severe yield losses. In addition, yield is negatively affected by abiotic stress, e.g. drought. Therefore, breeding research on improving resistance/tolerance to biotic stress and on adaptation to climate change is a prerequisite for facing future challenges.

Today genomic resources like the Infiniumi Select genotyping arrays, the Genome Zipper, comprising a virtual linear order of genes of different monocot species, next generation sequencing techniques, e.g. genotyping by sequencing (GBS), exome capture, or RNAseq and MACE, allow efficient marker development and gene identification in bi-parental populations as well as by genome wide association studies (GWAS). This tool box facilitates (a) a more efficient exploitation of genetic resources, (ii) an efficient marker development for genes and QTL involved in resistance/tolerance to biotic and abiotic stress, (iii) an enhanced identification of candidate genes followed by gene isolation, (iv) allele mining and allele based breeding, (v) a faster implementation of new breeding goals. Examples for genomics-based breeding research for improving resistance to biotic stress, e.g. on a *P. triticina* resistance derived from *T. monococcum*, to abiotic stress, e.g. drought, as well as for the implementation of new breeding goals, e.g. adaptation to rising CO_2 concentrations are given.

Dr Andrzej Kilian

Director
DArT Pty Ltd
Bruce
Australia
zej@diversityarrays.com

After completing in 1987 his PhD on population genetics of *Arabidopsis thaliana* in Poland, Andrzej was a Postdoctoral Fellow funded by FAO/IAEA at the Plant Breeding Institute (PBI) in Cambridge, UK. His work in Cambridge provided the first indication of synteny among cereal genomes. While at PBI, he worked on the first field release of a genetically engineered food crop (potato). From 1991 to 1996, while at WSU, Pullman, USA, he contributed the first proof of the synteny among grass genomes at the gene level and seminal work on telomerase activity in plants. After arriving in Australia to lead genomics at CAMBIA, a non-for-profit institute he co-founded, he led the work that resulted in the cloning of the catalytic subunit of human telomerase, a major biomedical target. Andrzej invented and lead development of Diversity Arrays Technology, DArT, a genotyping method with many applications in plant and animal genetics and breeding. He is a founder and the Director (President) of Diversity Arrays Technology Pty Ltd which is providing genetic and IT services to a global customer base.

He is primarily involved in further development of genome profiling and IT technologies for data storage and mining. While primarily leading DArT Pty Ltd Andrzej is frequently serving as a consultant for a range of private and public institutions, primarily in the area of molecular breeding and crop performance evaluation systems. In 2004 Andrzej was selected as one of the 10 top scientists in Australia by The Bulletin-Microsoft “Smart 100” competition and in 2007 he was the finalist of the Australian Ethnic Business Award in recognition of his achievements in business and contribution to Australia.

DArT PL's Support for Agricultural Research and Practice: Delivery Model and Technology Package

Andrzej Kilian

Diversity Arrays Technology Pty Ltd, Building 3 Level D, Kirinari Street, University of Canberra, Bruce ACT 2617, Australia
Email: a.kilian@diversityarrays.com

DArT PL was set up in 2001 with a vision to spread the benefits of genomics and information technologies across the agricultural sector in an equitable manner and to achieve substantial social and environmental gains in the process. Our initial technology (DArT™) enabled utilization of the whole genome profiling in crop breeding, thanks to drastic reduction in the cost and increase in throughput compared to alternative technologies. In the last four years we have launched a new service using DArT complexity reduction methods combined with Next Generation Sequencing platforms. DArTseq technology scans over 100,000 loci for DNA variation targeting primarily genic regions. DArTseq has been broadly adopted for a variety of applications in pre-breeding and crop improvement of practically all crops and is rapidly expanding to other organisms, especially animals. The demand for further genotyping cost reduction and increasing the throughput for breeding prompted us to develop additional technologies to cover small to medium marker densities.

We combine DNA profiling at the density most appropriate for the application with extensive support in data analysis and overall data management. Our support is tailored to specific clients' needs, thanks to a modular design of our software tools and their integration via web services. We have developed a robust data model for molecular, field and environmental data and an Application Programming Interface (API) which was recently released under GPL license. We are delivering our integrated services using open access model through partnerships with a number of large public institutions on several continents.

Session VII

Genomics-Assisted Breeding - II

Co-chairs

Dr Tim Sutton

Principal Scientist
South Australian Research and Development
Institute (SARDI)
Adelaide
Australia

Dr Bharat Chattoo

Senior Professor
Molecular Genetics
M.S. University of Baroda
Baroda
India

Dr Henry T Nguyen

MSMC Endowed Professor & Director
National Centre for Soybean Research
University of Missouri
Columbia
USA
nguyenhenry@missouri.edu

Henry T. Nguyen is Professor of Genetics, and the Missouri Soybean Merchandising Council Endowed Chair in Soybean Biotechnology. He serves as Director of the National Center for Soybean Biotechnology established by the United States Congress. Prior to the current position, he was a professor of genetics at Texas Tech University and Texas A&M University System for 18 years. The Board of Regents at Texas Tech University awarded him the Paul Whitfield Horn distinguished professorship. He has a distinguished career in plant genetics and biotechnology and is internationally recognized for his research in plant adaptation to stress environments. His research team conducts genetic analysis of major traits and applies molecular marker technology to soybean improvement. Dr. Nguyen has gained recognition through many awards such as the National Science Foundation's Presidential Young Investigator Award and the Young Crop Scientist Award. He was elected as Fellow of the Crop Science Society of America, Fellow of the American Society of Agronomy, and Fellow of the American Association for the Advancement of Science. He served as Chair of the Molecular Genetics, Genomics, and Biotechnology Division of the Crop Science Society of America and the Board of Directors of the CSSA. He has served on several editorial boards and published more than 200 refereed articles and 30 book chapters. He chairs the Abiotic Stress Workshop at the International Plant and Animal Genome Conference. He coordinates a large scale soybean genome re-sequencing project funded by the United Soybean Board and seed industry.

Accomplishments in Soybean Molecular Breeding and Future Perspectives

Valliyodan B, Nguyen HT*

Division of Plant Sciences and National Center for Soybean Biotechnology,
University of Missouri, Columbia, Missouri 65211, United States of America
*Email: nguyenhenry@missouri.edu

Development of new tools in molecular genetics and genomics has facilitated significant understanding of trait genetics and its application in plant breeding. DNA markers for major genes or QTL such as nematode resistance and seed composition traits are effectively used in soybean breeding programs. Marker-assisted selection for polygenic trait improvement requires innovative strategies that eliminate the bottlenecks in the current approaches. Next-generation sequencing technologies help build individual crop genomes for deeper investigation of genomic regions of interest. Large-scale sequencing of soybean genomes and transcriptomes helped us to discover the extent and distribution of genetic diversity in soybean gene pools, and its relationship to yield and quality traits. New genetic mapping strategies were developed to optimize genetic variations and discovery of genes and molecular markers for breeding programs. Also, investigation of recombination landscapes and dissecting the complex traits by re-sequencing recombinant inbred lines in soybean help to identify genome-wide distribution of crossovers and to characterize sequence motifs around crossover hotspots. A combination of individual plant genome comparisons, novel genetic mapping strategies including the genome wide association studies tapping maximum natural genetic variations, and whole genome prediction of complex traits will be the future path towards breeding by design for crop improvement.

Dr Trilochan Mohapatra

Director
ICAR-Central Rice Research Institute
Cuttack
India
tmnrcpb@gmail.com, directorcrri@sify.com

Dr. Trilochan Mohapatra is currently the Director of the Central Rice Research Institute, Cuttack, Odisha, India. Prior to this, he worked as a researcher and teacher for about 20 years at the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute (IARI), New Delhi. He has been working in the area of molecular genetics and genomics. Dr. Mohapatra has over 135 research papers in national and international journals of repute and several book chapters. His research accomplishments include the development of the first high-yielding Basmati rice variety resistant to bacterial leaf blight through molecular marker assisted selection, and physical mapping and genome sequencing of rice and tomato. He has received several honours and awards in recognition of his excellent academic and research contributions, including the INSA Young Scientist Award, Prof. LSS Kumar Memorial Award, NAAS-Tata Award, IARI BP Pal Award, DBT Bio-science Award and NASI-Reliance Industries Platinum Jubilee Award. He is a Fellow of the Indian National Science Academy, New Delhi, National Academy of Sciences-India, Allahabad, and the National Academy of Agricultural Sciences, New Delhi.

Genome-Wide Association of SNPs in Stress Responsive Genes with Salinity Tolerance in Rice

Vinod Kumar[1], Anshuman Singh[1], S.V. Amitha Mithra[1], Swarup K. Parida[1], S.L. Krishnamurthy[2], Sourabh Jain[1], Kapil K. Tiwari[1], Pankaj Kumar[1], A.R. Rao[3], S.K. Sharma[2], J.P. Khurana[4], N.K. Singh[1], T. Mohapatra[1,5,*]

[1]National Research Centre on Plant Biotechnology, New Delhi 110012, India; [2]Central Soil Salinity Research Institute, Karnal 132001, India; [3]Indian Agricultural Statistics Research Institute, New Delhi 110012, India; [4]University of Delhi, South Campus, New Delhi 110021, India; [5]Central Rice Research Institute, Cuttack, Odisha 753006, India
*Email: tmnrcpb@gmail.com

Rice growth is affected due to salinity stress, to a varying degree at all stages starting from germination through maturation. Reduction in major yield components, including tiller and spikelet numbers, has been reported to be the major cause of yield loss (27-50%) in rice during early reproductive panicle initiation stage under salinity stress. In Asia, 12 million ha of land area is thought to be salinity affected, with India having more than 50% of this area. We implemented global transcriptome profiling of control and salt stress (200 mM NaCl) seedlings of two rice genotypes (CSR30 and Taraori Basmati) using the next-generation Illumina Solexa Genome Analyzer. We identified 288 and 140 differentially expressed salinity-tolerant and sensitive transcripts/genes in CSR30 and Taraori Basmati, respectively. Functional annotation of these transcripts corresponded with different known (19%) and candidate (67%) salinity tolerance and unknown expressed (14%) rice genes. Pathway analysis enabled us to localize 128 known and candidate salinity tolerant genes in various known salinity stress-responsive pathways, including salt overly sensitive (SOS) and calcium signalling. Integration of differential expression profiling of genes with that of whole genome re-sequencing data enabled identification of single nucleotide polymorphism (SNP) in the salinity stress-responsive rice genes. In an alternative approach, the SNP information was utilized to carry out genome wide association studies (GWAS) to identify loci controlling salinity tolerance. A custom designed SNP array based on 6000 stress-responsive genes, distributed at an average physical interval of <100 kb on 12 rice chromosomes was used to genotype 220 rice accessions using Infinium assay. Genetic association was analysed with 12 different traits recorded on these accessions under field conditions at reproductive stage. We identified 20 SNPs (loci) significantly associated with Na^+/K^+ ratio, and 44 SNPs with other traits observed under stress condition. In addition to a known quantitative trait locus (QTL) for Na^+/K^+ ratio under stress near *Saltol* locus on chromosome 1, we found GWAS peaks representing new QTLs on chromosomes 4, 6 and 7. The current association mapping panel contained mostly *indica* accessions which can serve as source of novel salt tolerance genes and alleles. The study helped in unveiling genomic regions/candidate genes regulating salinity stress tolerance in rice.

Dr Petr Smykal

Assistant Professor
Department of Botany
Faculty of Sciences
Palacky University in Olomouc
Czech Republic
petr.smykal@upol.cz

Dr. Petr Smykal is Assistant Professor in the Department of Botany at the Palacky University, Olomouc, Czech Republic. He received his doctoral degree from the Charles University, Prague, in the Department of Plant Experimental Biology as a plant molecular biologist working on pollen embryogenesis and heat stress (1999). He conducted his postdoctoral research at the Swiss Institute of Technology (ETH), Zurich, on tobacco photoperiodic responses and MADS-box genes, followed by a second postdoc at the University of Freiburg, Germany, working on *Arabidopsis* meristem patterning in the context of Argonautgenes and miRNAs processing. From 2004 till 2011 he worked at Agritec Plant Research Ltd. on analysis of flax and pea germplasm diversity, developed retrotransposon based marker systems for various crops, and pea and flax transgenosis. He has an international reputation (recognized by Global Crop Diversity Trust) on *Pisum* and *Fabeae* tribe species phylogeny and genetic diversity and has been involved in the establishment of the world pea collection, providing methodology for efficient germplasm assessment for AEGIS (Bioversity International). He was among the founders of the International Legume Society and chaired the Grain Legume Technology Transfer Platform (2008-10). The main research focus is currently on the study of seed testa mediated dormancy and pod dehiscence, in the context of legume (pea) domestication using a combination of genomics, anatomical and chemistry approaches. The second focus (and project) is on the use of crop wild relatives (wild peas) to broaden the genetic diversity of bottlenecked cultivated pea by creation of introgression lines and finally combining genomics with ecology to study plant species adaptation.

Establishment of Wild Pea *Pisum Fulvum* Chromosome Segment Substitution Lines in Cultivated *P. Sativum* Genetic Background, as a Tool to Study Domestication and to Broaden Genetic Diversity

Petr Smykal*, Micová B.

Department of Botany, Palacký University in Olomouc, Šlechtitelů 11,
783 71 Olomouc, Czech Republic
*Email: petr.smykal@upol.cz

Plant evolution under domestication has altered numerous traits, including self-pollination which reinforced fertility barriers between wild and cultivated populations, facilitating fixation of the desired genotype. Domestication bottleneck has resulted in high degree of relatedness, leading to narrower genetic base of cultivated germplasm, prone to pests and diseases. The study of genetic diversity showed that although wide diversity is captured among cultivated pea, wild material provides yet broader diversity. The chromosome segment substitution lines containing genomic segments of wild pea (*Pisum fulvum* WL2140) in the cultivated pea (*P. sativum subsp. sativum* WL1238/cv. Terno) genetic background were developed. Twenty eight microsatellite and 44 gene-specific markers at 2 to 82 cM spacing, were used to make initial molecular characterization of 105 lines. The heterozygozity was detected in 533 (8%), *Pisum sativum* parent was present in 4552 (69%) and introgressed segments of *P. fulvum* in 1551 (23%). There were five to 14 segments per line, with a mean of 9.6. These lines were described for 14 traits (including branching, height, nodes, pod and seed numbers). Establishment of such permanent introgression library will allow phenotypic characterization of unlimited number of target traits, which, coupled together with higher density markers, will provide means for QTL and gene identification and subsequent incorporation in desired genotypes. In parallel the series of lines is being established with *Pisum sativum* subsp. *elatius* L100 and cv. Cameor parents.

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Session VIII

Climate Resilience Genomics Breeding

Co-chairs

Prof KHM Siddique

Hackett Prof of Agriculture Chair
& Director, Institute of Agriculture
The University of Western Australia
Perth
Australia

Dr Ajay Parida

Executive Director
M S Swaminathan Research Foundation
(MSSRF)
Chennai
India

Dr BM Prasanna

Director, Global Maize Program
International Maize and Wheat Improvement Center
(CIMMYT)
Nairobi
Kenya
b.m.prasanna@cgiar.org

Dr. B.M. Prasanna is the Director of the Global Maize Program of CIMMYT since March 2010. He is based at Nairobi, Kenya, and is leading a strong and multi-disciplinary team of scientists located in Sub-Saharan Africa, Latin America and Asia, with major focus on developing and delivering stress-resilient and nutritious maize for the tropics, besides application of novel tools and technologies for enhancing genetic gains and breeding efficiency. Prior to joining CIMMYT, Prasanna served as a faculty member and maize geneticist at the Division of Genetics, IARI, New Delhi, for nearly two decades. He led the Indian team under the Asian Maize Biotechnology Network (AMBIONET) during 1998-2005, and served as ICAR National Fellow during 2005-2010.

During his tenure at IARI and at CIMMYT, Prasanna has developed and successfully implemented several multi-institutional projects on maize genetics, breeding, biotechnology and seed systems. He was recognized with several awards and honors for his contributions to maize research and post-graduate teaching.

Climate-Resilient Maize Development and Delivery in the Tropics through Public-Private Partnerships: CIMMYT's Experiences and Perspective

BM Prasanna

CIMMYT (International Maize and Wheat Improvement Center), Nairobi, Kenya
Email: b.m.prasanna@cgiar.org

Innovative approaches as well as partnerships are required for accelerated development, evaluation and delivery of climate-resilient and nutritionally-enriched maize varieties in the stress-prone, tropical agro-ecologies. This warrants not only improved genetics, but also effective seed systems, improved agronomy and enabling policies. Effective integration of modern tools/strategies, including high-density genotyping, high throughput and precision phenotyping, doubled haploid (DH) technology, genomics-assisted breeding, and advanced computational tools for knowledge-led decision-support systems through public-private partnerships (PPPs), should be integral to our efforts towards increasing genetic gains, and enhancing the pace, precision and efficiency of breeding programs. The presentation will focus on an array of functional PPPs on maize R&D in the tropics in which CIMMYT plays a key role, including the Drought Tolerant Maize for Africa (DTMA), Water Efficient Maize for Africa (WEMA), Maize Doubled Haploid (DH) facility in Africa, Heat Tolerant Maize for Asia (HTMA), Masagro-Maize in Mexico, and the International Maize Improvement Consortium (IMIC) in Asia.

Intensive seed systems work is required to reduce the time to release new varieties (effectively replacing the older, less productive ones), deploy easy-to-produce hybrids, scale-up seed rapidly, and reach the unreached. DTMA in sub-Saharan Africa demonstrates the impact of such work. Through PPPs involving nearly 100 seed companies, NGOs, and farmer organizations, the project could facilitate production and delivery of about 30,000 tons of DT maize seed in 2013, benefiting an estimated2 million African households.The CIMMYT-led International Maize Improvement Consortium (IMIC) in Asia and in Latin America, especially in partnership with more than 75 SME seed companies, has also significantly strengthened the interface with both public and private institutions engaged in maize R&D. The underlying principles of this partnership include research prioritization that is client-determined, besides a more focused, demand-driven approach for product development, while drawing on the synergies through a collaborative testing network for targeted impacts. Experiences of CIMMYT in PPPs in the developing world so far indicate that appropriate government policies, adoption of progressive seed laws and regulations, and institutional innovations are vital for improving smallholder farmers' access to improved seed, and for overcoming key bottlenecks affecting maize seed value chain. PPPs are also neededin strategic areas, such as mechanization/automation of breeding operations, establishment of field-based precision phenotyping platforms, and provision of low-cost and efficient genotyping services, all of which have significant potential to enhance the efficiency of crop breeding programs in the developing world.

Dr Jauhar Ali

Senior Scientist & Plant Breeder
International Rice Research Institute (IRRI)
Los Baños
Philippines
j.ali@irri.org

Dr. Jauhar Ali is Senior Plant Breeder serving at IRRI, Los Baños, Philippines from 2009 onwards. Before joining IRRI headquarters, he was the National Coordinator for the Hybrid and Molecular Breeding Program of Iran, and a consultant for IRRI-Iran project for six years. Prior to that, he was the Project Scientist at IRRI under a Rockefeller project for the International Rice Molecular Breeding Program. He served the Tamil Nadu Agricultural University (TNAU) for five years as Assistant Professor after his postdoctoral research on hybrid rice at IRRI in 1994. He has successfully released 28 rice varieties, four hybrids and 15 TGMS lines. He has currently nominated 64 rice cultivars into different national testing programs in Asia and Africa. He bred and shared more than 195 promising multiple stress-tolerant GSR cultivars at IRRI. He is member of the 3K-rice genome project. He has developed several mapping populations and discovered many QTLs for varied target traits covering abiotic and biotic stresses. He has guided 10 PhD and seven MS students and systematically trained more than 950 researchers on seed production, heterosis, and molecular breeding. Jauhar published more than 50 peer-reviewed publications and three breeding manuals. He is also the Academic Editor for PLOS One journal and member of several scientific societies. His major part of research contribution over the last 22 years relates to raising the yield ceiling by exploitation of hybrid vigor and genetic enhancement of tolerances to unfavorable environments.

Advent of Climate Smart Rice Varieties through Genomics-Assisted Breeding

Ali J[1],*, Xu JL[2], Gao YM[2], Revilleza JE[1], Franje N[1], Li ZK[2]

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

Researchers need to develop crop varieties that combine higher grain yield potential with multiple stress tolerance to provide genetic crop insurance cover to farmers against sudden climatic disturbances. We developed 195 cultivars for testing, released 10 varieties and nominated 44 promising multiple abiotic and biotic stress tolerant materials across Asia and Africa within a short span of five years, adopting an innovative genomics assisted breeding strategy. Introgression breeding and designed QTL pyramiding (DQP) was employed for developing varieties with multiple abiotic and biotic stress tolerance without compromising on grain yield and quality. BC_1F_2 populations derived from HHZ and WTR1 (recipient parents) and 16 donors at IRRI were screened simultaneously for three rounds for different abiotic (drought, salinity, submergence and low fertilizer input conditions) and biotic stresses (blast, BLB, Tungro) and normal irrigated conditions, which resulted in identification of 1333 (HHZ-ILs) + 2232 (WTR 1-ILs) trait specific introgression lines (ILs) superior to tolerant checks. QTLs governing complex traits (drought, salinity, cold) were identified by genome sequencing 495 ILs in HHZ background. We nominated 35 promising pyramiding lines (PLs) to AYT (MET0) in DS2015 from 45 DQP crosses. Success of deriving high genetic gains may be attributed to combination of effective selection skills and innovative genomics-assisted breeding approach.

Dr Vincent Vadez

Assistant Program Director - Dryland Cereals
International Crops Research Institute for the Semi-Arid Tropics
Patancheru
India
v.vadez@cgiar.org

Vincent Vadez is a crop physiologist and agronomist, initially trained as an engineer. Prior to ICRISAT, he has worked for four years with a Bolivian lowland indigenous group to understand and measure the socio-economic drivers of deforestation and of new farming technology adoption. This was an enriching experience that showed him that beyond technologies, there are people with a say. Before that he did research on symbiotic nitrogen fixation at the University of Florida on drought in soybean, at CIAT Colombia on low soil P in bean, and at the National University of Singapore on low soil P in Acacia. At ICRISAT his group works on the genetic and mechanistic deciphering of plant traits, and of trait-environment interactions, contributing to drought adaptation. His research has *also contributed* a quantum leap in the approach to understand the role of roots in drought adaptation. Indeed he developed a large lysimetric platform (**LysiField**) for a direct, precise, rapid, *in-vivo* assay of water extraction (http://www.icrisat.org/bt-root-research.htm to tackle the functionality and highly dynamic nature of roots (rather than destructive root measurements). Currently he is developing another large platform (**LeasyScan**) combining the lysimetric approach of Lysifield to 3-D scanning of the crop canopy, to phenotype water-controlling traits. The current thrust of his team is now to decipher the genetic basis of water-controlling traits, and to combine trait phenotyping with field evaluation in representative locations. This part is supported by crop simulation modeling to characterize main stress scenarios and to predict trait effects on yield across time and geographical scales.

Adaptation to Water limitation and Climate Change: From Trait Dissection to Yield

Vadez V*, Kholova J, Kakkera A, Siva Sakhti K, Tharanya M, Medina S, Malayee S, Palakolanu S, Choudhary S, Baddam R, Dharani S, Deshpande S, Srivastava R, Hash T

International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Hyderabad, India
E-mail: v.vadez@cgiar.org

In the last few years we have acquired strong evidence across dryland legume and cereal crops species that small amount of water during the reproductive and grain filling period is critical for enhancing grain yield under water limited conditions. Water availability during grain filling is a consequence of a number of plant traits altering the plant water budget, and operating mostly in the absence of soil water stress. Our current thrust is then to crack the plant water budget into simpler "building blocks", more amenable to genetic analysis and breeding use. Data will be presented on the genetic variation in different species for one of these traits, the capacity to restrict transpiration under high vapor pressure deficit (VPD), which is highly relevant both for drought and climate change adaptation, and on high throughput methods to measure it. We'll talk about possible mechanisms underlying this trait, in particular its close relationship with differences in aquaporin gene expression in leaves and roots. For the breeding application we will show the close linkages between some of these "building blocks" and QTLs related to drought adaptation (staygreen in sorghum, terminal drought tolerance in pearl millet). Finally, we'll discuss the use of crop simulation modelling to characterize prevalent stress scenarios and test the effect of such traits/trait-by-management combinations on yield across locations, and how crop simulation has becomes an essential tool to bind together the pieces of a multi-disciplinary approach ("integrated breeding") to guide the choice of key breeding and agronomic management targets.

Session IX

Novel Breeding Approaches

Co-chairs

Dr EA Siddiq

Honorary Professor
Institute of Biotechnology
Acharya N G Ranga Agricultural University
Hyderabad
India

Dr Pooran Gaur

Asstt Res Prog Director-Grain Legumes
International Crops Research Institute for
the Semi-Arid Tropics (ICRISAT)
Patancheru
India

Prof. Mark Sorrells

Professor
Plant Breeding and Genetics Section
Cornell University
Ithaca
USA
mes12@cornell.edu

Dr. Mark E. Sorrells received his PhD in plant breeding and genetics from the University of Wisconsin – Madison in 1978 and then joined the faculty at Cornell University in the Department of Plant Breeding & Biometry. Since 1991 he has been Professor of Plant Breeding and from 2006 to 2008 he was Chair of the Department of Plant Breeding & Genetics. The primary focus of Dr. Sorrells' research program is on breeding methodologies and the development of small grains varieties. His breeding program has released 16 small grains varieties. Currently the focus of his research is optimizing genomic selection strategies. He has published 260 papers in peer-reviewed journals and is a fellow of the American Association for the Advancement of Science, the Crop Science Society of America, and the American Society of Agronomy. Dr. Sorrells has served as major advisor to 37 PhD students, nine M.S. graduate students and minor advisor to 22 students.

Genomic Selection in Plants: A New Tool for Crop Improvement

Sorrells, ME

Cornell University, Ithaca, NY 14853 USA
Email: mes12@cornell.edu

Inexpensive DNA sequencing and new statistical methods are revolutionizing plant breeding. Genomic selection (GS) is the simultaneous use of genome-wide markers to increase accuracy of performance prediction for both phenotyped and unphenotyped individuals. In GS, a training population related to the breeding germplasm is genotyped with genome-wide markers and phenotyped in the target set of environments. That data is used in a prediction model to estimate breeding values of unphenotyped candidates. Design of the training population is crucial to the accuracy of prediction models and can be affected by many factors, including population structure and composition. Prediction models can incorporate performance over multiple environments and assess GxE effects to identify a highly predictive subset of environments. We have developed a methodology for unbalanced datasets using genome-wide marker effects to group environments and identify outlier environments.

In addition, environmental covariates can be generated using a crop model; and used in a GS model to predict GxE in unobserved environments and to predict performance in climate change scenarios. Current research is focused on optimizing the training population to improve efficiency and increase prediction accuracy in terms of genotypes, experimental design and environment sampling.

Dr Jose Crossa

Biometrics and Statistics Unit
International Maize and Wheat Improvement Center (CIMMYT)
Texcoco
Mexico
j.crossa@cgiar.org

Dr. Jose Crossa was born in Uruguay and is a Distinguished Scientist at the Biometrics and Statistics Unit of CIMMYT. He is also Adjunct Professor in the Department of Plant Science at the University of Nebraska-Lincoln, and invited Professor at the Statistics Department of the Post-Graduate College in Mexico.

Jose has a basic background in statistical genetics and has more than 30 years of research in international agriculture. His contributions include developing statistical models for studying genotype by environment interaction, for modelling QTL by environment interaction and for genomic prediction in plant breeding. Jose has also developed quantitative genetics and population genetics models for genetic resources conservation and utilization. He has more than 250 articles in refereed journals and more than 30 book chapters.

Jose has won several awards/fellowships, including Elected Fellow of the Crop Science Society of America, and the American Society of Agronomy. In 2008 he was selected as the best Scientist in the CGIAR system for his contribution to developing mathematical genetic models for genetic resources conservation. He was elected member of the National Academy Society of Mexico, and has been, for several years, in the editorial board of *Crop Science*, *Theoretical and Applied Genetics,* and *Euphytica*. For five years he published articles in the division of Genetic Resources Conservation of Crop Science, which were selected within the best three articles published in each of those years.

New Developments in Genomic-Enabled Prediction Models

de los Campos G[2], Perez-Rodriguez P[3], Perez-Elizalde S[3], Cuevas J[3], Montesinos-Lopez O[4], Cuevas J[4], Lopez-Cruz M[1], Gianola D[5], Crossa J[1]*

[1]Biometrics and Statistics Unit, CIMMYT, Apdo. Postal, 6-641, 06600, Mexico DF, México
[2]Department of Biostatistics, School of Public Health, University of Alabama Birmingham, AL, 35294, USA.
[3]Colegio de Postgraduados, Montecillos. Edo de México, México.
[4]Universidad de Colima, Colima, México.
[5]Department of Animal Sciences, University of Wisconsin, Madison, WI 53706, USA
*Email: J.crossa@Cgiar.org

In this contribution we examine results from three areas of research that aim to increase genomic-enabled prediction accuracy in plant breeding: (1) inverse penalized regression models, (2) prediction models that incorporate genotype × environment interaction (GE), and (3) threshold models for ordinal traits commonly used in plant breeding for assessing various plant diseases. Recently, models were developed within the framework of inverse regression theory. Inverse solutions make it possible to visualize that noise is inversely proportional to singular values and graphics depict the shrinkage behavior according to the prior variance and weighting factor. Inverse Bayesian regression models deal well with the ill-conditioning and random noise problems arising in genomic prediction when $p>>n$. Results show that inverse Bayesian regression models increase prediction accuracy compared with standard Bayesian regression models. Prediction models incorporating genotype × environment interaction (GE) have been developed as extensions of the GBLUP. These models allow incorporating highly dimensional marker and environmental covariable data and increase prediction accuracy when incorporating GE. Another type of GBLUP model uses marker x environment interaction for modeling GE. The model marker x environment interaction provides substantial gains in prediction accuracy, provided that the environments analyzed are positively correlated. Threshold genomic predictions model for ordered categorical plant disease data incorporating GE and additive x additive interactions indicated increases in prediction ability as compared with GBLUP threshold model without GE and addtive x additive interactions.

Dr John Hickey

The Roslin Institute
University of Edinburgh
United Kingdom
hickeyjohn@gmail.com

Dr. John Hickey is a quantitative geneticist who works at The Roslin Institute in Edinburgh. His area of research spans animal breeding, plant breeding, and human geneticists. In particular he seeks to develop computational methods to generate and analyse huge data sets with whole genome sequence information, methods and breeding strategies that use genomic information to increase rates of genetic progress. The concept of Genomic Selection 2.0. Software and algorithms developed by John Hickey underpin aspects of several of the largest breeding programs globally.

Potential of Promotion of Alleles by Genome Editing for Improving Quantitative Traits in Livestock Breeding Programs

Hickey J[1*], Jenko J[1], Gorjanc G[1], Cleveland MA[2], Varshney RK[3], Bruce C[1], Whitelaw A[1], Woolliams JA[1]

[1]The Roslin Institute and Royal (Dick) School of Veterinary Studies,
The University of Edinburgh, Easter Bush, Midlothian, Scotland, UK
[2]Genus plc., 100 Bluegrass Commons Blvd., Suite 2200, Hendersonville, TN, 37075, USA
[3]International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
*Email: john.hickey@roslin.ed.ac.uk

Background: Genome editing (**GE**) is a method that enables specific nucleotides in the genome of an individual to be changed. To date, use of GE in livestock has focussed on simple traits that are controlled by a few quantitative trait nucleotides (**QTN**) with large effect. The aim of this study was to evaluate the potential of GE for improving quantitative traits that are controlled by many QTN, termed herein as promotion of alleles by genome editing (**PAGE**).

Methods: Different scenarios were simulated to test PAGE for quantitative traits. They differed in the (i) number of QTN defining the trait (1,000 or 10,000), (ii) number of edits per sire (0 to 100), (iii) number of edits per generation (0 to 500), and (iv) the strategy for the use of PAGE (editing all of the selected sires or only a proportion of them). A base line scenario involved selecting individuals on true breeding values (i.e., **GSonly** - genomic selection with perfect accuracy) for 10 generations. Alternative scenarios complemented this base line with PAGE (**GS+PAGE**).The effect of different PAGE strategies was quantified by comparing the response to selection, the change in the allele frequency, the number of distinct QTN edited, the sum of absolute effect of the edited QTN, and the inbreeding.

Results: Response to selection after 10 generations was between 1.04 and 4.24 times higher with GS+PAGE than with GSonly. Increase in genetic gain was larger with more edits per sire and more sires edited. When the total resources for PAGE were limited, editing a few sires for many QTN resulted in more genetic gain and inbreeding compared to editing many sires for a few QTN. Between the scenarios GSonly and GS+PAGE, there was little difference in the average change in QTN allele frequency but there was a major difference for the 20 QTN with largest effect. The sum of effects of the edited QTN decreased across the generations.

Conclusions: This study showed that PAGE hasa great potential for application in livestock breeding programs, but inbreeding needs to be managed.

Dr Jesse Poland

Assistant Professor
Kansas State University
Manhattan
USA
jpoland@ksu.edu

Dr. Jesse Poland is an Assistant Professor at Kansas State University, Director of the Feed the Future Innovation Lab for Applied Wheat Genomics, and Associate Director of the Wheat Genetics Resource Center. Research in Dr. Poland's group is focused on wheat genetics and germplasm improvement. They are currently developing new marker technologies for use in breeding, diversity studies, and association genetics. In collaboration with public breeding programs, Dr. Poland is exploring the use of genomic selection methods in wheat breeding. In the area of germplasm development, Dr. Poland's group is focused on developing new breeding lines with resistance to the major pests of wheat including stem rust, stripe rust, leaf rust and Hessian Fly. To complement advances in genomics, Dr. Poland's lab is developing high-throughput phenotyping approaches for field-based evaluation of breeding lines, with the primary focus being genetic characterization of heat and drought tolerance and development of improved germplasm.

Dr. Poland currently supervises six graduate students, two post-doctoral scholars and sits on the graduate committees of five other students at Kansas State University and two students at Colorado State University, where he holds affiliate faculty status.

Integration of Physiological Breeding and Genomic Selection for Wheat Improvement

Jesse Poland

Kansas State University
Manhattan, USA
Email: jpoland@ksu.edu

New breeding methodologies are needed to help accelerate the rate of genetic gain to meet the growing demand for food crops in the face of less favorable and increasingly volatile environments. Genomic selection, using whole-genome markers for breeding value prediction, is an approach that can accelerate genetic gain through decreasing the breeding cycle time and increasing the selection intensity through larger populations. At the same time, physiologically defined selection parameters, such as canopy temperature, have been demonstrated as valuable indexes for selection, particularly for stress environments. The integration of ecophysiological modeling and genomic prediction has the potential to enable more robust selection for a range of environments. Developing such approaches and making physiological measurements across the breadth of breeding programs will necessitate innovation and deployment of high-throughput phenotyping systems that can capture the temporal and spatial resolution needed to screen large sets of germplasm and build model parameters to integrate with genomic prediction.

Session X

New Horizons for Crop Improvement

Co-chairs

Prof SK Datta

Pro-Vice Chancellor
Visva-Bharati
Santiniketan
India

Dr KC Bansal

Director
National Bureau of Plant Genetic
Resources
New Delhi
India

Dr Gary Atlin

Senior Program Officer &
Crop Productivity Functional Team Lead
Agricultural Research and Development, Global Development
Bill & Melinda Gates Foundation
gary.atlin@gatesfoundation.org

Dr. Gary Atlin, a Canadian national, studied crop science at the University of Guelph, and was a technician in the maize breeding program there for several years. His first experience in international agricultural research was as a research associate in the potato program at CIP in Peru. His PhD work in oats at Iowa State focused on the design of breeding programs for stressful environments. After graduating, he worked as a commercial flax breeder in Canada. He then taught plant breeding at Nova Scotia Agricultural College for ten years, developing a theoretical framework for managing genotype x environment interaction in breeding programs. In 2000, he joined IRRI as upland rice and then rainfed lowland rice breeder, establishing IRRI's drought tolerance trait pipeline, which identified the first rice QTLs with large effects on yield under drought stress. He joined CIMMYT in 2006 as a maize breeder, and became technical breeding lead in 2009, coordinating efforts to optimize CIMMYT's maize pipelines to increase genetic gains. Throughout his career, he has combined practical cultivar development (his programs have released several widely-used rice, maize, and flax lines) with theoretical work on maximizing rates of genetic gain in stress-prone environments (over 50 publications in refereed journals). In 2012, he joined the Gates Foundation as a Senior Program Officer in the Agricultural Development Initiative. He is now the crop productivity lead within the R&D team, coordinating the foundation's investment's aiming to increase the rate of genetic gain delivered to smallholders in Sub-Saharan Africa and South Asia.

Bringing Genomic Data into Routine Use in Cultivar Development: Reducing Costs and Improving the Tools for Breeders

Gary Atlin

Bill & Melinda Gates Foundation
Email: gary.atlin@gatesfoundation.org

Despite progress in crop genetic analysis, there is little application of genomic data in breeding in the developing world. Application of genomic information in public sector breeding has been largely restricted to backcross introgression of haplotypes for quality and tolerance to biotic and abiotic stresses. In most breeding programs in the developing world, DNA markers are not used at all. By contrast, advanced private sector programs use whole-genome profiles extensively for both quantitative and qualitative traits in forward breeding. Routine use of genome profiling in forward breeding by the public sector is currently impossible due to high genotyping costs and lack of bioinformatics support; genome profiling costs for CGIAR and NARS programs are approximately 10-fold higher than they are for the multinational seed companies, due to both lack of access to high-throughput genotyping technologies and to inadequate bioinformatics support. The Gates Foundation is supporting efforts to reduce genotyping costs for the CGIAR and its partners, and provide breeders with tools for using genomic data in forward breeding. These include the Global Open-Source Breeding Informatics Initiative (GOBII), a partnership between Cornell University, CIMMYT, IRRI, and ICRISAT to develop easily-queried databases for five species to organize rapidly-accumulating GBS and sequence data on breeding materials and link it to lower-density marker platforms and phenotypic information, allowing the whole HapMap to be imputed onto selection candidates using low marker densities. GOBII will deliver the imputation and prediction tools allowing breeders to routinely exploit available genomic data in forward breeding.

Dr Steve Rounsley

Dow AgroSciences LLC
Indianapolis
USA
steve.rounsley@gmail.com

Dr. Steve Rounsley is the Genomics Leader for Dow Agrosciences where he leads the application of next generation sequencing technologies to breeding and biotech discovery across the company. He started his education in the UK, before moving to the US to obtain a PhD in developmental plant biology from UCSD. In 1995, realizing his lab skills left something to be desired, Steve moved into bioinformatics with a post-doc at TIGR just as the first bacterial genome was sequenced. While there, he helped develop the strategy and tools for eukaryotic projects and led the team sequencing the *Arabidopsis* genome as part of a large international consortium. Since those early days of plant genomics, he has worked on a range of plant species in non-profit research organizations, companies (big and small), and in his own lab at University of Arizona. He is passionate about the role that obtaining, sharing and exploiting genomic knowledge can play in improving agricultural productivity around the world - both in well-studied commodity crops, and less well resourced crops critical for the developing country agriculture.

Cassava Genomics - Applying Genomic Technologies to Benefit Smallholder Farmers in Africa

Steve Rounsley

University of Arizona, Tucson Arizona, USA
Dow Agrosciences, Indianapolis, Indiana, USA
Email: sdrounsley@dow.com

Cassava (*Manihot esculenta* Crantz) is a woody shrub with a large starchy root grown in many parts of the tropics, and plays a particularly important role in food security in Sub-Saharan Africa. It originated in South America and was introduced to Africa approximately 400 years ago. Many aspects of its genetics do not lend themselves to rapid research progress, and consequently cassava has lagged many of the more "traditional" crops in research funding and rates of improvement. The widespread use of clonal planting material has also made cassava cultivation more vulnerable to disease, such as the current outbreak of Cassava Brown Streak Disease. Genomics provides a suite of tools that can accelerate the understanding of germplasm resources and assist the cassava community to leapfrog decades of slow advances. I will discuss the recent advances in genomic resources available to cassava researchers and their impact.

Dr Peter Wenzl

Liaison
Diversity Seek (DivSeek) Initiative
Global Crop Diversity Trust
Bonn
Germany
peter.wenzl@croptrust.org

Peter joined the Global Crop Diversity Trust to work for the recently launched Diversity Seek initiative. DivSeek, for short, brings together a large number of organizations from almost 30 countries to harness genetic resources for food security and climate adaptation. Before joining the Crop Trust, he led efforts at CIMMYT to identify and mobilize useful genetic variation from maize and wheat genebanks. With a PhD from Vienna University, he has moved across a variety of research domains, both in the public and private sector, to develop and implement enabling technologies and innovative approaches to accelerate the genetic improvement of crops.

Diversity Seek (DivSeek): a community-driven effort to harness the genetic potential of the world's genebanks

Wenzl P[1],* Bastow R[2], Powell W[3], Manzella D[4], López F[4], Dempewolf H[1], McCouch S[5]

[1]Global Crop Diversity Trust, Bonn, Germany
[2]Global Plant Council, London, UK
[3]CGIAR Consortium Office, Montpellier, France
[4]Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture, Rome, Italy
[5]Cornell University, Ithaca, USA
Email: peter.wenzl@croptrust.org

Global genebanks conserve approximately seven million accessions of crop species and their wild relatives. These accessions are fundamental for global food security as they provide the 'genetic raw material' for crop improvement. Past efforts to identify and mobilize beneficial genetic variation from genebanks into breeding programs have been limited, compared to the size of this global resource. Clearly, the development of climate-ready, high-yielding and nutritious varieties for growing populations requires a more effective utilization of crop diversity. Fortunately, game-changing sequencing and phenotyping techniques as well as 'big data' approaches now enable a broad-based, comprehensive approach to harnessing genetic resources. The recently launched Diversity Seek initiative (DivSeek; http://www.divseek.org) aims to capture this opportunity. DivSeek provides a networking and cross-crop learning platform to promote synergies and add value to like-minded, but otherwise autonomous efforts or projects. The initiative is based on voluntary membership and will focus on common challenges encountered by individual projects, as prioritized collectively by all DivSeek partners. The main areas of work will likely include (i) data standards and interoperable data sets/repositories, (ii) genomics and high-throughput phenotyping platforms, (iii) a broadly accepted framework for 'rights management' that helps projects comply with data-sharing principles, and (iv) capacity-building efforts in all the areas above. We invite community members who are interested in the topic and share our vision to join the initiative.

Dr John Myles Axton

Editor-in-chief
Nature Genetics
New York
USA
m.axton@us.nature.com

Dr. Myles Axton is the editor of *Nature Genetics*. He was a university lecturer in molecular and cellular biology at the University of Oxford and a Fellow of Balliol College from 1995 to 2003. He obtained his degree in genetics at Cambridge in 1985, and his doctorate at Imperial College in 1990, and between 1990 and 1995 did postdoctoral research at Dundee and at MIT's Whitehead Institute. Myles's research made use of the advanced genetics of *Drosophila* to study genome stability by examining the roles of cell cycle regulators in life cycle transitions. His interests broadened into human genetics, genomics and systems biology through lecturing and from tutoring biochemists, zoologists and medical students from primary research papers. Helping to establish Oxford's innovative research MSc. in Integrative Biosciences led Myles to realize the importance of the integrative overview of biomedical research. As a full time professional editor he is now in a position to use this perspective to help coordinate research in genetics.

Trends in Agricultural Genomics and *Nature* Journal Standards

Myles Axton

Nature Genetics, Macmillan Scientific and Scholarly Publishing,
75 Varick St. 9th Floor, New York, NY, 10013, USA.
Email: m.axton@us.nature.com

We are particularly interested in attracting research articles on the genetic architecture of plant traits and crop plant performance, fundamental functional genomics of plant growth and development, natural and agricultural variation in plant species, and genomic methods for studying genetic and gene-environment variation. In seeking research papers, we will progressively move from the identification of mutations and quantitative trait loci, first reference genomes and new components of existing developmental pathways to emphasize in particular the use of genomic resources for new biology and for solving agricultural challenges. Whereas rapidly reproducing model organisms such as *Arabidopsis* are essential for interventional experiments and study of basic biology, model organisms grown by the billions as crops offer complementary experimental opportunities in basic and crop biology with readily translatable results. There is plenty more than agricultural productivity to be discovered in measuring genome variation in plants. There is the aim of understanding the architecture of traits, including the heterozygous advantage of F1 hybrids, gene-environment interactions and epistasis. Evolutionary and domestication analyses will lead to the preservation and reuse of crop diversity and the restoration of variants lost during domestication. Together with marker-assisted plant breeding, research and the development of genetically modified crop plants (GMOs) have an important place in the future of plant science since variation is variation and some of it is useful to us. Expanding upon the genetic discovery effort of which we are a part, our new journal *Nature Plants* will also engage with the social and economic dimensions of plant science, climate change, policy-ready science, food security and distribution, and the next green revolution.

Concluding Session

Dr Jean-Marcel Ribaut

Director
Generation Challenge Program
C/o CIMMYT
Texcoco
Mexico
j.ribaut@cgiar.org

Dr. Jean-Marcel Ribaut, Director of the Generation Challenge Program (GCP), a 10-year initiative of the Consultative Group on International Agricultural Research (CGIAR), is responsible for leading and coordinating a large network of partners in modern crop breeding for food security. Jean-Marcel has cumulative experience in agriculture biotechnology and plant science, as well as leadership skills for dispersed global R&D teams. Prior to becoming GCP Director in 2005, Jean-Marcel worked at CIMMYT, Mexico, where he held positions of increasing responsibility, rising to Deputy Director of the Applied Biotechnology Center in 2001, which became the Genetic Resources Programme in 2003; and to Biotechnology Group Leader in 2004. Jean-Marcel has been appointed recently as Director of the Integrated Breeding Platform (https://www.integratedbreeding.net). Jean-Marcel holds a PhD in plant physiology from Lausanne University, Switzerland. His scientific background is in plant physiology and genetics, and his main research interests are understanding the genetic basis and underlying physiological and metabolic pathways that influence plant performance under abiotic stress– particularly drought – as well as innovations in molecular breeding.

Jean-Marcel has a particular interest in promoting modern breeding methods to hasten crop improvement in the developing world, helping to weave effective and interactive communities of crop researchers at both the global and regional levels; and bridging the gap between basic and applied agricultural science. He believes in true partnership and solid capacity building to overcome some of the bottlenecks in R4D, with developing-country partners as key actors and leaders in the research arena.

Translating Biology: The Generation Challenge Programme- A Successful Case Study

Jean-Marcel Ribaut

Generation Challenge Program
C/o CIMMYT, Texcoco
Mexico
Email: j.ribaut@cgiar.org

The Generation Challenge Programme (GCP) began as part of the 2001 CGIAR reform aimed at fostering a programmatic approach to research. During its lifetime (2004-2014), the GCP has focused on promoting the use of genetic diversity and modern plant science for crop improvement in developing countries. The $170 M program has resulted in some very significant achievements, most notably in establishing true partnerships that have successfully linked upstream research with applied science.

The work of the GCP community has resulted in a number of research outputs including: genetic and genomic resources; genes and QTL; improved germplasm; and bioinformatics tools. The capacity for national programs in developing countries to conduct modern breeding has been enhanced through human capacity development, improved infrastructure, and access to analytical tools as well as data management systems. The GCP has resulted in more than 400 articles in refereed journals and 100 PhD and MSc students have received support to conduct their theses.

The overall lessons learned include: the importance of empowering national programs for effective collaboration and impact on the ground; the need for a flexible approach to research management, including a combined approach of competitive and commissioned projects; the indispensable need for capacity building embedded in research activities; and, the importance of having a product deployment strategy.

A major spin-off from the GCP has been the Integrated Breeding Platform (IBP), an initiative that works towards improving the efficiency of plant breeding programs in developing countries by enabling plant breeders to access modern technologies, breeding materials and related information.

List of Posters

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
1	Anandan, A	ICAR-Central Rice Research Institute (CRRI), Cuttack, India	Appraisal of diverse rice collections using morphological and molecular markers for early vigor trait in direct seeded condition	anandanau@yahoo.com	NGG-P01
2	Angannan, Suganya	ICAR-Sugarcane Breeding Institute, Coimbatore, India	Chromosome transmission patterns in interspecific hybrids of sugarcane derived with different cytotypes of *Saccharum spontaneum*, L.	harimuns@rediff.com	NGG-P02
3	Ansari, Mohd Jamal	ICAR-Indian Institute of Pulses Research (IIPR), Kanpur, India	Expression of a synthetic Bt gene in chickpea (*Cicer arietinum* L.) confers resistance to gram pod borer (*Helicoverpa armigera* H.)	jamalansari87@gmail.com	NGG-P03
4	Arumugam, Chandrasekar	ICAR-National Research Centre for Banana (NRCB),Tiruchirapalli, India	MusatransSSRDB – A transcriptome derived SSR database an advanced tool for banana improvement	chandrugcg_77@yahoo.co.in	NGG-P04
5	Atieno, Judith	Australian Centre for Plant Functional Genomics (ACPFG), University of Adelaide, Australia	Genotypic variation for salinity tolerance in the chickpea reference set	judith.atieno@acpfg.com.au	NGG-P05
6	Babbar, Anita	Jawaharlal Nehru Krishi ViswaVidyalaya (JNKVV), Jabalpur, India	Marker assisted backcrossing to introgress resistance to fusarium wilt race 4 in JG 74, an elite cultivar of chickpea	anitababbar@rediffinail.com	NGG-P06
7	Bhat, Ramesh S	University of Agricultural Sciences (UAS), Dharwad, India	Analysis of TMV 2 × NLM derived RIL population towards mapping genomic regions governing taxonomic and morphological traits in peanut	bhatramesh12@gmail.com	NGG-P07
8	Bhave, Mrinal	Swinburne University of Technology, Hawthorn, Australia	Identification of protein phosphatase 2C subgroup A in barley using mRNA-sequencing	mbhave@swin.edu.au	NGG-P08
9	Chandra, Saket	Birla Institute of Technology, Mesra, India	De novo transcriptome assembly and functional annotation of resistant and susceptible near-isogenic wheat (*Triticum aestivum* L.) in response to leaf rust pathogenesis	saket10to22@gmail.com	NGG-P09
10	Chaudhary, Spandhan	Kadi Sarva Vishwavidyalaya, Gandhinagar, India	Enhancement of secondary metabolite production in *Trigonella foenum graecum* (fenugreek)	spandan.chaudhary@gmail.com	NGG-P10
11	Chellapilla, Bharadwaj	ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India	Genomic approaches for breeding drought tolerant chickpea	drchbharadwaj@gmail.com	NGG-P11
12	Chetukuri, Anuradha	Prof. Jayshankar Telangana State Agricultural University (PJTSAU), Hyderabad, India	Tagging of gene for yellow mosaic virus (YMV) resistance in greengram (*Vigna radiata* (L).Wilczek)	anu_dna@rediffmail.com	NGG-P12

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S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
13	Das, Alok	ICAR- Indian Institute of Pulses Research (IIPR), Kanpur, India	Allele mining of two drought responsive factor (DRF) genes in pigeonpea (*Cajanus cajan* L.).	alokbio@gmail.com, adas@icar.org.in	NGG-P13
14	Deokar, Amit A	University of Saskatchewan, Saskatoon, Canada	From QTL to gene: Mapping QTLs and candidate genes for early flowering and photoperiod sensitivity in chickpea	aadeokar@gmail.com	NGG-P14
15	Deshpande, Sanjeev K	University of Agricultural Sciences (UAS), Dharwad, India	Phenotyping of available Indian germplasm, breeding lines for resistance to rust and mosaic virus in cowpea (*Vigna unguiculata* L. Walp)	sanjeevgpb@gmail.com	NGG-P15
16	Dharmaraj, PS	ARS-Gulbarga, University of Agricultural Sciences, Raichur, India	Genetic variability and path co-efficient analysis in minicore collections of pigeonpea (*Cajanus cajan*.L)	psdharmaraj@yahoo.com	NGG-P16
17	Dwiyanti, Maria S	International Rice Research Institute (IRRI), Los Banos, The Philippines	Potential of SNP density approach to identify unique variations of whole genome sequence	m.dwiyanti@irri.org	NGG-P17
18	Gaikwad, Priyanka	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Study of relative effectiveness of stay-green (stg) QTL combinations under stress conditions	priyankagaikwad00@gmail.com	NGG-P18
19	Gangashetty, Prakash	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger	Molecular and morphological diversity in Basmati and non-Basmati aromatic local short grain aromatic genotypes of rice (*Oryza sativa* L.): A study using standard panel of SSR and InDel markers	P.Gangashatty@cgiar.org; prakash.gangashetty@gmail.com	NGG-P19
20	Garg, Aditya Pratap	ICAR- Indian Institute of Pulses Research (IIPR), Kanpur, India	Introgression of resistance to *F. oxysporum* (Race 2) in Pusa 256 variety of chickpea (*C. arietinum* L.) through marker assisted backcross breeding	adityap@icar.org.in; adityapratapgarg@gmail.com	NGG-P20
21	Garg, Vanika	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Genome-wide identification of gene families involved in the regulation of small RNA expression in chickpea and pigeonpea	vanikag1@gmail.com	NGG-P21
22	Gemenet, Dorcus Chekesis	Kenya Agricultural and Livestock Research, Nairobi, Kenya	Association analysis of low-phosphorus tolerance in West African pearl millet using DArT™ markers	gemenet2014@gmail.com	NGG-P22
23	Gupta, Shashi K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Comparison of phenotypic and molecular distances to predict heterosis and F1 performance in pearl millet (*Pennisetum glaucum* L. (R.) Br.)	s.gupta@cgiar.org	NGG-P23

S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
24	Jaganathan, Deepa	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Fine mapping of "QTL-hotspot" for drought component traits in chickpea	j.deepa@cgiar.org	NGG-P24
25	Jain, Mukesh	National Insitute of Plant Genome Research (NIPGR), New Delhi, India	Resources for functional and applied genomics in chickpea for crop improvement	mjain@nipgr.ac.in	NGG-P25
26	Jhang, Tripta	CSIR-Central Institute of Medicinal and Aromatic Plants (CIMAP), Lucknow, India	Prediction of withanolide heterosis using RNA-seq in *Withania somnifera*	t.jhang@cimap.res.in	NGG-P26
27	Kamboj, Atul	Swinburne University of Technology, Hawthorn, Australia	Genome wide profiling of histone H3K4-trimethylation in barley under salt and drought stress conditions	akamboj@swin.edu.au	NGG-P27
28	Kapinga, Fortunus	International Institute for Tropical Agriculture (IITA), Nairobi, Kenya	Quantitative phenotyping of cassava brown streak disease root symptoms for QTL detection	fakapinga@yahoo.com	NGG-P28
29	Khan, Hammad	Australian Centre for Plant Functional Genomics (ACPFG), University of Adelaide, Australia	Salt sensitivity of chickpea is determined by sodium toxicity	hammad.khan@acpfg.com.au	NGG-P29
30	Koradi, Pranitha	Barwale Foundation, Hyderabad, India	Introgression of stigma exsertion trait into a maintainer rice line IR79156B by marker assisted backcross breeding	pranitha@barwalefoundation.org	NGG-P30
31	Korupalli, Usha K	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Genome wide association studies (GWAS) for shoot fly resistance component traits and stay-green traits on sorghum chromosome SBI-10	K.Kiranmayee@cgiar.org	NGG-P31
32	Kriti, Roopendra	ICAR-Indian Institute of Sugarcane Research (IISR), Lucknow, India	Perturbation of source-sink communication: a stepping stone for increasing sucrose productivity in sugarcane	kriti.roopendra@gmail.com	NGG-P32
33	Kumar, Ashok	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Introgression of shoot fly resistance QTLs into elite sorghum varieties using marker assisted backcrossing (MABC)	A.AshokKumar@cgiar.org	NGG-P33
34	Kumar, Manish	Birla Institute of Technology, Ranchi, India	Transcriptome-wide identification of long non-coding RNAs during leaf rust infection in wheat	manish@bitmesra.ac.in	NGG-P34
35	Kumar, Narendra	ICAR- Directorate of Groundnut Research (DGR), Junagadh, India	Phenotyping for seed coat resistance and aflatoxin production to *A. flavus* in groundnut	narendrapb09@gmail.com	NGG-P35

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S No	Presenter's name	Affiliation	Title of the poster	E-mail	Poster ID
36	Kumari, Varsha	formery with University of Agricultural Sciences, Dharwad, India	Introgression of foliar disease resistance using synthetic amphidiploids and identification of associated QTLs in groundnut (*Arachis hypogaea* l.)	varshagpb@gmail.com	NGG-P36
37	Krishnamohan, KAVS	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	NGS-QCbox and Raspberry for parallel, automated and rapid quality control analysis of large-scale next generation sequencing (Illumina) data	k.krishnamohan@cgiar.org	NGG-P37
38	Manickavelu, Alagu	Yokohama City University, Yokohama, Japan	Molecular drought adaptation nature of Afghan wheat landraces	manicks@yokohama-cu.ac.jp	NGG-P38
39	Manyasa, Eric	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	Genetic diversity in east African finger millet (*Eleusine coracana* (L.) Gaertn) landraces based on SSR markers and some qualitative traits	E.MANYASA@cgiar.org	NGG-P39
40	Motagi, Babu N	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger	Introgression lines with improved resistance to late leaf spot and rust in peanut	B.N.Motagi@cgiar.org	NGG-P40
41	Mukhopadhyay, Kunal	Birla Institute of Technology, Mesra, India	Transcriptome-wide detection of microRNAs and targets in wheat (*Triticum aestivum* L.): elucidating their role during leaf rust infection	kmukhopadhyay@bitmesra.ac.in	NGG-P41
42	Muniswamy, S	ARS-Gulbarga,University of Agricultural Sciences, Raichur, India	Phenotyping and validation of SCAR markers for fusarium wilt and sterility mosaic disease in minicore collections of pigeonpea (*Cajanus cajan*.L)	muniswamygpb@gmail.com	NGG-P42
43	Nayak, Spurthi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Identification of associated markers for aflatoxin contamination through genome-wide association studies in groundnut (*Arachis hypogaea* L.)	s.nayak@cgiar.org	NGG-P43
44	Nezhad, Khalil Z	Gorgan University of Agricultural Sciences and Natural Resources, Gorgon, Iran	A new QTL controlling plant height in bread wheat (*Triticum aestivu*m L.)	khalil1381@yahoo.com	NGG-P44
45	NVPR, Ganga R	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	Pigeonpea improvement in Eastern and Southern Africa through an effective use of unique local germplasm	N.Gangarao@cgiar.org	NGG-P45

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46	Obala, Jimmy	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Towards identification of genomic regions associated with seed protein content in pigeonpea (*Cajanus cajan* (L.) Millsp.)	jimmyobala@gmail.com	NGG-P46
47	Ojulong, Henry	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya	Screening for drought tolerance in finger millet germplasm	H.Ojulong@CGIAR.ORG	NGG-P47
48	Omoigui, Lucky O	University of Agriculture, Makurdi, Nigeria	SSR markers linked with *Alectra vogelii* resistance in cowpea [*Vigna unguiculata* (L.) Walp]	lomoigui@yahoo.co.uk	NGG-P48
49	Pandey, Dev	Birla Institute of Technology, Mesra, India	In silico study on prediction of miRNAs and their related SNPs in *Arachis hypogaea* L.	dmpandey@bitmesra.ac.in	NGG-P49
50	Pandey, Manish	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Ridge Regression-BLUP and Bayesian LASSO identified as the appropriate genomic selection (GS) models for predicting genomic values in groundnut (*Arachis hypogaea* L.) GS breeding	m.pandey@cgiar.org	NGG-P50
51	Parupalli, Swathi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Development of nested association mapping (NAM) population in pigeonpea (*Cajanus cajan* L. Millsp.)	p.swathi@cgiar.org	NGG-P51
52	Pasupleti, Janila	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Enhanced resistance to foliar fungal diseases and improved oil quality in peanut using MABC approach	P.Janila@cgiar.org;	NGG-P52
53	Patil, BR	University of Agricultural Sciences (UAS), Dharwad, India	Pigeonpea transcriptome expression analysis for the discovery of new genes implicated in fusarium wilt resistance	patilbhuvaneshwara@gmail.com	NGG-P53
54	Patil, Suyash	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Photo and thermo insensitive super early maturing pigeonpea [*Cajanus cajan* (L.) Millspaugh]: prospectus and opportunities	P.Suyash@cgiar.org	NGG-P54
55	Pattanashetti, SK	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Identification of quantitative trait loci associated with iron absorption efficiency in groundnut (*Arachis hypogaea* L.)	S.Pattanashetti@cgiar.org	NGG-P55
56	Poornima, KN	ICAR-Indian Institute of Pulses Research, Kanpur, India	Chloroplast targeting: Potential tool for functional genomics in pulses	poornimakn04@gmail.com	NGG-P56

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57	Puppala, Naveen	New Mexico State University (NMSU), Las Cruces, USA-	Valencia peanut breeding for increased shelf life, enhanced drought tolerance and improved disease resistance	npuppala@nmsu.edu	NGG-P57
58	Rathore, Abhishek	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	ISMU 2.0: A multi-algorithm pipeline for genomic selection	a.rathore@cgiar.org	NGG-P58
59	Rohini, MK	University of Agricultural Sciences (UAS), Dharwad, India	Mapping late leaf spot and rust resistance using an improved map from the RILs of TAG 24 × GPBD 4 in peanut (*Arachis hypogaea*)	rohini_bt45@rediffmail.com	NGG-P59
60	Roorkiwal, Manish	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Selection of appropriate genomic selection model for yield related traits in chickpea	m.roorkiwal@cgiar.org	NGG-P60
61	Santra, Dipak K	University of Nebraska, Lincoln, USA	Mapping genes for agronomic traits in proso millet (*Panicum milliacum* L.)	dsantra2@unl.edu	NGG-P61
62	Sehgal, Deepmala	International Maize and Wheat Improvement Center (CIMMYT), Texcoco, Mexico	CIMMYT wheat molecular breeding: Achievements and progress	D.Sehgal@cgiar.org	NGG-P62
63	Seleman, Kaoneka	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Towards identification of genomic regions associated with yield and yield related traits in pigeonpea (*Cajanus cajan* (L.) Millsp)	K.Seleman@cgiar.org	NGG-P63
64	Sharma, Ram Kumar	CSIR-Institute of Himalayan Bioresource Technology (IIHBT), Himachal Pradesh, India	Exploiting next generation sequencing for creation of genomic resource in Tea	ramsharma@ihbt.res.in	NGG-P64
65	Singh, Akhilesh K	Barwale Foundation, Hyderabad, India	QTL mapping for stigma exsertion traits under *indica* genetic background in F_2 population of rice (*Oryza sativa* L.)	akhileshsingh@barwalefoundation.org	NGG-P65
66	Singh, Arpan	ICAR- Indian Institute of Pulses Research (IIPR), Kanpur, India	Kanamycin based screening of putative transgenic pigeonpea (*Cajanus cajan* L.) lines based on lateral root inhibition (LRI)	arpan.biotech@gmail.com	NGG-P66
67	Singh, Jang Bahadur	ICAR- Indian Agricultural Research Institute (IARI), Indore, India	Marker assisted selection – a fast tract in plant breeding to introgress resistance for stem rust race 117-group in durum wheat	jangbsingh@gmail.com	NGG-P67
68	Singh, Nand	Motilal Nehru National Institute of Technology, Allahabad, India	Introduction and characterization of potential mutants genotypes of basmati rice (*Oryza sativa* L.)	singhnand@gmail.com	NGG-P68
69	Singh, Vikas	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	QTL-seq reconfirms the presence of major QTLs for 100-seed weight and root / total plant dry weight ratio in the "*QTL-hotspot"* in chickpea	Vikas.Singh@cgiar.org	NGG-P69

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70	Singh, Vikash K	National Insitute of Plant Genome Research (NIPGR), New Delhi, India	Transcriptome dynamics during flower development and genome-wide analysis of GH3 gene family in chickpea	tovikashalone@gmail.com	NGG-P70
71	Singhal, Tripti	ICAR- Indian Agricultural Research Institute, New Delhi, India	Variability for seedling salinity tolerance in chickpea	triptisinghal16@gmail.com	NGG-P71
72	Sinha, Pallavi	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Evaluation of housekeeping genes as reference for gene expression studies under heat and salt stress conditions in pigeonpea (*Cajanus Cajan*)	p.sinha@cgiar.org	NGG-P72
73	Tathineni, Revathi	Prof. Jayshankar Telangana State Agricultural University (PJTSAU), Hyderabad	Towards development of a SCAR marker linked to sterility mosaic disease resistance in pigeonpea (*Cajanus cajan* L. Millsp.)	revathi.biotech87@gmail.com	NGG-P73
74	Thammineni, Chakradhar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Fine mapping and introgression Of '*ms*3' loci in rabi sorghum for ease of population development	T.Chakradhar@cgiar.org	NGG-P74
75	Thirumalaisamy, PP	ICAR-Directorate of Groundnut Research (DGR), Junagadh, India	Relationship of post-harvest handling of groundnut and aflatoxin contamination in processing units	thirumalaisamypp@yahoo.co.in	NGG-P75
76	Tripathi, Shailesh	ICAR- Indian Agricultural Research Institute (IARI), New Delhi, India	Targeting root traits for improving drought tolerance in chickpea (*Cicer arietinum* L.)	shaitri@rediffmail.com	NGG-P76
77	Verma, Indu	ICAR-Indian Institute of Sugarcane Research (IISR), Lucknow, India	Inter-nodal sugar and expression profiling of early and late maturing sugarcane varieties	indu.verma8718@gmail.com	NGG-P77
78	Verma, Subodh	National Insitute of Plant Genome Research (NIPGR), New Delhi, India	Utilization of genotyping by sequencing (GBS) approach for high density linkage map construction and identification of QTLs controlling seed and pod traits in chickpea (*Cicer arietinum* L.)	subodhshanky@gmail.com	NGG-P78
79	Yaduru, Shasidhar	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Construction of dense genetic maps and identification of quantitative trait loci controlling oil content and different fatty acids in groundnut (*Arachis hypogaea* L.)	y.shasidhar@cgiar.org	NGG-P79
80	Yeri, Sharanabasappa B	University of Agricultural Sciences (UAS), Dharwad, India	Marker assisted backcrossing to improve foliar disease resistance in JL 24 and TMV 2 varieties of peanut	vishalyeri@gmail.com	NGG-P80

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81	Hingane, Anupama	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Development of super early maturing hybrids in pigeonpea [(Cajanus cajan (L.) Millspaugh] using A4 cytoplasm	h.anupama@cgiar.org	NGG-P81
82	Sameerkumar,CV	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India	Cleistogamous flowering a novel trait in pigeonpea [(Cajanus cajan (L.) Millspaugh] with ensured self-pollination	C.Sameerkumar@cgiar.org	NGG-P82
83	Vyas, Darshna	LGC Genomics, Hertfordshire, UK	Molecular tools for plant breeding – "Success starts at the plant"	darshna.vyas@lgcgroup.com	NGG-P83
84	Smykal, Petr	Palacky University, Olomouc, Czech Republic	Establishment of wild pea Pisum fulvum chromosome segment substitution lines in cultivated P. sativum genetic background, as a tool to study domestication and to broaden genetic diversity.	petr.smykal@upol.cz	NGG-P84
85	Adarsh, MN	Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Solan, India	Marker assisted gene introgression: A rapid method to incorporate rust resistant Ur-3 gene into the genetic background of french bean	adarshm464@gmail.com	NGG-P85
86	Apoorva, MJ	ICAR- Central Rice Research Institute (CRRI), Cuttack, India	Microsatellite based DNA finger prints for elucidation of genetic diversity in rice (Oryza sativa L.)	apoorvamj565@gmail.com	NGG-P86
87	Islam, Shahinul	University of Rajshahi, Rajshahi, Bangladesh	Production of doubled haploids through androgenesis and identification of plants by molecular markers in maize (Zea mays L.)	shahin_ibsc@ru.ac.bd	NGG-P87
88	Kujur, Alice	National Insitute of Plant Genome Research (NIPGR), New Delhi, India	An efficient integrated genomic approach for rapid delineation of potential candidate transcription factor genes/ QTLs regulating seed weight in chickpea	alice1.kujur@nipgr.ac.in	NGG-P88
89	Kumari, Poonam	Dr. Yashwant Singh Parmar University of Horticulture and Forestry, Solan, India	Molecular and morphological characterization of variation related to fusarium wilt resistance in gladiolus (Gladiolus x hybridus Hort.)	poonamjaswalfls@gmail.com	NGG-P89
90	Sheikh, Imran	Eternal University, Baru Sahib Via Rajgarh, India	Characterization of radiation induced precise transfer of genes for high grain micronutrients from non-progenitor Aegilops species into wheat	imransheikh485@gmail.com	NGG-P90

Appraisal of Diverse Rice Collections Using Morphological And Molecular Markers for Early Vigor Trait in Direct Seeded Condition

Anandan, A*[1], Mahender, A and Singh ON[1]

[1]Crop Improvement Division, Central Rice Research Institute, Cuttack, India
*E mail: anandanau@yahoo.com

Aerobic and dry direct seeded rice (DDSR) are technologies that effectively addresses the problem of water and labor shortage through reduced utilization of water for land preparation as well as water saving through better irrigation management and introduction of mechanized practices for sowing, weed control and harvesting. Therefore, this scenario demands development of rice varieties better suited to aerobic and dry direct seeded through precision breeding. Non-uniform emergence and reduced ability of the rice to compete with weeds under dry direct seeded situations are important factors determining reduced yield under DDSR. Early vigour (biomass accumulation) is a useful trait in DDSR. In the present study we have characterized a panel of 607 diverse rice genotypes. The early vigor traits were observed on 14th, 28th and 56th days after sowing. Pearson correlation analysis indicated that seedling vigor index (SVI) on 14th, 28th and 56th days after sowing correlated with 7 traits, 10 traits and 5 traits respectively. Of the 607, 96 genotypes were selected based on SVI and analyzed further with 45 QTL linked SSR markers of early vigor traits. Based on the 45 molecular marker data analyses, 7 markers showed high polymorphism with an average PIC value of 0.378 and 4 markers (RM9, RM3839, RM258, RM340) have more than 5 alleles. Therefore, these promising markers can be utilized in breeding program to development genotypes with early vigor suitable for DDSR.

Chromosome Transmission Patterns in Interspecific Hybrids of Sugarcane Derived with Different Cytotypes of *Saccharum spontaneum* L.

Suganya A*, Selvi A

Sugarcane Breeding Institute, Coimbatore, Tamil Nadu, India
*Email: suganyamuns @rediff.com

*Saccharum spontaneum,*L. founded a schematic pave for sugarcane breeding through its exploitation in the inception of first man-made interspecific hybrid 'Co 205' in 1918. It is a polymorphic wild relative of sugarcane and exists with 41 cytotypes with 2n=40-128, of which the cytotype 2n=64 is predominant. In order to analyse the cytological performance of the hybrids involving different cytotypes, chromosome transmission pattern of 450 hybrids derived from 47 crosses involving commercial varieties of sugarcane and different cytotypes of *S. spontaneum* (2n=40, 56, 60, 64, 72, 80, 88 and 112) was studied. Cytological data indicated n+n, n+2n and 2n+n transmission and elimination of chromosomes. The progenies of the cytotype 2n = 64 were stable (n+n) with the expected chromosome number in majority of the hybrids. The hybrid, 04-359 of BO 102 x IND 84 - 338 (2n=60) possessed the least chromosome number with 2n=72 with the elimination of 12 chromosomes. However, loss of chromosomes was higher in crosses with the cytotype 2n=72, 80, 88 and 112.The hybrid (04-1326) from the cytotype 2n=80 had maximum elimination of 15 chromosomes. The hybrids derived with cytotype 2n=40 had n+2n transmission. A rare occurrence of 2n+n transmission was observed in three hybrids with 2n=166,153 and142 derived with the cytotypes 2n=112, 88 and 64 respectively. Molecular analysis of 60 hybrids with SSR markers revealed higher frequency of male specific fragments with 2n=64. Selection of stable progenies with desired traits will be advantageous to incorporate all the available genes from both the parents.

Expression of a Synthetic *Bt* Gene in Chickpea (*Cicer arietinum* L.) Confers Resistance to Gram Pod Borer (*Helicoverpa armigera* H.)

Ansari MJ, Shukla A, Kumar M, Das A*, Sujayanand GK, Datta S, Singh NP

ICAR-Indian Institute of Pulses Research, Kanpur 208 024, Uttar Pradesh, India
*Email: adas@icar.org.in

Chickpea (*Cicer arietinum* L.) is the most important grain legume of India, and constitutes an important component of protein intake in human diet. The gram pod borer (*Helicoverpa armigera* H.) is the most destructive insect pest of chickpea, accounting for 10-40 % loss annually. The insecticidal gene derived from *Bacillus thuringiensis* (Bt) was shown to confer resistance against Lepidopteron pests in many crop species. A synthetic *Bt* gene under constitutive promoter (CaMV35S), mobilized into *Agrobacterium* was used for genetic transformation of chickpea. Constitutive expression of the insecticidal gene in chickpea exhibited high neonate mortality (80-90%). Elite lines with stable expression can be used as donors in insect resistance breeding programme.

Musatransssrdb – A Transcriptome Derived SSR Database: An Advanced Tool for Banana Improvement

Backiyarani S*, Uma S, Chandrasekar A, Saravanakumar A S, Saraswathi M S

National Research Centre for Banana, Thogamalai Road, Thayanur PO,
Trichy – 620102, Tamil Nadu, India
*Email: backiyarani@gmail.com

Availability of transcriptome datasets for use in accelerated molecular-based breeding in banana is limited. Illumina Hiseq technology was employed to determine differential gene expression between contrasting cultivars for three different stresses -- Eumusae leaf spot caused by *Mycosphaerella eumusa,* the root lesion nematode *Pratylenchus coffea,* and moisture deficit stress -- under challenged and unchallenged conditions. An average of 34.72 million reads was assembled into 47629 contigs and we identified 7426 simple sequence repeats (SSR) from each library. GO annotation and KEGG pathway analysis were carried for all the transcripts, and SSRs and SNPs were also detected. Based on this information, a MusatransSSRDB has been developed. Currently, the database consists of 48,298 SSRs with unique information such as the putative function of the SSR-containing genes and their metabolic pathway, and expression profiling under various stress conditions. This database provides information on *in-silico* polymorphic SSRs (2830 SSRs) between the contrasting cultivars for each stress and within stress. Information on *in-silico* polymorphic SSRs specific to differentially expressed genes under challenged conditions for each stress can also be accessed. The database facilitates the retrieval of results by navigating the tabs for cultivars, stress and polymorphism. The database was developed using HTML, Java and PHP, datasets are stored in MySQL database and are public domain (http://nrcb.res.in/nrcbbio/). This unique information facilitates banana breeders to select SSR primers based on the specific objectives. The MusatransSSRDB along with other genomics databases will facilitate genetic dissection and breeding for complex traits in banana. Thus, this database is a step forward in economizing cost, time, manpower and other resources.

Genotypic Variation for Salinity Tolerance in the Chickpea Reference Set

Atieno J[1*], Li Y[1], Langridge P[2], Sutton T[1, 3]

[1] Australian Centre for Plant Functional Genomics, School of Agriculture, Food and Wine, University of Adelaide, Waite Campus, PMB 1, Glen Osmond, SA 5064, Australia
[2] School of Agriculture, Food and Wine, University of Adelaide, Waite Campus, PMB 1, Glen Osmond, SA 5064, Australia
[3]Current Address: South Australian Research and Development Institute, GPO Box 397 Adelaide, South Australia, 5001, Australia
Email: Judith.atieno@acpfg.com.au

Salinity is a major abiotic stress in arid and semi-arid environments as well as in intensively irrigated lands. Solutions to allow utilisation of saline lands for chickpea production are urgently needed. Salinity management options are expensive, which necessitates a genetic approach. The focus of this study is to dissect the genetic basis of salinity tolerance in chickpea. The first step towards this is to generate high quality phenotypic data. To this end, an assembly of 245 chickpea accessions with a diverse genetic background from ICRISAT in India was phenotyped under 0 and 40 mM NaCl in potting mix containing 1:1 cocopeat and UC mix (v/v). The experimental design consisted of (nearly) trend free design with plots randomised and replicated two or three times. To quantify relative growth rate due to salinity, plant growth was imaged in a glasshouse at the Australian Plant Phenomics Facility commencing 28 days after sowing for three days, after which salt was added in increments over a period of two days. The plants were then further imaged for 25 days after salt application. In addition to data extracted from high resolution imaging, data on yield and yield components were also taken. The results show a wide range of variation for relative growth rate and seed yield under both control and salinity treatments. 40 mM NaCl reduced relative growth rate, shoot biomass and seed yield, with some genotypes affected more than others. Phenotypic data from this experiment combined with SNP data generated from whole-genome resequencing will be used to identify genomic regions controlling salinity tolerance in chickpea through genome wide association analysis.

Marker Assisted Backcrossing to Introgress Resistance to *Fusarium* Wilt Race 4 in JG 74, an Elite Cultivar of Chickpea

Babbar A*, Pandey S

Department of Plant Breeding & Genetics, JNKVV, Jabalpur , MP-482004, India
*Email: anitababbarjnkvv@gmail.com

Chickpea is one of the important cool-season food legumes grown extensively by poor farmers throughout the Indian subcontinent. India alone contributes about 67% of the global chickpea production; however, there has been little improvement in the crop productivity. Several biotic and abiotic stresses impose adverse effects on plants at most of the growth stages, leading to low productivity. Among the biotic stresses, fusarium oxy [*Fusarium oxysporum* f. sp. ciceris (foc)], causing 10-90% yield loss is the most severe constraint in central India. Till date, two pathotypes (yellowing and wilting) and eight pathogenic races (races 0, 1A, 1B/C, 2, 3, 4, 5and 6) have been described for *Fusarium* wilt. Therefore, marker-assisted backcrossing (MABC) programs by targeting foc4 locus were undertaken to introgression resistance to FW in JG 74, an elite cultivar of chickpea at JNKVV, Jabalpur. Foreground selection (FGS) was conducted with two markers (GA16 and TA 96) linked to foc4 in the cross JG 74 × WR 315 (FW resistant). Background selection (BGS) was employed with 40 SSR markers in the chickpea genome to select plant (s) with higher recurrent parent genome (RPG) recovery. By using three backcrosses and three rounds of selfing, 168 BC3F4 lines were generated for JG 74 × WR 315 cross. Phenotyping of these lines has identified forty four resistant lines (with 99.2-99.8% RPG) to race 4 of FW that may be evaluated for yield and other agronomic traits under multiplication trials for possible release and cultivation.

Analysis of TMV 2 × NLM Derived RIL Population Towards Mapping Genomic Regions Governing Taxonomic and Morphological Traits in Peanut

Hake AA, Gowda MVC, Bhat RS*

College of Agriculture, University of Agricultural Sciences, Dharwad-580005, India
*E-mail: bhatramesh12@gmail.com

Mapping of traits like growth habit, main stem flowering, branching pattern, 50% flowering, presence of secondary branches and leaflet shape in peanut is of great utility in breeding. TMV 2 (Spanish type) and its Virginia type mutant, narrow leaf mutant (NLM) differed significantly for these traits. A mapping population consisting of 432 RILs was previously developed. RILs were evaluated for these traits during the rainy season of 2014. A considerably high variability was recorded for the traits among the RILs. Both alternate and sequential branching pattern was observed with a frequency of 36.40% and 63.60%, respectively among the RILs. Similarly, 0.012%, 69.45% and 29.40% of the RILs had decumbent-2, decumbent-3 and erect type of growth habit, respectively. In general, RILs with sequential branching pattern had flowers on the main stem, while those with alternate branching pattern lacked flowers on the main stem. High variability was also observed for leaf shape; RILs with linear lanceolate, oblong lanceolate, ovate and wide elliptic leaves were observed with a frequency of 0.5%, 14%, 0.5% and 85%, respectively. Number of secondary branches per plant exhibited highest (146.74% and 121.72%) phenotypic coefficient of variation (PCV) and genotypic coefficient of variation followed by number of primary branches per plant (PCV: 31.45% and GCV: 19.42%) and plant height (PCV: 21.14% and GCV: 18.41%). In attempt to develop a genetic map, the parents were screened with 159 Arachis hypogaea transposable element-specific markers, of which 78 (49.05%) were polymorphic. Effort is being made to develop the map, and to detect the genomic regions governing taxonomic and morphological traits for use in peanut breeding.

Identification of Protein Phosphatase 2C Subgroup A in Barley Using mRNA-Sequencing

Kamboj A[1], Ziemann M[2], Bhave M[1*]

[1]Faculty of Science Engineering and Technology, Swinburne University of Technology, Hawthorn, Victoria, 3122, Australia.
[2]Baker IDI Heart and Diabetes Institute, 75 Commercial Road, Melbourne, Victoria 3004, Australia
*Email: mbhave@swin.edu.au

Salt and drought are the two most important environmental stresses which limit plant growth and development. The phytohormone abscisic acid (ABA) is crucial for plant's adaptive response to salinity and drought stresses. ABA accumulates in plant cells to protect vegetative tissues and regulates developmental events. The protein phosphatase 2C subgroup A (PP2CA) enzymes have been implicated to act as negative modulators of the ABA-mediated abiotic stress signaling pathway. A genome-wide analysis of the PP2CA gene family has been conducted in *Arabidopsis* and rice, but this family is poorly defined in the major crops, wheat and barley. Thus the present study aimed to identify and characterise the PP2CA-encoding transcripts genes in barley. The expressed barley PP2CAs were identified using next generation mRNA-seq data and searches in the International Barley Genome Sequencing Consortium database. Twenty three barley PP2CAs were identified. Their encoded proteins were analysed for the conserved motifs and key residues involved in the binding to the soluble ABA receptors of the Pyrabactin-resistance family (PYR/PYL/RCAR). The residues shown to form a bond with the active site of PYR/PYL/RCAR of *Arabidopsis* were found to be strictly conserved in all PP2CAs in barley. PP2CAs were found to be up-regulated under both abiotic stresses studied. The sequences of barley PP2CAs and their expression changes under stress conditions provide an important step in their functional testing, allele identifications and development of stress-tolerant lines through genetic screening and/or modifications.

De novo Transcriptome Assembly and Functional Annotation of Resistant and Susceptible Near-Isogenic Wheat (*Triticum aestivum* L.) in Response to Leaf Rust Pathogenesis

Chandra S, Singh D, Poddar R, Kumar M, Mukhopadhyay K*

Birla Institute of Technology, Mesra, Ranchi 835215, India
*E-mail: kmukhopadhyay@bitmesra.ac.in

Wheat represents the largest volume of agricultural production. Pathogen attack poses major threats to wheat yield and food security. *Puccinia triticina,* the causal organism for leaf rust, incites extensive losses to wheat production. The interaction between wheat and *P. triticina* is complicated and not much is known at molecular level involving this interaction. In this study induced response to *P. triticina* was analyzed at 24 h. Four SAGE (Serial Analysis of Gene Expression) libraries were prepared from resistant and susceptible near-isogenic wheat lines involving seedling resistance *Lr28* gene that were either inoculated with *P. triticina* or mock inoculated. This study resulted 165,767,777 SOLiD SAGE reads, each of 35 bases. The reads were processed and multiple k-mers were attempted for *de novo* assembly; 22 k-mer presented the most satisfactory result. A total of 21,345 contigs were generated. Functional annotation predicted 6,122 contigs had sequence similarity with known wheat genes. The contigs were further mined for transcription factors, resistance genes and expression analysis. Expression analysis of the four libraries based on Reads Per Kilobase of transcripts per Million mapped reads (RPKM) showed major alterations in the transcriptome in response to pathogen-infection reflecting reorganizations in major biological processes and metabolic pathways. A total of 1329 contigs showed homology with 51 transcription factor families and 416 resistant genes whose sequences are available at Plant Transcription Factor Database and Plant Resistant Gene Database respectively. This study will provide valuable resource that can be used for molecular breeding of wheat to develop leaf rust resistance.

Enhancement of Secondary Metabolite Production in *Trigonella foenum-graecum* (Fenugreek)

Chaudhary S[1*], Pandey M[2], Chaudhary A[2], Shah P[2], Sharma MC[1] and Chikara.SK[2]

[1]Department of Biotechnology, Kadi Sarva Vishwavidyalaya, Gandhinagar, Gujarat, India
[2]Xcelris Labs Limited, Ahmedabad, Gujarat, India
*E-mail: spandan.chaudhary@xcelrislabs.com

Having numerous therapeutic applications, saponins (secondary metabolites) are commercially very important compounds for manufacturing various drugs. The aim of the study is to enhance the production of secondary metabolite synthesis in fenugreek. We have targeted two genes, 3-hydroxy-3-methylglutaryl-CoA reductase (HMG) and sterol-3-Beta glucosyl transferase (STRL), from the 11 key genes involved in secondary metabolite synthesis pathway identified in our transcriptome sequencing data published earlier.

HMG is involved in the rate limiting step of the cholesterol synthesis pathway which is the route to steroid synthesis, and STRL gene is involved in the synthesis of diosgenin via synthesis of sterol 3-β-D-glucoside (saponin). Six different varieties of *Trigonella foenum-graecum (fenugreek)* GM-1, Kasuri-1 and Kasuri-2, PEB, RMT-1 and MMT-5, have been selected for the study and were treated with methyl jasmonate which is commonly used as inducers of triterpene saponin production and a key elicitator of enzymes leading to secondary metabolite accumulation. To study the expression levels of HMG and STRL genes, methyl jasmonate was applied in concentrations of 0 µl/l, 50 µl/l, 100 µl/l, 200 µl/l, 300 µl/l, 500 µl/l, 1000 µl/l on the seedlings. Gene expression analysis was conducted using syber green chemistry by real time polymerase chain reaction method using Roche LightCycler 480 II. Due to direct involvement of STRL gene in the secondary metabolite production, it was hypothesized that its expression will affect the saponin biosynthesis. In present study we report that the methyl jasmonate treatment has enhance the expression of STRL gene significantly in all the varieties as 22 fold in GM2, 3.5 fold in Kasuri-I, 28 fold in Kasuri-II, 7.74 fold in PEB, 2.15 fold in RMT and 73 fold in MMT. It is concluded that methyl jasmonate treatment can significantly enhance the yield of secondary metabolites in fenugreek plant.

Genomic Approaches for Breeding Drought-Tolerant Chickpea

Bharadwaj C[1*], Kumar S[1], Singhal T[1], Kumar T[1], Singh P[1], Tripathi S[1], Pal M[1], Hegde VS[1], Jain PK [2], Chauhan SK[1], Verma AK[1], Roorkiwal M[3], Gaur PM[3], Varshney RK[3]

[1]Indian Agricultural Research Institute, Delhi, India
[2] National Research Centre for Plant Biotechnology, Pusa, New Delhi
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*Email: chbharadwaj@yahoo.co.in

Genomic selection (GS), marker assisted backcross (MABC), and marker-assisted recurrent selection (MARS) are now being routinely used in chickpea for yield improvement and stabilization. Development of intraspecific maps, identification of QTLs for yield, identification of stress responsive genes and the sequencing of chickpea genome (Varshney et al) have made this genomic orphan crop into a genomic resource rich crop. NARS partners and CGIAR institutes are working together in harnessing this potential. The training population consisting of elite lines has been evaluated in both rain-fed and normal sown conditions to identify superior lines. Seedling screening through hydroponics, and root phenotyping has confirmed the presence of drought tolerance in these genotypes. Sequence similarity approaches with stress responsive genes identified the up regulation of genes like *Myb transcription factor, DHN and CAD*. A relative relationship between canopy temperature depression (CTD) and grain yield was worked out.

Since many workers have already established the relationship between CTD and drought tolerance, ie., the cultivars with greater CTD had greater tolerance to drought, using maximax-minimax approach scatter, the genotype ICCV 03408 with high CTD and high yield under terminal drought conditions has been identified as a drought-tolerant line and the lines ICCV03104, ICCV00202, ICCV01102, ICCV10112 and ICCV04106 with high CTD values have been identified as donors for drought tolerance.

Tagging of Gene for Yellow Mosaic Virus (YMV) Resistance in Greengram (*Vigna radiata* (L).Wilczek)

Anuradha Ch*, Srinivas AMN

Institute of Biotechnology, Professor Jayashankar Telangana State Agriculture University, Rajendranagar, Hyderabad-500030
*Email: anu_dna@rediffmail.com

Mungbean (*Vigna radiata* (L.) Wilczek) is one of the important pulse crops which contain about 25% of protein of high digestibility. It is a soil building crop which fixes atmospheric nitrogen through symbiotic action. Mungbean Yellow Mosaic Virus (MYMV) is a whitefly (*Bemisia tabaci*) –transmitted by Begomovirus, causes disease in a variety of leguminous crops, but the most seriously affected are blackgram, mungbean and soybean . it causes significant yield losses in mungbean, leading to a yield penalty of cent percent under; and the disease occurs throughout the Asian countries.Molecular markers linked with YMV can improve the process of identification of resistant genotypes. Simple Sequence Repeats (SSR) and Bulk segregant analysis (BSA) techniques were used to analyse the F_2 individuals of resistant LGG 460 × susceptible PM 115 to screen and identify the yellow mosaic virus (YMV) resistant gene in mungbean. Parental survey study was carried out by using fiftynine SSR markers of which thirteen showed polymorphism between the parents. SSR marker MB14 was found to be tightly linked to yellow mosaic virus resistance gene. To the best of our knowledge, this is the first report of YMV-resistance linked marker in greengram. This marker MB14 could be utilized in the marker assisted breeding programme.

Allele Mining of Two Drought Responsive Factor (DRF) Genes in Pigeonpea (*Cajanus cajan* L.)

Das A*, Kumar N, Thakur S, Soren KR, Shanmugavadivel PS, Basu PS, Singh NP

ICAR-Indian Institute of Pulses Research, Kanpur 208 024, Uttar Pradesh, India
Email: adas@icar.org.in

Pigeonpea (*Cajanus cajan* L.) is a major grain legume crop of the semi-arid tropics, but several abiotic stresses such as drought, heat and cold stresses are major constraints which affect productivity adversely. Identification of genes/better alleles involved in environmental stress response offers scope for genetic improvement of pigeonpea for enhanced tolerance against abiotic stresses. CYP (cyclophilin) and Cc HyPRP (hybrid proline-rich protein encoding) genes are well characterized, known to be stress inducible factors. In the present study, we prospected the allelic variants of two drought-responsive factors, CYP and CcHyPRP, from a set of pigeonpea genotypes of mini core set, to determine nucleotide diversity and phylogenetic relationship. This is a maiden initiative of mining alleles of stress inducible genes from pigeonpea genotypes, which help in selection of better/ more powerful alleles for drought tolerance in future.

From QTL to Gene: Mapping QTLs and Candidate Genes for Early Flowering and Photoperiod Sensitivity in Chickpea

Deokar A, Daba K, Ridge S, Tar'an B*

Crop Development Centre, Department of Plant Sciences, University of Saskatchewan,
51 Campus Dr, Saskatoon, SK S7N 5A8, Canada
*Email: bunyamin.taran@usask.ca

Chickpea is considered a good example of the most successful crop adaptation outside of its origin. More than 90% of chickpea production came from short growing season areas of Asia and Africa. Natural allelic variation for loci associated with adaptive response, including time of flowering and photoperiod sensitivity in chickpea played an important role in the successful adaptation of chickpea in areas with short-growing seasons. Four major genes (designated as *elf-1, elf-2, elf-3* and *elf-4*) controlling early flowering have been identified in chickpea. In this study, we identified QTLs for early flowering and photoperiod sensitivity in ICCV 96026 X CDC Frontier RIL (CPR-01) mapping population on Chr4 and Chr5. The QTLs explained for 71% of phenotypic variation for sensitivity to photoperiod. Single-nucleotide polymorphisms (SNPs) between ICCV 96029 and CDC Frontier were detected for GIGANTIA (GI), flowering locus D (FLD), and cryptochrome (CRY2) on Chr4. A short deletion resulting in a frame-shift and a premature termination codon of Early Flowering 3 (ELF3) gene on Chr5 was detected in ICCV 96029. All the SNPs were converted into KASP SNP markers and mapped on CPR-01 genetic map. The candidate genes GI and ELF3 mapped in the QTLs region on Chr4 and Chr5 respectively. We screened a subset of chickpea mini-core collection for ELF3 allele, using allele-specific SNP markers and found *elf3* as a rare allele, only detected in four accessions including ICCV96029 and ICCV 2, which shares a common source for *elf-1* gene.

Phenotyping of Available Indian Germplasm, Breeding Lines for Resistance to Rust and Mosaic Virus in Cowpea (*Vigna unguiculata* L. Walp)

Deshpande SK*, Patil BR

Department of Genetics and Plant Breeding, University of Agriculture Sciences, Dharwad-580005, Karnataka, India
*Email: sanjeevgpb@gmail.com

A total of 160 germplasm lines of cowpea (*Vigna unguiculata*. L. Walp) and 22 stabilized breeding lines were evaluated in augmented block design along with checks C152, DCS47-1, and GC3, for resistance to cowpea rust and cowpea mosaic virus (CMV); and yield *per se* for two seasons during *kharif* (summer) 2013 and 2014 at Dharwad. Disease epiphytotic conditions were created. Disease scoring was done for rust on 0-9 scale and for cowpea mosaic virus (CMV) on 1-9 scale (1=0% DI (R), 3=0.1-10% DI (MR), 5=10.1-25% DI (AI), 7=25.1 – 50% DI (MS), 9= >50% DI (HS) for virus). Promising germplasm lines for yield *per se* and resistant to CMV (1 score) compared to checks C152 and GC3 are as follows: IC15567, IC199701, IC201079, IC201087, IC15567, IC199701, IC201079, IC201087. The germplasm lines exhibiting resistance (1 score) to rust are IC97787, IC198333, IC202781, IC257420, IC202786, IC27502, IC202924, IC249140 compared to checks. Check entry DCS 47-1 and stabilized line DC15 showed high yield *per se* (1200 kg/ha and 1350kg/ha seed yield respectively) and also displayed resistance to rust and tolerance to CMV.

Advanced breeding lines identified for higher yield, multiple disease resistance (Rust and CMV) are (V118 x IC97767)IC97767 (BC2F5), (GC3 x IC97767) IC97767 (BC2F5), (GC3 x IC97767)(F6), (V118 x IC97767)(F4), (GC3 x IC97767)IC97767(BC1F5) and GC3 x Goa Local (F4).

Genetic Variability and Path Co-Efficient Analysis in Minicore Collections of Pigeonpea (*Cajanus cajan.* L)

Dharmaraj PS*, Muniswamy S, Yamanura R, Girish G

Agricultural Research Station (ARS), Gulbarga - 585 101, Karnataka, India
*Email: psdharmaraj@yahoo.com

A study was undertaken at the Agriculture Research Station, Gulbarga, during 2013-14 to analyse variability in 191 minicore collections along with five check varieties in pigeonpea which were obtained from ICRISAT Telangana, IIPR, Kanpur and local collections around Gulbarga. Moderate PCV and GCV coupled with high heritability was observed for days to 50% flowering, number of seeds per pod, and 100 seed weight, indicating that a little improvement in yield can be achieved through selection for these traits. Days to maturity and plant height, though, have high heritability but their contribution to yield improvement was low as indicated by low GCV and PCV values. High rate (0.30 to 0.99) of positive direct effect on yield was observed by means of days to 50% flowering, number of pods per plant and 100 seed weight at genotypic and phenotypic level, indicating that emphasis can be laid on these three characters during selection of genotypes for improvement of yield. Further, low rate (0.10 to 0.91) of positive direct effects was observed through pod bearing length at genotypic and phenotypic level, suggesting that it is also an important trait for yield improvement. Days to maturity registered negative direct effects on yield, indicating that this trait is not the criterion for yield improvement. High rate of positive indirect effect on yield was observed through days to maturity, *via* days to 50% flowering, pod bearing length *via* days to maturity. Moderate and positive indirect effects (0.2 to 0.29) on yield was observed through number of pods per plant *via* number of branches per plant and pod bearing length.

Potential of SNP Density Approach to Identify Unique Variations of Whole Genome Sequence

Dwiyanti MS[1], Ulat VJ[1], Koh HJ[2], Mauleon R,[1] Chin JH,[1]* and Thomson MJ [1]*

[1]International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines
[2]Plant Molecular Breeding Center, College of Agriculture and Life Sciences,
Seoul National University, 151-921, Seoul, Korea
*Emails: m.thomson@irri.org, j.chin@irri.org

The availability of whole-genome sequence of donors for biotic and abiotic stress tolerance will accelerate the characterization of genes underlying QTLs and the development of molecular markers for marker-assisted breeding. For this purpose, we sequenced rice donors for abiotic and biotic stress tolerance, and several major recipient varieties. Raw reads from all sequences were aligned to japonica reference genome Nipponbare MSU 7.0 using Bowtie2. SNPs and small indels were called using GATK pipeline. In general, *indica* and *aus* varieties have more variants compared to *japonica* varieties, because *indica* and *aus* varieties are more distantly related to Nipponbare than *japonica* varieties. Variation block approach has been used to identify candidate gene of hilum color in soybean. A similar approach is used to explore regions that show unique variation in rice genome.

The distribution of SNPs and small indels along the chromosomes is shown as number of SNPs and indels per 10-kb bin (SNP density). SNP density patterns in chromosome 5 and 11 across 11 varieties are shown as examples. Japonica varieties show low SNP density in chromosome 11, except 22.4 – 28.9 Mb, where high SNP density was observed. Many disease resistance-related genes are located in this region. The 9.6-13.3 Mb region of chromosome 5 of N 22 has high SNP density, while SNP density of this region is low in other varieties. Further exploration of these unique regions may help in candidate gene identification and marker development for rice breeding.

Study of Relative Effectiveness of Stay-Green (Stg) QTL Combinations under Stress Conditions

Gaikwad PS[1,2], Mehtre SP[2], Vadez V[1], Hash CT[3], Deshpande SP[1*]

[1]International Crops Research Institute for the Semi-Arid Tropics, Patancheru,502324, Hyderabad, India
[2]Department of Genetics and Plant Breeding, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, 413402, Maharashtra, India
[3]International Crops Research Institute for the Semi-Arid Tropics, Niamey, Niger
*Email: s.deshpande@cgiar.org

Breeding experiments have shown that any single stay-green QTL alone does not effectively protect sorghum yield from terminal drought. For this study, a combination of 7 and 8 stg Introgression Lines (IL) were developed in half diallel fashion, both in R16 and S35 backgrounds, respectively. F_2 seeds were produced by selfing of confirmed F_1s. The resulting 49 progenies (21 and 28 in R16 and S35, respectively) were field evaluated in 2013 summer along with the parents and F_1s in RCBD design with three replications. Observations were recorded on green leaf area (GLA) % and on important yield-contributing traits such as days to 50% flowering, grain dry weight (g) (GDW) and 100 grains mass (g) (HGM). Genetic variation among all the crosses was highly significant for all the traits in both backgrounds, except for GLA (%) 28 days after flowering (DAF) in S35 background. Operative repeatabilities were high for all traits (62-92%), except 34; and 54 % in S35 background for GLA (%) at 28 and 35 DAF. In F_2 population for both backgrounds, correlations were highly positive between all GLA (%) traits in maximum crosses. Positive correlations between GLA (%) and yield-contributing traits indicates that stg QTLs combinations play an important role in increased HGM and GDW under stress conditions in sorghum. Frequency distribution graphs show that in R16 background, positive transgressive segregation is observed in crosses, involving stg3, stg4 and stgB QTL combinations. For further evaluation diallel analysis is underway to estimate interaction and combining ability of stay-green QTLs.

Molecular and Morphological Diversity in Basmati and Non-basmati Aromatic Local Short Grain Aromatic Genotypes of Rice (*Oryza sativa* L.): A Study using Standard Panel of SSR and InDel Markers

Gangashetty PI[1,2*], Salimath PM[2], Steele KA[3], Hanamaratti NG[2], Nadaf HL[2]

[1]International Crop Research Institute for Semi-Arid Tropics (ICRISAT), Niamey, Niger (Via Paris), BP12404
[2]Department of Genetics and Plant Breeding, UAS Dharwad, India-580005
[3]CARIAD, Bangor University. LL57 2UW, United Kingdom.
*Email: P.Gangashetty@cgiar.org

Genetic diversity in crop plants plays a vital role in crop breeding and helps in maintaining and creation of new novel genetic variability in the breeding populations. The characterization of local basmati and non-basmati aromatic short grain rice genotypes for different morphological characters and molecular characterization with SSR (Simple sequence Repeats) and InDels (Insertion-Deletion) markers was attempted. The morphological genetic diversity analysis indicated that inter cluster distance was not consistent with the geographic distribution of land races. The land races belonging to diverse ecological regions were clustered together, whereas, land races of the same region were grouped into separate clusters. Morphological characterization of fourty two landraces revealed that, landrace Gandhasali was superior for test weight and grain yield per plant, Pusa suganda-4 was superior for grain yield per plant while, Kalanamak and Ambemohor were rich in Fe and Zn in grains. Grain yield per plant had maximum contribution towards the genetic divergence followed by grain length and plant height. Molecular characterization with SSR and InDels markers revealed presence of variation between basmati and non-basmati short grain aromatic genotypes. Most of the basmati genotypes were grouped to one cluster while, all the local short grain aromatic genotypes were grouped into another cluster. These standard set of markers can be can further used for distinguishing basmati and non-basmati aromatic genotypes.

Introgression of Resistance to *F. oxysporum* (Race 2) in Pusa 256 Variety of Chickpea (*C. arietinum* L.) through Marker Assisted Backcross Breeding

Pratap A[1*], Chaturvedi SK [1], Tomar R[1], Varshney RK [2]

[1]ICAR-Indian Institute of Pulses Research, Kanpur-208024, Uttar Pradesh, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, Telangana
*Email: adityapratapgarg@gmail.com

Fusarium wilt caused by *F. oxysporum* f. sp. *ciceri* causes extensive damage to chickpea (*Cicer arietinum* L.). In central part of India, race *2 (Foc* 2) of this pathogen causes severe yield losses to this crop. We initiated molecular marker assisted breeding using Vijay as a donor to develop *Fusarium* wilt race 2 (*foc2)* resistant Pusa 256 variety of chickpea. To confirm introgression of resistance for this race, foreground selection was done using two SSR markers (TA 37 and TA110), while background selection to observe the recovery of recurrent parent genome was done using 45 SSRs accommodated in eight multiplexes. The true F_1 plants identified through molecular markers were backcrossed with Pusa 256 and selfed, assisted by foreground and background selection at each stage to generate 161 plants in BC_3F_2 generation during the period 2009-2013. Similarly 46 BC_3F_1 plants were also generated. On the basis of foreground selection, 46 plants were found homozygotes in BC_3F_2 generation. Among them 17 plants recorded >91% background recovery with the highest recovery percentage of 96%. Similarly in BC_3F_1 generation also, 14 true plants recorded a background recovery of >85% with the highest background recovery percentage of >94%. The identified plants were selfed to obtain 1341 BC_3F_3 and 2,198 BC_3F_2 seeds which have been screened phenotypically. This has led to development of Pusa 256 lines with *Foc* 2 gene introgressed in them. Development of such lines will help in horizontal as well as vertical expansion of chickpea crop in central India.

Genome-Wide Identification of Gene Families Involved in the Regulation of Small RNA Expression in Chickpea and Pigeonpea

Garg V[1,2], Agarwal G[1], Khan AW[1], Doddamani D[1], Kudapa H[1], Pazhamala LT[1], Kavi Kishor PB[2], Varshney RK[1,3*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Department of Genetics, Osmania University, Hyderabad, India
[3]School of Plant Biology and Institute of Agriculture, The University of Western Australia, Crawley, Australia
*Email: r.k.varshney@cgiar.org

Small RNAs have emerged as one of the most important regulators of gene expression in both plants and animals. DCL (Dicer-like), RDR (RNA-dependent RNA polymerase) and AGO (Argonaute) gene families are known to be essential for the biogenesis and function of small RNAs. It is therefore imperative to investigate the role of protein/gene families involved in regulation of expression of small RNAs in important legume crops like chickpea and pigeonpea. HMM (Hidden Markov Model), blastp searches followed by domain scanning identified a total of 4 DCL, 5 RDR, 13 AGO proteins in chickpea and 5 DCL, 5 RDR, 13 AGO proteins in pigeonpea. Phylogenetic analysis provided insights into the evolutionary aspects and resulted in clustering of these members into different groups based on their orthologs from other species. Motif analysis, promoter prediction, functional annotation and gene structure analysis of these families in both chickpea and pigeonpea were carried out. These results were in concurrence with the previous reports in arabidopsis, rice, maize and soybean indicating the conservation of small RNA function and structure in plants. Our study unraveled 17 out of 22 and 20 out of 23 identified proteins as potential targets for the microRNAs (miRNAs) in chickpea and pigeonpea, respectively. This study has not only identified the genes involved in regulation of gene expression in these two crops, but also would result in identification of probable candidate genes imparting resistance against different stresses.

Association Analysis of Low-phosphorus Tolerance in West African Pearl Millet Using DArT™ Markers

Gemenet DC[1,7], Leiser WL[1], Zangre RG[2], Angarawai II[3], Sanogo MD[4], Sy O[5], Thudi M[6], Hash CT[3], Haussmann BIG*[1]

[1]University of Hohenheim, Stuttgart, Germany
[2]Institut de l'Environnement et de Recherches Agricoles (INERA), Ouagadougou, Burkina Faso
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Sahelian Center, BP 12404, Niamey, Niger
[4]Institut d'Economie Rurale (IER), Cinzana, Mali
[5]Institut Sénégalais de Recherches Agricoles (ISRA), Bambey, Senegal
[6]Center of Excellence in Genomics (CEG), ICRISAT, Hyderabad 502 324, India
[7]Kenya Agricultural and Livestock Research Organization, PO Box 57811, Nairobi 00200, Kenya
*Email: Bettina.haussmann@uni-hohenheim.de

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] (PM) is the food security crop of the world's harshest crop-livestock production environments. Low soil-phosphorus availability (LSPA) is the major abiotic constraint to PM production but information on genomic regions responsible for PM LSPA-tolerance is generally lacking. This is the first report on genetic polymorphisms underlying PM LSPA-related parameters, flowering time (FLO) & grain yield (GY) under LSPA-limiting conditions based on 384 diversity array technology (DArT™) markers & 155 West African PM inbred lines from ICRISAT's West & Central African Pearl Millet inbred Germplasm Association Panel (WCA-PMiGAP) phenotyped in six environments in West Africa (WA) under both high-P & low-P conditions. Sixteen markers were significantly associated with LSPA-related traits, fifteen markers with FLO, & 21 markers with GY, each explaining between 4.6% and 12.3% of the observed variation in WCA-PMiGAP. Both constitutive & adaptive associations were observed for FLO & GY, with markers *PgPb11603* & *PgPb11459* being associated with the most stable effects on FLO & GY, respectively, across locations. There were shared polymorphisms, especially for P-uptake efficiency & GY, implying possible co-location of genomic regions responsible for these two traits. Our findings help bridge the gap between quantitative & molecular methods for complex traits like LSPA tolerance in WA. However, validation of these markers is necessary to assess their potential applicability in marker-accelerated breeding (MAB) programs targeting low-P environments, which are especially important in WA where resource-poor farmers are expected to be the hardest hit by the approaching global P crisis.

Comparison of Phenotypic and Molecular Distances to Predict Heterosis and F1 Performance in Pearl Millet (*Pennisetum glaucum* L. (R.) Br.)

Gupta SK*[1], Nepolean T[1,2], Rai KN[1], Das RR[1], Ghouse SKC[1], Rathore A[1]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2] Indian Agricultural Research Institute, New Delhi, India
*E-mail: s.gupta@cgiar.org

Pearl millet is cultivated on about 27 million ha in Asia and Africa. India, the largest grower (about 9 m ha) of pearl millet cultivates its hybrids on about 6 million ha. This study aimed at determining the relationship between parental distance estimated from phenotypic traits or molecular markers with heterosis for grain and stover yield. 101 hybrid parents of diverse parentage were assessed for molecular diversity using 28-38 SSRs. These lines and their 51 hybrids grouped into two sets (43 lines and 22 hybrids in set-I; and 58 lines and 28 hybrids in set-II) were evaluated for grain and stover yield, and 7 phenotypic traits for 2 seasons at ICRISAT, Patancheru. Results showed that neither phenotypic nor molecular genetic distance was correlated to better parent heterosis or hybrid performance for both the sets of hybrids. Interestingly, the correlation between phenotypic and molecular distance was also very low (r=0.20). Phenotypic distance was highly significantly correlated with mid-parent heterosis for grain yield for Set-I (r=0.59, P<0.01) and for Set–II (r=0.50, P<0.01). Molecular distance was not significantly correlated with mid-parent heterosis for grain-yield, fresh stover yield, and dry stover yield for both the sets of hybrids. In conclusion, parental distances estimated from phenotypic or molecular diversity couldn't predict hybrid performance or better parent heterosis, while phenotypic traits could predict mid-parent heterosis for grain yield than estimated from molecular markers.

Fine Mapping of "*QTL-hotspot*" for Drought Component Traits in Chickpea

Jaganathan D[1,2], Kale SM[1], Ruperao P[3], Ramu P[4], Thudi M[1], Roorkiwal M[1], Kavi Kishor PB[2], Gaur PM[1], Singh NP[5], Chaturvedi SK[5], Venkatesh MS[6], Revanappa[6], Batley J[3], Edwards D[3,7], Sutton T[8], Varshney RK[1,9*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India,
[2]Osmania University, Hyderabad, India
[3]University of Queensland, Brisbane, Australia
[4] Cornell University, Ithaca, USA
[5]Indian Institute of Pulses Research (IIPR), Kanpur, India
[6]Indian Institute of Pulses Research (IIPR) - Regional research centre, Dharwad, India
[7]Australian Centre for Plant Functional Genomics (ACPFG), University of Queensland, Brisbane, Australia
[8]South Australian Research and Development Institute (SARDI), Urrbrae, Australia
[9]School of Plant Biology and the Institute of Agriculture, The University of Western Australia (UWA), Crawley, Australia
*E-mail: r.k.varshney@cgiar.org

A "*QTL-hotspot*" region for drought component traits was identified on CaLG04 using a RIL population (ICC 4958 × ICC 1882) in chickpea. This region spanned 29 cM on genetic map and 7 Mb on physical map. Genotyping-by-sequencing (GBS) method was used which further refined the region into 14 cM and ~3 Mb on genetic and physical map respectively. Additionally, whole genome re-sequencing of RILs identified 62,370 SNPs. Using these SNPs, recombination break points were determined by sliding window approach. A total of 1,610 bins were identified and used as molecular markers for mapping. Genetic map with 1,557 bins was used for QTL analysis. Detailed analysis of QTL results revealed two refined genomic regions within the "*QTL-hotspot*". Region I spans 0.23 cM on genetic map and 139.22 kb on physical map for 5 traits (100SDW, RLD, PHT, DC and POD), similarly region II spans 0.22 cM and 153.36 kb on genetic and physical maps respectively for two traits (SDW and RTR). In order to fine map these regions, a high resolution mapping population was developed by crossing a NIL^{+} line (introgression line with "*QTL-hotspot*" from ICC 4958) with ICC 1882 genetic background. Further F2 population with 3,818 lines was generated. KASPar assays were developed for 6 SNPs flanking and within the target regions. Genotyping analysis of F2 lines revealed 78 recombinants. Progeny testing will be carried out on the selected recombinants in F3 generation. These efforts are expected to narrow down the target region into few kb regions which can directly link to specific genes for the traits of interest.

Resources for Functional and Applied Genomics in Chickpea for Crop Improvement

Jain Mukesh

Functional and Applied Genomics Laboratory, National Institute of Plant Genome Research (NIPGR),
New Delhi – 110067, India
Email: mjain@nipgr.ac.in

The availability of genomic resources provides an opportunity for devising strategies for crop improvement by facilitating the scientific community towards understanding the molecular basis of various cellular processes and important agronomic traits. Chickpea is an important crop legume plant not only for its high nutritional value, but also for its ability to maintain soil fertility by fixing atmospheric nitrogen. The availability of limited genomic resources and very low levels of genetic diversity have been important constraints in chickpea improvement. We sequenced the transcriptomes of cultivated (*desi* and *kabuli*) and wild chickpea using next generation sequencing technologies and generated optimized assemblies to reveal the gene space. The comprehensive functional annotation identified genes involved in various cellular processes and transcription factor encoding genes. We performed global gene expression analysis also to identify genes expressed in tissue-specific manner. In addition, several genetic variations (simple sequence repeats and single nucleotide polymorphisms) among the cultivated and wild chickpea have been identified. Many of these variations were found to be present in the tissue-specific and transcription factor encoding transcripts. All these data have been integrated into the Chickpea Transcriptome Database (CTDB). We have analyzed the chickpea genome sequence also to reveal gene space, gene expression and genetic variations.

Recently, we analyzed the global transcriptome dynamics using RNA-seq to identify novel genes/ pathways involved in chickpea flower development and abiotic stress responses. Genome-wide discovery and differential regulation analysis of microRNAs from different tissues in chickpea has been performed via deep sequencing to gain insights into the regulatory aspects of various developmental processes. These genomic resources will surely facilitate research in various areas of functional and applied genomics in chickpea for crop improvement.

Prediction of Withanolide Heterosis using RNA Seq in *Withania somnifera*

Arpan, Gupta AK, Jhang T*

Department of Genetics and Plant Breeding
Central Institute for Medicinal and Aromatic Plants (CSIR)
Lucknow, India
*Email: t.jhang@cimap.res.in

Withania somnifera a tetraploid (2n=4x=48) pivotal medicinal plant of Indian Ayurveda. It is the chief source of withanolides and withanosides which can reverse the Alzheimers disease pathology and inhibit breast cancer cell growth, besides having diverse pharmacological potential for which it is in use as traditional medicine since 300 years. To meet the growing demands of pharmaceutical industries for bioactive withanolides through *in planta* production, withanolides-targeted breeding programme is being undertaken at CSIR-CIMAP.

For strategic introgression of metabolite QTLs, two diverse chemotypes -- a well-adapted, good root-quality, withaferrin A-rich recipient accession from Nagore, and a high withanolide A content, high biomass and biotic stress-tolerant donor accession collected from Patna -- were selected as potential parental stocks. Leaf transcriptome from the strand specific libraries were subjected to PE 100bp HiSeq 2000 Illumina sequencing and *de novo* assembled using Trinity. ~300 hybrids were generated. Heterosis has been observed for earliness, short height, good root quality, berry size along with calyx inflation, leaf length/breadth ratio, root length and content of withaferrin A, withanolide A, 12-deoxywithastramonolide, withanoside V, withanoside IV, withanone, total leaf alkaloids, and total root alkaloids in various recombinations. Here we report the unique gene present in either parent which might have complemented to answer for the presence of heterotic withanolide QTLs in *Withania somnifera* hybrids in the desirable combinations for *Withania* genetic improvement programme.

Genome Wide Profiling of Histone H3k4-Trimethylation in Barley Under Salt and Drought Stress Conditions

Kamboj A[1], Ziemann M[2], Bhave M[1*]

[1]Faculty of Science Engineering and Technology, Swinburne University of Technology, Hawthorn, Victoria, 3122, Australia.
[2]Baker IDI Heart and Diabetes Institute, 75 Commercial Road, Melbourne, Victoria 3004, Australia
*E-mail: mbhave@swin.edu.au

Histone modifications affect gene expression level. Several studies have shown that they may play key roles in regulating gene expression in plants under abiotic stress, but genome-wide surveys of such stress-related modifications are very limited, especially for crops. By using chromatin immune-precipitation (ChIP)-seq and mRNA-seq, we investigated the genome-wide distribution pattern of histone H3 lysine4 tri-methylation (H3K4me3) and the pattern's association with whole genome expression profiles of barley (*Hordeum vulgare* L.) under salt and drought stresses, the major and representative abiotic stresses. mRNA-Seq reads were able to align with 20,537 and 20,702 sequences in the International Barley Genome Sequencing Consortium (IBSC) et al. 2012) database for salt and drought stressed plants respectively. Furthermore, 19,015 and 19,005 genes were differentially H3K4me3-modified (H3K4M), under salt and drought stress conditions respectively. 7,816 and 7,792 genes were significantly identified only in mRNA-seq and 4,261 and 4,247 only in ChIP-seq under salt and drought stresses respectively. Differential H3K4 tri-methylation only affects a small proportion of stress-responsive genes, and the H3K4me3 modification level was significantly and positively correlated with transcript level only for a subset of genes showing changes both in modification and expression with salt (4322) and drought (4296) stresses. Of these genes, 51% and 50% genes have shown same direction of expression and H3K4 tri-methylation. Similar to rice, for the H3K4me3-regulated stress-related genes, the H3K4me3 modification level was mainly increased in genes with low expression and decreased in genes with high expression under abiotic stresses. The comprehensive data of H3K4me3 and gene expression profiles in barley under salt and drought stresses provide a useful resource for future epigenomic regulation studies in plants under abiotic stresses.

Quantitative Phenotyping of Cassava Brown Streak Disease Root Symptoms for QTL Detection

Kapinga FA[1*], Masumba E[2], Salum K[3], Mkamilo G[1], Kulembeka HP[3], Herselman L[4], Labuschgne MT[4], Kanju E[5], Muranaka S[6], Matsumoto R[6], Ferguson ME[7]

[1]Naliendele Agricultural Research Institute, Mtwara, Tanzania
[2]Sugar Research Institute, Kibaha, Tanzania
[3]Ukiriguru Agricultural Research Institute, Mwanza, Tanzania
[4]University of the Free State, Bloemfontein, South Africa
[5]International Institute of Tropical Agriculture (IITA), Dar-es-Salaam, Tanzania
[6]IITA, Ibadan
[7]IITA, Nairobi, Kenya
*Email: fakapinga@yahoo.com

Cassava (*Manihot esculenta* Crantz) is a crop which can potentially provide Africa with sufficient food despite prevailing climate changes. However, in southern, eastern and central Africa cassava brown streak disease (CBSD) can cause up to 100% yield loss. Breeding and use of resistant varieties is one of the methods of combating CBSD. This can be done more efficiently through the use of marker-assisted breeding. For this, quantitative trait loci (QTL) associated with CBSD resistance must be identified. This process is underway in Tanzania through genotyping and phenotyping of a biparental F_1 mapping population developed from crosses between NDL06/132 (resistant female) and AR37-80 (susceptible male). Accurate phenotyping is an important aspect of this process. Currently, the disease severity assessment is subjective, whereby severity is qualitatively categorized into classes ranging from 1 to 5 (no symptoms to severe symptoms).

An improved quantitative phenotyping methodology was developed whereby cassava root samples were sliced in a cross-sectional way using a root cutter designed to cut roots at equal lengths of 5 cm, to expose cross sectional areas. A digital camera was used to capture images of the exposed cross-sectional areas which were then processed using the software Image-J to determine a quantitative score of CBSD root necrosis. Data from this new phenotyping methodology based on imaging will be analyzed to identify QTL associated with CBSD tolerance in NDL06/132.

Salt Sensitivity of Chickpea is Determined by Sodium Toxicity

Khan HA[1,2*], Siddique KHM[1], Sutton T[2,3], Colmer TD[1]

[1]The University of Western Australia, Crawley, WA 6009, Australia
[2]The University of Adelaide, Waite Campus, Urrbrae, SA 5064, Australia
[3]South Australian Research and Development Institute, GPO Box 397 Adelaide, South Australia, 5001, Australia
*Email: hammad.khan@acpfg.com.au

Chickpea (*Cicer arietinum* L.) is sensitive to salinity, however, the responses of chickpea to the main components of salt stress (osmotic stress and Na^+ and/or Cl^- toxicity) were not known. This study dissected the responses to these components of salt stress in two chickpea genotypes. Sensitive (Rupali) and tolerant (Genesis836) genotypes were exposed to osmotic treatment, Na^+ or Cl^- only, or with NaCl at 0, 30 or 60 mM. Plants were grown for 42 days under treatments with six harvests (0, 4, 7, 14, 28 and 42 days of treatments) to measure growth, tissue ion concentrations and leaf gas-exchange. The osmotic treatments did not reduce growth of either genotype whereas the NaCl treatments severely reduced growth (Rupali more affected than Genesis836). Growth reduction was similar in Na^+ only and NaCl treated plants, whereas Cl^- treated plants did not differ from the controls. Both genotypes had similar shoot concentrations for each of the individual ions (Na^+, Cl^- or K^+) in each of the various treatments; shoot Na^+ concentrations were similar for plants with Na^+ only or NaCl. A negative correlation was found between shoot dry mass and shoot Na^+ concentration (r^2 = 0.88) whereas shoot Cl^- concentration had no correlation with shoot dry mass. Genesis836 achieved higher photosynthetic rate compared with Rupali at the same leaf Na^+ concentrations (~135 ± 10 mM). We conclude that salt sensitivity of chickpea is determined by Na^+ toxicity and two contrasting genotypes had similar Na^+ concentrations in leaves, but appear to differ in tissue tolerance.

Introgression of Stigma Exsertion Trait Into a Maintainer Rice Line IR79156B By Marker Assisted Backcross Breeding

Koradi P[1] , Singh AK[1], Priyadarshi R[1], Khandekar D[1], Shanti ML[1], Khera P[1, 2], Barthwal M[1, 3] Patil V[1, 4], Kemparaju KB[5], Subba Rao LV[5], Jayaramulu K[5], Madhav MS[5], Hariprasad AS[5], Ulaganathan K[6], Shenoy V[1,*]

[1]Barwale Foundation Research Centre, Hyderabad, India
[2]International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India
[3]Bayer Biosciences Pvt. Ltd., Hyderabad, India
[4]Mahindra and Mahindra Ltd., Agribusiness, Secunderabad, India
[5]Indian Institute of Rice Research, Hyderabad, India
[6]Centre for Plant Molecular Biology, Osmania University, India
*Email: vvshenoy123@gmail.com

For long, India's acreage under hybrid rice has been struggling to increase from 4% to more. Thus, to make hybrid rice technology practically feasible and adoptable, a strong system capable of reducing the commercial hybrid seed cost is required. One of the possible ways to achieve this would be to improve the outcrossing in rice CMS lines by increasing the overall stigma exsertion (SE) rate. The objective of the present study was to transfer SE trait from *indica* cultivar BF-16B (90% total SE) into IR79156B (46% total SE), a wild-abortive maintainer line of rice hybrid parent, via marker-assisted backcross breeding. Since, the reported markers failed to validate in our backcross population, phenotypic selection for SE trait was followed. Fourteen plants with high stigma exsertion, and desired phenotypic and genetic characteristics were selected in each generation (BC_1F_1, BC_2F_1, BC_3F_1). The selected plants were subjected to molecular profiling with 65 polymorphic SSR markers evenly distributed across the 12 chromosomes to identify plants with the highest level of genetic similarity with the recurrent parent. Only the final selected BC_3F_1 plants showing high SE were advanced to BC_3F_2 and BC_3F_3 generation through selfing. The improved IR56B line in BC_3F_3 generation showed an increase of 65-70% in SE trait, as compared to native IR79156B parent. Thus, the improved IR56B line would be utilized for developing A line with SE trait which would prove to be significantly useful in hybrid rice breeding programs.

Genome Wide Association Studies (GWAS) for Shoot Fly Resistance Component Traits and Stay-Green Traits on Sorghum Chromosome SBI-10

Usha kiranmayee KNS[1,2], Sharma HC[1], Kavi Kishor PB[2], Ramu P[3],Sivasubramani S[1], Munghate RS[1], Sakhale SA[1], Hash CT[4], Deshpande SP[1]*

[1]International Crop Research Institute for the Semi-Arid Tropics, Patancheru PO, Hyderabad, India
[2]Department of Genetics, Osmania University, Hyderabad, India
[3]Cornell University, Ithaca, New York, United States of America
[4]International Crop Research Institute for the Semi-Arid Tropics, Niamey, Niger.
*Email: s.deshpande@cgiar.org

The productivity of sorghum in semi-arid tropics is mainly affected by both biotic, i.e shoot fly stress; and abiotic, i.e drought stress. In order to dissect the genetic basics of shoot fly resistance (SFR) component traits and stay-green traits (stg) QTL mapping studies were conducted followed by development of a high-resolution cross - (RSG4008 × J2614). F2 homozygous double recombinants for favorable alleles on chromosome SBI-10 derived from a high-resolution cross were skim sequenced by Genotyping By Sequencing (GBS) approach. For shoot fly resistance and stay-green, the exact marker trait associations can be studied with the help of GWAS. Nearly 1500 SNPs were used along with two seasons of phenotypic data for glossiness (Gs), trichome density on adaxial (TDU), trichome density on abaxial (TDL) for shoot fly resistance; and days to 50% flowering (DAF), plant height (PlHt), grain dry weight per plot (GDW/plot), panicle harvest index (PHI), 100 grain mass (HGM (g)) and stay-green weekly scores (GLA (%) 15, 30, 45 days after flowering) for stay-green /drought tolerance. A total of 165 significant SNPs were identified for eight traits, of which 19 SNPs were common for TDU and TDL with p-value of 6.4×10^{-5} to 5.5×10^{-6} and phenotypic variance ranging from 45-48%. Thirteen SNPs for glossiness, 49 SNPs for yield-related traits, and 15 SNPs for agronomic traits were reported to be associated. These results provide insights into the genetic basis of shoot fly resistance and drought tolerance in sorghum chromosome SBI-10; and facilitate efficient marker assisted breeding of these traits.

Perturbation of Source-Sink Communication: A Stepping Stone for Increasing Sucrose Productivity in Sugarcane

Roopendra K[1], Chandra A[1*], Saxena S[2], Solomon S[1]

[1] Indian Institute of Sugarcane Research, Lucknow-226002, U.P., India
[2]Babasaheb Bhimrao Ambedkar University, Lucknow-226025, U.P., India
*Email: amaresh_chandra@rediffmail.com

Sugarcane is a C4 species, wherein storage of assimilate occurs at exceptionally high concentrations in the form of sucrose, with higher sucrose concentrations in the mature internodes and lesser accumulation in the younger internodes. Sugarcane is considered a unique source (leaf)–sink (culm parenchyma tissue) system, wherein the major storage tissue (culm), is also the growing stalk. The co-ordination between source activity and sink demand is crucial for plant growth and sugar accumulation. In addition to the sink demand for growth, respiration and storage, the import and immobilization of sucrose in vacuolar storage in culm parenchyma cells causes a high sink demand for sucrose. Also, the activity of various sugar signaling enzymes and expression of associated gene transcripts, is, perhaps, modified by sink demand. The concentration of sucrose is principally regulated by the cycle of degradation–synthesis of sucrose occurring in the culm.

Overall, limitation of source supply through partial shading or defoliation treatments have been found to result in increase in photosynthetic rates in the remaining source leaves, indicating that sugarcane leaves have a strong capacity for adapting to increased demand from the culm sink. This stands as evidence that there is scope to further the maximum limit of photosynthesis in leaves. Thus, perturbation of source-sink communication and study of the consequent changes can facilitate better understanding of the mechanism of sucrose accumulation in sink tissue and its regulation thereof, offering considerable scope for increasing the ceiling of sucrose concentration in the culm.

Introgression of Shoot Fly Resistance QTLs into Elite Sorghum Varieties using Marker Assisted Backcrossing (MABC)

Gorthy S[1,2], Deshpande SP[1], Sharma HC[1], Narasu ML[2], Ashok Kumar A[1,*]

[1]Research Program-Dryland Cereals, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, 502324. Telangana, India, [2]Jawaharlal Nehru Technological Institute, Hyderabad, Telangana , India
*Email: a.ashokkumar@cgiar.org

Sorghum is a staple food to more than 600 m people across Sub-Saharan Africa and South Asia. Shoot fly is the most damaging pest on sorghum, causing severe yield losses. Development of host plant resistance is the cheapest and sustainable method for managing shoot fly. Shoot fly resistance is a complex trait and number of QTLs controlling components of shoot fly resistance (leaf glossiness, presence of trichomes and plants with fewer shoot fly eggs) reported. They include four validated QTLs imparting shoot fly resistance (QTL A on sorghum chromosome SBI-10, QTL E on SBI-07, QTL G on SBI-10, and QTL J on SBI-05) governing leaf trichome density (QTL G), reduced oviposition & dead hearts incidence (QTL A and QTL E) and leaf glossiness (QTL G and QTL J). In this study we introgressed these four shoot fly resistance QTLs in to an elite sorghum variety SPV 1411(Parbhani Moti) and a popular B-line ICSB 29004. The F_1s were generated by emasculating florets of recurrent parents SPV-1411 and ICSB 29004 and crossing those with QTL donor lines (J2658 and J2698 = QTL A donors; J2714 and J2743 = QTL E donors; 2614-3 and J2614-5 = QTL G donors; and J2799 and J2834 = QTL J donors) in BT×623 background. Foreground selection with QTL linked SSR markers was employed in each backcross generation to select positive plants for crossing and selfing. Background selection using genome wide SSR markers is being employed to identify lines with maximum recurrent parent genome.

A set of 58 SSRs distributed across genomic region of our target QTLs on linkage groups SBI-01 (A), SBI-07 (E), SBI-10 (G) and SBI-05 (J) were tested for polymorphism between the donor lines (introgression lines with QTLs from IS 18551 in BTx623-background), and recurrent parents. Thirty three out of 58 SSRs were polymorphic and used for foreground selection across donor-recurrent parent combination for each QTL. The differences in allele size among parents varied between 3 base pairs (bp) to 100bp. These polymorphic markers were used for selecting true hybrids in F_1 and further backcross generations. The F_1 plants confirming the hybridity were backcrossed to their respective recurrent parents SPV1411 and ICSB 29004 to produce BC_1F_1 plants. Starting from BC_1F_1 till BC_2F_3, PCR based molecular markers were used to select individual segregants with heterozygote allele constitution for QTL flanking SSRs. The BC_2F_3 lines (based on QTL flanking marker genotype) were expected to be homozygous for individual QTL flanking SSR based on marker analysis and field screening trials.

We phenotyped 20 QTL introgression lines (BC_2F_3) and their respective elite recurrent and QTL donor parents along with shoot fly resistant and susceptible checks. Preliminary results showed significant differences among the introgression lines for all shoot fly resistance traits. The mean performance of some of the introgression lines in the study showed significantly low number of dead-hearts when compared to their recurrent parents. Introgression lines 6018-15, 5135-8 and 6018-5 containing QTL for reduced oviposition showed lesser percentage of plants with shoot fly eggs 10%, 22% and 25% less (respectively) compared to the recurrent parent carrying 39% shoot fly eggs. Similarly, the line 6026-13 carrying QTL for trait oviposition non-preference and dead hearts percentage, showed 5% shoot fly eggs and 10% shoot fly dead hearts compared to the recurrent parent ICSB 29004 showing 20% shoot fly dead hearts. All the entries carrying QTL for trait glossiness showed glossy character. These lines can be further validated and used in shoot fly resistance improvement programs and in commercialization.

Transcriptome-Wide Identification of Long Non-Coding RNAs during Leaf Rust Infection in Wheat

Kumar D [1], Adhikari M[1], Namrata[1], Singh D[2], Mukhopadhyay K[1], Kumar M[1*]

[1] Birla Institute of Technology, Mesra, Ranchi 835215, Jharkhand, India
[2] Eternal University, Baru Sahib 173001, Himachal Pradesh, India
*Email: manish@bitmesra.ac.in

Long non-coding RNAs (lncRNAs) are a large and diverse class of transcribed RNA molecules having a length of more than 200 nucleotides that do not encode proteins. Their expression is developmentally regulated and can be tissue- and cell-type specific. Therefore, transcriptome-wide identification of lncRNAs and expression profiling in response to leaf rust infection using mock and pathogen-inoculated resistant (HD2329+*Lr28*) and susceptible (HD2329) near-isogenic wheat plants was performed. **A** pipeline for detecting novel lncRNAs from *de novo* assembled transcriptome data was constructed. The possible partial transcripts and artefacts are filtered according to the quantified expression level. Novel lncRNAs are detected by further filtering known transcripts and those with high protein coding potential, using an ORF finder. We identified 951 novel lncRNA candidates, which have shorter transcript length, fewer exons, shorter putative open reading frame, compared with known protein-coding transcripts. After analyzing, 131, 537 and 283 differentially- expressed putative lncRNAs were identified that were common to all four libraries, susceptible mock and pathogen-inoculated; and resistance mock and pathogen-inoculated libraries respectively. On the basis of lncRNAs indentified in all libraries, their expression increased after pathogen inoculation in both susceptible and resistant near-isogenic wheat lines. Quantitative Real Time PCR was used to profile 11 highly differentially expressed lncRNAs identified from *de-novo* assembled sequence data. The spatio-temporal expression profiling at different time points of infection progression, validated the differential expression of lncRNAs between the isolines as well as in retort to pathogen infection.

Phenotyping for Seed Coat Resistance and Aflatoxin Production to *A. flavus* in Groundnut

Kumar N*, Rathnakumar AL, Jadon KS, Dagla MC, Ajay BC, Thirumalaisamy PP, Chikani BM

ICAR-Directorate of Groundnut Research, P.B.No.5, Ivnagar road, Junagadh – 362 001, Gujarat, India
*Email: narendra@nrcg.res.in

Groundnut (*Arachis hypogaea* L.) is an important oilseed as well as food crop and valued as a rich source of oil (48–50%) and protein (25–28%). Groundnut has a distinct position among the oilseeds as it can be consumed and utilized for edible oil and confectionery purposes. India has become the major exporter of groundnut but aflatoxin contamination is becoming a big obstacle in export. Thus a study was carried out to identify groundnut genotypes resistance to aflatoxin by *A. flavus* through *in vitro* seed and pod colonisation and aflatoxin production methods. A total 54 groundnut genotypes were studied for *in vitro* colonization by *A. flavus* at pod as well as kernel levels, using modified progressive 1- 4 scale and aflatoxin production (AFB1 in ppb) during post-rainy (summer) season of 2013. Seed infection among the genotypes ranged from 1.5 (PBS-18055) to 4.0 (TG37A) score on a 1-4 scale. Pod infection ranged from 1.0 (PBS-12066) to 2.8 (PBS-12167).

The aflatoxin content in kernel was in the range of 0 to 4 ppb and most of the genotypes were found to be aflatoxin-free in the kernel. This study revealed that two genotypes PBS-12195 and PBS-18055 had less than 2 score on 1- 4 scale for *in vitro* seed and pod colonisation and no aflatoxin production in the kernel. Hence, the experiment will be repeated in one more season to identify resistant genotypes for seed and pod infection and low aflatoxin production by *A. flavus*.

Introgression of Foliar Disease Resistance Using Synthetic Amphidiploids and Identification of Associated QTLs in Groundnut (*Arachis hypogaea* L.)

Kumari V[1]*, Gowda MVC[1], Tasiwal V[1], Bhat RS[1], Pandey MK[2], Varshney RK[2, 3]

[1]University of Agricultural Sciences (UAS), Dharwad 580 005, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[3]CGIAR Generation Challenge Programme (GCP), CIMMYT, Mexico DF, Mexico
*Email: varshagpb@gmail.com

In an attempt to broaden the genetic base and variability for late leaf spot (LLS) and rust resistance in groundnut, three introgression line (IL) populations, ICGS 76 × ISATGR 278-18 (IL1), DH 86 × ISATGR 278-18 (IL2) and DH 86 × ISATGR 5 (IL3) were developed by crossing disease-susceptible varieties with the resistant synthetic amphidiploids (ISATGR 278-18 and ISATGR 5) and backcrossing twice with the recurrent parents. In total, 164, 51 and 32 BC_2F_4 ILs constituted IL1, IL2 and IL3, respectively. Field evaluation of the ILs during *kharif* 2011, summer 2012 and *kharif* 2012 showed considerable variability and heritability for disease resistance, agronomic and productivity traits. Linkage mapping with 136 SSR markers in IL1 resulted in map of 1103.2 cM with 19 linkage groups and 8.62 cM inter-marker distance. Single marker analysis showed significant association of a few markers with R^2 ranging from 3.94% to 94.34% for LLS and 3.96% to 68.337% for rust. GM1954 was consistent across the populations for both the diseases. Composite interval QTL mapping identified 26 QTL for disease resistance, and 16 for agronomic and productivity traits. Major QTL consistent across seasons included GM1996-IPAHM103 (31.12%-67.45%), gi-4925-GM2144 (9.70%-14.99%) and TC6E01-GM1409 (9.84%-12.39%) for LLS, gi-4925-GM2144 (10.40%-16.52%), GM2009-GM2301 (7.88%-16.03%) and GM900-GM2082 (5.74%-11.04%) for rust and GM900-GM2082 (13.15%-24.89%) for test weight. The markers flanking the major QTL carried the favorable alleles contributed by ISATGR 278-18, indicating the utility of wild diploids. QTL and the markers identified here need to be validated before deployed for marker assisted selection.

NGS-QCbox and Raspberry For Parallel, Automated and Rapid Quality Control Analysis of Large-Scale Next Generation Sequencing (Illumina) Data

Katta AVSKM[1], Khan AW[1], Doddamani D[1], Varshney RK[1,2]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, Telangana, India
[2]School of Plant Biology and Institute of Agriculture,The University of Western Australia, Crawley, WA 6009, Perth, Australia
*Email: r.k.varshney@cgiar.org

Rapid popularity and adaptation of next generation sequencing approaches has generated huge volumes of data. High throughput platforms like Illumina HiSeq produce terabytes of raw data that requires quick processing. Quality control of the data is an important component prior to the downstream analyses. To address these issues, we have developed a quality control pipeline, NGS-QCbox that scales up to process hundreds or thousands of samples. Raspberry is an in-house tool developed in C language utilizing HTSlib (v1.0) (http://htslib.org) towards computing read/base level statistics. It can be used as standalone application and can process both compressed and uncompressed FASTQ format files. NGS-QCbox integrates Raspberry with other open-source tools for alignment (Bowtie2), SNP calling (SAMtools) and other utilities (bedtools) towards analyzing raw next generation sequencing (NGS) data at higher efficiency and in high-throughput manner. The pipeline implements batch processing of jobs using Bpipe (https://github.com/ssadedin/bpipe) in parallel and internally, a fine grained task parallelization utilizing openmpi. It reports read and base statistics along with genome coverage and variants in a user friendly format. The pipeline developed presents a simple menu driven interface and can be used in either quick or complete mode. In addition, the pipeline in quick mode outperforms in speed and memory required against other similar existing QC pipeline/tools. The NGS-QCbox pipeline, Raspberry tool and associated scripts are made available at the URL https://github.com/CEG-ICRISAT/NGS-QCbox and https://github.com/CEG-ICRISAT/Raspberry for rapid quality control analysis of large-scale next generation sequencing (Illumina) data.

Molecular Drought Adaptation Nature of Afghan Wheat Landraces

Manickavelu A[1*], Marta L[2], Amin E[3], Ban T[1]

[1] Kihara Institute for Bio. Res., Yokohama City University, Yokohama, Japan
[2] CIMMYT-Turkey, Ankara, Turkey
[3] Arid-Land Research Centre, Tottori University, Japan
* Email: manicks@yokohama-cu.ac.jp

Wheat (*Triticum aestivum* L.) is an important cereal crop feeding most parts of world. The current and anticipated climatic vulnerability requires finding new genetic material for wheat improvement. The Afghan wheat landraces stored in Japan is the base of this study where the germplasm was genomically characterized (Genotyping By Sequencing) and thoroughly screened under drought conditions (both natural and artificial). Various characters were recorded and statistically analysed. A Genome wide association mapping (GWAS) approach was attempted and the identified markers were linked with traits of interest.

The sequence of linked markers was analysed *in silico* and possible functions of the characters were found. Selected lines were further re-screened under growth chambers and confirmed for possible adaptive mechanism. The results of association mapping, linked markers, molecular function and new direction of research will be presented.

Genetic Diversity in East African Finger Millet (*Eleusine coracana (L.)* Gaertn) Landraces Based on SSR Markers and Some Qualitative Traits

Manyasa EO*, Tongoona P, Shanahan P, Mgonja MA, de Villiers S

*Email: e.manyasa@cgiar.org

Genetic diversity in 340 finger millet accessions from Kenya, Tanzania and Uganda and 15 minicore accessions was assessed using 23 SSR markers and five qualitative traits. Nineteen markers were polymorphic with mean PIC value of 0.606 and a range of 0.035 to 0.889 with allele size range of 148-478. A total of 195 alleles were detected (range of 3-23 and average of 10.3 alleles per locus) with 57.7% being rare and 17.4% being private. Differentiation between the three countries' accessions was weak with most of the genetic variability explained within countries and sub-regions than among countries and sub-regions. The highest genetic diversity was observed in Kenyan accessions (0.638±0.283) and the least in Ugandan accessions (0.583±0.264). The widest differentiations based on Wright's fixation index were between Ugandan and Tanzanian accessions (F_{ST} = 0.117: P<0.001). There was no association between the morphological traits assessed and the genetic classes observed. The low variability between the countries could be attributed to a shared gene pool since the crop originated from the east African region. Farmers' selection for adaptation and end use could have contributed to the high diversity within countries. Concerted efforts need to be made to characterize the large germplasm stocks in East Africa for its effective conservation and utilization. Lack of representation of the three countries' accessions in all global minicore diversity clusters points to the need to explore the east African germplasm to identify the diversity not earlier captured to be included in the global repository.

Introgression Lines with Improved Resistance to Late Leaf Spot and Rust in Peanut

Paratwagh SA[1], Madhumitha DV[1], Sukruth M[1], Chougale DB[1], Varshakumari[1], Motagi BN[1, 2*], Gowda MVC[1], Bhat RS[1]

[1]College of Agriculture, University of Agricultural Sciences, Dharwad-580005, India
[2]ICRISAT, Kano, Nigeria
*E-mail: b.n.motagi@cgiar.org

In an effort to simultaneously transfer and map the genomic regions governing resistance to late leaf spot (LLS) and rust in peanut, two susceptible varieties (ICGS 76 and DH 86) were crossed to two resistant synthetic tetraploids; an amphidiploid, ISATGR 278-18 (*Arachis duranensis* × *Arachis batizocoi*) and an autotetraploid, ISATGR 5B (*Arachis magna* × *Arachis batizocoi*). Two cycles of backcrossing with the recurrent parents resulted in the development of a large number of introgression lines (ILs). They (BC_2F_6 and BC_2F_7) were evaluated during the rainy season of 2013 and 2014. ILs differed significantly for LLS and rust resistance, and productivity traits. Twenty seven introgression lines superior over ICGS 76, and three ILs superior over DH 86 for pod yield were selected from respective crosses. Many of them were highly resistant to both LLS and rust. Majority of them carried resistant allele at marker loci linked to LLS and rust. A few ILs also combined high test weight, shelling percentage and sound mature kernel percentage. Of these introgression lines, eleven were also superior over GPBD 4, a national check variety. These genetic resources can be of immense use in peanut breeding or for commercialization.

Transcriptome-Wide Detection of MicroRNAs and Targets in Wheat (*Triticum aestivum* L.): Elucidating their Role during Leaf Rust Infection

Kumar D [1], Singh D[2], Kumar M[1], Mukhopadhyay K[1*]

[1] Birla Institute of Technology, Mesra, Ranchi 835215, Jharkhand, India
[2] Eternal University, Baru Sahib 173001, Himachal Pradesh, India
*Email: kmukhopadhyay@bitmesra.ac.in

The major threat to wheat production has been the rust epidemics. The present study was targeted towards identification and functional characterizations of micro(mi)RNAs of wheat in response to leaf rust ingression to decipher their roles in disease development. Recent studies indicate involvement of miRNAs in plant development, growth and response to biotic and abiotic stresses, adaptive responses, metabolism, and signal transduction. Therefore, transcriptome-wide identification of miRNAs and their expression profiling in response to leaf rust infection using mock- and pathogen-inoculated resistant (HD2329+*Lr24*) and susceptible (HD2329) near-isogenic wheat plants was performed. A total of 1056 mature miRNAs were identified, of which 497 were conserved, and 559 were novel. The pathogen-inoculated resistant plants manifested more miRNAs compared to the pathogen-infected susceptible plants. It was also noted that the miRNA counts increased in susceptible isoline due to leaf rust infection; conversely, the counts decreased in the resistant isoline in response to pathogenesis illustrating precise spatial tuning of miRNAs during compatible and incompatible interaction. Quantitative Real Time PCR was used to profile 10 highly differentially expressed miRNAs obtained from high throughput sequencing data. The spatio-temporal profiling validated the differential expression of miRNAs between the isolines, as well as in retort to pathogen infection. Degradome sequencing predicted 701 target genes. The identified targets were associated with development, metabolism, defense response, signal transduction and transcriptional regulation. It was found that the target-specific identified miRNAs also expressed differentially among mock and pathogen inoculated susceptible and resistant plants.

Phenotyping and Validation of SCAR Markers for *Fusarium* Wilt and Sterility Mosaic Disease in Minicore Collections of Pigeonpea (*Cajanus cajan* L)

Muniswamy S*[1], Lokesha R[2], Dharmaraj PS[1], Fakrudin B[3], Kantaraju V[4], Diwan JR[2]

[1]Agricultural Research Station, (ARS) Gulbarga-585 101, Karnataka, India
[2]College of Agriculture, UAS, Raichur-584 102, Karnataka, India
[3] College of Horticulture, UHS, Bagalkot, Karnataka, India
[4] Krishi Vigyan Kendra, Gangavati, Karnataka, India
*Email: muniswamygpb@gmail.com

Fusarium wilt and sterility mosaic disease (SMD) are major bottlenecks in pigeonpea. Hence, a study was undertaken to screen 191 minicore collections along with five check varieties, which were obtained from the International Crop Research Institute for Semi Arid Tropics (ICRISAT) Telangana, IIPR, Kanpur and local collection from Gulbarga district. *Fusarium udam* pathogen load of 4.5 x 10^3 Cfu/gm of soil was maintained in the wilt sick plot of ARS, Gulbarga. SMD screening was carried out at ARS, Bidar, Karnataka. All the genotypes were sown during *kharif* (summer) 2012-13 and 2013-14, and a row length of 4 metres each was maintained with spacing of 75 cm and 10 cm between the rows and plants respectively. Two years of field screening for wilt yielded 11 resistant genotypes *viz*.,ICP-8793, GRG-811, GRG-333, BWR-153, ICP-13304, ICP-11320,GRG-2009, TS-3R (Ch), WRP-1 (Ch), ICPL-87119 (Ch) and ICP-8863 (Ch). Further, the genotypes ICP-8793, GRG-2009, ICP-11320, GRG-811 and GRG-333 were wilt-resistant and high-yielding as indicated by their *per se* performance. A total of 69 genotypes showed moderate resistance to wilt reaction. SMD screening results revealed four resistant genotypes *viz.,* Bahar, ICP-7035, ICP-11910 and Raja. The genotype Bahar was asymptomatic for SMD. These genotypes serve as donor parent for resistant variety development or contrasting parent in developing mapping population.

Validation of Sequence Characterised Amplified Region (SCAR) markers indicated that SCAR-N-18 had strong association with sterility mosaic disease, as indicated by a significant Kruskal test co-efficient (HC=33.01 p=0.0001). Whereas, SCAR-704 exhibited non significant test co-efficient (HC=3.61 p=0.112), indicating less association of the marker with *Fusarium* wilt.

Identification of Associated Markers for Aflatoxin Contamination through Genome-wide Association Studies in Groundnut (*Arachis hypogaea* L.)

Nayak SN[1], Hamidou F[2], Rathore A[1], Pandey MK[1], Das RR[1], Upadhyaya HD[1], Vadez V[1], Sudini HK[1], Desmae H[3], Ozias-Akins P[4], Guo B[5], Varshney RK[1,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey, Niger
[3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Bamako, Mali
[4]The University of Georgia (UGA), Tifton, USA
[5]CPMRU, USDA-ARS, Tifton, USA
*Email: r.k.varshney@cgiar.org

Groundnut is considered as the major protein source for the rural poor especially in sub-Saharan Africa. The cause of concern for its consumption comes with its susceptibility to cancer causing aflatoxin contamination caused by fungi *Aspergillus flavus* and *A. parasiticus*. Aflatoxin contamination is more prevalent under rainfed conditions making produce unfit for human and animal consumption, affecting the international trade adversely. In order to address the problem of aflatoxin contamination, the global 'reference set' comprising of 300 diverse genotypes was screened for aflatoxin contamination in four seasons at different temperature regimes namely, two moderate temperature (rainy season) and two high temperature (dry season) experiments under well-watered and water stress conditions at Niger. The genotypic data (154 SSR markers and 4,567 polymorphic DArT markers) and phenotyping data on aflatoxin contamination were generated on 'reference set'. After considering the population structure, marker-trait association (MTA) was carried out using genome association prediction integrated tool (GAPIT). Genome-wide association analysis identified a total of 12 significant marker-trait associations involving five microsatellite markers and seven DArT markers at p-value < 0.01. The resistant cultivars identified can be used to generate genetic resources to combat aflatoxin contamination while the markers associated can aid in marker-assisted breeding to develop improved varieties resistant to aflatoxin contamination.

A New QTL Controlling Plant Height in Bread Wheat (*Triticum aestivum* L.)

Nezhad KZ[1,5], Weber WE[2], Khlestkina E[1,3], Roder MS[1], Sharma S[1,4], Lohwasser U[1], Borner A[1]

[1]Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstrasse 3, D-06466 Gatersleben, Germany
[2]Institute of Agricultural and Nutritional Sciences, Martin-Luther-Universität, Halle-Wittenberg, Julius-Kühn-Str. 25, D-06099 Halle, Germany
[3]Institute of Cytology and Genetics, Siberian Branch, Russian Academy of Sciences, Lavrentjeva Ave. 10, Novosibirsk 630090, Russia.
[4]Department of Fingerprinting, College of Biotechnology, SVBPUA&T, Modipuram; Meerut, India
[5]Department of Plant Breeding and Biotechnology, Faculty of Plant Production, Gorgan University of Agricultural Sciences and Natural Resources, Postcode 49138-15739, Gorgan, Golestan, Iran
Email: khalil1381@yahoo.com

Plant height is a complex trait and is inherited quantitatively. The present study was conducted to identify genes determining this trait in bread wheat through Quantitative Trait Loci (QTLs) analysis. QTL study was performed using 133 $F_{2:3}$ families and a SSR-based genetic linkage map derived from an intraspecific cross between HTRI 11712 and HTRI 105, two winter wheat accessions from Pakistan and Sweden, respectively. Phenotypic evaluation was performed through two experiments under field and greenhouse conditions at IPK-Gatersleben. QTL analysis using composite interval mapping revealed seven QTLs distributed over seven chromosomes of which three were repeated on both experiments as well as based on the mean of the two experiments. Current study detected a new QTL (*QPhe.ipk-5B*) on the long arm of chromosome 5B near to centromere which is reported for the first time in this study and also revealed six QTLs which were reported previously by other authors.

Pigeonpea Improvement in Eastern and Southern Africa through an Effective use of Unique Local Germplasm

Ganga Rao NVPR*, Siambi M, Lyimo S, Kananaji GAD, Amane M, Kimurto P, Obong Y, Odeny D, Salim S, Sameerkumar CV, Upadhyaya HD, Saxena R, Varshney RK

International Crops Research Institute for the Semi-Arid Tropics, P O Box 39063, Nairobi, Kenya
*Email: n.gangarao@cgiar.org

Eastern and Southern Africa (ESA) is the secondary centre of diversity for pigeonpea. At present, pigeonpea area and production in ESA is about 1 million ha and 700,000 t, respectively. During the last fifteen years, area and production in ESA have increased dramatically by 92% and 95%, respectively. Tanzania and Malawi are showcasing a path to success that guides other regional countries to follow. Pigeonpea is the crop of smallholder farmers, about 5-7 million families growing and depending on pigeonpea sub-sector through its multiple benefits to cropping systems, fuel wood supply, source of cash, food and nutritional security. Pigeonpea improvement in ESA started in 1992 however, major impetus came in last 15 years and during this period 19 high yielding varieties were released that led to productivity gains, and the highest productivity recorded was in Malawi with 1300 kg/ha. The major breeding thrust was on high grain yield, inter-cropping compatibility, photo-period insensitivity, grain quality, resistance and/or tolerance to *Fusarium* wilt and *Helicoverpa* pod borer and resilience to climate change. Pigeonpea improvement in ESA, is mostly relies on native germplasm. ICRAISAT's global and regional genebanks holding about 1200 unique germplasm accessions collected from the ESA region. Pigeonpea, being an often-cross pollinated crop, it is more dynamic in genetic diversity and efforts are being made to capture this through germplasm gap analysis and followed by germplasm collection. Pigeonpea germplasm/elite lines derived through hybridization program in ESA have unique traits like tolerance to *Fusarium* wilt, tolerance to pests and consumer preferred grain traits.

Towards Identification of Genomic Regions Associated with Seed Protein Content in Pigeonpea (*Cajanus cajan* (L.) Millsp.)

Obala J [1,2], Saxena RK [1], Kumar V[1], Singh VK[1], Khan AW[1], Kale SM[1], Tongoona P[2], Sameerkumar CV[1], Varshney RK[1,3,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]School of Agricultural, Earth and Environmental Sciences, University of KwaZulu-Natal, Scottsville 3209, South Africa
[3]School of Plant Biology and Institute of Agriculture, The University of Western Australia, Crawley, WA, Australia
*E-mail: r.k.varshney@cgiar.org

Pigeonpea is an important source of protein to the vegetarian and poor families around the globe. Despite the importance of seed protein content in pigeonpea, very little is known about the genes or genomic segments controlling this trait. With an objective to reveal the genetics and identify molecular markers associated with seed protein content, we have developed segregating mapping populations. As the first step towards the development of mapping populations a set of 24 diverse pigeonpea genotypes were evaluated for total seed protein content using a Skalar Autonalazer. Genotypes showed highly significant differences ($P < 0.001$) in seed protein content ranging from 18% to 28%. Based on the contrast in total seed protein content of the parental genotypes, five crossing combinations were selected to develop mapping populations. The populations are being evaluated under field conditions at ICRISAT, India. Two parents and 188 F_2 individuals per population are being genotyped-by-sequencing, and will also be phenotyped for total seed protein content. Genotyping data together with the phenotyping data will be used to identify marker-trait associations through quantitative trait loci (QTL) analysis. In parallel, through the use of comparative genomics and whole genome re-sequencing approaches, we have identified putative candidate SNPs associated with protein content in pigeonpea. Identified markers through above-mentioned approaches will be used in genomics-assisted breeding for seed protein content in pigeonpea.

Screening for Drought Tolerance in Finger Millet Germplasm

Ojulong H*, Manyasa E, Sheunda P, Letayo F, Mgonja F

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Nairobi, Kenya
*Email: h.ojulong@cgiar.org

Drought is the most limiting abiotic stress in finger millet production. Finger millet is believed to have special mechanisms for drought resistance and some varieties are believed to possess this; there is a need to explore more germplasm/varieties to discover their drought resistance and also study the mechanisms of the resistance. A kit of 29 promising drought tolerant varieties selected from the previous drought trials and an improved drought tolerant check, U15 were constituted into a regional drought trial. The trials were established at KALRO-Kiboko, Kenya and DRD-Miwaleni, Tanzania during the 2013 short rains (2013SR) and 2014 long rains (2014LR) and agronomic data taken. Across locations fourteen varieties had days to 50% flowering (DAP) lower than improved check, U15 (62days). All except two varieties had above average agronomic scores (≤ 3.0). Eight varieties yielded better than the improved check (2.3 t/ha). Combined analysis revealed genotype to be highly significant for all the traits. Location was highly significant for DAF, plant height and grain yield and significant ($P<0.05$) for number of tillers. Highly significant interaction between Genotype and Location (G x L) was observed in plant height, days to flowering and number of tillers, with grain yield being significant ($P<0.05$). Drought tolerance lines are taken as those that yield relatively well when water is scarce (Fleury *et al*. 2010). Based on that five accessions; IE6072, IE2183, IE2957 IE501 and IE3547 were selected for drought tolerance; and they are being crossed to farmer preferred varieties to develop populations for identifying molecular markers.

SSR Markers Linked with *Alectra vogelii* Resistance in Cowpea [*Vigna unguiculata* (L.) Walp]

Omoigui LO[1],*, Ugba MS[1], Bello LL[1], Gowda BS[2], Timlo MP[2], Motagi BN[3]

[1]Department of Plant Breeding and Seed Science, College of Agronomy, University of Agriculture, P.M.B. 2373, Makurdi, Nigeria
[2]Department of Biology, University of Virginia, Charlottesville, Virginia 22903, U.S.A.
[3]International Crop Research for the Semi-Arid Tropics (ICRISAT), Kano, Nigeria
*Email: luckyomoigui@gmail.com

Cowpea [*Vigna unguiculata* (L.) Walp.] is an important food legume grown in tropical and subtropical regions of the world, primarily in Sub-Saharan Africa. Despite the importance of cowpea, yield on farmers' field is still low due to variety of biotic and abiotic stresses that constrain its production. Among the biotic constraints, the parasitic flowering plant, *Alectra vogelii* (Benth.) is one of the more formidable limitations to cowpea production in the dry Savannas of West and Central Africa, a region which accounts for over 64 % of world cowpea production. Several control measures have been suggested for the control of the parasite. These include: cultural practices, application of ethylene chemicals, and host plant resistance. Among these control measures, the use of resistance cultivars appears to be the most attractive option to the resource poor farmers in sub-Saharan Africa Breeding resistance cultivars would be facilitated by marker-assisted selection (MAS). The objective of this study was to identify molecular markers tightly linked to *Alectra* resistance gene that would be useful in MAS in breeding cowpea for resistance to *Alectra vogelii*. F_2 population of a single cross, Banjar (susceptible parent) × B301 (resistant parent) was screened for reaction to *Alectra* using pot culture technique. DNA was extracted from parental genotypes and F_2 lines from young leaves of plant at 14 days after planting using FTA® PlantSaver cards. 50 SSR cowpea, 40 SSR rice bean and 50 SSR asparagus bean primers, previously reported to give amplification products in cowpea, were used to screen DNA from B301 and Banjar for polymorphism. Of the 140 primers screened 20 primers were polymorphic between B301 and Banjar and these were used in the technique of BSA performed with DNA bulks of highly resistant and highly susceptible F_2 lines to select those that co-segregate with the resistant gene. Two of the markers (RB16 from rice bean and CLM0356 from asparagus bean) were found to be consistently associated with the resistance gene. The utility of these two markers were validated using 150 F_2 lines for marker segregation and association analysis. Similarity index (SI) revealed that these markers were closely linked (90.23%) with *Alectra* resistance gene. Cluster analysis as depicted by dendogram also showed a tight association (>0.75) between these markers, suggesting that these markers can be explored in MAS targeting breeding for *Alectra* resistance in cowpea.

In silico Study on Prediction of miRNAs and their Related SNPs in *Arachis hypogaea* L.

Kumari D, Kumari S, Ram MK, Kumari A, Pandey DM*

Birla institute of Technology, Mesra, Ranchi-835215, Jharkhand, India
*Email: dmpandey@bitmesra.ac.in

MicroRNAs (miRNAs) are a novel growing family of endogenous, small, non-coding, single-stranded RNA molecules which regulate gene expression at the post-transcriptional level. High conservation of miRNAs in plants provides the foundation for identification of new miRNAs in other plant species through homology alignment. Here, previously known and unique miRNA sequences of other plants miRNA are subjected to BLAST against the Expressed Sequence Tag (EST) database of *Arachis hypogaea*, and according to a series of filtering criteria, two miRNAs showing similarities with other plant species were predicted. Our study also includes the prediction of 26 SNPs associated with previously known miRNA sequences of peanuts. Overall, our findings lay the foundation for further researches of miRNAs function in *A. hypogaea.*

Ridge Regression-BLUP and Bayesian LASSO Identified as the Appropriate Genomic Selection (GS) Models for Predicting Genomic values in Groundnut (*Arachis hypogaea* L.) GS Breeding

Pandey MK[1], Rathore A[1], Das RR[1], Khera P[1], Upadhyaya HD[1], Jannink J-L[2], Hickey JM[3], Varshney RK[1,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Cornell University, Ithaca, USA
[3]The Roslin Institute, University of Edinburgh, Midlothian, Scotland, UK
*Email: r.k.varshney@cgiar.org

Genomic selection (GS) has emerged as the most potential modern breeding approach which can facilitate development of improved cultivars with increased yield and promises to improve other such complex traits. The main strength of GS is that it can capture several small-effect genetic factors and can also improve multiple traits simultaneously. With an objective to deploy GS breeding in groundnut, the global 'minicore collection' with 184 genotypes was phenotyped for three important agronomic traits (days to flowering, seed weight and pod yield) and genotyped with 15,360 diversity array technology (DArT) features. The prediction of genomic values with better accuracy is the key to success in GS breeding. Phenotypic data analysis revealed lowest coefficient of variation, genetic variance, genotypic coefficient of variation for days to flowering followed by seed weight and pod yield. In contrast, the heritability was found highest for days to flowering (78.85%) followed by seed weight (75.46%) and pod yield (62.53%). Phenotypic data analysis together with genotypic data (2,356 polymorphic DArT markers) using six GS models showed higher cross-validation values for days to flowering than seed weight and pod yield. Ridge Regression-BLUP and Bayesian LASSO provided better correlation and cross-validation estimates as compared to Random Forest Regression, Kinship GAUSS, BayesCπ and BayesB. In summary, the Ridge Regression-BLUP and Bayesian LASSO performed better for high heritable (days to flowering and seed weight) as well as moderate heritable (pod yield) traits. The above results suggest that these two best performing GS models may be used for predicting genomic values in groundnut GS breeding.

Development of Nested Association Mapping (NAM) Population in Pigeonpea (*Cajanus cajan* L. Millsp.)

Parupalli S[1,3], Saxena RK [1], Singh VK[1], Vechalapu S[1], Kumar V [1], Samerkumar CV [1], Kavi Kishor PB[3], Varshney RK[1, 2,*]

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

To overcome the limitations associated with linkage mapping and association studies, a family based mapping approach is being used in pigeonpea. In this context, nested association mapping population (NAM) is being developed, in which Asha (ICPL 87119) as nested parent was crossed with 10 diverse founder parents (MN-1, ICP 7035, ICP 7263, ICP 8863, ICPL 87, ICP 28, ICPL 88039, ICPL 85063, HPL 24 and ICPL 85010). As a result, a total of 10 different F_1 combinations were generated which were further selfed in controlled conditions to develop 10 F_2 mapping populations or NAM-F_2. NAM-F_2 population has been genotyped using genotyping-by-sequencing (GBS) approach whereas, NAM-$F_{2:3}$s will be phenotyped for FW and SMD resistance in disease nursery. Disease phenotyping data along with genotyping data will be used for the identification of marker traits associations (MTA), which would ultimately lead to the development of genomics assisted breeding driven FW and SMD resistant pigeonpea varities/ parental lines.

Enhanced Resistance to Foliar Fungal Diseases and Improved Oil Quality in Peanut Using MABC Approach

Janila P[1*], Pandey MK[1], Variath MT[1], Manohar SS[1], Shasidhar Y[1], Radhakrishnan, T[2], Sudini HK[1], Rathnakumar AL[2], Manivannan N[3], Dobariya KL[4], Vasanthi R[5], Upadhyaya HD[1], Nagesh P[1], Nigam SN[1], Varshney RK[1],

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
[2]Directorate of Groundnut Research (DGR), Junagadh, Gujarat
[3]Tamil Nadu Agricultural University (TNAU), Coimbatore
[4]Junagadh Agricultural University (JAU), Junagadh
[5]Acharya N G Ranga Agricultural University (ANGRAU), Tirupathi,

*E-mail: p.janila@cgiar.org

Peanut varieties with resistance to foliar fungal diseases and improved oil quality can meet farmer's need and industry demand. Foliar fungal diseases cause 15-20% of peanut pod yield losses in Asia and Africa and it is possible to increase pod and haulm yield and quality by growing disease resistant varieties. Enhanced oleic acid content of oil has benefits to consumer's health and processing industry. Disease resistant introgression lines in the background of three popular varieties were derived using marker assisted backcrossing (MABC) approach. Introgression lines recorded a pod yield increase of 56-96% over their respective recurrent parents. Combining foliar fungal disease resistance with early maturity was the most significant outcome of MABC. Following screening of these lines in disease hot spots, multilocation trials are planned in 2015. Gene pyramiding was initiated to improve resistance to rust and late leaf spot diseases and oil quality. Drought tolerant genotypes are used as recurrent parents. The oleic to linoleic acid ratio (O/L) in normal peanut is 2-4, which can go >20 in case of *FAD* mutants. *FADA* and *FADB* mutant alleles were selected using allele specific and cleaved amplified polymorphic sequence (CAPS) markers. Phenotyping for O/L ratio was done using near infrared reflectance spectroscopy and gas chromatography, and superior performing progenies with O/L ratio (8 to >20) were selected for preliminary yield trials. Lines homozygous for both *FADA* and *FADB* mutation had relatively higher O/L ratio than the lines that are homozygotes to one or either of the alleles.

Pigeonpea Transcriptome Expression Analysis for the Discovery of New Genes Implicated in *Fusarium* Wilt Resistance

Patil BR[1]*, Jaggal L[1], Thimmaraju[1], Nethravathi K H[1], Lokesh H[1], Saxena RK[2], Naik PM[1], Dodamani S[1], Rajendra B[1],

[1]University of Agricultural Sciences, Dharwad, 580 005, Karnataka, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*Email: patilbhuvaneshwara@gmail.com

Pigeonpea is a major legume crop of rain-fed agriculture in the semi-arid tropics. In recent years, a novel, high-throughput, deep-sequencing transcriptome analysis, termed RNA-seq, has made it possible to efficiently generate large-scale expressed sequence tag (EST) libraries which improved the speed of gene discovery. Though genomic resourcesziz., RNA seq analysis is available, the molecular mechanism of *Fusarium* wilt resistance is not well understood. Therefore, an effort was made to screen and characterize a mini core collection set during the 2010 *kharif* (summer crop) season a in wilt sick plot at the Agricultural Research Station (ARS), Gulbarga, with ICP2376 as a susceptible check. The results revealed that the accessions ICP348, ICP1071, ICP2577, ICP3451, ICP3576, ICP4575 were resistant, while ICP14368, ICP14801, ICP16309 and ICP2376 were susceptible to *Fusarium* wilt. The present investigation will subject two contrasting genotypes for their resistance against *Fusarium* wilt, and carry out the RNA-Seq analysis. This new technology makes it possible to identify exons and introns and helps to understand the complexity of eukaryotic transcriptome. RNA-Seq enables identification of transcription initiation sites (TSS's) and new splicing variants, permitting precise quantitative determination of exon, splicing isoform expression and also variation analysis such as SNP, Indels, mutations etc. The present study permits to employ an SNP marker as a Marker Assisted Selection (MAS) strategy or isolate, characterize and clone the genes which impart resistance against *Fusarium* wilt upon transformation in a suitable genotype

Photo and Thermo Insensitive Super Early Maturing Pigeonpea [(*Cajanus cajan* (L.) Millspaugh]: Prospectus and Opportunities

Sameerkumar CV[1*], Singh IP[2], Patil SB[1], Hingane AJ[1], Mula MG[1], Kumar RV[1], Ganga Rao NVPR[1], Saxena RK[1], Singh VK[1], Lekha P[1], Sinha P[1], Vinay Kumar[1], NageshKumar MV[3], Sudhakar C[3], Varshney RK[1]

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

Pigeonpea is an important food legume of the semi-arid tropics and sub-tropical regions. It is rich in protein content and plays a crucial role in the food and nutritional security of mostly vegetarian population of India. Photo and thermos sensitivity of this crop restricted its expansion to wider latitudes and altitudes. Considering this, a breeding program initiated at ICRISAT in 2006 to develop super-early maturing (< 100 days) pigeonpea lines. This resulted in very stable photo and thermo insensitive lines in determinate (ICPL 20340, ICPL 20338, ICPL 11255) and non-determinate group (ICPL 20325, ICPL 20326, ICPL 11301). These lines provide number of opportunities like pigeonpea–wheat cropping system since pigeonpea matures by 100 days provides time to prepare the land for the following wheat crop which is not possible with traditional medium duration varieties. It escapes diseases, drought, and pod borer attacks if planted early in June and harvested before those stresses occur. Introduction of super-early pigeonpea in rice fallows not only generates additional income but also improve soil health and productivity. Due to its shorter growth period, it saves irrigation water, promote long-term sustainability of agriculture, and improve human nutrition. Other advantages of having super-early materials for breeding and genetic analysis purposes include faster generation turnover. Mapping populations suitable to study the genetics of biotic and abiotic stresses could also be developed faster (< 2 years to get recombinant inbred lines); however, a prerequisite would be to have contrasting parents for the traits of interest in the super-early maturity group.

Identification of Quantitative Trait Loci Associated with Iron Absorption Efficiency in Groundnut (*Arachis Hypogaea* L.)

Pattanashetti SK[1,2], Pandey MK[1], Naidu G[2], Boodi IH[2], Shasidhar Y[1], Singh OK[2], Biradar BD[2], Vishwakarma MK[1], Upadhyaya HD[1], Vadez V[1], Varshney RK[1,*]

[1]International Crops Research Institute for the Semi-Arid tropics (ICRISAT), Hyderabad, India
[2]University of Agricultural Sciences (UAS), Dharwad, India
*Email: r.k.varshney@cgiar.org

Iron deficiency chlorosis is mostly prevalent in major groundnut growing states of India including Maharashtra, parts of Rajasthan, Tamil Nadu and Karnataka causing considerable yield reduction. Alleviation of chlorosis through soil/foliar application of iron have inherent problems including lack of economic feasibility. Development of iron absorption efficient cultivars is the best economical and durable approach. In this context, effort has been made to identify quantitative trait loci (QTLs) associated with visual chlorotic rating (VCR) and SPAD chlorophyll meter reading (SCMR). A recombinant inbred line population with 318 individuals from the cross TAG 24 (inefficient) × ICGV 86031 (efficient) were phenotyped during two consecutive rainy seasons under iron deficient calcareous soils (Fe < 4 ppm) at Bijapur, Karnataka. The phenotypic observations were recorded for VCR (1-5 scale: 1-highly efficient, 5-highly inefficient) and SCMR at 30, 60 and 90 days after sowing (DAS). QTL analysis using the genotypic data for 191 SSR marker loci together with above mentioned phenotyping data identified a total 14 QTLs for VCR (4, 5 and 5 QTLs for VCR30, VCR60 and VCR90, respectively) with the phenotypic variance (PV) ranging from 12.6 to 34.1%. Similarly, 12 QTLs were identified for SCMR (2, 5 and 5 QTLs for SCMR30, SCMR60 and SCMR90, respectively) with the PV ranging from 12.2 to 45.3%. Interestingly, out of total 26 QTLs identified for both VCR and SCMR, nine QTLs were found located on the linkage group AhV. These QTLs after validation could be deployed in genomics-assisted breeding (GAB) for the improvement of groundnut cultivar with high iron absorption efficiency.

Chloroplast Targeting: Potential Tool for Functional Genomics in Pulses

Poornima KN*, Das A, Singh NP

Division of Plant Biotechnology, ICAR-Indian Institute of Pulses Research, Kanpur-208 024, Uttar Pradesh, India
*Email: poornimakn04@gmail.com

Genes require different *cis*-acting elements for their expression and localisation. Chloroplast has been a very important organelle constituting many photosynthetic proteins. Majority of these proteins are encoded by the nucleus and then transported into the chloroplast. The chloroplast transport is aided by a *cis*-element called the chloroplast Transit Peptide (cTP) that localises all the essential proteins into chloroplast. The present study focuses on isolation of genes encoding chloroplast targeting proteins, including transit peptide sequences from chickpea and pigeonpea genome. All the transit peptide sequences were aligned, their conserved motifs identified, and their phylogeny deciphered. Sequence analysis revealed several signature consensus sequences that marks chloroplast targeting, such as the conserved 'homology block' Gly-X-Arg-XXX-Val and the presence of valine and alanine at -3 and -1 sites of all the analysed peptides. The current study will help understand the structural and functional aspects of chloroplast targeting in pulses. Further, foreign proteins expressed at very low levels or toxic to the cytoplasm can be localised to intracellular compartments of chloroplast by fusing with cTP. It can also facilitate the genome editing of chloroplast genome, and also for targeting of different cellular proteins into the chloroplast with higher and stable expression.

Valencia Peanut Breeding for Increased Shelf Life, Enhanced Drought Tolerance and Improved Disease Resistance

Puppala N[1],*, Payton P[2], Rowland D[3], Kottapalli R[4], Burow M[5], Barkley N[6], Chenault K[7], Sanogo S[8], Xavier A[1], Sandhu G[1]

[1]New Mexico State University, Plant and Environmental Science, College of Agricultural, Consumer, and Environmental Sciences, PO Box 30003 MSC 3Q, Las Cruces, NM 88003-8003, USA
[2]USDA-ARS Cropping Systems Research Laboratory, Lubbock, TX 79415 USA;
University of Florida, Agronomy Department, PO Box 110500, Gainesville, FL 32611-0500, USA
[3]Center for Biotechnology and Genomics, Texas Tech University, Lubbock, TX 79409 USA
[4]Texas A&M AgriLife Research and Department of Plant and Soil Science Texas Tech University, Lubbock, TX 79409, USA
[5]USDA-ARS, Plant Genetic Resource Conservation Unit, Griffin, GA, USA
[6]USDA-ARS, Research Biologist, Wheat, Peanut and Other Field Crops Research Unit
1301 N. Western Rd. Stillwater, OK 74075, USA
[7]New Mexico State University, Entomology, Plant Pathology and Weed Science, College of Agricultural, Consumer, and Environmental Sciences, PO Box 30003 MSC 3Q, Las Cruces, NM 88003-8003, USA
*Email: npuppala@nmsu.edu

Valencia peanuts are specialty nuts that are grown mainly in eastern New Mexico and west Texas mainly for its sweet taste and three to four seeded pods. The acreage is about less than 1% of the US peanut acreage. They are mainly sold as in-shell peanuts. This presentation will focus on three major traits of Valencia peanut breeding: longer shelf life, drought tolerance, and diseases resistance. Shelf life of the peanut product is influenced by variation in oleic (O) and linoleic (L) fatty acid ratio: higher the O/L ratio longer the product stability. The high oleic trait is controlled by two recessive genes, *FAD2A* and *FAD2B*. Use of marker assisted selection in breeding programs helps plant breeders reduce the time and cost in selection thereby increasing the precision. We have developed NuMex-01 high Oleic Valencia peanut using oil trait in peanut that was originally designated Ol_1-ol_1 and Ol_2-ol_2 by Moore and Knauft along with conventional breeding approach. The associations of ol_1 and ol_2 with the A and B genomes of *Arachis hypogaea* were utilized in selection of initial breeding lines. As climate change become inevitable the future of peanut production in the U.S. as well as in other areas of the world will rely upon the peanut crop's ability to yield under decreased water availability. For this reason, selection specifically for improved drought tolerance will be needed, and selection for yield under optimal conditions will not be sufficient. Drought at harvest results in aflatoxin infection which is a serious quality constraint as contaminated peanut kernels/cake, if eaten, is a potential health hazard (carcinogenic) to animal and human health. We have developed a mapping population using C76-16 and 308-2 advanced breeding line from Valencia peanut breeding program. Pod rot and Sclerotinia blight are a serious constraint to Valencia peanut production worldwide. Additionally, it also reduces the quality of edible grade peanut. Valencia peanuts with distinct bright color (< 25% discoloration) are paid an additional premium price of US $ 50/ton by the New Mexico processors while dark colored peanuts with black hull and pod rot diseases receive trade penalty (i.e. low price and possibly rejected). Peanut is widely used in the food and confectionery industry due to its high nutritive value.

ISMU 2.0: A Multi-Algorithm Pipeline for Genomic Selection

Rathore A[1],*, Das RR[1], Roorkiwal M[1], Doddamani D[1], Telluri M[1], Edwards D[2], Sorrells ME[3], Jenko J[4], Hickey J[4], Jannink J-L[3], Varshney RK[1],*

[1]ICRISAT, Hyderabad, India
[2]University of Queensland, Brisbane, Australia
[3]Cornell University, Ithaca, NY
[4]The University of Edinburgh, Scotland, United Kingdom
*Emails:a.rathore@cgiar.org; r.k.varshney@cgiar.org

Genomic selection (GS) is getting immense popularity in modern breeding especially for complex traits. In the GS, marker effects, after deploying genome-wide and high-density marker datasets, are estimated without testing for their statistical significance and used to predict genomic breeding values (GEBVs). Although some groups have developed algorithms for calculating GEBVs, these algorithms are often coded in R, FORTRAN and C++ languages that require understanding of programing environment and large-scale data handing. In addition, breeding community may have a challenge in applying several algorithms together due to their limited expertise in different algorithms. To overcome these challenges, as part of the Integrated Breeding Platform, ICRISAT and its partners are in process of developing "ISMU 2.0" pipeline after integrating several GS algorithms in Java. For instance, the pipeline incorporates seven popular GS algorithms namely RR-BLUP, Kinship Gauss, Bayesian LASSO, BayesA, BayesB, BayesCπ and Random Forest written in FORTAN and R languages. RR-BLUP and BayesA algorithms implemented in FORTRAN language in the ISMU have been found faster in terms of analyzing large datasets. Additionally, the pipeline has modules to check quality of marker datasets such as % missing data, minor allele frequency (MAF) and polymorphism information content (PIC). The pipeline has been optimized for running MS-Windows, Linux, CentOS and Ubuntu platforms.

Mapping Late Leaf Spot and Rust Resistance using an Improved Map From the RILs of TAG 24 x GPBD 4 in Peanut (*Arachis hypogaea*)

Kolekar RM[1], Sujay V[1], Shirasawa K[2], Yeri SB[1], Chougale DB[1], Asha B[1], Gowda MVC[1], Varshney RK[3], Bhat RS[1*]

[1]College of Agriculture, University of Agricultural Sciences, Dharwad-580005, India
[2]Department of Frontier Research, Kazusa DNA Research Institute, Chiba 292-0818, Japan
[3]Center of Excellence in Genomics (CEG), International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502 324, India
*Email: bhatramesh12@gmail.com

An effort was made to map late leaf spot (LLS) and rust resistance using the recombinant inbred line population of TAG 24 × GPBD 4 with additional genotypic and phenotypic data in peanut. The new genetic map constructed based on the 266 RILs of TAG 24 × GPBD 4 carried 109 AhTE markers in addition to previously mapped 188 SSR markers. The new map of 1730.8 cM had an average inter-marker distance of 5.4 cM. The phenotypic data on LLS and rust reaction collected from 3 seasons in addition to previously recorded data from 8 seasons were used to detect the QTL for these traits. In addition to the previously identified QTL for LLS and rust resistance, a few more minor QTL were detected. QTL at major genomic region on LG XV were linked to new AhTE markers like AhTE0498, AhTE0928, AhTE0621 and AhTE0200 in addition to already mapped SSR markers. Apart from their use in marker assisted selection, these AhTE markers could be useful in dissecting the QTL based on the transpositions of AhMITE at marker loci.

Selection of Appropriate Genomic Selection Model for Yield Related Traits in Chickpea

Roorkiwal M[1], Rathore A[1], Das RR[1], Singh MK[1], Srinivasan S[1], Gaur PM[1], Bharadwaj C[2], Tripathi S[2], Hickey JM[3], Lorenz A[4], Jannink J-L[5], Varshney RK[1],*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Indian Agricultural Research Institute, Delhi, India
[3]The Roslin Institute, The University of Edinburgh, Scotland, UK
[4]University of Nebraska, Lincoln, USA}
[5]Cornell University, Ithaca, USA
*Email: r.k.varshney@cgiar.org

Genomic selection (GS) unlike MABC (marker assisted backcross) or MARS (marker-assisted recurrent selection), predicts breeding values of lines and makes selection prior to phenotyping using genome-wide marker profiling. To address the low productivity in chickpea owning to several biotic and abiotic stresses, a collection of 320 elite breeding lines was selected as the "training population". Training population was phenotyped extensively for yield and yield related traits at ICRISAT, Patancheru and IARI, Delhi during crop season 2011-12 and 2012-13 under rain-fed and irrigated conditions. In parallel, the training population was genotyped using KASPar assays (for 651 SNPs) and DArT arrays (15,360 features). Phenotypic data and genome-wide marker profiling data as mentioned above were used with six statistical models including RR-BLUP, kinship based ridge regression, BayesCπ, BayesB, Bayesian LASSO and random forest to predict genomic estimated breeding values (GEBVs). GS models were tested for four yield related traits namely seed yield, 100 seed weight, days to 50% flowering and days to maturity. Correlation inside training (CIT) for the models tested varied from 0.138 to 0.912. Heat map analysis using genotyping data to understand the relationship within these lines suggested possibility of two different groups similar to cluster analysis. In order to understand the effect of population structure on accuracy, analysis was re-performed by implementing population structure for calculation of GEBV. Population structure significantly affected the CIT that varied from 0.001 to 0.745 for desi group, and 0.004 to 0.727 for kabuli group.

Mapping Genes for Agronomic Traits in Proso Millet (*Panicum milliacum* L)

Santra DK*, Rajput SG

Panhandle Research and Extension Center, University of Nebraska, Scottsbluff, NE USA
*Email: dsantra2@unl.edu

Proso millet is an allotetraploid cereal crop grown in China, Russia, USA and Europe. It is a short season, shallow-rooted, and low water-requiring crop. This makes it as an ideal alternative crop for wheat-based dryland cropping systems in semiarid high plains of the USA. There is no report of a genetic map and gene mapping in proso millet. The objectives are to: (1) develop DNA markers and genetic linkage map and (2) identify and map genes for important agronomic traits in proso millet. Mapping populations consisted of 157 and 250 $F_{6:7}$ recombinant inbred lines (RILs) form 'Huntsman' x 'Rise' and 'Huntsman' x 'Minsum'. The RILs were evaluated for agronomic traits (heading date, plant height, number of internodes, Fe chlorosis, neck length, lodging, panicle length, shattering, 100 seed weight, inflorescence and seeds/panicle) in 2013 and 2014 field trials at Sidney and Scottsbluff, NE, USA. The RILs were genotyped with 15,000 SNP markers and 100 simple sequence repeat (SSR) markers ('Huntsman x Rise' only).The agronomic traits were segregated in both populations, indicating segregation of the genes controlling the traits. Many of the traits seem to have polygenic/quantitative inheritance.

Eight traits except internode number and seed weight showed significant differences among the RILs in both populations. Transgressive segregation was observed for most the traits. A preliminary genetic linkage map was developed for mapping the genes/QTLs for these agronomic traits. This is the first report of this kind in proso millet, which will be useful in proso millet breeding.

CIMMYT Wheat Molecular Breeding: Achievements and Progress

Sehgal D, Dreisigacker S

CIMMYT Headquarters, Km. 45, Carretera,Méx-Veracruz, El Batán, Texcoco, México, CP 56130
Emails: s.dreisigacker@cgiar.org, d.sehgal@cgiar.org

The CIMMYT Global Wheat Program has a more than 10 years of history in the use of molecular markers to assist wheat improvement. Molecular markers associated with loci or causal genes for traits with relatively larger phenotypic effects are routinely used at CIMMYT in diverse ways: characterization of parents and predicting the progeny performance; monitoring the shift in frequency of loci in advanced breeding material; facilitating the introgression of chromosome segments via backcrossing; and to pyramid several genes in one single genotype. The molecular characterization of lines, being candidates to be distributed by CIMMYT international nurseries, has become a common practice. Markers used are mainly associated to seedling and adult-plant resistance genes to wheat rust and other diseases, quality genes, and genes related to plant height and flowering time. With the revolution brought about by advent of next generation sequencing, the number of SNP markers in wheat databases has increased from 1536 in 2010 to over 90,000 in 2014. A core subset of these SNPs has been integrated into wheat molecular breeding by converting them to KASP assays for variety identification or marker enrichment of targeted chromosome regions. CIMMYT has also adopted the latest genotyping-by-sequencing (GBS) technology as a common platform for genotyping annually up to 10,000 advanced lines. Both high throughput platforms (SNPs and GBS) are currently being used for diversity analysis, gene discovery (for disease resistance and more complex traits e,g., stable regions associated with yield and yield components)using genome wide association mapping, and genomic selection.

Towards Identification of Genomic Regions Associated with Yield and Yield Related Traits in Pigeonpea (*Cajanus cajan* (L.) Millsp)

Kaoneka SR [1,2], Shimelis HA[2], Singh VK[1] ,Kumar V[1], Parulpalli S[1], Saxena RK[1], Varshney RK [1,3]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]School of Agricultural, Earth and Environmental Sciences,
University of KwaZulu-Natal, Private Bag X01, Scottsville 3209,South Africa
[3]School of Plant Biology and Institute of Agriculture, The University of Western Australia,
35 Stirling Highway, Crawley, WA, 6009, Australia
*Email: r.k.varshney@cgiar.org

Pigeonpea is an important legume crop grown in tropics and sub tropics regions of the world. Despite the past and ongoing breeding efforts the crop productivity remains <1 ton/ha in farmers' fields. In order to break the yield plateau, genomics assisted breeding (GAB) for yield and yield related traits seems to be a better option. To deploy the GAB we are identifying genomic regions associated with yield and related traits in segregating mapping populations. Three mapping populations (AL 201 × ICPL 20325, ICP 8863 × ICPL 87119 and ICP 5529 × ICP 7035) representing three different maturity groups (short, medium and long)were developed. These mapping populations (F_2) are being phenotyped for yield and related traits in cropping season of 2014-2015. In parallel 188 F_2s and parents from each mapping population will be subjected to genotyping by sequencing (GBS) to construct the genetic linkage maps. Genotyping data together with the yield and yield related traits data will be used for the identification of marker trait associations (MTAs). Generated information will be used in deploying genomics assisted breeding for enhancing the yield in pigeonpea.

Exploiting Next Generation Sequencing for Creation of Genomic Resource in Tea

Sharma RK*, Parmar R, Singh G, Raina AS, Kuldip, Bhandawat A, Seth R, Sharma H, Singh AK, Ahuja PS

Biotechnology Division, CSIR - Institute of Himalayan Bioresource Technology, Palampur, 176061, Himachal Pradesh, India

*Email: mrk_sharma@yahoo.com, ramsharma@ihbt.res.in

Tea is one of the most popular natural beverages worldwide because of its taste and health benefits, with major cultivation confined to Southeast Asian countries. Perennial nature, high heterozygosity and a long gestation period limits genetic improvement of tea through conventional means. Although critical for trait dissection and identification of key pathway genes, except for a few transcriptomes, larger genomic resources are non-existing in tea. With an aim to enrich genomic resource, 15 diverse tea accessions capturing considerable trait diversity for biotic, abiotic and quality traits were sequenced at transcriptome level using high-throughput Illumina platform. Utilizing current transcriptome and public sequence data, a markers genomic resource was created, which so far contains 28298 SSRs, 242846 SNPs and 26331 Indels. A total of 19213 flanking SSR primers were designed out of which 6449 SSR markers found to be polymorphic in e-PCR. A set of 1500 SSR markers having detected functional relevance in annotations (GO, KEGG, EC) were experimentally validated in selected tea accessions.Furthermore, localization of SNPs to different genome components identified 153151 in UTRs and 41792 in CDS. These functionally relevant SNPs can be utilized for developing an SNP array. Our current efforts will provide an unprecedented sequence based marker data base, which will enable marker-trait association, identification of key pathway genes, investigation of functional variation, and genome mapping in tea.

QTL Mapping for Stigma Exsertion Traits under indica Genetic Background in F_2 Population of Rice (*Oryza sativa* L.)

Singh AK[1], Priyadarshi R[1], Koradi P[1], Khandekar D[1], Shanti ML[1], Khera P[1, 2], Barthwal M[1, 3] Patil V[1, 4], Kemparaju KB[5], Subba Rao LV[5], Jayaramulu K[5], Madhav MS[5], Hariprasad AS[5], Ulaganathan K[6,] Shenoy V[1]*

[1]Barwale Foundation Research Centre, Hyderabad, India
[2]International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, India
[3]Bayer Biosciences Pvt. Ltd., Hyderabad, India
[4]Mahindra and Mahindra Ltd., Agribusiness, Secunderabad, India
[5]Indian Institute of Rice Research, Hyderabad, India
[6]Centre for Plant Molecular Biology, Osmania University, India
*Email: vvshenoy123@gmail.com

Hybrid rice technology has been found to be one of the most practical and pragmatic options to increase yield potential. Increased hybrid seed production can be achieved by improving the outcrossing rate in rice CMS lines which, in turn, would reduce the overall seed cost of hybrid seed. Among various traits that influence outcrossing, stigma exsertion (SE) is a key factor contributing to the efficient improvement of seed set in male sterile lines of rice. The goal of this study was to identify QTL for SE trait, based on F_2 mapping population by using two *indica* cultivars, namely IR58025B, a well-known maintainer line for WA-CMS IR58025A and BF-16B, a newly identified maintainer line for high SE traits, identified at the Barwale Foundation, Hyderabad. We mapped the genomic region and QTL influencing the four SE traits and identified a major QTL for total stigma exsertion (TSE) (R^2=18.25%, LOD=5.99), dual stigma exsertion (DSE) (R^2=17.19%, LOD=3.46), and single stigma exsertion (SSE) (R^2=28%, LOD=3.52) using composite interval mapping. Out of the nine QTL identified, six were contributed by the parent, BF-16B, while three QTL by were contributed by IR58025B. Also, a marker interval (RM3480-RM6948) on chromosome 8 harboring major QTL for the three traits was identified. These results would be of great use in the development of parental lines with high stigma exsertion trait. Furthermore, it is feasible to transfer these positive QTLs into WA-CMS maintainer lines to improve the natural outcrossing rate, thereby increasing the seed production in hybrid rice.

Kanamycin Based Screening of Putative Transgenic Pigeonpea (*Cajanus cajan* L.) Lines Based on Lateral Root Inhibition (LRI)

Arpan, Singh AK, Kumar M, Srivastava J, Das A*, Datta S, Singh NP

Division of Plant Biotechnology, ICAR-Indian Institute of Pulses Research,
Kanpur 208 024, Uttar Pradesh, India
*Email: adas@icar.org.in

Successful screening of putative transgenic lines is an absolute necessity for the establishment of true transgenic plants. To screen large numbers of putative transgenic seeds, it is imperative to grow each and every seed up to plantlet level for molecular characterization. This is not only labour intensive, but also time consuming and requires large space for containment. It would be quite useful if there is some initial indication of their transgenic status. Hence, a novel and simple approach has been used for primary screening of seeds of pigeonpea harvested from different primary lines (genetically transformed with plant selectable marker gene, neomycin phosphotransferase II (*nptII*) gene from *E coli*) based on effect of minimum inhibitory concentration of Kanamycin on lateral root initiation. Lateral roots, being single celled in origin, could be a very useful tool for primary screening of transgenic seeds based on kanamycin resistance. This will help to transfer and establish only kanamycin-resistant plants in greenhouse, obviating the ardours job of screening after establishment.

Marker Assisted Selection – a Fast Track in Plant Breeding to Introgress Resistance for Stem Rust Race 117-group in Durum Wheat

Singh JB[1*], Sai Prasad SV[1], Singh SK[1], Vinod[2], Prem K[1], Sandeep KC[1], Kantwa SL[1], Dubey VG[1], Divya A[1], Prakasha TL[1], Mishra AN[1]

[1] ICAR- Indian Agricultural Research Institute – Regional Station, Indore, MP, India
[2] ICAR- Indian Agricultural Research Institute, New Delhi, India
*Email: jangbsingh@gmail.com

Molecular marker-assisted selection, often simply referred to as marker-assisted selection (MAS), offers such a possibility by adopting a wide range of novel approaches to improving the selection strategies in agricultural crop breeding. Stem rust (*Puccinia graminis* f. sp. *tritici)* has historically been one of the major constraints in realizing stabilized durum wheat yields in central India. Pyramiding of genes into a single genotype has been one of the preferred strategies in wheat rust management. Currently, HI 8498 (Raj 6070/ Raj 911) is the most popular durum wheat cultivar in central India. However, it is susceptible to a number of Indian pathotypes of stem rust race 117-group. Hence, a planned breeding programme was taken up to develop derivatives of HI 8498 with improved resistance by pyramiding stem rust resistance genes *Sr36* and *Sr2* through marker assisted selection. The markers being used for foreground selection in the HI 8498 derivatives are '*pbc*' and CAPS marker *cssr2* for the gene *Sr2*, and SSR marker *Xstm773-2* for the gene *Sr36*. Stem rust resistance in the 'HI 8498' derivatives (BC_3F_1) carrying *Sr2* and *Sr36* individually has improved significantly (terminal disease severity 0 to 5S), compared to the background cultivar HI 8498 (30S – 40S).

Additionally, 177 markers out of 730 SSR primers showed polymorphism and are being used as effective markers in Marker Assisted Background Selection (MABS) to identify 99 % of recurrent parent genome (RGP) i.e., HI 8498 in BC_3F_1 generation of both the populations involving *Sr36* and *Sr2* genes to facilitate their pyramiding in common recipient parent background. *Sr36* and *Sr2* genes were detected in 49 and 46 plants respectively, but only 19 plants were found to be having both *Sr36* and *Sr2* genes.

Introduction and Characterization of Potential Mutants Genotypes of Basmati rice (*Oryza sativa* L.)

Singh NK*, Rani M, Raj TS

Department of Biotechnology
Motilal Nehru National Institute of Technology Allahabad-211004 India
*Email: singhnand@gmail.com

Rice is stable cereal food crop for more than 60% of world's population. Quality of rice grain is important because of its commercial value. Rice growing farmer are less attracting to growing of basmati rice due to less yield, intensive agronomical practices, high insect past and disease management as compare to normal rice cultivars. Therefore present requirement to develop new genotype that reduce above mentioned demerit in existing basmati genotypes. In present study, two basmati mutants genotype were developed through chemical mutagenesis using EMS(0.24%). These mutants are subjected to morphological screening by using qualitative parameters such as Leaf blade colour, auricle colour, panicle extension and collar colour shows anthocyanin pigmentation at basal leaf sheath as compared to control. Biochemical analysis of these mutants done for phytic acid content work as anti-nutrients, poly unsaturation such as omega-3 fatty acid used in cardiovascular disease prevention and glycemic index.BM 6 mutant showed 25 days early, MB 9 mutant are 10 days early from control. These mutants are high yielding and requires less agronomical practice.These mutants under processing for characterization of gene expression for early flowering gene family containing MADS-box (OsMADS 14,15,18 and 45) by micro array and real time PCR, compactness of starch molecule analysis was done by using SEM.

QTL-seq Reconfirms the Presence of Major QTLs for 100-seed Weight and Root / Total Plant Dry Weight Ratio in the "*QTL-hotspot*" in Chickpea

Singh VK[1], Khan AW[1], Jaganathan D[1], Thudi M[1], Takagi H[2], Garg V[1], Kumar V[1], Chitikineni A[1], Gaur PM[1], Terauchi R[2], Varshney RK[1,3,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]Iwate Biotechnology Research Center, Kitakami, Japan
[3]School of Plant Biology and Institute of Agriculture,The University of Western Australia, Crawley, Australia
*Email: r.k.varshney@cgiar.org

Next-generation sequencing technologies, in the recent past, have revolutionized the efficiency of establishing the marker-trait associations and identification of candidate genes for crop improvement. Terminal drought has been major constraint to chickpea production and productivity especially in the arid and semi-arid regions across the globe. 100-seed weight (100SDW) and total dry root weight to total plant dry weight ratio (RTR%) are important yield contributing and drought tolerance related traits, respectively. Identification of genomic regions and candidate genes in the genomic regions will help defining breeding strategies for reducing the yield losses in chickpea. In this direction, bulked segregant analysis based whole genome re-sequencing approach referred as "QTL-seq" was used for identification of candidate genomic regions and genes for 100SDW and RTR%. Based on precise phenotyping data generated on the recombinant inbred line population developed from the cross ICC 4958 × ICC 1882, extreme bulks were constructed for both the traits. Genome-wide SNP profiling of the extreme bulks for 100SDW provided two significant genomic regions, one on CaLG01 (1.4 Mb region between 3.07 - 4.47 Mb) and another on CaLG04 from (2.7 Mb region between 11.12 - 13.82 Mb). Similarly, one genomic region (1.10 Mb between12.73 - 13.83 Mb) for RTR% on CaLG04 was identified. Further, analysis of candidate genomic regions revealed eight and five putative candidate genes for 100SDW and RTR%, respectively. Thus, this study demonstrates the usefulness of QTL-seq in precisely identifying candidate genomic regions and genes in a high throughput manner which can be deployed for chickpea improvement.

Transcriptome Dynamics during Flower Development and Genome-wide Analysis of *GH3* Gene Family in Chickpea

Singh VK, Garg R, Jain M*

Functional and Applied Genomics Laboratory, National Institute of Plant Genome Research, New Delhi, India
*Email: mjain@nipgr.ac.in

Flower development is one of the major developmental processes that regulates seed setting in angiosperms. However, little is known about the molecular mechanisms underlying flower development in legumes. Employing RNA-seq for various stages of flower development and a few vegetative tissues, we identified a large number of differentially expressed genes during flower development in chickpea. Further, we identified several genes expressed in a stage-specific manner during flower development. Various transcription factor families and metabolic pathways involved in flower development were also elucidated. The members of MADS-box family were highly enriched among the transcription factor genes up-regulated during various stages of flower development. Our data provides a resource for exploring the complex molecular mechanisms underlying flower development and identification of gene targets for functional genomics in legumes. In addition, we performed genome-wide analysis of GH3 gene family members in legumes. *GH3* genes maintain endogenous auxin homeostasis by conjugating excess of auxin with amino acids and regulate flower development. A comprehensive expression analysis revealed that many of *GH3* genes were expressed in a tissue-specific manner in different vegetative and reproductive tissues/stages in chickpea. Several members were found to be differentially regulated under different abiotic stress conditions also. Furthermore, analyses of three-dimensional protein structures, active site residues and ligand preferences provided molecular insights into functions of *GH3* genes in legumes. These results would help in investigation of precise functions of *GH3* genes in legumes during development and stress conditions.

Variability for Seedling Salinity Tolerance in Chickpea

Singhal T[1*], Bharadwaj C[1], Kumar T[1], Neeraj[1], Singh P[1], Tripathi S[1], Pal M[1], Roorkiwal M[2], Gaur M[2], Varshney RK[2]

[1]Indian Agricultural Research Institute, Delhi, India
[2] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*Email: triptisinghal16@gmail.com

Chickpea (*Cicer arietinum* L.) is considered a salt sensitive species, but some genetic variation for salinity tolerance exists. The present study was initiated to determine the degree of salt tolerance among chickpea genotypes. The saline treatment was applied as an 80 mM solution of NaCl in a sufficient volume to saturate the soil at field capacity at sowing. Thereafter, pots were watered with distilled water containing no significant amount of salt, and maintained close to field capacity (gravimetrically) to avoid an increase in salt concentration. Non-saline treated controls were watered with non-saline water. Ten chickpea genotypes; namely Pusa 362, Pusa 1103, Pusa 72, L550, JG 11, CSG 8962, ICC 1431, ICC 4958, ICCV98944, and Pusa green 112; were evaluated for seedling stress tolerance. Under salt stress conditions Pusa 72, Pusa 362 and Pusa 1103 outperformed the others. Salinity impairs seed germination, reduces nodule formation, retards plant development and reduces crop yield. It significantly decreased shoot and root dry weight of the seedlings. The effect of salinity on germination of seeds can be either by creating osmotic potential which prevents water uptake, or by toxic effects of ions on embryo viability of the seeds. Shoot growth is also reduced by salinity due to the inhibitory effect of salt on cell division and enlargement in the growing point. Considerable genotypic variation for salt tolerance exists in chickpea germplasm. Selection for genotypes with high pod and/or seed numbers that accumulate low concentrations of salt in the seed will be beneficial.

Evaluation of Housekeeping Genes as Reference for Gene Expression Studies Under Heat and Salt Stress Conditions in Pigeonpea (*Cajanus cajan*)

Sinha P[1], Saxena RK[1], Singh VK[1], Suryanarayana V[1], Krishnamurthy L[1], Varshney RK[1, 2,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2]School of Plant Biology and Institute of Agriculture, The University of Western Australia, Stirling Highway, Crawley, WA, Australia.
*Email: r.k.varshney@cgiar.org

Gene expression studies through quantitative real-time PCR (qRT-PCR) depend on the stable performance of reference gene(s) or housekeeping genes. However, the expressions of housekeeping genes were found to be highly inconsistent under different stress conditions. Therefore, it is recommended to use appropriate housekeeping gene in specific expression studies. Despite the fact that genome sequence has become available for pigeonpea (*Cajanus cajan*) no specific housekeeping genes have been reported for stress specific expression studies. To identify the stable housekeeping genes in pigeonpea for expression analysis under heat and salt stress conditions, the relative expression variations of 10 commonly used housekeeping genes (*EF1α, UBQ10, GAPDH, 18SrRNA, 25SrRNA, TUB6, ACT1, IF4α, UBC* and *HSP90*) were studied on root, stem and leaves tissues of Asha (ICPL 87119). Three statistical algorithms geNorm, NormFinder and BestKeeper were used to define the stability of candidate genes. Under heat stress condition, *EF1α, UBC* and *HSP90* were found to be the most stable reference genes. In case of salinity stress *GAPDH* followed by *UBC* and *ACT1* were identified as the most stable reference genes. Above mentioned stable housekeeping genes will facilitate gene expression studies in pigeonpea especially under heat and salt stress conditions.

Towards Development of a SCAR Marker Linked to Sterility Mosaic Disease Resistance in Pigeonpea (*Cajanus cajan* L. Millsp.)

Revathi T[1,2], Joshi S[1], Rajani G[1], Anuradha G[1,*], Yamini KN[1], Suresh M[1], Sameerkumar CV[2], Singh VK[2], Sharma M[2], Saxena RK[2], Varshney RK[2]

[1]Institute of Biotechnology, PJTSAU, Rajendranagar, Hyderabad, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[3]Agricultural Research Station, Tandur, India
*Email: saps_61@yahoo.com

Pigeonpea (*Cajanus cajan* L. Millsp) is one of the important grain legumes and is a rich source of protein. The major bioticstresses causing economic losses in pigeonpea are *Fusarium*wilt, sterility mosaic disease (SMD) and phytopthora blight. In case of SMD yield losses can reach up to 95 per cent. The causal agent of SMD is pigeonpeasterility mosaic virus (PPSMV) which is transmitted by a vector, eriophyid mite (*Aceriacajani*Channabasavanna). In order to implement genomics assisted breeding (GAB) for SMD resistance in pigeonpea,the present study was undertaken to identify markers associated with SMD resistance in RIL mapping population derived from ICP 8863(susceptible) xICPL20097(resistant). A total 96 RAPD primers were surveyed for identification of polymorphism between the resistant and susceptible parents, of which 18 were found polymorphic. Based on phenotypic screening for SMD resistance ten each of the extremely resistant and susceptible RILs were identified and respective bulks were constituted. Bulked segregant analysis (BSA) was employed using the 18 polymorphic markers using extreme bulks and both of the parents. Of these, one marker (OPI-13) was found co-segregating between resistant and susceptible bulks. Further screening of the individual RILs with OPI-13 differentiated resistant and susceptible lines, indicating that OPI-13 could be associated with SMD resistance in these lines. The RAPD band obtained in the resistant parent was cloned and sequenced. Development of a SCAR marker from this sequence is in progress and would be very useful in implementing GAB for SMD resistance in pigeonpea.

Fine Mapping and Introgression Of '*ms*3' Loci in Rabi Sorghum for Ease of Population Development

Thammineni C, Deshpande SP*

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru-502324, Hyderabad, India
*Email: s.deshpande@cgiar.org

Development of locally adapted and drought tolerant cultivars in a farmer preferred genetic background will go a long way in deploying the drought tolerant cultivars that will ultimately improve sorghum production globally. The back-cross derived genetically diverse population will serve as both pre-breeding population and genetic population to achieve above target and dissect trait genetics. An efficient cross pollination system is required to achieve the above target. Hence we took the advantage of "ms3" mediated genic male sterile strategy to convert locally adapted familiar varieties to male sterile lines. Initially Parbhani Moti (SPV1411) was selected for development of genetic male sterile conversion. Sterile genotypes of M35-1 from a segregating population were selected as donor parent. Considering the photosensitivity issues we took up a staggered sowing of the recurrent parent SPV1411 (3 plantings with one week gap between each sowing date) and non-recurrent parents (2 sowing dates separated by one week, with first sowing date matching with second sowing of recurrents). Crossings were made initially by making recurrent parent as pollen donor to access the genetic male sterile gene. Following this, two successive rounds of back crossings (plant X plant) involving SPV1411 as recurrent parent/female parent were made to increase recurrent back ground. Based on preliminary analysis nine SSR markers in the region of 70 Mbp to 73 Mbp with map distance of 17cM, were selected to identify the parental polymorphism for the trait sterility and fertility. Among nine markers used, *Xtxp*423 was found showing clear polymorphism between fertile and sterile parents when analysed on capillary electrophoresis.

Relationship of Post-Harvest Handling of Groundnut and Aflatoxin Contamination in Processing Units

Thirumalaisamy PP*, Dobaria JD, Sukhadiya BJ

ICAR - Directorate of Groundnut Research, Junagadh, Gujarat, India
*Email: thirumalaisamypp@yahoo.co.in

Groundnut (*Arachis hypogaea* L.) is an important food crop of the world and is used for production of edible oils, groundnut butter and a host of other food products. Groundnut and maize (*Zea mays* L.) are two specific commodities which get easily infected by aflatoxin producing fungi, *Aspergillus flavus* and *A. parasiticus* and are major dietary sources of aflatoxin in humans. *A. flavus* infection can occur at pre-harvest stages, during harvest, post-harvest curing, processing and storage. Pre-harvest, harvest and post-harvest integrated aflatoxin management packages have been made available to the farmers. However, information on aflatoxin build-up within the processing units in India and measures to be undertaken for its control is hardly there. The present studies carried on post-harvest handling of groundnut in different processing units, infection of *A. flavus* on pods & kernels and aflatoxin contamination in kernels at various stages of processing. Fourteen groundnut processing units were surveyed during 2012 and 2013, and samples from each stages of the processing were collected for analysis of moisture content, *A. flavus* infection and aflatoxin contamination. The estimated moisture content in the pods collected from different processing units (dry processing) ranged from 3.1 to 6.7% and in kernels, it ranged from 2.9 to 6.6%. None of the samples at these moisture content support the *A. flavus* growth when artificially spores were dusted on the pods and kernels, and incubated in a temperature (29-32^{O}C) and humidity (about 70%) controlled chamber. However, pod and kernel samples collected from the wet processing units supported the *A. flavus* growth. In addition to infection of *A. flavus* in groundnut, the frequency of detection of aflatoxin contamination in groundnut was high in discarded kernels (rejected materials from manual or mechanical sortex) in each stage of the processing. The information generated will be useful to the groundnut processing units for production groundnut free of aflatoxin.

Targeting Root Traits for Improving Drought Tolerance in Chickpea (*Cicer arietinum* L.)

Singh RK[1], Chauhan SK[1], Thudi M[2], Bharadwaj C[1], Gaur PM[2], Varshney RK[2], Hegde VS[1], Tripathi S[1*]

[1]Division of Genetics, Indian Agricultural Research Institute, New Delhi 110012, India
[2]International Crops Research Institute for the Semi-Arid Tropics, Patancheru (A.P.) 502324, India
*Email: shaitri@rediffmail.com

Chickpea (*Cicer arietinum* L.) is the second most important grain legume in the world after dry beans. Globally, it is cultivated on over 13.2 m ha with an annual production of 11.6 m t (FAOSTAT, 2013). India is the major chickpea producing country contributing more than 75% of the total global production (9 m t in 2010-13). The chickpea genome has been recently sequenced and is estimated to be 738 Mb in size (Varshney *et al*., 2012). One of the major constraints in chickpea production is drought which accounts for upto 50% reduction in yield. Studies have revealed that drought tolerance in plants is a complex trait and the underlying mechanism may be due to drought escape, avoidance and tolerance. Molecular breeding can be deployed by targeting drought tolerance component traits with help of closely linked markers. The aim of the present study is to develop drought tolerant chickpea cultivars with higher yield using MABB (Marker Assisted Backcross Breeding). Extensive phenotyping and genotyping of two recombinant inbred lines (RIL) populations (ICC 4958 x ICC1882 and ICC 283 x ICC 8261) by ICRISAT in collaboration with NARS partners, a 'QTL hotspot' region was identified in the chickpea genome harbouring QTLs for drought tolerance related traits including root traits. MABB was initiated at IARI, New Delhi using ICC 4958 as donor for root traits and Pusa 362, an elite cultivar as recurrent parent. Pusa 362 and ICC 4958 were screened with 194 SSR markers and 50 polymorphic markers covering 8 linkage groups (CaLG) were selected for background selection. For foreground selection QTL based marker NCPGR 21 was used. During rabi 2013-14, BC_3F_1 (51) and BC_2F_2 (340) plants were screened with NCPGR 21. In BC_3F_1, 14 plants were heterozygous while in BC_2F_2 51 plants were homozygous for allele from donor parent. Introgression lines (BC_2F_3) are being phenotyped for root traits and yield.

Inter-Nodal Sugar and Expression Profiling of Early and Late Maturing Sugarcane Varieties

Verma I, Chandra A*, Jain R, Solomon S

Indian Institute of Sugarcane Research, Lucknow-226002, India
*Email: amaresh_chandra@rediffmail.com

Sugarcane is one of the most important cash crops, which accumulates high concentrations of sucrose. Sugarcane lines differ in their sucrose accumulation capacity that can be further improved by breeding programmes. Sucrose content distinctly varies between the source and sink tissue, and shows variation among internodes too. Sucrose synthesis and its storage in sugarcane is a complex process and it involves many genes; among these soluble acid invertase (SAI), sucrose synthase (SS), sucrose phosphate synthase (SPS) are critical in controlling the biochemical events in the source and sink tissue. Sucrose synthase and sucrose phosphate synthase play important role in regulating sucrose accumulation. Sucrose phosphate synthase helps in sucrose synthesis in leaves and initiates the transfer of photosynthate from the source tissue to the sink. Sucrose synthase shows reversible reaction, primarily causing cleavage of sucrose in the sink tissue, with sufficient sucrose and with high demand from carbon biosynthetic and respiratory pathway. Sucrose content varies with growth stages; in mature internodes it is found to be around 25% of the stalk fresh weight. Internodal maturation progresses towards the base of stalk, with an increasing concentration of sucrose at the lower internodes. Lower concentration of sucrose is found in the young internodes and in the source tissue, where reducing sugar content is predominantly high.

Utilization of Genotyping By Sequencing (GBS) Approach for High Density Linkage Map Construction and Identification of QTLs Controlling Seed and Pod Traits in Chickpea (*Cicer arietinum* L.)

Verma S, Bhatia S*

National Institute of Plant Genome Research, New Delhi, 110067 India
*Email: sabhyatabhatia@gmail.com

Expeditious development of high density linkage maps is needed to aid genetic improvement of crops, which, in turn, is facilitated by the discovery of large numbers of molecular markers. Among the various categories of molecular markers, SNPs are the markers of choice due to their genome wide presence, biallelic nature and cost-effective discovery. Recently, next generation sequencing technology has contributed substantially to SNP discovery. The Genotyping By Sequencing (GBS) approach utilizes restriction enzymes for genome complexity reduction and high throughput sequencing platforms for simultaneous discovery and genotyping of genetic variants. Therefore, we demonstrated the utility of GBS in chickpea for SNP discovery and genotyping and implemented these markers for saturated linkage map construction in order to identify QTLs controlling seed and pod traits. A total of 119,672 SNPs were identified and genotyping data of 3,977 SNPs across 93 recombinant inbred lines (RILs) from an intra-specific mapping population (SBD377 × BGD112) was utilized. These markers were assigned to eight linkage groups with a resolution of 0.33 cM. The map was utilized for the identification of QTLs, which revealed a total of 27 QTLs for seed and pod traits. Sequence information of markers associated with these QTLs was utilized to extract defined genomic regions from the whole genome sequence of chickpea in order to predict candidate genes related to seed weight and seed number.

Construction of Dense Genetic Maps and Identification of Quantitative Trait Loci Controlling Oil Content and Different Fatty Acids in Groundnut (*Arachis hypogaea* L.)

Shasidhar Y, Vishwakarma MK, Pandey MK, Janila P, Manohar SS, Upadhyaya HD, Varshney RK*

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*E-mail: r.k.varshney@cgiar.org

Development of dense genetic maps is the pre-requisite for conducting quantitative trait locus (QTL) analysis to locate the genomic region controlling traits of interest. The first generation molecular markers such as random amplified polymorphic DNA and simple sequence repeats have shown low polymorphism which hindered in developing dense genetic maps. The oil content and different fatty acids are the important traits in groundnut preferred by both traders and consumers. In this context, the Diversity Array Technology (DArT) and DArTseq genotyping platform was used to genotype 188 F_2 individuals of each mapping population segregating for oil content (ICGV 07368 x ICGV 06420) and fatty acids (ICGV 06420 × SunOleic 95R). High density genetic map was constructed for fatty acids and oil content with 1,452 marker loci and 854 marker loci, respectively covering the total map distance of 3,524 and 2,423 cM, respectively. The highest map density could be achieved for the genetic map constructed for fatty acids (3.0 cM/loci) and oil content (4.1 cM/loci). QTL analysis using the genotyping and phenotyping data resulted in identification of 8 QTLs explaining 5.6-22.12% phenotyping variance (PVE) for oil content while 69 QTLs explaining 1.0-39.53% PVE for fatty acids. These identified linked markers upon validation may be used in genomics- assisted breeding for development of superior groundnut cultivars with optimum levels of oil content and different fatty acids.

Marker Assisted Backcrossing to Improve Foliar Disease Resistance in JL 24 and TMV 2 Varieties of Peanut

Yeri SB[1], Kolekar RM[1], Sukruth M[1], Meghashree HM[1], Nadaf HL[2], Bhat RS[1*]

[1]College of Agriculture, University of Agricultural Sciences, Dharwad-580005, India
[2]AICRP on oilseeds, University of Agricultural Sciences, Dharwad-580005, India
*E-mail: bhatramesh12@gmail.com

JL 24 and TMV 2, two elite varieties of peanut were improved for late leaf spot (LLS) and rust resistance using marker assisted backcrossing (MABC). JL 24 and TMV 2 were crossed to a Spanish bunch variety GPBD 4 and two interspecific derivatives, ICGV 86699 and ICGV 99005 which were resistant to LLS and rust. A large number of backcross lines were developed, and the selection for the QTL governing LLS and rust resistance was assisted with linked markers (GM2301 and IPAHM103). Ten BC_3F_2 homozygous plants, one from JL 24 × GPBD 4, seven from JL 24 × ICGV 86699 and two from JL 24 × ICGV 99005 were selected by foreground selection. Selfed generations of these plants (BC_3F_3 and BC_3F_4) were evaluated in summer 2013-14 and *kharif* 2014. Selected BC_3F_4 families were resistant to LLS and rust, and they carried resistant allele at linked markers like IPAHM103 and GM2301. These homozygous lines were *on par* with the recurrent parent (JL 24) for pod yield (kg/ha), shelling percentage, test weight and sound mature kernel percentage. The background genome recovery in a selected family (JG_BC_3F_3_18) of JL 24 × GPBD 4 was up to 86.6% when checked with 30 polymorphic transposable element (TE) based markers covering all linkage groups. A few homozygous BC_1F_2 plants of TMV 2 × GPBD 4 were also identified. These genetic resources will be useful in identifying the backcross lines of JL 24 and TMV 2 with resistance to LLS and rust.

Development of Super Early Maturing Hybrids in Pigeonpea [*Cajanus cajan* (L.) Millspaugh] Using A_4 Cytoplasm

Hingane AJ*, Patil SB, Sameer kumar CV, Saxena KB

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
*Email: h.anupama@cgiar.org

In India, pigeonpea is mainly grown as intercrop, limiting significant increase in area and production. Considering the ever-increasing domestic demand of pigeonpea, several efforts were attempted to increase productivity of pigeonpea through development of hybrids. But, available pigeonpea hybrids are mainly of medium duration (160-180 days) which does not fit in wider cropping systems. There is need to promote pigeonpea in new production niches, like pigeonpea-wheat and pigeonpea –rice cropping pattern. Super early maturing pigeonpea that matures in 90-100 days and found to be less sensitive to photoperiod and temperature finds, potential in these areas. Considering this scenario, a crossing program was initiated to develop super early CMS lines during rainy season 2012. A set of 12 diverse super early testers were identified on the basis of *per se* performance and were crossed with ICPA 2156 as a prominent source of A_4 cytoplasm. The F_1 seeds were grown in the off-season to check their pollen fertility. Twenty-five plants were grown in each cross and all of them were completely sterile, indicating maintenance of sterility. The F_1 plants were again backcrossed with their respective maintainers to get the BC_1F_1 seeds. Out of which, ICPL 11335 gave maintainer reaction, while; ICPL 11336 was identified as restorer in super early group. Plant to plant crosses were made between the male sterile and maintainer line. Based on the performance of new experimental hybrids using early duration lines on selected male sterile plants, ICPL 149 and PAU 881 are identified as good restorers, which contribute for good vigor and yield in the super early hybrid combinations. The super early, identified restores were further crossed with the early restorers (ICPL 11336) for transferring desired agronomic traits.

Cleistogamous Flowering a Novel Trait in Pigeonpea [(*Cajanus cajan* (L.) Millspaugh] with Ensured Self-pollination

Sameerkumar CV[1*], Singh IP[2], Patil SB[1], Mula MG[1], Hingane AJ[1], Kumar RV[1], Gangarao NVPR[1], Singh VK[1], Saxena RK[1], Nageshkumar MV[3], Sudhakar C[3] and Varshney RK[1]

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

Pigeonpea (*Cajanus cajan* L.) is an often cross pollinated species and out crossing extent up to 25-30 %. It is considered to be a prime constraint in maintaining genetic purity of cultivars and genetic stocks. Once a variety is released for commercial cultivation, it deteriorates over time due to out-crossing, mechanical mixtures, mutations etc. and out crossing plays important role in it. To maintain a variety true to type especially in partially out-crossed species, it needs lot of resources in terms of isolation distance, installation of insect proof cages where isolation is not possible, labor charges for rouging and seed cleaning operations. Considering these facts attention was paid on natural mutant with wrapped flower morphology or cleistogamy. Cleistogamy trait is governed by single recessive gene and very easy to transfer in the background of commercial lines. A partial cleistogamous line ICPL 87154 was developed earlier with low natural out crossing (<1 %). Similar effort was initiated to develop early maturing cleistogamous lines in the background of elite lines and super early stable breeding lines. Crosses were made in year 2007 using ICPL 87154 (DT) as female with early and super early maturing genotypes. It is observed that cleistogamous flowering is linked with shriveled seeds and very few recombinants recovered with bold seeds in the advanced generation. At present ICPL 12337 is selected as best early maturing line with bold seeds in this group and can be used as donor for development of self-pollinated lines in this crop.

Molecular Tools for Plant Breeding – "Success Starts at the Plant"

Darshna Vyas *et al**

[1]LGC, Genomics Division, Hertfordshire, UK
*Email: darshna.vyas@lgcgroup.com

Sample preparation is key in all areas of science to ensure high-quality data and to reduce time spent revalidating results. Generating high quality data from applications such as sequencing or genotyping to support plant breeding programmes, requires strong and robust plant tissue sample preparation procedures. Achieving this can often be challenging as material has to be sourced and processed from remote locations.

Whilst DNA extraction in laboratories is processed in controlled environments, events upstream of this are varied and prone to mistakes and degraded samples are common by the time samples get to the lab. This means that valuable samples often give poorer sequencing / genotyping data than is desired. Whilst it may be possible to go back and re-sample, this is not always an option, and it can add weeks to finite breeding cycles. Increasingly plant breeders around the world are now looking to access molecular techniques for breeding and selection programs; and sampling processes are vital to ensure this can happen effectively.

LGC has worked closely with the plant breeding community to develop a robust and simple a plant sampling kit and protocol that is suitable for all cultivars. The kit is designed to get tissue safely back to laboratory in an optimal state and also overcomes phytosanitary regulations when crossing international borders.

In this poster we will present data to demonstrate the clear advantages of ensuring that truly "Success does starts at the plant".

Establishment of Wild Pea *Pisum fulvum* Chromosome Segment Substitution Lines in Cultivated *P. sativum* Genetic Background, as a Tool to Study Domestication and to Broaden Genetic Diversity

Smýkal P., Micová B.

Department of Botany, Palacký University in Olomouc,
Šlechtitelů 11, 783 71 Olomouc, Czech Republic
Email: petr.smykal@upol.cz

Plant evolution under domestication has altered numerous traits, including self-pollination which reinforced fertility barriers between wild and cultivated populations, facilitating fixation of the desired genotype. The domestication bottleneck has resulted in high degree of relatedness, leading to narrower genetic base of the cultivated germplasm which is prone to pests and diseases. The study of genetic diversity showed that although wide diversity is captured among cultivated peas, the wild material provides yet broader diversity. The chromosome segment substitution lines containing genomic segments of wild pea (*Pisum fulvum* WL2140) in the cultivated pea (*P. sativum subsp. sativum* WL1238/cv. Terno) genetic background were developed. Twenty eight microsatellite and 44 gene-specific markers at 2 to 82 cM spacing were used for initial molecular characterization of 105 lines. Heterozygozity was detected in 533 (8%), *Pisum sativum* parent was present in 4552 (69%), and introgressed segments of *P. fulvum* in 1551 (23%). There were 5-14 segments per line, with a mean of 9.6. These lines were described for 14 traits (including branching, height, nodes, pod and seed numbers). Establishment of such permanent introgression library will allow phenotypic characterization of unlimited number of target traits which, coupled together with higher density markers, will provide means for QTL and gene identification and subsequent incorporation in desired genotypes. In parallel, a series of lines is being established with *Pisum sativum* subsp. *elatius* L100 and cv. Cameor parents.

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Marker Assisted Gene Introgression: A Rapid Method to Incorporate Rust Resistant *Ur-3* Gene into the Genetic Background of French Bean

Adarsh MN[2], Aghora TS[1]*, Mohan N[1] Ravishankar KV[1]

[1]Indian Institute of Horticultural Research (IIHR), Bangalore, India
[2]University of Horticultural Sciences, Bagalkot, India
*E-mail: aghor@iihr.ernet.in

Rust (*Uromyces phaseoli* L.) is one of the most important fungal diseases of bean which has become epidemic in bean growing areas and especially in locations where humid to moderately humid conditions, long dew periods and cool conditions prevail during the growing season of beans. Accession IC-525236, maintained at IIHR, is a valuable source of rust resistance carries *Ur-3* gene conferring resistance to rust which is effective in bean introgressions and their derivatives. The *Ur-3* gene was validated using SCAR marker SK-14 which is strongly linked to the gene was mapped earlier and used for introgression in F_2 population derived from crosses of susceptible parent Arka Sharath and its resistant parent. The marker was also mapped and validated at the same position in another independent F_2 plants derived from crosses of IC-525236 with the susceptible parent IC-525260. In both the F_2 crosses, segregation was similar according to Mendelian fashion.

The marker segregated at (n = 620) for a gene. SK-14, defining *Ur-3*, was found to be reliable and robust co-dominant marker in a wide range of bean lines. The marker is useful in tagging in marker-assisted bean breeding programs that aim to incorporate *Ur-3* into elite bean lines and cultivars for durable resistance to rust.

Microsatellite Based DNA Finger Prints for Elucidation of Genetic Diversity in Rice (*Oryza sativa L.*)

Behera L[1], Mukherjee AK[2], Kulakarni K[3], Apoorva MJ[4]*

[1]Central Rice Research Institute, Odisha, India
[2] Central Rice Research Institute, Odisha, India
[3]Directorate of Rice Research, Hyderabad, India
[4] Narendra Dev University of Agriculture and Technology, Uttar Pradesh, India
*Email: apoorvamj565@gmail.com

Rice is the predominant dietary energy source in India as well as one third of world's population. Numerous varieties have been developed till date in order to meet the demands of mushrooming population. Genotypes considered for the present study have been previously characterized based on morphological characters but not at molecular level. Molecular markers can be employed for assaying genetic diversity, varietal identification, for protection of released varieties by intellectual property rights, to predict genetic fidelity of germplasm accessions during storage and conservation. This technique can be aptly called DNA Fingerprinting.

The present study was undertaken to assess genetic diversity among twenty two elite genotypes of rice at molecular level employing panel of forty five rice microsatellite markers. Among these, thirty primers revealed clear unambiguous polymorphism. These thirty primers generated 69 alleles i.e. on an average 2.833 alleles per locus. Polymorphic Information Content values ranged from 0 to 0.9 with an average of 0.726 per polymorphic locus. Genetic similarities among these genotypes varied from 0.43 to 0.80 with an average of 0.767. Three unique alleles were identified which can be ascribed as important source of genetic diversity and also in the development of diagnostic markers, serving as yardstick in differentiating genotypes. Cluster analysis revealed low genetic diversity amongst 22 rice genotypes considered under study. Hence, highly diverse genotypes need to be utilized for breeding program in order to exploit heterosis. Present study reflects the reliability of SSR markers to assess the molecular polymorphism, phylogenetic relationships and also in germplasm conservation.

Production of Doubled Haploids Through and Rogenesis and identification of Plants by Molecular Markers in Maize (*Zea mays* L.)

Morshed S, Hossain M, Islam SMS*

Plant Genetic Engineering Lab., Institute of Biological Sciences, University of Rajshahi, Rajshahi-6205, Bangladesh
*E-mail: shahin_ibsc@ru.ac.bd/shahinul68@gmail.com

The *in vitro* production of doubled haploids through androgenesis (anther & microspore culture) is an efficient system for production of fully homozygous plants rapidly. Through anther culture complete homozygous plants can be achieved within a year compared to long inbreeding methods. Significant advantage is that the system is not only speed up the advance to homozygosity, but also to increase selection efficiency. Under this study, seeds of four maize varieties (Barnali, Kohi Bhutta, Mohar, Shuvra) were collected from BARI, Gazipur, Bangladesh and cultured in three induction media *viz.* 6N1, N6 and Zheng-14. All media was supplemented with 0.1 mg/l TIBA, 1.5 mg/l 2, 4-D, 2.5 mg/l kinetin and activated charcoal. Cold pretreatment at 4ºC~ 6ºC to maize tassel from 3-21 days and as drought stress pre-treatments to precised anthers were applied for 1-9 hrs. Microspores at early to late uni-nucleate stages were cultured in IMM (modified MS). Highest embryoids (12-18%) were obtained in YP medium that supplement with 0.1 mg/l TIBA. Molecular screening of desired alleles combined with doubled haploid (DH) technology allows traits of interest to be fixed early in the breeding process are simple and efficient systems. RAPD (random amplified polymorphic DNA) and SSR (simple sequence repeats) marker-based analysis is under progress for the identification of plants that developed anther and microspore derived embryoids in comparison of control genotypes. Our main goals are to develop pure homozygous maize line and its proper identification through molecular marker analysis

An Efficient Integrated Genomic Approach For Rapid Delineation Of Potential Candidate Transcription Factor Genes/ Qtls Regulating Seed Weight In Chickpea

Kujur A[1], Bajaj D[1], Saxena MS[1], Tripathi S[2], Upadhyaya HD[3], Gowda CLL[3], Singh S[3], Jain M[1], Tyagi AK[1], Parida SK[1]*

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

Marker-assisted genetic improvement in crop plants requires large-scale validation and high-throughput genotyping of numerous informative genetic markers at genome-wide scale in order to identify and fine map (map-based isolation) the genes/ QTLs (quantitative trait loci) regulating important agronomic traits. The screening and genotyping of these informative markers in association panel (core and minicore germplasm lines) and advanced generation bi-parental mapping populations involve massive costs in terms of resources, time, and labour due to low intra-specific polymorphism in chickpea. This necessitates the development and use of a cost-effective association/ genetic mapping approach to expedite the genomics-assisted breeding application in chickpea. The whole genome and global transcriptome sequences of diverse *desi* and *kabuli* chickpea accessions however, generated huge genomic information such as microsatellite and single nucleotide polymorphism (SNP) markers, useful known/candidate genes, transcription factors (TFs) and regulatory sequences. These genomic information led to develop 1269 genic microsatellite markers including 1108 TFGMS (transcription factor gene-derived microsatellite) and 161 TFFDMS (transcription factor functional domain-associated microsatellite) informative markers from 707 TF genes at a genome-wide scale, which were further genotyped in seed weight-specific natural association mapping panel and bi-parental mapping population of chickpea. To accelerate this process of marker genotyping, an alternative time-saving and cost-effective pool-based trait association mapping approach integrated with genetic/QTL mapping, differential expression profiling, and high-resolution microsatellite-SNP marker-based haplotyping/LD (linkage disequilibrium) mapping was employed. This integrated approach helped us to delineate four candidate TF genes regulating seed weight in *desi* and *kabuli* chickpea. The evolutionary history derivation of one of the strong seed weight-associated TF gene based on natural allelic variations and haplotype-sharing among *desi*, *kabuli* and wild accessions unravelled useful information having implication for seed weight/size trait evolution during chickpea domestication. The seed weight-associated functionally relevant molecular tags (novel TF genes/ QTLs, alleles and haplotypes) identified have potential for marker-assisted genetic enhancement of chickpea.

Molecular and Morphological Characterization of Variation Related to *Fusarium* wilt Resistance in Gladiolus (*Gladiolus* x *hybridus* Hort.)

Poonam K[1]*, Manjunatha RT[2] and Anuradha S[1]

[1] University of Horticultural Sciences, Bagalkot, India
[2] Indian Institute of Horticultural Research (IIHR), Bangalore, India
*E-mail: poonamjaswalfls@gmail.com

Discovery of superior gladiolus lines conferring resistance to *fusarium* wilt from genetically diverse germplasm through combined approach of molecular marker and morphological analysis could provide its usefulness in breeding programs. Four gladiolus (*Gladiolus* x *hybridus* Hort.), accessions were screened for resistance to *fusarium* wilt. Two accessions (Arka Amar and IIHRG-11) from IIHR were identified with resistance to *fusarium* earlier. Twenty nine polymorphic inter-simple sequence repeat (ISSR) markers were screened for the ability to generate reproducible polymorphic bands for genetic diversity analysis. The polymorphic information content (PIC) values for these markers ranged from 0.66–0.85 with a mean of 0.75 per marker. Cluster analysis performed using generated by using Ward's method (UPGMA) determined that high genetic similarity was observed between genotypes 'Arka Amar' and 'Pink Friendship'. Genotypes 'IIHRG-11' and 'IIHRG-12' were closely related to each other. The present findings suggest that ISSR markers are useful for detection of resistant bands and also genetic relationship in gladiolus species. The identified ISSR marker from investigation will help in screening the gladiolus population for *fusarium* wilt resistance. Further tagging the gene, cloning and sequencing these desirable polymorphic DNA fragment in the future will verify the presence of specific genes related to *fusarium* resistance for gladiolus improvement programs.

Key words: Gladiolus, *Fusarium* wilt, ISSR markers, Polymorphism

Characterization of Radiation Induced Precise Transfer of Genes for High Grain Micronutrients from Non-Progenitor Aegilops Species into Wheat

Sheikh I[1], Sharma P[1], Verma S K[2], Kumar S[2], Malik S[3], Kumar S[3], Chugh V[1] and Dhaliwal HS[1*]

[1]Eternal University, Sirmour, Himachal Pradesh, India
[2]Indian Institute of Technology Roorkee, Roorkee, Uttarakhand, India
[3]GB Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India
*hsdhaliwal07@gmail.com

Radiation hybridization is very efficient physical mapping approach which can be used for precise transfers of useful genes from non-progenitor species into wheat cultivars. In the present study pollen and seeds of selected wheat-*Aegilops* substitution lines with enhanced grain micronutrients were irradiated at 1.75 Krad and 40 Krad, respectively. Only the healthy F_1 plants with better yield, good harvest index and bold seeds were screened for grain micronutrients and molecular marker retention. GISH analysis and SSR molecular markers data of the selected radiation hybrid plants indicated stable introgression of U^k and S^k chromosome fragments in the wheat genome. Some of the irradiation induced transfers showed higher grain Fe and Zn content indicating that some fine and compensating transfers carrying the genes for high grain iron and zinc without linkage drag could be obtained. Approximately forty genes are involved in the process of micronutrient uptake, translocation and sequestration e.g. *IDS, NAAT, NAS, Nramp, YSL, ZIP* and *FRO*. Introns, the non-coding sequences of genes, are interspersed throughout the eukaryotic genome. Compared with exons, the introns are much more variable and suitable for DNA marker development. For intron targeted amplified polymorphic marker development, full mRNA sequences of the genes were retrieved from the NCBI database, and on BLASTn against the wheat genome in Ensembl Plants got the genomic sequences for the mRNAs revealing the exonic and intronic sequences of the genes. These markers amplifying intronic regions of the genes are being used for characterization and validation of precise transfer with least linkage drag.

List of Participants

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(Ralph W Cummings Auditorium)

List of Participants

Australia

Atieno, Judith
Australian Centre for Plant Functional Genomics (ACPFG)
University of Adelaide
Adelaide
judith.atieno@acpfg.com.au

Batley, Jacqueline
University of Western Australia
Perth
jacqueline.batley@uwa.edu.au

Bhave, Mrinal
Swinburne University of Technology
Hawthorn
mbhave@swin.edu.au

Colmer, Tim
University of Western Australia
Perth
timothy.colmer@uwa.edu.au

Edwards, Dave
University of Western Australia
Perth
dave.edwards@uwa.edu.au

Henry, Robert J
University of Queensland
Brisbane
robert.henry@uq.edu.au

Huang, Emma
Commonwealth Scientific and Industrial Research Organisation
(CSIRO)
Brisbane
emma.huang@csiro.au

Jordan, David R
University of Queensland
Brisbane
david.jordan@uq.edu.au

Kamboj, Atul
Swinburne University of Technology
Hawthorn
akamboj@swin.edu.au

Khan, Hammad
Australian Centre for Plant Functional Genomics (ACPFG)
University of Adelaide
Adelaide
hammad.khan@acpfg.com.au

Kilian, Andrzej
Diversity Arrays Technology Pty Ltd (DArT)
Bruce
zej@diversityarrays.com

Li, Yongle
Australian Centre for Plant Functional Genomics (ACPFG)
University of Adelaide
Adelaide
yongle.li@acpfg.com.au

Mace, Emma
University of Queensland
Brisbane
emma.mace@daff.qld.gov.au

Pang, Jiayin
University of Western Australia
Perth
jiayin.pang@uwa.edu.au

Ruperao, Pradeep
University of Western Australia
Perth
p.ruperao@uq.edu.au

Siddique, Kadambot
UWA Institute of Agriculture, University of Western Australia
Perth
kadambot.siddique@uwa.edu.au

Spangenberg, German C
DEPI, La Trobe University
Melbourne
German.Spangenberg@depi.vic.gov.au

Sutton, Tim
South Australian Research and Development Institute (SARDI)
Adelaide
tim.sutton@sa.gov.au

Bangladesh

Islam, Shahinul
University of Rajshahi
Rajshahi
shahin_ibsc@ru.ac.bd

Mohd, Atikur R
Advanced Seed Research and Biotech Center (ASRBC),
Advanced Chemical Industries (ACI) Ltd
Dhaka
atikur@aci-bd.com

Benin

Ramaiah, Venuprasad
Africa Rice Center (AfricaRice)
Cotonou
r.venuprasad@cgiar.org

Burkina Faso

Zongo, Adama
University of Ouagadougou
Ouagadougou
zongoss@yahoo.fr

Canada

Deokar, Amit A
University of Saskatchewan
Saskatoon
aadeokar@gmail.com

Sharpe, Andrew G
National Research Council of Canada
Saskatoon
andrew.sharpe@nrc-cnrc.gc.ca

China

Yu, Yue
Millennium Genomics Inc.
Shenzhen
yuyue@macrogencn.com

Zhang, Gengyun
BGI – Shenzhen
Shenzhen
zhanggengyun@genomics.org.cn

Czech Republic

Smykal, Petr
Palacky University
Olomouc
petr.smykal@upol.cz

Egypt

Hamwieh, Aladdin
International Center for Agricultural Research in the Dry Are as (ICARDA)
Cairo
a.hamwieh@cgiar.org

Ethiopia

Fenta, Berhanu A
Ethiopian Institute of Agricultural Research (EIAR)
Melkassa
berhanufenta@gmail.com

Ojiewo, Christopher O
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Addis Ababa
c.ojiewo@cgiar.org

France

Berges, Helene
French Plant Genomic Resources Center
Toulouse
helene.berges@toulouse.inra.fr

Sorokin, Alexander
Aglentech
Evry
asorokin@algentech.com

Germany

Ordon, Frank
JKI- Federal Research Centre for Cultivated Plants
Quedlinburg
frank.ordon@jki.bund.de

Stein, Nils
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
Gatersleben
stein@ipk-gatersleben.de

Wenzl, Peter
Global Crop Diversity Trust
Bonn
peter.wenzl@croptrust.org

Ghana

Danquah, Eric Y
West Africa Centre for Crop Improvement (WACCI), University of Ghana
Legon
edanquah@wacci.edu.gh

Ifie, Beatrice E
West Africa Centre for Crop Improvement (WACCI), University of Ghana
Legon
bifie@wacci.edu.gh

India

Adarsh, MN
Dr. Yashwant Singh Parmar University of Horticulture and Forestry
Solan
adarshm464@gmail.com

Agarwal, Gaurav
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
gaurav.agarwal@cgiar.org

Aggarwal, Ramesh
CSIR-Centre for Cellular and Molecular Biology (CCMB)
Hyderabad
rameshka@ccmb.res.in

Agrawal, Pawan K
National Agricultural Science Fund
Ministry of Agriculture
New Delhi
nationalfund1011@gmail.com

Alo, Fedaa
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
f.alo@cgiar.org

Anand Kumar, P
DSS Takara Bio India Pvt. Ltd
New Delhi
anand_kumar@dsstakarabio.com

Anandan, A
ICAR-Central Rice Research Institute (CRRI)
Cuttack
anandanau@yahoo.com

Angannan, Suganya
ICAR-Sugarcane Breeding Institute
Coimbatore
harimuns@rediff.com

Ansari, Mohd Jamal
ICAR-Indian Institute of Pulses Research (IIPR)
Kanpur
jamalansari87@gmail.com
Apoorva, MJ
ICAR- Central Rice Research Institute (CRRI)
Cuttack
apoorvamj565@gmail.com

Arumugam, Chandrasekar
ICAR-National Research Centre for Banana (NRCB)
Tiruchirapalli
chandrugcg_77@yahoo.co.in

Babbar, Anita
Jawaharlal Nehru Krishi Viswa Vidyalaya (JNKVV)
Jabalpur
anitababbar@rediffmail.com

Babu, Raman
CIMMYT-India
Patancheru
r.babu@cgiar.org

Bahuguna, Ashish
Ministry of Agriculture
New Delhi
secy-agri@nic.in

Bajaj, Deepak
National Institute of Plant Genome Research (NIPGR)
New Delhi
deepak_bajaj19@yahoo.com

Bajaj, Prasad
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.bajaj@cgiar.org

Balyan, Harindra S
Ch Charan Singh University
Meerut
hsbalyan@gmail.com

Bansal, Kailash C
ICAR-National Bureau of Plant Genetic Resources (NBPGR)
New Delhi
kailashbansal@hotmail.com

Bedis, Madhukar R
Mahatma Phule Krishi Vidyapeeth (MPKV)
Rahuri
pulses.mpkv@gmail.com

Bera, Biswajit
Tea Board of India
Kolkata
drteaboard@gmail.com

Bergvinson, David
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
d.bergvinson@cgiar.org

Bhat, Ashraf
Sher-e-Kashmir University of Agri. Sciences and Technology of Kashmir
Shalimar
mashrafbhat@skuastkashmir.ac.in; mashrafbhat@gmail.com

Bhat, Ramesh S
University of Agricultural Sciences (UAS)
Dharwad
bhatramesh12@gmail.com

Bhatia, Chittranjan
Former Secretary, Department of Biotechnology, Government of India
Mumbai
crbhatia.bhatia@gmail.com

Bhatia, Sabhyata
National Institute of Plant Genome Research (NIPGR)
New Delhi
sabhyatabhatia@nipgr.ac.in

Bhardwaj, Vinay
Reliance Industries
Mumbai
vbhardwaj902@gmail.com

Bhattacharya, Parthasarathi
Tierra Seed Science Pvt Ltd.
Hyderabad
partha@tierraseedscience.com

Biradar, Sunil K
Monsanto Holdings Pvt Ltd
Hyderabad
sunil.kumar.biradar@monsanto.com

Chakraborthy, Niranjan
National Institute of Plant Genome Research (NIPGR)
New Delhi
nchakraborty@nipgr.ac.in; nchakraborty@hotmail.com

Carberry, Peter
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.carberry@cgiar.org

Chandra, Saket
Birla Institute of Technology
Mesra
saket10to22@gmail.com

Chattoo, Bharat B
M.S.University of Baroda
Baroda
bharat.chattoo@bcmsu.ac.in

Chaturvedi, Sushil K
ICAR- Indian Institute of Pulses Research (IIPR)
Kanpur
sushilk.chaturvedi@gmail.com

Chaudhary, Spandan
Kadi Sarva Vishwavidyalaya
Gandhinagar
spandan.chaudhary@gmail.com

Chellapilla, Bharadwaj
ICAR-Indian Agricultural Research Institute (IARI)
New Delhi
drchbharadwaj@gmail.com

Chetukuri, Anuradha
Prof. Jayshankar Telangana State Agricultural University (PJTSAU)
Hyderabad
anu_dna@rediffmail.com

Chinchole, Laxuman
Bayer Crop Science
Hyderabad
laxuman.chinchole@bayer.com

Chitikineni, Anu
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
a.chitikineni@cgiar.org
Dadakhalandar, Doddamani
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
d.doddamani@cgiar.org

Dan, Debasis
DuPont Pioneer
Hyderabad
debasis.dan@pioneer.com

Das, Alok
ICAR- Indian Institute of Pulses Research (IIPR)
Kanpur
alokbio@gmail.com, adas@icar.org.in

Das, Sandip
University of Delhi
New Delhi
sandipdas04@gmail.com

Datta, Karabi
University of Calcutta
Kolkata
krbdatta@yahoo.com

Datta, Swapan K
Visva-Bharati University
Santiniketan
swpndatta@yahoo.com

Deshpande, Sanjeev K
University of Agricultural Sciences (UAS)
Dharwad
sanjeevgpb@gmail.com

Deshpande, Santosh
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.deshpande@cgiar.org

Devi, Pooja
Bisco BioSciences Pvt Ltd
Hyderabad
pooja.devi@limagrain.in

Dhaliwal, Harcharan S
Eternal University
Baru Sahib Via Rajgarh
hsdhaliwal07@gmail.com

Dhande, Gaurav A
Nirmal Seeds Pvt. Ltd.
Pachora
gadhande@nirmalseedsindia.com

Dharmaraj, PS
ARS-Gulbarga, University of Agricultural Sciences
Raichur
psdharmaraj@yahoo.com

Easdown, Warwick
AVRDC/South Aisa, The World Vegetable Center
Patancheru
warwick.easdown@worldveg.org

Ellis, Noel
CGIAR Research Program on Grain Legumes
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
n.ellis@cgiar.org

Gaikwad, Priyanka
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
priyankagaikwad00@gmail.com

Garg, Aditya P
ICAR-Indian Institute of Pulses Research (IIPR)
Kanpur
adityapratapgarg@gmail.com

Garg, Vanika
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
vanikag1@gmail.com

Garladinne, Mallikarjuna
Agri Biotech Foundation
Hyderabad
mallikb4u@gmail.com

Gaur, Pooran
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.gaur@cgiar.org

Ghana, Pallavi
DuPont Pioneer
Hyderabad
pallavi.ghana@pioneer.com

Ghosh, Raju
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
r.ghosh@cgiar.org

Gopinath, Ashok
Illumina Inc. India
Bengaluru
agopinath@illumina.com

Gowda, Malali
Centre for Cellular and Molecular Platforms
Bengaluru
malalig@ncbs.res.in

Grando, Stefania
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
S.Grando@cgiar.org

Gupta, Hari S
Borlaug Institute for South Asia (BISA)
New Delhi
h.s.gupta@cgiar.org

Gupta, Pushpendra K
Ch Charan Singh University
Meerut
pkgupta36@gmail.com

Gupta, Rajeev
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
g.rajeev@cgiar.org

Gupta, Sanjeev
ICAR-Indian Institute of Pulses Research (IIPR)
Kanpur
saniipr@rediffmail.com

Gupta, Shashi K
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.gupta@cgiar.org

Gupta, Shilpa
Punjab Agricultural University
Ludhiana
shilpagupta09@gmail.com

Hingane, Anupama
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
h.anupama@cgiar.org

Jaganathan, Deepa
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
j.deepa@cgiar.org

Jain, Ankit
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
A.Jain@cgiar.org

Jain, Mukesh
National Institute of Plant Genome Research (NIPGR)
New Delhi
mjain@nipgr.ac.in

Jhang, Tripta
CSIR-Central Institute of Medicinal and Aromatic Plants (CIMAP)
Lucknow
t.jhang@cimap.res.in

Kale, Sandip
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.kale@cgiar.org

Kancharla, Nagesh
Reliance Industries Limited
Mumbai
nagesh.kancharla@ril.com

Karwa, Anup
Krishidhan Seeds Pvt. Ltd
Jalna
anupkarwa@krishidhanseeds.com

Kashikar, Pratiksha M
Ankur Seeds Pvt Ltd
Nagpur
pratiksha@ankurseeds.com

Kavikishor, PB
Osmania University
Hyderabad
pbkavi@yahoo.com

Kedareswar, Pradhan
Orissa University of Agriculture & Technology (OUA&T)
Bhubaneswar
kdrcsp@gmail.com

Khan, Aamir W
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
a.khan@cgiar.org

Khera, Pawan
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
k.pawan@cgiar.org

Konda, Kotilingam
Bayer Crop Science
Hyderabad
kotilingam.konda@bayer.com

Koradi, Pranitha
Barwale Foundation
Hyderabad
pranitha@barwalefoundation.org

Korupalli, Usha K
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
k.kiranmayee@cgiar.org
Kothari, SL
Amity University
Jaipur
slkothari@jpr.amity.edu

Kotla, Anuradha
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
a.kotla@cgiar.org

Krishnamohan, KAVS
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
k.krishnamohan@cgiar.org

Krishnamurthy, Nandini
DuPont Pioneer
Hyderabad
krishnamurthy.nandini@pioneer.com

Kriti, Roopendra
ICAR-Indian Institute of Sugarcane Research (IISR)
Lucknow
kriti.roopendra@gmail.com

Kudapa, Himabindu
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
k.himabindu@cgiar.org

Kujur, Alice
National Institute of Plant Genome Research (NIPGR)
New Delhi
alice1.kujur@nipgr.ac.in

Kulwal, Pawan L
Mahatma Phule Krishi Vidyapeeth (MPKV)
Rahuri
pawankulwal@gmail.com

Kumar, Arvind
IRRI South Asia Hub
Patancheru
a.kumar@irri.org

Kumar, Ashish
Jawaharlal Nehru Krishi Viswa Vidyalaya (JNKVV)
Jabalpur
ashishashish2612@gmail.com

Kumar, Ashok
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
a.ashokkumar@cgiar.org

Kumar, Bhavnesh
DSS Takara Bio India Pvt. Ltd
New Delhi
bhavnesh_kumar@dsstakarabio.com

Kumar, Jitendra
ICAR- Indian Institute of Pulses Research (IIPR)
Kanpur
jitendra73@gmail.com

Kumar, Manish
Birla Institute of Technology
Ranchi
manish@bitmesra.ac.in

Kumar, Narendra
ICAR- Directorate of Groundnut Research (DGR)
Junagadh
narendrapb09@gmail.com

Kumari, Poonam
Dr. Yashwant Singh Parmar University of Horticulture and Forestry
Solan
poonamjaswalfls@gmail.com

Kumari, Varsha
formerly with University of Agricultural Sciences
Dharwad
varshagpb@gmail.com

Kundapura, Ravishankar
Indian Institute of Horticultural Research
Bengaluru
kv_ravishankar@yahoo.co.in

Maganti, Sheshu Madhav
ICAR- Indian Institute of Rice Research (IIRR)
Hyderabad
sheshu_24@yahoo.com

Mahala, Rajendra S
DuPont Pioneer
Hyderabad
r.s.mahala@pioneer.com

Mahto, Arunima
National Institute of Plant Genome Research (NIPGR)
New Delhi
arunimamahto@yahoo.com

Manda, Sriswathi
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
m.sriswathi@cgiar.org

Mani, Elangovan
Advanta India Limited
Hyderabad
elangovan.m@advantaseeds.com

Mani, Vetriventhan
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
m.vetriventhan@cgiar.org

Manivannan, N
Tamil Nadu Agricultural University
Coimbatore
nmvannan@gmail.com; nm68@tnau.ac.in

Menon, Sai
Ganga Kaveri Seeds Pvt. Ltd.
Hyderabad
jm.rao@gangakaveri.in

Modala, Venkateshwarlu
Seribiotech Research Laboratory
Bengaluru
modalavenkat@yahoo.com

Mohanty, Amitabh
DuPont Pioneer
Hyderabad
amitabh.mohanty@pioneer.com

Mohapatra, Trilochan
ICAR-Central Rice Research Institute (CRRI)
Cuttack
tmnrcpb@gmail.com; directorcrri@sify.com

Mukherjee , Arijit
Bayer Crop Science
Hyderabad
arijit.mukherjee@bayer.com
Mukhopadhyay, Kunal
Birla Institute of Technology
Mesra
kmukhopadhyay@bitmesra.ac.in

Muniswamy, S
ARS-Gulbarga, University of Agricultural Sciences
Raichur
muniswamygpb@gmail.com

Nadaf, HL
University of Agricultural Sciences (UAS)
Dharwad
hlnadaf892@yahoo.com

Nagabandi, Tulasi
Premas Life Sciences Pvt. Ltd
New Delhi
tulasi.nagabandi@premasbiotech.com

Narayanan, Eswar
DuPont Pioneer
Hyderabad
narayanan.eswar@pioneer.com

Narayanan, KK
Metahelix Life Sciences Limited
Bengaluru
narayanan@meta-helix.com

Nayak, Spurthi
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.nayak@cgiar.org

Neelagiri, Jagan Mohan Rao
Ganga Kaveri Seeds Pvt. Ltd.
Hyderabad
jm.rao@gangakaveri.in

Obala, Jimmy
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
jimmyobala@gmail.com

Palchamy, Kadirvel
ICAR- Directorate of Oilseeds Research
Hyderabad
kadirvel.palchamy@gmail.com
Pandey, Arun K
University of Hyderabad
Hyderabad
pandeyarun80@gmail.com

Pandey, Dev
Birla Institute of Technology
Mesra
dmpandey@bitmesra.ac.in

Pandey, Manish
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
m.pandey@cgiar.org

Parida, Ajay
M S Swaminathan Research Foundation
Chennai
ajay-ed@mssrf.res.in

Parupalli, Swathi
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.swathi@cgiar.org

Pasupuleti, Janila
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.janila@cgiar.org

Patel, Kishan K
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.kishan@cgiar.org

Pathak, Dharminder
Punjab Agricultural University
Ludhiana
dharminderpathak@pau.edu

Patil, Bhuvaneshwaragouda R
University of Agricultural Sciences (UAS)
Dharwad
patilbhuvaneshwara@gmail.com

Patil, Sanjiv S
Mahatma Phule Krishi Vidyapeeth (MPKV)
Rahuri
sanjivspatil@gmail.com

Patil, Sudam C
Mahatma Phule Krishi Vidyapeeth (MPKV)
Rahuri
sudampatil59@gmail.com

Patil, Suyash
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
p.suyash@cgiar.org

Pattanashetti, Santosh
International Crops Research Institute for the Semi-Arid Tropics
Patancheru
s.pattanashetti@cgiar.org

Pattnaik, Swetansu
DuPont Pioneer
Hyderabad
swetansu.pattnaik@pioneer.com

Pental, Deepak
University of Delhi- South Campus
New Delhi
dpental@gmail.com

Polumetla , Ananda Kumar
Prof. Jayshankar Telangana State Agricultural University (PJTSAU)
Hyderabad
polumetla@hotmail.com

Poornima, KN
ICAR-Indian Institute of Pulses Research
Kanpur
poornimakn04@gmail.com

Pradhan, Akshay K
University of Delhi- South Campus
New Delhi
pradhancgmcp@gmail.com

Prasad, Manoj
National Institute of Plant Genome Research (NIPGR)
New Delhi
manoj_prasad@nipgr.ac.in

Prashant, Ramya
CSIR- National Chemical Laboratory (NCL)
Pune
rm.dixit@ncl.res.in
Prashant, S
Osmania University
Hyderabad
prashantsingam@gmail.com

Pazhamala , Lekha T
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
l.pazhamala@cgiar.org

Purohit, Shilp
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.purohit@cgiar.org

Radhakrishnan, T
ICAR-Directorate of Groundnut Research (DGR)
Junagadh
radhakrishnan.nrcg@gmail.com

Mousam, Ram Kumar
Birla Institute of Technology
Mesra
mousam.kr@gmail.com

Ramalingam, Abirami
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
a.ramalingam@cgiar.org

Rajani , G
Prof. Jayshankar Telangana State Agricultural University (PJTSAU), Hyderabad
rajani071@gmail.com

Rathnakumar, Arulthambi Luke
ICAR-Directorate of Groundnut Research (DGR)
Junagadh
rathnakumar169@gmail.com

Rathore, Abhishek
International Crops Research Institute for the Semi-Arid Tropics
Patancheru
a.rathore@cgiar.org

Ratnaparkhe, Milind B
ICAR-Directorate of Soybean Research (DSR), Indore
milind.ratnaparkhe@gmail.com

Reddy, Arjula R
University of Hyderabad
Hyderabad
arjulsl@yahoo.com

RM, Sundaram
ICAR-Indian Institute of Rice Research (IIRR)
Hyderabad
rms_28@rediffmail.com

Robin, S
Tamil Nadu Agricultural University (TNAU)
Coimbatore
robin.tnau@gmail.com

Rohini, MK
University of Agricultural Sciences (UAS)
Dharwad
rohini_bt45@rediffmail.com

Roorkiwal, Manish
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
m.roorkiwal@cgiar.org

Sameerkumar, CV
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
c.sameerkumar@cgiar.org

Samineni, Srinivasan
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.srinivasan@cgiar.org

Sanampudi, Venkata R
Bisco BioSciences Pvt Ltd
Hyderabad
ramireddyag@gmail.com

Sandhu, JS
Indian Council of Agricultural Research
New Delhi
ddgcs.icar@nic.in

Saraswathi, Abhiman
DuPont Pioneer
Hyderabad
abhiman.saraswathi@pioneer.com

Saifulla, M
University of Agricultural Sciences (UAS)
Bengaluru
saifullasaifulla@rediffmail.com

Saxena, Rachit
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
r.saxena@cgiar.org

Seleman, Kaoneka
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
k.seleman@cgiar.org

Senapathy, Senthilvel
ICAR-Directorate of Oilseeds Research (DOR)
Hyderabad
senasenthil@yahoo.com

Sharma, Amita
ICAR-Indian Institute of Sugar Cane Research
Lucknow
amitanamita@gmail.com

Sharma, Mamta
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
mamta.sharma@cgiar.org

Sharma, Pankaj
DuPont Pioneer
Hyderabad
psgeneticist@gmail.com;
pankaj.sharma@pioneer.com

Sharma, Pradeep K
Ch Charan Singh University
Meerut
Pks264@rediffmail.com

Sharma, Prakash C
Guru Gobind Singh Indraprastha University
New Delhi
prof.pcsharma@gmail.com

Sharma, Ram K
CSIR-Institute of Himalayan Bioresource Technology (IIHBT), Himachal Pradesh
ramsharma@ihbt.res.in
Sharma, Rameshwar
University of Hyderabad
Hyderabad
rameshwar.sharma@gmail.com

Sharma, Rameshwer P
ICAR-National Research Centre for Plant Biotechnology
New Delhi
rpsnrcpb@yahoo.co.in

Shedage, Sambhaji
Bayer Crop Science
Hyderabad
sy.shedge@bayer.com

Shehzad , Anwar
Aligarh Muslim University (AMU)
Aligarh
shahzadanwar@rediffmail.com

Sheikh, Imran
Eternal University
Baru Sahib Via Rajgarh
imransheikh485@gmail.com

Sheshshayee, MS
University of Agricultural Sciences (UAS)
Bengaluru
msheshshayee@hotmail.com

Shukla, Vivek
NRGene
Hyderabad
moran@nrgene.com

Siddiq, Ebrahimali A
Prof. Jayshankar Telangana State Agricultural University (PJTSAU)
Hyderabad
easiddiq@rediffmail.com; easiddiq@gmail.com

Singh, Akhilesh K
Barwale Foundation
Hyderabad
akhileshsingh@barwalefoundation.org

Singh, Anandita
The Energy and Resources Institute (TERI)
New Delhi
anandita107@gmail.com
Singh, Anil K
CSIR- Institute of Himalayan Bioresource Technology
Palampur
anil@ihbt.res.in

Singh, Arpan
ICAR- Indian Institute of Pulses Research (IIPR)
Kanpur
arpan.biotech@gmail.com

Singh, BD
Banaras Hindu University (BHU)
Varanasi
brahmadsingh@gmail.com

Singh, Jang B
ICAR- Indian Agricultural Research Institute (IARI)
Indore
jangbsingh@gmail.com

Singh, Muneendra
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
singhmk_23@yahoo.co.in

Singh, Nand
Motilal Nehru National Institute of Technology
Allahabad
singhnand@gmail.com

Singh, Narendra P
ICAR-Indian Institute of Pulses Research (IIPR)
Kanpur
npsingh.iipr@gmail.com

Singh, Rana DP
ICAR- Sugarcane Research Station
Gorakhpur
singhranadp@gmail.com

Singh, Servejeet
Rajasthan Agricultural Research Institute (RARI)
Durgapura
singhservejeet@yahoo.co.in

Singh, Vikas K
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
vikas.singh@cgiar.org

Singh, Vikash
National Institute of Plant Genome Research (NIPGR)
New Delhi
tovikashalone@gmail.com

Singh, Uma Maheshwar
IRRI South Asia Hub
Patancheru
uma.singh@irri.org

Singhal, Tripti
Indian Agricultural Research Institute (IARI)
New Delhi
triptisinghal16@gmail.com

Sinha, Pallavi
International Crops Research Institute for the Semi-Arid Tropics
Patancheru (ICRISAT)
p.sinha@cgiar.org

Sivaprasad, V
Central Sericultural Research & Training Institute (CSRTI)
Mysuru
csrtimys@gmail.com

Sivasankar, Shobha
CGIAR Research Program on Dryland Cereals
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
s.sivasankar@cgiar.org

SM, Balachandran
ICAR-Indian Institute of Rice Research (IIRR)
Hyderabad
balasena@yahoo.com

Sonti, Ramesh V
CSIR-Centre for Cellular and Molecular Biology (CCMB)
Hyderabad
sonti@ccmb.res.in

Srinivas, A
Osmania University
Hyderabad
srinivasmessage@gmail.com

Srivastava, Rakesh
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
r.k.srivastava@cgiar.org

Sujatha, M
ICAR-Directorate of Oilseeds Research (DOR)
Hyderabad
sujatador@gmail.com

Swaminathan, MS
M S Swaminathan Research Foundation
Chennai
founder@mssrf.res.in

Tathineni, Revathi
Prof. Jayshankar Telangana State Agricultural University (PJTSAU)
Hyderabad
revathi.biotech87@gmail.com

Thammineni, Chakradhar
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
t.chakradhar@cgiar.org

Thirumalaisamy, PP
ICAR-Directorate of Groundnut Research (DGR)
Junagadh
thirumalaisamypp@yahoo.co.in

Thudi, Mahendar
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
t.mahendar@cgiar.org

Tiwari, Onkar N
Department of Biotechnology
Ministery of Science & Technology
onkart@gmail.com

Tomer, Vinay K
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
vinay.kumar@cgiar.org

Tripathi, Shailesh
ICAR- Indian Agricultural Research Institute (IARI)
New Delhi
shaitri@rediffmail.com

Turlapati, Phanikanth
DuPont Pioneer
Hyderabad
phanikanth.turlapati@pioneer.com

Upadhyaya, Hari D
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
h.upadhyaya@cgiar.org

Upputuri, Siva P
DuPont Pioneer
Hyderabad
siva.upputuri@pioneer.com

Vadez, Vincent
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
v.vadez@cgiar.org

Varshney, Alok
Reliance Industries Limited (RIL)
Mumbai
alok.varshney@ril.com

Varshney, Rajeev
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
r.k.varshney@cgiar.org

Vasal, Surinder
CIMMYT-India
New Delhi
s.vasal@cgiar.org

Veera, Jayalakshmi
Regional Agricultural Research Station, Acharya N G Ranga Agricultural University
Nandyal
veera.jayalakshmi@gmail.com

Verma, Indu
ICAR-Indian Institute of Sugarcane Research (IISR)
Lucknow
indu.verma8718@gmail.com

Verma, Subodh
National Institute of Plant Genome Research (NIPGR)
New Delhi
subodhshanky@gmail.com

Vishwakarma, Manish

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru
manishvis@gmail.com

Viswanathan, Sadhasivam
DuPont Pioneer
Hyderabad
sadhasivam.viswanathan@pioneer.com

Yadav, Om P
ICAR-Directorate of Maize Research (DMR)
New Delhi
pdmaize@gmail.com

Yadav, Shailesh
IRRI South Asia Hub
Patancheru
shailesh.yadav@irri.org

Yaduru, Shasidhar
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru
y.shasidhar@cgiar.org

Yamini, KN
Prof. Jayshankar Telangana State Agricultural University (PJTSAU), Hyderabad
yaminikn@yahoo.com

Yeri, Sharanabasappa B
University of Agricultural Sciences (UAS)
Dharwad
vishalyeri@gmail.com

Iran

Nezhad, Khalil Z
Gorgan University of Agricultural Sciences and Natural Resources, Gorgon
khalil1381@yahoo.com

Israel

Ronen, Gil
NRGene
Ness Ziona
moran@nrgene.com

Japan

Manickavelu, Alagu
Yokohama City University
Yokohama
manicks@yokohama-cu.ac.jp

Kenya

Boddupalli , Prasanna M
International Maize and Wheat Improvement Center (CIMMYT)
Nairobi
b.m.prasanna@cgiar.org

Djikeng, Appolinaire
Biosciences Eastern and Central Africa (BecA) Hub, C/o ILRI
ILRI, Nairobi
a.djikeng@cgiar.org

Ferguson, Morag
International Institute for Tropical Agriculture (IITA)
Nairobi
m.ferguson@cgiar.org

Gemenet, Dorcus Chekesis
Kenya Agricultural and Livestock Research
Nairobi
gemenet2014@gmail.com

Kapinga, Fortunus
International Institute for Tropical Agriculture (IITA)
Nairobi
fakapinga@yahoo.com

Kimurto, Paul
Egerton University
Nakura
kimurtopk@gmail.com

Manyasa, Eric
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Nairobi
e.manyasa@cgiar.org

Monyo, Emmanuel S
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Nairobi
e.monyo@cgiar.org

NVPR, Ganga R
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Nairobi
n.gangarao@cgiar.org

Ojulong, Henry
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Nairobi
h.ojulong@cgiar.org

Olsen, Mike S
International Maize and Wheat Improvement Center
Nairobi
m.olsen@cgiar.org

Yao, Nasser K
Biosciences Eastern and Central Africa (BecA) Hub
C/o ILRI
Nairobi
n.yao@cgiar.org

South Korea

Lee, Suk-Ha
Seoul National University
Seoul
sukhalee@snu.ac.kr

Wu , Tingting
Macrogen Inc.
Seoul
ttwu@macrogencn.com

Mexico

Crossa, Jose
International Maize and Wheat Improvement Center (CIMMYT)
Texcoco
j.crossa@cgiar.org

Hearne, Sarah J
International Maize and Wheat Improvement Center (CIMMYT), Texcoco
s.hearne@cgiar.org
Ribaut, Jean-Marcel
Generation Challenge Programme
C/o CIMMYT, Texcoco
j.ribaut@cgiar.org

Sehgal, Deepmala
International Maize and Wheat Improvement Center (CIMMYT), Texcoco
D.Sehgal@cgiar.org

Niger

Gangashetty, Prakash
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Niamey
p.gangashatty@cgiar.org; prakash.gangashetty@gmail.com

Nigeria

Motagi, Babu N
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Kano
b.n.motagi@cgiar.org; bnmotagi@rediffmail.com

Omoigui, Lucky O
University of Agriculture
Makurdi
lomoigui@yahoo.co.uk

Ousmane, Boukar
International Institute for Tropical Agriculture (IITA)
Kano
o.boukar@cgiar.org

The Netherlands

Dixit, Shital
Keygene N V
Wageningen
shital.dixit@keygene.com

The Philippines

Ali, Jauhar
International Rice Research Institute (IRR)
Los Banos
j.ali@irri.org

Dwiyanti, Maria S
International Rice Research Institute (IRRI)
Los Banos
m.dwiyanti@irri.org

Thomson, Michael
International Rice Research Institute (IRRi)
Los Banos
m.thomson@irri.org

Senegal

Faye, Issa
Institut Sénégalais de Recherches Agricoles (ISRA)-
Centre National de Recherches Agronomiques (CNRA)
Bambey
issafaye2001@yahoo.fr

Sri Lanka

Perera, Chandrika N
Coconut Research Institute
Lunuwila
chandrikaperera2003@yahoo.com

Uganda

Mugisha, Mukankusi C
International Center for Tropical Agriculture
Arusha
c.mukankusi@cgiar.org

United Kingdom

Anthony, Jeffrey
LGC Genomics
Hoddesdon
jeffrey.anthony@lgcgroup.com

Asquith, Steven
LGC Genomics
Hoddesdon
steven.asquith@lgcgroup.com

Hickey, John M
University of Edinburgh
Edinburgh
hickeyjohn@gmail.com

Marshall, David F
The James Hutton Institute
Scotland
David.Marshall@hutton.ac.uk

United States of America

Atlin, Gary
Bill & Melinda Gates Foundation (BMGF)
Seattle
gary.atlin@gatesfoundation.org

Axton, Myles
Nature Genetics
New York
m.axton@us.nature.com

Bell, Matt
LGC Genomics
Beverly
matt.bell@lgcgroup.com

Cook, Douglas R
University of California
Davis
drcook@ucdavis.edu

Ehlers, Jeffrey
Bill & Melinda Gates Foundation (BMGF)
Seattle
jeff.ehlers@gatesfoundation.org

Fountain, Jake C
USDA-ARS/University of Georgia
Tiffton
jfount1@uga.edu

Guo, Baozhu
United States Department of Agriculture-Agricultural
Research Services
Tiffton
baozhu.guo@ars.usda.gov

Harms, Dan
Douglas Scientific
Minneapolis
dan.harms@douglasscientific.com

Higgins, William
Douglas Scientific
Minneapolis
ross.higgins@douglasscientific.com

King, Matthew
DuPont Pioneer
Urbandale
matt.king@pioneer.com

Kota, Raja
Syngenta Biotechnology Inc
Greensboro
raja.kota@syngenta.com

Lawley, Cindy
Illumina Inc.
San Francisco
clawley@illumina.com

Miller, Mailyn
University of Nebraska
Lincoln
mmiller3@unl.edu

Moran, Emily
Bill & Melinda Gates Foundation (BMGF)
Seattle
emily.moran@gatesfoundation.org

Nguyen, Henry T
University of Missouri
Columbia
nguyenhenry@missouri.edu

Pegadaraju, Venkatramana
Douglas Scientific
Minneapolis
venki.pegadaraju@douglasscientific.com

Penmetsa, Varma R
University of California
Davis
rvpenmetsa@ucdavis.edu

Poland, Jesse
Kansas State University
Manhattan
jpoland@ksu.edu

Puppala, Naveen
New Mexico State University (NMSU)
Las Cruces
npuppala@nmsu.edu

Rounsley, Steve
Dow AgroSciences
Indianapolis
steve.rounsley@gmail.com

Santra, Dipak K
University of Nebraska
Lincoln
dsantra2@unl.edu

Schnable, Patrik S
Iowa state University
Ames
schnable@iastate.edu

Shapiro, Howard-Yana
MARS Inc. & University of California
Davis
howard.shapiro@effem.com

Sorrells, Mark E
Cornell University
Ithaca
mes12@cornell.edu

Valliyodan, Babu
University of Missouri
Columbia
valliyodanb@missouri.edu

Wallace, Jason
Cornell University
Ithaca
jgw87@cornell.edu

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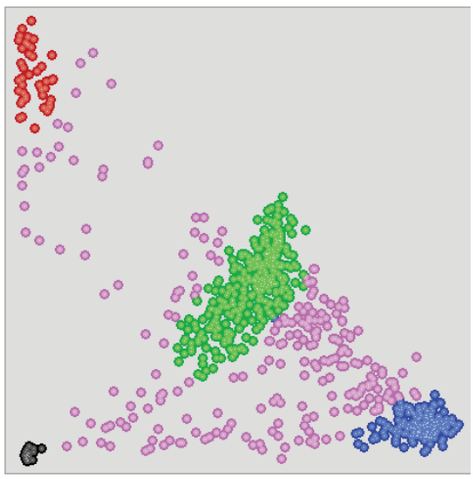

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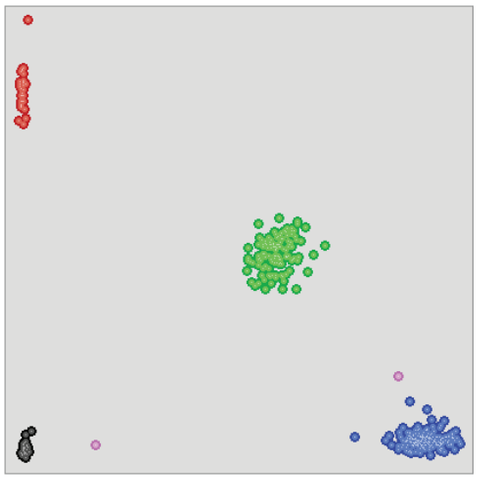

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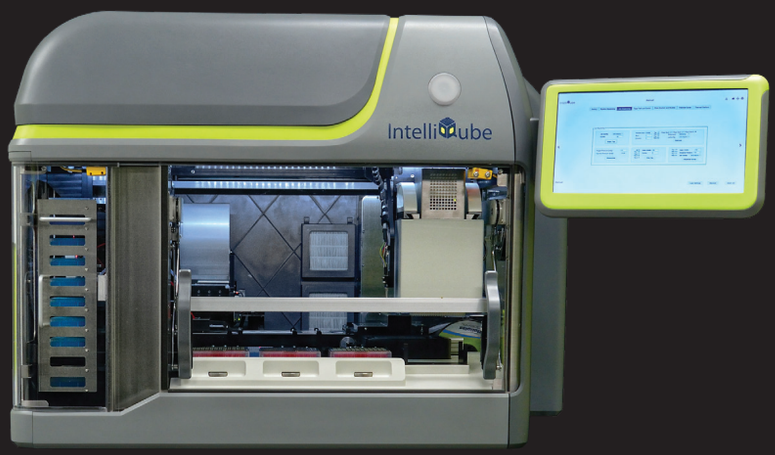

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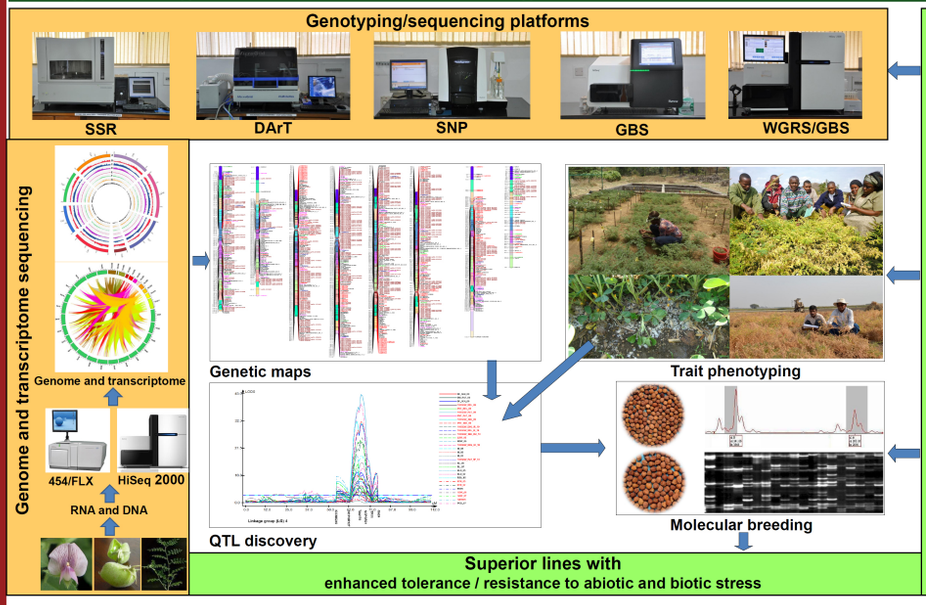


Genomics

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)
- Groundnut (Announced on 2 April 2014)
- >1000 legume genomes sequenced
- Pearl millet (in progress)

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

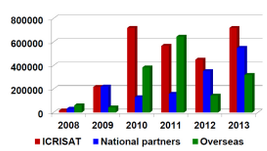
- Chickpea
- Pigeonpea
- Groundnut
- Sorghum
- Pearl millet
- Finger millet
- Rice
- Wheat
- Maize
- Barley
- Oats
- Sweet potato
- Tomato
- Potato
- Onion
- Garlic
- Cassava
- Tobacco
- Cotton
- Mango
- Guava
- Litchi
- Banana
- Mulberry

Projects

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

Beneficiaries

- NARS partners in Africa, Asia, Europe and Latin America
- Agricultural research institutes
- Research foundations
- Universities
- Small-scale breeding companies

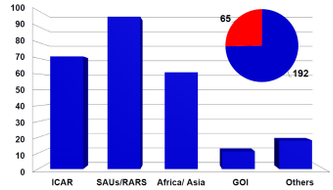


Overview on data generated for SSR, DArT and SNP markers

Capacity building

Students from sub-Saharan Africa and South Asia

Participants in training courses



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