CROP GENOMICS: PRESENT & FUTURE

nature INDIA

VI NEXT GENERATION GENOMICS & INTEGRATED BREEDING FOR CROP IMPROVEMENT CONFERENCE

ON

CROP GENOMICS: PRESENT & FUTURE

CELEBRATING THE 10TH ANNIVERSARY OF CEG

ICRISAT, HYDERABAD, INDIA

DECEMBER 6-8, 2017

Centre of Excellence in Genomics (CEG) ANNIVERSARY (2007-2017)

1972-2017 ICRISAT

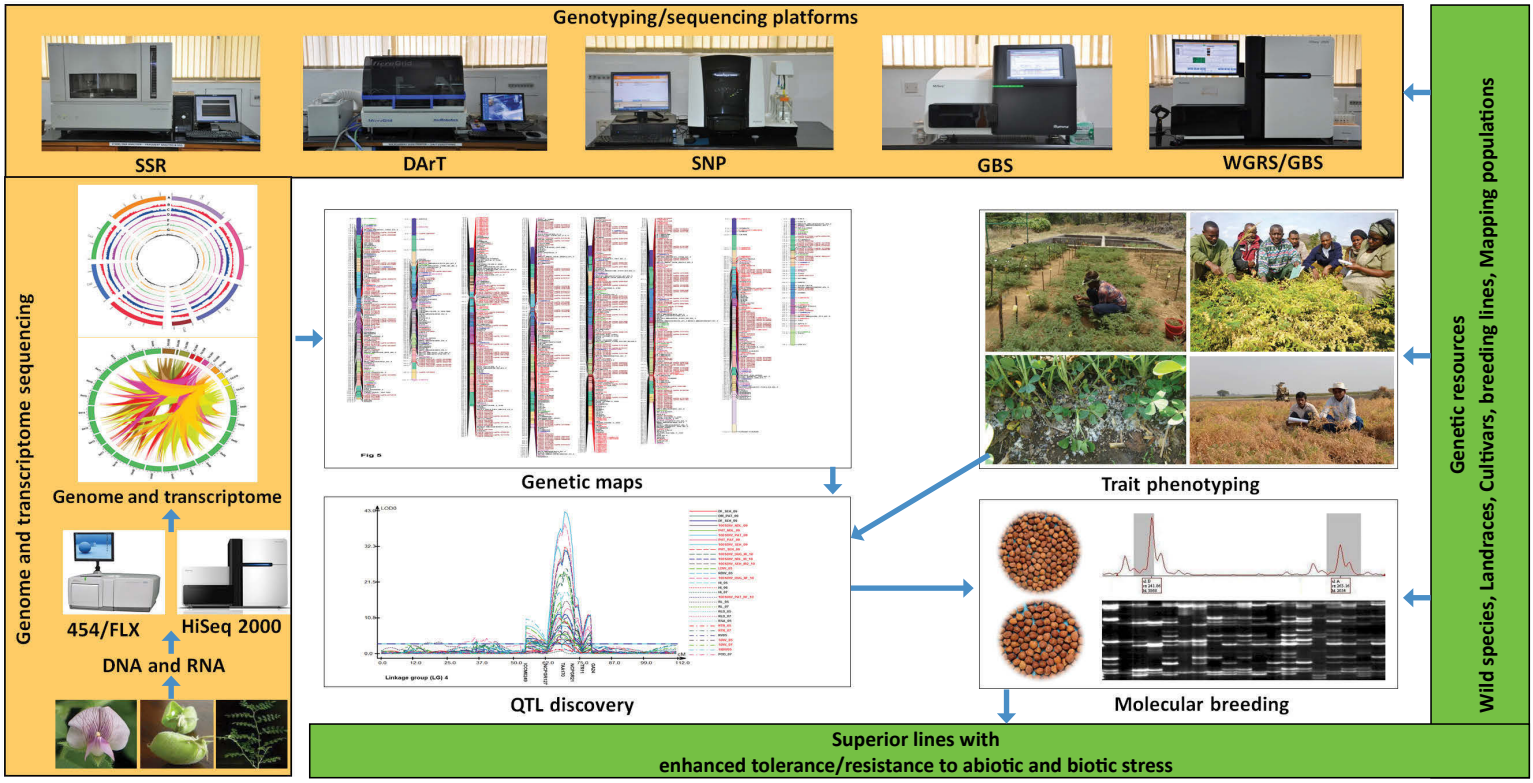
ICRISAT

INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

nature INDIA

Accelerating Genetic Gains in Crop Breeding Programs through Center of Excellence in Genomics (CEG)

Integrated genomics and breeding activities



Genome sequences

- Pigeonpea (Nature Biotech 2012, 30:83-89)
- Chickpea (Nature Biotech 2013, 31:240-246)
- Groundnut – A & B genomes
  (Nature Genetics 2016, 48:438-446), (PNAS 2016, 113: 6785-6790)
- Sorghum (Nature 2009, 457:551-556)
- Pearl millet (Nature Biotech 2017, 35:969-976)
- 3000 chickpea genome sequencing
- 1000 pearl millet genome sequencing
  (Nature Biotech 2017, 35:969-976)
- Re-sequencing initiatives in sorghum, groundnut and pigeonpea
  (Nature Genetics 2017b, 49:1082-1088)

Molecular breeding

- Chickpea: drought tolerance and resistance to Fusarium wilt and Aschochyta blight
- Groundnut: resistance to rust and oil quality
- Sorghum: drought tolerance, resistance to shoot fly and Striga
- Pearl millet: resistance to blast, downy mildew and Fe and Zn
- Pigeonpea: markers for enhancing precision and efficiency of hybrid breeding

Marker resources

- Diagnostic markers for key traits
- >10,000 SSRs across mandate crops
- >10,000 SNPs across mandate crops
- High density DArT arrays for chickpea, pigeonpea and groundnut
- Affymetrix 50K+SNP arrays in chickpea, pigepnpea and groundnut
- High throughput & low cost genotyping platform
  (US$ 1.5 per sample including DNA sample for 10 markers)

High performance computational genome analysis

- Number of cores 408
- Storage ~805 TB
- RAM 6 TB

Decision support tools

- ISMAB for molecular breeding
- GDMS for data management
- ISMU for mining SNPs based on NGS
- ISMU v 2 for deploying Genomic Selection
- GOBII for high-density genotyping data

ICRISAT
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Dec 2017

ICRISAT INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

Welcome !

We are very excited to have you in VI Next Generation Genomics & Integrated Breeding Conference on "Crop Genomics: Present & Future" to celebrate the 10th Anniversary of the Center of Excellence in Genomics (CEG). On behalf of Team CEG and my personal behalf, I would like to welcome you here. We very much hope that you will have a productive and enjoyable stay during the conference.

CEG is completing its 10 glorious years of excellence in science and partnership. We started this journey in 2007 from one CoE grant from the Department of Biotechnology, Government of India with an objective to provide marker genotyping services and train scientists in the area of molecular breeding. After ICRISAT institutionalized it as a Center, CEG started undertaking high-quality science and translate it in crop improvement programmes both at ICRISAT and national programs in developing countries. While working in close collaboration with scientists from different Themes/ Programs/ Regions of ICRISAT and 184 partner institutes from 35 countries, CEG has emerged as a high-quality research, service and training center at international level. Team CEG feels very satisfied while looking its efforts and achievements made during last 10 years in the area of generation of genomic resources, development of superior lines, empowerment of national partners by providing sequencing and genotyping services and training scientists in genome analyses and molecular breeding and creation of a next generation of scientists.

We are grateful to all our partners especially donors for their generous support as well as national and international agencies to keep Team CEG motivated and inspired by recognizing their efforts through honours/awards and appreciation. We are grateful to all current and previous members of the Governing Board and the Management Group of ICRISAT who have been nourishing CEG in the best possible way. Thanks are also due to a number of mentors and well-wishers who have always been there to guide us especially in challenging time. A number of congratulatory and best wishes messages received from several senior persons as mentioned above have been included in this book. We would also like to recognize the hard work and contributions of the current Team CEG and ca. 200 CEG alumni for making the 10 years journey successful.

This conference has brought 362 colleagues from 139 institutes (including 8 CGIAR institutes) from 34 countries together. We will have 22 presentations in 5 sessions, 2 panel sessions and 79 posters. This conference is expected to discuss the current status and future landscapes of genomics. As mentioned by Dr Nigel Poole and Dr David Bergvinson in their messages, the CEG is embarking in the area of Systems Biology. We are looking for partners for using Systems Biology approaches to analyze human gut microbiome as well as soil microbiome to improve human and plant health, respectively. The understanding of trait biology will be further strengthened by using Systems Biology approaches.

In the end, we are grateful to you for accepting our invitation and participating in this conference. We look forward for your contributions in this conference and receive your continuous support and collaboration.

Rajeev K. Varshney, *ML, FTWAS, FCSSA, FNA, FNASc, FNAAS*
Director, Center of Excellence in Genomics, &
Research Program Director, Genetic Gains

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ICRISAT INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

On behalf of the Governing Board I would very much like to welcome you both to ICRISAT and to the "Crop Genomics: Present and Future" conference. We hope that your participation in the conference and stay at ICRISAT will be stimulating and rewarding. Please accept my sincere apologies for being unable to attend the conference and meet with you in person but I believe that the conference (together with the CEG alumni meeting) will lead to the strengthening old partnerships and the development of new ones.

The Crop Genomics: Present and Future Conference celebrates 10 outstandingly productive years of the Centre of Excellence in Genomics (CEG) at ICRISAT. The CEG has made some very important findings which are significantly helping ICRISAT and its partners modernise their breeding programmes. While the CEG is celebrating its tenth anniversary, this year ICRISAT is celebrating its 45th anniversary. During these 45 years, ICRISAT together with our partners, have transformed the lives and livelihoods of many of the world's most vulnerable people. The title of our conference Crop Genomics: Present and Future made me consider what genomics was like 45 years ago and what it might be like in 45 years. In 1972 when I was an undergraduate studying Botany, Walter Fiers and his team at the University of Ghent were the first to establish and publish in Nature the complete nucleotide sequence of a gene (bacteriophage MS2 coat protein). Since 1995 we have witnessed an exponential growth in the number of genomes that have been sequenced due to improved techniques and massive cost reductions. Today genomics is helping us understand both agricultural and human traits with applications in human and animal disease and enhancing agricultural productivity. The pace of technological advances will continue and significantly impact diverse disciplines such as synthetic biology and species conservation as well as revolutionising plant and crop breeding to address the challenges of future sustainable food security, hunger and malnutrition. During the last 10 years and facilitated by its CEG, ICRISAT has become a leading international CGIAR centre that has championed the sequencing (and re-sequencing) of genomes of several crops like chickpea, pigeonpea, groundnut and pearl millet. A plethora of genotyping platforms have been established that cater for the different needs of researchers both in ICRISAT and NARS programs for both understanding plant biology as well as modernising breeding approaches. I believe that 10 years from today, we will have genome blue prints of all of our germplasm collections that will enable the tailoring of nutritionally rich climate smart (resilient) crops. The combination of mobile ICT technologies and genomics may well allow us to predict varietal performance at farm, field and within field scales, maximising resources.

We must through the meeting of minds and disciplines continue to significantly accelerate the conversion of genetic information into knowledge and the translation of this knowledge into new and better products and services that are "good for the consumer, producer and environment. We need to consider new thinking and approaches and will need to forge enduring partnerships to realise our collective potential. Genome projects have played an important role in developing systems thinking. Systems Biology with its integrative approach will in the next 10 years significantly increase the impact of our knowledge. I am delighted that ICRISAT is pursuing such approaches.

Congratulations CEG on your 10th anniversary I wish the conference every success.

Nigel Kerby

Governing Board Chair

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ICRISAT INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

Smallholder farmers across the drylands of sub-Saharan Africa and Asia face challenges of poverty, high levels of malnutrition specially for women and children, and uneconomic livelihoods based on agriculture. Climate change is worsening these challenges. Under the circumstances, ensuring food and nutrition security is complex and challenging requiring a holistic approach to address malnutrition, improve profitability of smallholder farmers, improve resilience of agri-food systems and ensure sustainable use of genetic resources and biodiversity.

Next-generation genomics technologies have revolutionized medical science and agriculture. The Center of Excellence in Genomics (CEG) at ICRISAT, while working with partners from around the world, has achieved a unique milestone in assembling draft genomes and large-scale re-sequencing of several important crops. CEG has also been at the forefront in genome sequence analysis and utilizing this information in crop improvement. ICRISAT is building on the work done by CEG as we embark with partners on a 'Systems Biology' framework to work across diverse disciplines to achieve nutritional security in service of realizing the Sustainable Development Goals (SDGs).

One Health – soil health, plant health and consumer (livestock and human) health – along with Systems Biology offers a framework to understand the interactions between these biophysical domains to support the design of modern agri-food systems that deliver nutrition within the ecological boundaries of the planet.

While CEG is celebrating its 10th Anniversary by organizing the VI NGGIBCI conference on Crop Genomics: Present & Future, ICRISAT is celebrating its 45th Anniversary in its journey to serve society through 'Science of Discovery' to 'Science of Delivery' for the drylands.

A warm welcome to ICRISAT and wish you a productive meeting to chart out the next 10 years!

David Bergvinson
Director General

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सत्यमेव जयते

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सचिव एवं महानिदेशक

TRILOCHAN MOHAPATRA, Ph.D.
FNA, FNASc, FNAAS
SECRETARY & DIRECTOR GENERAL

भारत सरकार
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MESSAGE

I am glad to note that the Centre of Excellence in Genomics (CEG) of International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) is celebrating its 10th Anniversary and to mark the occasion, the Centre is organizing 6th Next Generation Genomics and Integrated Breeding for Crop Improvement (VI NGGIBCI) Conference on Crop Genomics: Present and Future during December 6-8, 2017.

Deficiency in technology adoption and negative imports of various abiotic and biotic factors contribute to the decline in agricultural productivity especially in developing countries. Improved and climate resilient crop varieties need to be developed to cope with the increasing demand for food and other plant-based products. However, a better understanding of crop genetics is necessary to breed such varieties. In combination with automated phenotyping assays, genomics is providing new foundation for crop breeding. DNA sequence information is extremely valuable for identifying key genes controlling important agronomic traits and for adequately understanding the genetic variability among the cultivars. Sequencing of large and complex genomes of crop species, facilitated by new sequencing technologies and bioinformatics approaches, has provided new opportunities for crop improvement. In this context, ICRISAT's CEG has made significant advances by sequencing genomes of several crops, mapping of various traits and deployment of molecular breeding to develop better lines. CEG is making the impact on research and breeding not only in India but across the globe and I would like to congratulate Dr Rajeev Varshney and Team CEG for all breakthrough research they have made during the last 10 years. I am also excited to see an impressive list of speakers and participants for the VI NGGIBCI Conference. I do hope that the deliberations during the conference will focus as new developments as well as applications of genomics that will immensely benefit the researcher community.

I wish the Conference a grand success.

(T. MOHAPATRA)

Dated the 6th November, 2017
New Delhi

S.K. PATTANAYAK
SECRETARY

भारत सरकार
कृषि एवं किसान कल्याण मंत्रालय
कृषि, सहकारिता एवं किसान कल्याण विभाग
Government of India
Ministry of Agriculture & Farmers Welfare
Department of Agriculture, Cooperation
& Farmers Welfare

MESSAGE

It gives me great pleasure to know that the Center of Excellence in Genomics (CEG) of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, is celebrating its 10th Anniversary by organizing **VI NGGIBCI Conference on Crop Genomics: Present & Future** during December 6-8, 2017.

We have already witnessed several epoch making contributions of Genetics to revolutionise agriculture production by raising agriculture productivity. The "Green Revolution" in India is an example of such a success story that materialized due to the introduction of improved varieties developed through novel genetics and breeding approaches combined with a visionary policy support, liberal public funding and rapid absorption of new technology by the farmers of our country. Now the time has come for India to chalk out a new and innovative strategy using modern genomics to not only enhance the crop productivity but also to achieve the goal of doubling farmers' income by 2022.

Genomics-based technologies are instrumental in enhancing global food production at an accelerated pace by increasing crop yield and reducing post-production cost. CEG housed in ICRISAT is at the forefront of developing the deploying genomics technologies in agriculture. Having visited CEG several times in the past, I am deeply impressed with the pioneering work carried out by the CEG scientists in decoding genomes and using genome information in breeding programs. The CEG team and ICRISAT leadership deserve compliments for their sincere and dedicated efforts.

I wish CEG and ICRISAT the very best in all their future endeavours and wish the Conference all success.

(S.K. Pattanayak)

New Delhi
9th November, 2017

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Happy 10th – CEG, ICRISAT & Nature India

When their resequencing of the pearl millet genome was announced a couple of months ago (September 2017)[1], scientists from the Center of Excellence in Genomics (CEG) at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) were not overtly ecstatic about the feat that was going to change the lives of millions. Their composure was to be expected. It is now routine for the lab to sequence and re-sequence crops as part of a large international consortia and, in turn, quietly trigger major benefits in large swaths of resource-poor countries.

For instance, the CEG team is now resequencing 3,000 diverse lines of chickpea, phenotyping them at six locations in India. They plan to use this data to identify superior variants of genes that may be put to use to increase yields, impart stress-tolerance to the crops or enhance one of their desirable features.

In May 2017, the team led the re-sequencing of the genome of 292 pigeonpea varieties to discover important traits such as resistance to various diseases and its insensitivity to photo-period (the duration of daylight hours required for reaching maturity)[2]. Their research also traced the probable origin of the domesticated pigeonpea to Madhya Pradesh in central India. The crop geneticists took a fresh look at the humble peanut's ancestor, *Arachis duranensis*, resequening its genome to unravel significant genes responsible for peanut-allergy, the plant's unique capacity to reproduce beneath the ground (geocarpy) and oil formation[3].

Improving yields and traits of some of the important crops for the developing world — pigeonpea, chickpea, groundnut, adzuki bean, mung bean, sesame and pearl millet — CEG scientists have been at the helm of some intensive and high-throughput endeavours that provide low-cost high-density genotyping.

Nature India has been associated with CEG, ICRISAT for the last 10 years of its existence, coincidentally *Nature India*'s 10th year too. With the common mandate of 'bringing science to people', *Nature India* has been proudly associated with ICRISAT's InterDrought

series of conferences, which have debated and discussed genomics-based solutions for drought affected regions over the years.

Through its incisive editorial, *Nature India* continues to seek answers to the unique challenges that researchers and policy makers in India face, in line with CEG, ICRISAT's goal of finding solutions in technologies to render greater resilience to agricultural production in low-income countries.

Happy 10th to both of us.

1. Varshney, R. K. *et al*. Pearl millet genome sequence provides a resource to improve agronomic traits in arid environments. *Nat. Biotechnol*. (2017) doi: 10.1038/nbt.3943
2. Varshney, R. K. *et al*. Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. *Nat. Genet.* (2017) doi: 10.1038/ng.3872
3. Chen, X. *et al*. Draft genome of the peanut A-genome progenitor (*Arachis duranensis*) provides insights into geocarpy, oil biosynthesis, and allergens. *P. Natl. Acad. Sci. USA* (2016) doi: 10.1073/pnas.1600899113

Subhra Priyadarshini
Editor

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VI NGGIBCI Conference

on

Crop Genomics : Present & Future

to celebrate

10th Anniversary of CEG

ICRISAT, Hyderabad, India

December 6-8, 2017

Programme

(Venue: Ralph W Cummings Auditorium)

Wednesday, December 6, 2017		
17:00 – 18:45 hrs	**Inaugural Session**	
17:00 – 17:15 hrs	Welcome	**Rajeev Varshney** Research Program Director – Genetic Gains, *ICRISAT*
17:15 – 17:30 hrs	Opening address	**David Bergvinson** Director General, *ICRISAT*
17:30 – 17:45 hrs	Inaugural address	**T Mohapatra** Director General, *Indian Council of Agricultural Research (ICAR)*
17:45 – 18:00 hrs	Agricultural science perspectives	**Panjab Singh** President, *National Academy of Agricultural Sciences*
18:00 – 18:45 hrs	Inaugural Lecture: ***Genomics-based approaches to elevating crop disease resistance***	**Jonathan Jones** Fellow of Royal Society *The Sainsbury Laboratory* UK
19:00 – 20:00 hrs	***10th CEG Anniversary Video, celebrations*** ***Anniversary messages*** ***(David Bergvinson, Peter Carberry, Dave Hoisington, CLL Gowda, Mike Butterfield, Oscar Riera-Lizarazu*** *and others****)***	
20:00 – 21:30 hrs	*Dinner- IMOD Plaza, ICRISAT*	
Thursday, December 7, 2017		
08:30 – 10:30 hrs	**Session I: Advances in genomics** **Co-Chairs: Swapan Datta, *Visva-Bharati University, India*** **Mike Olsen, *CIMMYT-Kenya, Kenya***	
08:30 – 09:00 hrs	A 3D code in the human genome	**Erez Aiden** *Baylor College of Medicine* USA
09:00 – 09:30 hrs	Progress in wheat genomics	**Mike Bevan** *John Innes Centre* UK

09:30 – 10:00 hrs	Germline reprogramming and epigenetic inheritance: how to avoid *BadKarma*	**Rob Martienssen** *Cold Spring Harbor Laboratory* USA
10:00 – 10:30 hrs	Green systems biology – the need for ecological thinking in modern biology	**Wolfram Weckwerth** *University of Vienna* Austria
10:30 – 11:00 hrs	*Tea / Coffee Break*	
11:00 – 13:00 hrs	**Session II: Genome & germplasm diversity** **Co-Chairs: Kadambot Siddique, *Uni of Western Australia, Australia*** **Kuldeep Singh, *ICAR-NBPGR, India***	
11:00 – 11:30 hrs	High resolution genome sequence of mungbean using long read assembly and its utilization	**Suk-Ha Lee** *Seoul National University* Korea
11:30 – 12:00 hrs	Genomics driven activation of germplasm collections	**Andreas Graner** *IPK-Gatersleben* Germany
12:00 – 12:30 hrs	Genome harvest: deciphering mosaic genome diversity patterns as pathways to crop improvement	**JC Glaszmann** *CIRAD, the French Agricultural Research Centre for International Development* France
12:30 – 13:00 hrs	Reaching back through the domestication bottleneck to feed a hot and crowded planet	**Benjamin Kilian** *The Crop Trust* Germany
13:00 – 14:00 hrs	*Lunch-204 Banquet Hall, ICRISAT*	
14:00 – 16:00 hrs	**Session III: Sequencing based trait mapping** **Co-Chairs: Ajay Parida, Institute of Life Sciences (ILS), India** **Baozhu Guo, *University of Georgia, USA***	
14:00 – 14:30 hrs	Flowering time regulation in a vegetative crop and application in breeding	**Christian Jung** *University of Kiel* Germany
14:30 – 15:00 hrs	Genomics based valorization of genetic resources for improving disease resistance in cereals	**Frank Ordon** *Julius Kühn-Institut (JKI)* Germany
15:00 – 15:30 hrs	Using genomics to boost wheat grain yield	**Jochen Reif** *IPK-Gatersleben* Germany

15:30 – 16:00 hrs	Accessing genetic variation outside the primary gene pool	**Scott Jackson** *University of Georgia* USA
16:00 – 16:30 hrs	*Tea / Coffee Break*	
16:30 – 18:00 hrs	**Panel Session: Writing a high quality science paper** **Co-Chairs: PK Gupta, *Chaudhary Charan Singh University, India*** **Hon-Ming Lam, *The Chinese Uni of Hong Kong, Hong Kong***	
	Panelists: **Susan Jones**, Nature Biotechnology **Henry Daniell**, Plant Biotechnology Journal **Albrecht Melchinger**, Theor Appl Genet **Frank Ordon**, Plant Breeding	
18:00 – 19:00 hrs	***Poster Session (with soft drinks)***	
	Poster Evaluating Committee for Session I & II	Ramesh K Agarwal, Jacqueline Batley, Bhagirath Chaudhary, Rajeev Gupta, Eng Hwa Ng, Damaris Odeny, Rattan Yadav
	Poster Evaluating Committee for Session III, IV &V	HS Balyan, Anuradha Ch, Chris Ojiewo, Patrick Okori, RP Sharma, Hari Upadhyaya, Eric Bishop von Wettberg
19:00 – 21:30 hrs	*Cultural Program, Cocktails & Dinner-Anniversary Lawns*	
Friday, December 8, 2017		
08:30 – 10:30 hrs	**Session IV: Genomics-assisted breeding** **Co-Chairs: Deepak Pental, *University of Delhi, India*** **Arvind Kumar, *IRRI-Philippines, Philippines***	
08:30 – 09:00 hrs	Unlocking genetic basis of complex traits and heterosis in rice	**Bin Han** *Shanghai Institute for Biological Sciences* China
09:00 – 09:30 hrs	Libraries of doubled-haploid lines from landraces: a new tool for maize breeding and genomic research	**Albrecht Melchinger** *University of Hohenheim* Germany
09:30 – 10:00 hrs	BGI's efforts on crop breeding towards precision nutrition	**Shancen Zhao** *BGI Institute of Applied Agriculture* China
10:00 – 10:30 hrs	Challenge to genomic, genetic analysis and molecular breeding in allo-octoploid species, strawberry	**Sachiko Isobe** *Kazusa DNA Research Institute* Japan
10:30 – 11:00 hrs	*Tea / Coffee Break*	

1100 – 13:00 hrs	**Session V: Decision support tools and databases** **Co-Chairs: Ivo Grosse, *Martin Luther University Halle-Wittenberg, Germany*** **BM Prasanna, *CIMMYT-Kenya, Kenya***	
11:00 – 11:30 hrs	Genomics and bioinformatics requirements for future crop breeding	**Dave Edwards** *University of Western Australia* Australia
11:30 – 12:00 hrs	Computational tools for better crops	**Mario Caccamo** *NIAB* UK
12:00 – 12:30 hrs	Exploiting comparative genomics	**David Marshall** *The James Hutton Institute* UK
12:30 – 13:00 hrs	Unity through diversity: Building a legume federation with legume information system and friends	**Andrew Farmer** *National Center for Genome Resources (NCGR)* USA
13:00 – 14:00 hrs	*Lunch-204 Banquet Hall, ICRISAT*	
14:00 – 16:30 hrs	**Panel Session: Genomics applications perspective** **Co-Chairs: R B Singh, *Central University, Imphal*** **Eric Danquah, *University of Ghana, Ghana***	
	India	**B Rajender** *Ministry of Agriculture, Cooperation and Farmers Welfare* India
	China	**Liao Boshou** *Oil Crops Research Institute, Chinese Academy of Agricultural Sciences* China
	Kenya	**Paul Kimurto** Egerton University Kenya
	UAE	**Khaled Amiri** *Khalifa Center for Genetic Engineering and Biotechnology* UAE
	FAO	**Chikelu Mba** *Food and Agricultural Organization (FAO)* Italy

	MARS Inc.	**Victor Nwosu** *MARS Inc.* USA
	Dow AgroSciences	**Oscar Rierra-Lizarazu** *Dow AgroSciences* *USA*
	Centro de Tecnologia Canavieira (Sugarcane Research Center)	**Mike Butterfield** *CTC* *Brazil*
16:30 – 17:00 hrs	*Tea / Coffee Break*	
17:00 – 18:45 hrs	**Closing Session**	
	Genomics to Address Sustainable Development Goals	**RS Paroda** *Trust for Advancement of Agricultural Sciences, India*
	Inspirational Address	**Shobhana K Pattanayak** Secretary, *Department of Agriculture, Cooperation and Farmers Welfare, Ministry of Agriculture and Farmers Welfare, Govt. of India*
	Way Forward	**David Bergvinson** Director General, *ICRISAT*
	Closing remarks	**Peter Carberry** *Deputy Director General - Research, ICRISAT*
	Vote of thanks	**Rajeev Varshney** *Research Program Director - Genetic Gains* *ICRISAT*
18:45 hrs onwards	*Dinner- Mary Cummings Park, ICRISAT*	

Inaugural Session

Dr. Rajeev Varshney

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

Dr. David Bergvinson

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National Academy of Agricultural Sciences
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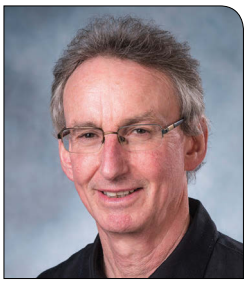
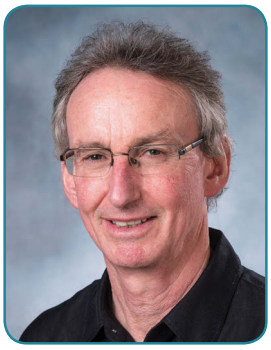


Prof. Jonathan Jones

Fellow of Royal Society
The Sainsbury Laboratory
UK



Professor Jonathan Jones
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Jonathan Jones is a leading researcher in plant/microbe interactions. He graduated in Botany from Cambridge (1976) and his PhD (1980) on cereal chromosomes was supervised by Dick Flavell at the PBI, Cambridge.

After a postdoc with Fred Ausubel at Harvard 1981-2 on symbiotic nitrogen fixation, he worked at agbiotech company AGS, founded to use GM for crop improvement. In 1988, he became one of the first recruits at The Sainsbury Laboratory, Norwich, UK. He was elected a Professor at UEA in 1997, to EMBO in 1998, as FRS in 2003, and Foreign Associate of US NAS in 2015.

He has contributed to Royal Society working groups on food security. His interests include disease resistance genes and protein mechanisms, how pathogens suppress host defences to cause disease, and exploiting knowledge of resistance mechanisms to reduce crop losses to disease.

He is a strong advocate of using GM or editing methods to move resistance genes between plant species to increase disease resistance in crops.

Genomics-based approaches to elevating crop disease resistance

Jonathan Jones

Jonathan Jones, Zane Duxbury, Yan Ma, Panagiotis Sarris, Sung Un Huh, Kee Sohn, Kamil Witek, Hari Karki and Oliver Furzer,
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Diverse microbes cause plant disease, and plants have evolved a robust innate immune system that recognises pathogen molecules and then activates defence. Immunity involves cell surface receptors and also intracellular Nucleotide-binding, Leucine-rich Repeat (NLR) immune receptors, encoded by Resistance (R) genes.

Some resistances require two co-functioning NLR proteins. The adjacent, divergently transcribed Arabidopsis RPS4 and RRS1 genes, encoding TIR-NLR proteins, are both required for resistance to bacteria that deliver AvrRps4 or PopP2 effectors, and for resistance to certain *Colletotrichum* strains. Both RRS1 and RRS1B carry a C-terminal WRKY domain targeted by AvrRps4 and PopP2, suggesting these effectors target WRKY domains. We investigate how the RPS4/RRS1 complex activates defence upon effector recognition. Many R gene pairs exist in which one of the two carries an "integrated decoy" domain that corresponds to a pathogen effector target.

R gene enrichment sequencing, ('RenSeq') involves sequence capture to enrich for NLR genes prior to sequencing (Jupe et al, 2013). We use RenSeq to discover whether new R genes in diverse *Solanum* sp against *Phytophthora infestans* could provide useful protection against blight in potato. We also use RenSeq to define new R genes against various pathogens of the Brassicaceae, in particular the 'White Rust'-causing *Albugo* species, and to investigate NLR gene diversity in Arabidopsis. NB-LRR gene clusters are complex and difficult to resolve using Illumina reads, but PacBio long reads enable us to define the diversity of NB-LRRs in *Arabidopsis*, and to better understand the evolutionary history of these fascinating genes (Witek et al 2016). These methods are of broad utility and have the potential to accelerate the isolation of useful disease resistance genes from wheat and its relatives. In addition, sequence capture methodology can facilitate investigation into the genomes and gene expression of obligate plant pathogens. Recent applications will be discussed.

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Session I

Advances in Genomics

Co-chairs

Prof. Swapan Datta

Vice Chancellor
Visva-Bharati University
India

Dr. Mike Olsen

Coordinator
Trait Pipeline and Upstream Research
CIMMYT-Kenya
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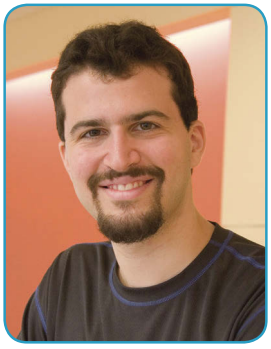

Dr Erez Lieberman Aiden
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Erez Lieberman Aiden received his PhD from Harvard and MIT in 2010. After several years at Harvard's Society of Fellows and at Google as Visiting Faculty, he became Assistant Professor of Genetics at Baylor College of Medicine and of Computer Science and Applied Mathematics at Rice University.

Dr Aiden's inventions include the Hi-C method for three-dimensional DNA sequencing, which enables scientists to examine how the 2-metre-long human genome folds up inside the tiny space of the cell nucleus (Lieberman-Aiden & Van Berkum *et al*., *Science*, 2009). In 2014, his laboratory reported the first comprehensive map of loops across the human genome, mapping their anchors with single-base-pair resolution (Rao & Huntley *et al*., *Cell*, 2014). In 2015, his lab showed that these loops form by extrusion, and that it is possible to add and remove loops and domains in a predictable fashion using targeted mutations as short as a single base pair (Sanborn & Rao *et al*., *PNAS*, 2014). In 2017, his lab showed that it is possible to use 3D maps, generated using Hi-C, to assemble mammalian genomes, entirely from scratch, from short reads alone, at a total cost of under $10,000 (Dudchenko *et al*., *Cell*, 2014). Using this methodology, the Aiden lab reported the first end-to-end genome of the *Aedes aegypti* genome, which carries the Zika virus. Assembling the *Aedes aegypti* genome from end to end had been highlighted as essential to the worldwide Zika response by a front page article in *The New York Times*.

In addition, together with Jean-Baptiste Michel, Dr Aiden also developed the Google Ngram Viewer, a tool for probing cultural change by exploring the frequency of words and phrases in books over the centuries. Now a product at Google, the Ngram Viewer is used every day by millions of people worldwide.

Dr Aiden's research has won numerous awards, including recognition for one of the top 20 'Biotech Breakthroughs that will Change Medicine', by *Popular Mechanics*, membership in *MIT Technology Review*'s 2009 TR35, recognizing the top 35 innovators under 35; and in *Cell*'s 2014 40 Under 40. His work has been featured on the front page of *The New York Times*, *The Boston Globe*, *The Wall Street Journal*, and *The Houston Chronicle*. One of his talks has been viewed more than one million times at TED.com. Three of his research papers have appeared on the cover of *Nature* and *Science*. In 2012, he received the President's Early Career Award in Science and Engineering, the highest government honour for young scientists, from Barack Obama. In 2014, Fast Company called him "America's brightest young academic". In 2015, his laboratory was recognised on the floor of the US House of Representatives for its discoveries about the structure of DNA.

A 3D Code in the Human Genome

Erez Lieberman Aiden

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Stretched out from end-to-end, the human genome — three billion chemical letters inscribed in a molecule called DNA — is over 2 metres long. Famously, short stretches of DNA fold into a double helix, which wind around histone proteins to form the 10nm fibre. But what about longer pieces? Does the genome's fold influence function? How does the information contained in such an ultra-dense packing even remain accessible?

In this talk, I describe our work developing 'Hi-C' (Lieberman-Aiden *et al*., *Science*, 2009; Aiden, *Science*, 2011) and 'in-situ Hi-C' (Rao & Huntley *et al*., *Cell*, 2014), which use proximity ligation to transform pairs of adjacent DNA loci into chimeric DNA sequences. Sequencing a library of such chimeras makes it possible to create genome-wide maps of physical contacts between pairs of loci, revealing features of genome folding in 3D.

Next, I will describe recent work using in situ Hi-C to construct haploid and diploid maps of nine cell types. The densest, in human lymphoblastoid cells, contains 4.9 billion contacts, achieving 1 kb resolution. We find that genomes are partitioned into contact domains (median length, 185 kb), which are associated with distinct patterns of histone marks and segregate into six subcompartments. We identify ~10,000 loops.

Next, I will discuss the mechanism that underlies chromatin looping. Specifically, our data is consistent with the formation of loops by extrusion (Sanborn & Rao *et al*., *PNAS*, 2015).

Finally, I will show that by modifying CTCF motifs using CRISPR, we can reliably add, move and delete loops and domains. Thus, it possible not only to "read" the genome's 3D architecture, but also to write it.

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Mike Bevan studied cell biology and biochemistry at the University of Auckland, New Zealand, and completed post-graduate studies in plant biochemistry in the Biochemistry Department at the University of Cambridge. Mike studied plant tissue culture differentiation, leading to an interest in *Agrobacterium tumefaciens* — mediated crown gall formation. Mike did his first post-doc with Mary-Dell Chilton at Washington University in St Louis, MO, where he worked on the structure, expression and functions of T-DNA genes. This work led to the identification of T-DNA promoters, which they used for the first demonstration of foreign gene expression in plants. Mike carried on this type of work at the Plant Breeding Institute in Cambridge, UK. Upon moving to the John Innes Centre, Mike initiated and coordinated the sequencing of the *Arabidopsis thaliana* genome. Currently Mike is working on analysing multiple wheat lines and understanding interactions between their component genomes.

Progress in wheat genomics

Mike Bevan

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Recent advances in genome sequencing technologies, coupled to radically improved assembly and annotation methods, have revolutionized genomics. These approaches are now being used to sequence the large and complex genomes of crop plants, and to access and understand genetic variation in populations of crop wild relatives. I will describe innovations in DNA sequencing and assembly that we have used to generate more complete assemblies of the wheat genome. We are analysing pedigrees of multiple UK wheat lines in order to understand how breeders' choices have shaped genomes and to identify key haplotypes commonly used in UK wheat breeding. This will provide breeders with unprecedented understanding of the genetic variation they are using to develop new varieties, and help develop new ways of selecting desired combinations of haplotypes. I will also describe recent progress in characterising the epigenomes of wheat and how these change upon the formation of new hybrids. This knowledge may contribute to understanding how polyploidy gives rise to altered gene expression and new traits.

Prof Rob Martienssen
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Rob Martienssen is a professor at Cold Spring Harbor Laboratory, and a Howard Hughes Medical Institute and Gordon and Betty Moore foundation Investigator in Plant Biology. Dr Martienssen obtained his PhD at the Plant Breeding Institute, Cambridge University. He received his postdoctoral training at the University of California, Berkeley, and joined the faculty at Cold Spring Harbor in 1989.

Research in Dr Martienssen's laboratory focuses on epigenetic mechanisms that shape and regulate the genome, and their impact on development and inheritance. His work on transposable elements in plants and repetitive sequences in fission yeast revealed a link between heterochromatin and RNA interference, for which he received the AAAS Newcomb Cleveland Award in 2003.

Professor Martienssen was made a Fellow of the Royal Society in 2006, and an associate member of EMBO in 2011.

Germline reprogramming and epigenetic inheritance: how to avoid Bad Karma

Rob Martienssen[1], Filipe Borges[1], Joe Calarco[1], Milos Tanurdzic[1], Kate Creasey[1], Jose Feijo[2], Jorg Becker[2], Bill Thompson[3], Meilina Ong-Abdullah[4], Nathan Lakey[5], Jared Ordway[5], Steve Smith[5], Raviga Sambanthamurthi[4]

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Epigenetic inheritance is more widespread in plants than in mammals, in part because mammals erase epigenetic information each generation by germline reprogramming. To assess the extent of germline reprogramming in plants, we sequenced the methylome from sperm cells (SC), the vegetative nucleus (VN), and the precursor microspore from developing haploid pollen. We found that asymmetric CHH methylation is lost in microspores and sperm cells, but restored in the VN and in fertilised seed. In the VN symmetric CG methylation is lost from targets of the DNA glycosylases DEMETER (DME) and REPRESSOR OF SILENCING 1 (ROS1) including transposons near imprinted genes, which contributes to imprinting via RNA-directed DNA methylation and 24nt siRNA. In contrast, most active transposons give rise to 21nt "epigenetically activated" small RNA in DECREASE IN DNA METHYLATION 1 (DDM1) mutants, in tissue culture and in the VN, which loses heterochromatin. Loss of heterochromatin in the VN is not only due to the loss of DNA methylation but also to histone replacement with variants resistant to modification. Thus genome reprogramming in pollen contributes to epigenetic inheritance, transposon silencing and imprinting, guided by small RNA. In a real-world example, micropropagation of oil palm clones from somatic cells circumvents germline reprogramming of Karma retrotransposons, and results in heritable epigenetic changes reminiscent of paramutation.

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Wolfram Weckwerth working since 2000 in the research field of plant metabolomics, Dr Weckwerth is a pioneer in applying integrative metabolomics, proteomics and computer-based systems biology techniques in plant biology and ecophysiology. In 2008, he moved as a full professor to the University of Vienna and founded the Department of Molecular Systems Biology (MOSYS). Since 2013 Dr Weckwerth has been Head of the Department of Ecogenomics and Systems Biology (ECOSYS). Since 2015 he has been Chair of the Vienna Metabolomics Center (VIME).

Dr Weckwerth is the protagonist of Green Systems Biology, an ecological concept of modern biology. The aim of Green Systems Biology is to extend studies on single model systems up to whole ecosystems and to define the organismal genotype-phenotype-relationship based on system-theoretical data-driven statistical-mathematical models.

Dr Weckwerth has produced more than 150 publications and several books (9000 citations, H-factor 52), and serves on many international boards as an expert in systems biology.

Green Systems Biology — the need for ecological thinking in modern biology

Wolfram Weckwerth

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Plants have shaped human life from the outset. With the emerging recognition of world population feeding pressures, global climate change and limited energy resources with fossil fuels, the relevance of plant biology and biotechnology is becoming dramatically important. One key issue is to improve plant productivity and abiotic/biotic stress resistance in agriculture due to restricted land area and increasing environmental pressures. Another aspect is the development of CO_2-neutral plant resources for fibre/biomass and biofuels: a transition from first-generation plants such as sugar cane, maize and other important nutritional crops, to second- and third-generation energy crops such as Miscanthus and trees for lignocellulose and algae for biomass and feed, hydrogen and lipid production.

At the same time we have to conserve and protect natural diversity and species richness. Here, biodiversity banks are discussed as a foundation of current and future plant-breeding research. Consequently, it can be anticipated that plant biology and ecology will play indispensable future roles. We therefore need an in-depth understanding of the physiology of single plant species for practical applications as well as the translation of this knowledge into complex natural as well as anthropogenic ecosystems. Latest developments in biological and bioanalytical research will lead into a paradigm shift towards understanding organisms at a systems level and in their ecosystemic context.

Systems biology combines these molecular data, genetic evolution, environmental cues and species interaction with the understanding, modelling and prediction of active biochemical networks up to whole species populations. This process relies on the development of new technologies for the analysis of molecular data, especially genomics, metabolomics and proteomics data. The ambitious aim of these non-targeted 'omic' technologies is to extend our understanding beyond the analysis of separated parts of the system, in contrast to traditional reductionistic hypothesis-driven approaches. The consequent integration of genotyping, pheno/morphotyping and the analysis of the molecular phenotype using metabolomics, proteomics and transcriptomics will reveal a novel understanding of plant metabolism and its interaction with the environment.

The analysis of single model systems — plants, fungi, animals and bacteria — will finally emerge in the analysis of populations of plants and other organisms and their adaptation to the ecological niche. In parallel, this novel understanding of ecophysiology will translate into knowledge-based approaches in crop plant biotechnology and marker- or genome-assisted breeding approaches.

In this lecture the foundations of green systems biology are described and applications in ecosystems research are presented. Knowledge exchange of ecosystems research and green biotechnology merging into green systems biology is anticipated based on the principles of natural variation, biodiversity and the genotype–phenotype environment relationship as the fundamental drivers of ecology and evolution.

Session II

Genome & Germplasm Diversity

Co-chairs

Prof. Kadambot Siddique

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

Dr Kuldeep Singh

Director
ICAR-National Bureau of Plant
Genetic Resources
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Dr Suk-Ha Lee
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Suk-Ha Lee, a well known legume geneticist, is Dean at Seoul National University, South Korea. Lee's main research area is the breeding, genetics and genomics of legume crops, with a specific emphasis on soybean crops including the development and application of SNP markers.

His group identified QTLs for some agronomic traits such as disease-resistant genes and seed protein content, and used fine mapping and RNA-seq technology to identify a BLP resistance gene.

Using NGS technology, his group has re-sequenced a *G. soja* genome, a wild relative of cultivated soybean (*Glycine max*), to understand the soybean crop domestication history.

Recently, Lee has been sequencing the whole genome of mungbean as well as its relative *vigna* species.

High-resolution genome sequence of mungbean using long read assembly and its utilisation

Suk-Ha Lee

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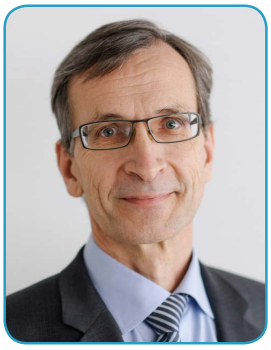
Mungbean is an important legume crop as a source of proteins and carbohydrates for human consumption.

The reference genome of *V. radiata* var. radiata VC1973A was assembled by Pacbio long reads. A total of 475 Mbp (N50=5.2 Mb) was estimated to cover 88% of the genome size. The scaffolds were anchored into 11 pseudochromosomes using high-resolution genetic map constructed by whole genome re-sequencing of 187 recombinant inbred lines (RILs).

Using genotyping by sequencing (GBS), 12,673 single nucleotide polymorphisms (SNP) were detected from cultivated and wild mungbean accessions from more than 20 countries. Nucleotide diversity among cultivated accessions decreased to 45% of nucleotide diversity among wild accessions. Several loci were identified as candidate regions that had undergone positive selection during mungbean domestication. Among the SNPs obtained from GBS, 7,179 SNPs were used for genome-wide association study to dissect the genetic background of several agronomic traits.

Phenotyping was performed for several important agronomic traits on 222 cultivated accessions and 48 markers were significantly associated with the traits. These data will be highly helpful for mungbean breeding programs.



Prof Dr Andreas Graner
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Andreas Graner is a pioneer in barley genomics at international level. His leadership has facilitated the establishment of the genome sequence of barley. He is internationally known for the development of one of the first RFLP maps in crop plants, the first set of large scale ESTs and EST-derived SSR and SNP markers in barley, the first set of SNP arrays, the first transcript map and physical map, genetic mapping of various qualitative and quantitative agronomic traits, map-based isolation of the first disease resistance genes and gene expression atlas in barley. Prof Graner's group has recently decoded inflorescence patterening, genetic architecture of plant stature, etcetera.

Prof Graner is a scientist of exceptional quality and great human values. As Science Manager, he was successful in establishing the Federal ex situ genebank of Germany in 2003, as a merger of the former ex situ genebanks of East and West Germany; created a novel standard for ex situ conservation management via the introduction of a quality management system certified according to DIN/ISO in 2007; and establishing IPK Gatersleben as a world leader in Triticeae Genomics with partners in 30 different countries.

He currently provides guidance and services to the international science community with his presence on various boards.

Genomics-driven activation of germplasm collections

Andreas Graner

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Crop breeding rests on repeated cycles of crossing and selection. However, this process is sustainable only if the genetic diversity that is lost by selection is adequately replenished by introducing novel diversity into the gene pool.

Ex-situ conservation of plant genetic resources represents the major backbone to maintaining the intraspecific diversity of many important crop plant species. At present, about seven million seed samples are stored in far more than 1000 *ex-situ* collections worldwide.

Undeniably, the vast diversity resting on the shelves of genebanks has been tapped into only marginally. Benefitting from genomics technologies, the conservation management of individual collections can be optimised (i) to monitor the authenticity of a given accession and (ii) to activate a collection to provide informed access to genetically defined material.

Technical advances in several key areas including (i) structural and functional genomics, (ii) phenotypic cataloguing of accessions using automated imaging, and (iii) novel biotechnological approaches will provide entry points for crop improvement.

While the application of novel technology opens up a wealth of entry points for genetic analyses, it also generates and amasses large streams of data. Therefore, integrated concepts of data management and analysis are instrumental when aiming at the exploitation of novel technologies for the systematic phenotypic and genotypic characterisation of genebank collections.

I will give examples of how conservation management of *ex-situ* collections will benefit from genomics analysis and how automated imaging technologies can be exploited for turn mapping.

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Jean-Christophe Glaszmann is researcher at CIRAD, the French Agricultural Research Centre for International Development, in Montpellier.

Initially trained in plant breeding and ecological genetics, he has conducted research on the assessment and use of genetic diversity in diverse crops such as rice, sugar cane, sorghum and banana.

He has been director of AGAP, a major joint research unit in Montpellier, focussed on tropical and Mediterranean plant genetic improvement and adaptation (2010-2014). Before that he was Scientific Director at CIRAD (2007-2010) and led the Sub-Programme on crop genetic diversity of the CGIAR Generation Challenge Programme from 2004 to 2010.

He is a member of the Scientific Advisory Board member at the IPK Gatersleben Leibniz Institute.

His current area of research is the use of phylogeographic approaches for assessing genetic diversity in crop germplasm. He is also leading CultiVar, an Agropolis initiative for linking research across continents through training and capacity building in plant breeding.

GenomeHarvest: deciphering mosaic genome diversity patterns as pathways to crop improvement

Jean Christophe Glaszmann

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We undertake a collective effort to analyse crop genetic diversity coordinated in the GenomeHarvest project supported by Agropolis Fondation in Montpellier. In concert with several CGIAR centres and programmes, we expand genomic initiatives that have recently led to the production of crop reference genome sequences. The current possibility for massive resequencing data production has opened new opportunities to understanding, with unprecedented resolution, the organization and dynamics of these genomes and the related keys to a more efficient exploitation of their diversity in breeding programs.

The full exploitation of these data requires development of new biomathematic/bioinformatic concepts, methods and tools to be made available in the SouthGreen platform. We tackle this challenge with a collaborative framework, making use of carefully selected representative, economically important and scientifically attractive biological models, including banana, citrus, coffee and rice.

We specifically address the impact of the frequent inter(sub) specific events involved in the history of crops. This will be illustrated with recent developments leading to new representations of current diversity as mosaics derived from ancestral founder populations. The first instance, in banana, highlights large genome structural variations that result in segregation distortions and restricted recombination. The second instance depicts introgression among rice varietal groups and highlights the massive contribution of alien sources of diversity.

Dr Benjamin Kilian
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Benjamin Kilian is a scientist and project manager, and in charge of all pre-breeding projects at the Global Crop Diversity Trust. Benjamin has a particular interest in exploring ways in which crop wild relatives and landrace diversity can be used in breeding programmes more effectively by better linking of genebanks to breeders.

Benjamin completed his PhD training at the Max Planck Institute for Plant Breeding Research (MPIPZ), Cologne, Germany. He has led various research projects at the Leibniz Institute for Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany, on genetics and genomics of plant genetic resources, especially in wheat and barley and their wild relatives.

Subsequently, Benjamin worked in the private sector aiming at making crop diversity available to breeding.

His scientific interest focuses on the domestication, conservation and use of agrobiodiversity, and the role it can play for sustainable development and food security.

Reaching back through the domestication bottleneck to feed a hot and crowded planet

Benjamin Kilian

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Crop wild relatives (CWR) represent a large pool of genetic diversity from which to draw beneficial allelic variation required in breeding programs. CWR have been extremely valuable in adapting crop varieties to changing disease pressures, farming practices, market demands, and climatic conditions. This talk will provide examples on how wild species have contributed to the development of improved crop varieties and where efforts must be concentrated in order to harness their value in the future. Introducing the global initiative "*Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives*" and drawing on it's current results, the role that CWR play in modern crop breeding will be documented. Activities that promise to facilitate the use of CWR, and what constraints continue to hinder increased utilization of plant genetic resources in breeding, will be discussed.

Session III

Sequencing-Based Trait Mapping

Co-chairs

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Dr. Baozhu Guo

Research Plant Pathologist
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Christian Jung is a plant breeder and molecular biologist working at the Plant Breeding Institute, Kiel University. From 1976 to 1981, he studied agriculture with a specialisation in plant production and microbiology at the University of Göttingen. In 1984, he received a doctoral degree with a thesis on "per se-performance and interaction between wheat and rye genomes in triticale".

From 1987-1992, he worked on plant molecular genetics and genomics at the Institute of Botany, University of Munich, where he received a habilitation degree in 1992.

Since 1993, he has been the director of the Plant Breeding Institute in Kiel. He is working on the molecular mechanisms of plant pathogen resistance and flowering time regulation.

Sugar beet, oilseed rape and barley are his main crops of interest.

Flowering time regulation in a vegetative crop and application in breeding

Christian Jung, Nadine Dally, Nadine Höft

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Sugar beet is a biennial species where floral transition is initiated after exposure to extended cold. Key regulators for bolting time control have been cloned.

Two homologs of the Arabidopsis *FT* gene have contrasting effects on flowering time. *BvFT1* is a floral repressor whereas *BvFT2* induces bolting and flowering. *BTC1* and *BvBBX19* are both acting upstream of *FT* perceiving signals form the photoperiod pathway. Single nucleotide mutations in either *BTC1* or *BvBBX19* have a strong impact on the function of the encoded protein turning an annual into a biennial genotype.

Our recent activities are focused on the interaction between *BTC1* and *BvBBX19,* and their transcriptional regulation of both *BvFT* genes. We reason that the *BTC1/BvBBX19 BTC1* module established a function like the CO gene from Arabidopsis because a functional CO ortholog is missing in beet. We selected double mutants (btc1 and Bvbbx19) from segregating beet offspring that displayed strong non-bolting phenotypes. These studies pave the way for breeding vegetative crops in which orthologs of the floral activator *FT* are completely downregulated even after cold treatment, giving rise to 'never bolting' crops.

Putative applications are winter beets sown before winter or vegetables such as lettuce or Chinese cabbage, which have a strong tendency for early bolting if they experience cold temperatures in early spring cultivation.

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Frank Ordon is vice-president of the JKI, head of the Institute for Resistance Research and Stress Tolerance of the JKI, 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 (Dr. habil.). He is the editor in chief of *Plant Breeding* and is a member of several editorial boards — for example, *Theoretical and Applied Genetics* and *Journal of Applied Genetics*, as well as scientific advisory boards. He is chair of the Research Committee of the Wheat Initiative.

Dr Ordon 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 contribution includes genetic analyses of resistance and the development of molecular markers for major resistance genes and QTL, especially against viral diseases, up to gene isolation.

Besides this, he is working on improving tolerance to abiotic stress in several crop species.

Dr Ordon has published the results of his studies in more than 100 papers in peer reviewed journals.

Genomics based valorization of genetic resources for improving disease resistance in cereals

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Barley and wheat are of special importance for feeding the earth´s growing population. However, both are hit by many pathogens causing severe yield losses. Therefore, identifying sources of resistance in genetic resources in order to broaden the genetic basis of resistance followed by marker development and the marker based exploitation of these resistances is a prerequisite to ensure an ecological sound cereal production and to avoid high yield losses. Based on screening programmes for resistance followed by genetic analyses, molecular markers have been developed for many major genes and QTLs for resistance in wheat and barley. While in the past marker development was time consuming and laborious, today genomic tools (e.g. GBS, chip technology, RNAseq etc.) and the availability of the sequence of wheat and barley facilitate efficient marker development and marker saturation of genes and QTL as well as gene isolation via map based cloning. Examples of using these genomic tools to harness resistances to fungal (e.g. *P. hordei, P. triticina, P. teres* etc.) and viral pathogens (BYDV, WDV, BaMMV, BaYMV) derived for exotic germplasm, landraces and crop wild relatives of wheat and barley are given.

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Jochen Reif is the head of the Department of Breeding Research of the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) in Gatersleben, Germany.

Dr Reif was awarded a PhD in Plant Breeding from the University of Hohenheim.

Prior to his appointment as head of the Department of Breeding Research, he served as head of the State Plant Breeding Institute at the University of Hohenheim.

Dr Reif manages a vigorous research program on basic and applied research to provide knowledge and enable new approaches to improve plant breeding in a sustainable manner.

Dr Reif coordinates the worldwide largest public-private partnership on establishing hybrid breeding in wheat. More than 6,000 wheat hybrids and their parental lines are currently evaluated using state-of-the-art genomic tools and their yield potential is assessed in comprehensive field trials. The data is used for a deeper understanding and improved valorization of heterosis for the selfing species wheat.

Using genomics to boost wheat grain yield

Jochen Christoph Reif

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Wheat (*T. aestivum* L.) is one of the most important crops, providing 20% of the total calories for the world's population. In contrast to maize and rice, wheat provides higher protein content and serves as the major ingredient in producing a wide variety of food. Worldwide wheat production needs to be doubled to feed an estimated world population of nine billion by 2050.

Nevertheless, it is becoming increasingly difficult to satisfy this rising global demand because arable land and water are increasingly becoming scarce, average living standards are rising, and investments in increasing agricultural productivity are growing slowly. Wheat breeding is one viable and sustainable solution to increase grain yield and to improve yield stability.

In this contribution, several genomics-based breeding strategies that hold the potential to boost wheat grain yield are reviewed. These include marker-assisted and genomic selection in multi-stage selection programs, genomics-aided implementation of hybrid wheat breeding, and genomics-based exploitation of wheat genetic resources.

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Scott A Jackson is the Georgia Research Alliance Eminent Scholar and Professor of Plant Functional Genomics at the University of Georgia. He is the Director of the Center for Applied Genetic Technologies and has appointments in the Institute for Bioinformatics, Plant Biology and Crop and Soil Sciences. His research focuses on the application of genomics for crop improvement and the understanding of basic biological processes, such as chromosome and genome evolution, domestication and polyploidy. His lab works primarily with rice and several legumes, and is international in scope with work in Asia, Africa and South America. His recent work has focused on sequencing the genomes of crops such as peanut, common bean and soybean wild relatives as well as elucidating the evolution of polyploid genomes including the role of epigenetics in these processes.

Accessing genetic variation outside the primary gene pool

Scott Jackson

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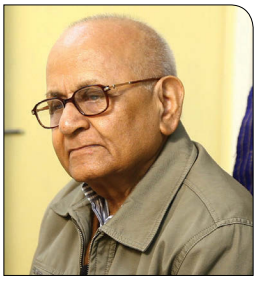
Using two legume crops, peanut and soybean, I will discuss i) our efforts to understand and describe genetic/epigenetic variation, and ii) approaches for moving useful variation into plant improvement programs. Both crops have undergone extensive genetic bottlenecks: in addition to domestication, soybean in the US can be traced to just a few founder lines, an extreme bottleneck. In peanut, polyploidy was coincident with domestication and is likely a result of a single polypoid event. Thus, both species are genetically depauperate and new genetic material is required to increase and protect yields. In soybean, undomesticated soybean (*Glycine soja*) has about twice the amount of genetic diversity as the domesticate. We have also shown that polyploidy has resulted in diversity within domesticated soybean that is often overlooked — for example, differentially methylated genes, presence-absence variation facilitated by genetic redundancy, and fixed hybridity between duplicated genes. In peanut, we are actively re-creating the cultivated allopolyploid, thereby moving new genes into the cultivated gene pool. This is done by mapping traits in the ancestral diploids and then making neo-allopolyploids that are interfertile with peanut. Both approaches have as their goal the use of existing genetic variation to solve agronomic problems.

Panel Session

Writing A High Quality Science Paper



Prof. PK Gupta
Hon. Emeritus Professor &
INSA Senior Scientist Professor
& INSA Senior Scientist
Chaudhary Charan Singh
University
India

Born in Saharanpur, UP on December 14, 1936, Professor **PK Gupta** had his early education there. Later, after completing his MSc (Meerut College, Meerut) from Agra University (1958), he mainly served Gorakhpur University (1960-69) and Meerut University (1969-1996) and also earned his PhD degree (1967) from University of Manitoba (Canada). Taken together, during the period of his active service and after his retirement, he supervised ~80 PhD students, and published ~440 research papers. For post-doctoral research work, and for attending international conferences, he also travelled world-wide in different countries (e.g., Canada, USA, Mexico, UK, France, Germany, Switzerland, Syria, Australia, Japan, Thailand, China, Australia, etc.).

Professor Gupta has also written more than two dozen university level text-books, which are widely read, and also edited a couple of volumes (Macmillan, Elsevier and Springer) that are used as reference material in the field of genetics, cytogenetics and biotechnology. He is a fellow of all the national Academies in the area of Science and Agriculture in India (FNA, FNASc, FASc, FNAAS), and also earned various academic awards including the prestigious Birbal Sahni Gold Medal of the Indian Botanical Society and the "ABLE Award for Excellence in Agricultural Research, 2013" for Significant Contribution in the Area of Marker Assisted Selection for Crop Improvement.

Prof. Hon-Ming Lam
Professor
The Chinese University of Hong
Kong
Hong Kong

Hon-Ming Lam, a Professor in the School of Life Science and the Director of the Partner State Key Laboratory of Agrobiotechnology, The Chinese University of Hong Kong (PSKLA), has been working on the identification of stress tolerance genes in soybean for more than 20 years. In 2010, Prof. Lam published an article in *Nature Genetics*, reporting the decoding of 31 wild and cultivated soybean genomes that revealed a much higher biodiversity in wild soybeans. In 2014, his team has successfully identified and cloned a major salt tolerance gene from wild soybeans, leading to a paper published in *Nature Communications*. This is a milestone in the mass production of high quality salt tolerant soybeans, a stage reached which will eventually benefit agriculture worldwide.

Using the finding from basic science research, Prof. Lam has also been working with soybean breeders in China to produce salinity and drought tolerant soybeans that can be grown on saline and/ or arid lands, via non-GM methods. In 2016, two new stress tolerant soybean cultivars gained provincial approval in China, and were cultivated in arid regions to restore arable land and help the local farmers.

Prof. Lam also published important reviews related to food security and agricultural sustainability, including a first-authored analytical review to The Lancet in 2013 and a co-authored perspective article to *Nature Plants* in 2016.

Panelists

Dr. Susan Jones
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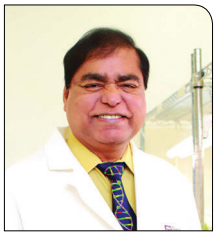
Susan Jones obtained a PhD at the University of Warwick, UK, where she studied quorum sensing in a plant pathogenic bacterium. She left the lab in 2003 to join *Nature Reviews Microbiology*, becoming Chief Editor in 2008, then joined the *PLOS Medicine* team and became Senior Research Editor in 2011. Susan joined *Nature Biotechnology* in 2012 and oversees manuscripts in plant biotechnology, microbial technology, genomics and synthetic biology.



Dr. Henry Daniell
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Henry Daniell is the Fellow of the AAAS and a foreign member of the Italian National Academy of Sciences (14th American to be inducted in the past 250 years) and the Editor in Chief of the *Plant Biotechnology Journal*, Oxford, UK. He pioneered chloroplast genetic engineering to enhance agronomic traits and produce and orally deliver low cost vaccines and biopharmaceuticals bioencapsulated in plant cells. He is recipient of several awards for his outstanding contributions.

Prof. Dr. A. E. Melchinger
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Albrecht Melchinger holds the Chair for Applied Genetics and Plant Breeding at the University of Hohenheim. He served as Dean of the Agricultural Faculty for several years and is a member of the scientific advisory board of several prestigious institutions. He has supervised more than 45 PhD and 120 MSc students and has published more than 320 peer-reviewed research articles in journals of repute. Dr Melchinger has received several awards for his contributions to maize research and breeding including Fellow of (i) the Crop Science Society of America, (ii) the Agronomy Society of America, and (iii) the Indian National Society of Agriculture. The major focus of his research is on selection theory in plant breeding and quantitative research, where he focuses on mapping of QTL by various methods, and genomic selection. His team has developed new tools for increasing the efficiency of maize breeding, most notably improvements of double-haploid technology.

Prof. Dr. Frank Ordon
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Frank Ordon is vice-president of the JKI, head of the Institute for Resistance Research and Stress Tolerance of the JKI, 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 (Dr. habil.). He is the editor in chief of *Plant Breeding* and is a member of several editorial boards — for example, *Theoretical and Applied Genetics* and *Journal of Applied Genetics*, as well as scientific advisory boards. He is chair of the Research Committee of the Wheat Initiative.

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Besides this, he is working on improving tolerance to abiotic stress in several crop species.

Dr Ordon has published the results of his studies in more than 100 papers in peer reviewed journals.

Session IV

Genomics-Assisted Breeding

Co-chairs

Prof. Deepak Pental

INSA Senior Scientist and former Vice-Chancellor
University of Delhi-South Campus
India

Dr. Arvind Kumar

Senior Scientist
IRRI
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Prof Dr Bin Han
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Bin Han obtained his bachelors degree in Biology from Anhui Normal University in 1985, masters degree in Biology from Guangxi Agricultural College in 1988, and PhD in Molecular Genetics from the Sainsbury Laboratory at John Innes Centre in UK in 1992. Between 1992 and 1998, he did postdoctoral work at the Department of Plant Sciences of University of Cambridge. In 1998, he returned to China and served as the director of the National Center for Gene Research, Chinese Academy of Sciences (CAS).

From 2002, he also served as a vice-director of the Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, CAS. In 2013, he was elected a member of the CAS.

Professor Han's area of focus is rice genome sequencing, comparative genome analysis of rice subspecies, and rice functional genomics. With second-generation sequencing technology, he and his laboratory have developed a high-throughput genotyping platform for both high-resolution linkage mapping and genome-wide association studies, and used these approaches to dissect complex traits in rice.

He and his laboratory have also used RNA-Seq technology for a global survey and comparison of cultivated rice transcriptomes.

Unlocking genetic basis of complex traits and heterosis in rice

Bin Han

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Most agronomic traits, which are called complex traits, are usually controlled by multiple genes and affected by various environmental conditions. Although a lot of quantitative trait locus (QTL) and genes related to rice complex traits have been cloned and functionally characterised, genetic basis and regulatory mechanisms underlying these complex traits are still unclear.

We have implemented an integrated approach of genome-wide association study (GWAS) and phenomics with functional analysis to catch up on agronomic trait genes or QTLs in a diverse cultivated rice population. This approach informs us that the associated loci with agronomic traits such as panicle length, grain sizes, grain weight and grain filling rate can be further characterised through expressional profiling, in-depth genome analysis, transgenic study, genome editing, and population genetic analysis.

We believe that allelic genetic variations responsible for complex traits can be effectively explored.

Exploitation of heterosis is one of the most important applications of genetics in agriculture. However, the genetic mechanisms of heterosis are only partly understood, and a global view of heterosis from a representative number of hybrid combinations is lacking. We have developed an integrated genomic and forward genetic approach to constructing a genome map for elite hybrid rice varieties and their inbred parental lines. We identified that the accumulation of numerous rare superior alleles with positive dominance is an important contributor to the heterotic phenomena.

We have further done large-scale genomic mapping for yield-related traits and heterotic effects by analysing more than 10,000 rice lines produced from 17 elite rice lines. The large data of genomics and phenomics from the well-designed populations enabled us, for the first time, to identify the genetic contributors and find out the exact causes of heterosis using "a composite interval-mapping method". For the individual yield components, the heterozygous state of the heterosis-related genes generally acted through dominance complementation.

Taking all the components into account, the hybrids with yield heterosis resulted from an optimal combination of multiple yield-related components, meaning better performance of overall yield in crop productions. These results inform the genomic architecture of heterosis for yield traits in rice, useful information for crop improvement program.

Prof Dr Albrecht E. Melchinger
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Albrecht Melchinger holds the Chair for Applied Genetics and Plant Breeding at the University of Hohenheim. He served as Dean of the Agricultural Faculty for several years and is a member of the scientific advisory board of several prestigious institutions. He has supervised more than 45 PhD and 120 MSc students and has published more than 320 peer-reviewed research articles in journals of repute. Dr Melchinger has received several awards for his contributions to maize research and breeding including Fellow of (i) the Crop Science Society of America, (ii) the Agronomy Society of America, and (iii) the Indian National Society of Agriculture. The major focus of his research is on selection theory in plant breeding and quantitative research, where he focuses on mapping of QTL by various methods, and genomic selection. His team has developed new tools for increasing the efficiency of maize breeding, most notably improvements of double-haploid technology.

Libraries of doubled-haploid lines from landraces: a new tool for maize breeding and genomic research

Albrecht E Melchinger, Juliane Böhm and Wolfgang Schipprack

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Landraces of maize evolved over centuries of multiplication and selection by farmers. Molecular data show that they represent a huge reservoir of untapped genetic variation. Since landraces in allogamous crops are open-pollinated populations, they represent conglomerates of highly diverse, heterozygous individuals with a high genetic load. This entails problems for their characterisation and exploitation in line development by recurrent selfing for hybrid breeding.

Production of DH line libraries (DHL) from landraces by *in vivo* haploid induction could overcome these problems. To test this hypothesis, we developed 389 lines from six DHL and evaluated their line *per se* performance for 14 agronomic traits in four locations. We found a much larger genotypic variance (σ^2_G) within DHL than among DHL. Usefulness of the best 20% lines was for individual DHL comparable to that of elite lines.

The DH lines were also genotyped with a 50k SNP chip and analysed for 288 metabolites. We found a rapid decay of linkage disequilibrium (LD) in most DHL, indicating their potential for high-resolution association mapping (AM). A proof-of-concept for this hypothesis was tested in a joint AM study of metabolites and agronomic traits. AM revealed significant associations for four of 16 agronomic traits as well as for 60 of the 288 metabolites. For certain metabolites, we found clear peaks in regions harboring gene(s) involved in the respective biochemical pathway.

Altogether, our results demonstrate that DHL are a promising tool for harnessing the genetic diversity of landraces for maize breeding and also for AM studies.

Dr Shancen Zhao
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Shancen Zhao is a research scientist and the deputy director of BGI Institute of Applied Agriculture. Dr Zhao graduated from the College of Life Sciences in Peking University, and then obtained a PhD at The Chinese University of Hong Kong. At the beginning of his PhD period, he joined BGI and dealt with several cooperative projects — for example, panda populations, wheat genomes, rice and soybean genomics.

He is widely interested in plant evolution, polyploid genomes, crop domestication and crop breeding. These projects resulted in several papers published in high-impact journals such as *Nature*, *Nature Genetics* and *PNAS*.

He now works as a consultant and research scientist for plant and animal projects in BGI, and directs the newly founded institute, focusing on applied agriculture.

BGI's efforts on crop breeding towards precision nutrition

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New advances in genomics and biotechnologies have offered new opportunities as well as challenges in the application of crop breeding for precision nutrition.

Nutrigenomics is the prospective analysis of differences among nutrients in the regulation of gene expression, while nutrigenetics is the analysis of genetic variations among individuals with respect to the interaction between diet and disease. Molecular breeding includes marker-assisted selection, marker-assisted backcross breeding, along with other newer breeding approaches, such as marker-assisted recurrent selection and genomic selection.

The integration of these technologies into crop breeding can enhance our understanding of biological mechanisms underlying diet and human health.

Recently, BGI-Shenzhen set up a non-profit research institute together with local government, named the BGI Institute of Applied Agriculture. The target is to promote translation and application of BGI's research achievements in the field of agriculture. The institute has constructed four public platforms, including Molecular Breeding, Advanced Biotechnologies, Biological Big Dataand Precision Nutrition, based on which, new research data and services are provided. Here, I will briefly introduce our efforts and designs on crop breeding towards precision breeding, taking rice, foxtail millet and soybean as examples.

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Sachiko Isobe started her career as a conventional red clover breeder. Currently she is a plant molecular biologist, and lab head of Plant Genomics and Genetics at Kazusa DNA Research Institute. The research group has performed genome sequencing and molecular genetics, including DNA marker development, linkage map construction, QTL identification and marker assisted selection. More than 30 model and crop species have been targeted, including strawberry, sweet potato, tomato, Lotus *japonicus*, groundnut, and clovers. Of these, strawberry is one of the main species, and comprehensive analysis on it has been performed, such as genome sequencing, RNA-Seq and genomic selection.

Challenge to genomic, genetic analysis and molecular breeding in allo-octoploid species, strawberry

Kenta Shirasawa[1], Hideki Hirakawa[1], Soichiro Nagano[1], Fumi Maeda[2], Manabu Watanabe[2], Yuji Noguchi[3], Sono Kataoka[3], Takuya Wada[4], Kouichiro Oku[4], Kiyoshi Namai[5], Kimihisa Tasaki[5], Akihiro Nakaya[6], Tomohiro Yanagi[7], Sachiko Isobe[1]

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[3]NARO Institute of Vegetable and Tea Science
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The complex structure of the polyploid genome has inhibited advances in genomics and genetic analysis in polyploid species. Strawberry (*Fragaria* × *ananassa*) is cultivated and consumed across the world. It is an allo-polyploidy species (2n = 8X = 56) with an estimated genome size of 1C = 708–720 Mb.

Strawberry was artificially generated in 16th century Europe by crossing between two octoploid species, *F. chiloensis* and *F. virginiana*. The construction of high quality subgenome-specific reference sequences in *F* × *ananassa* has been a long-dreamt goal, due to its potential for analyzing gene expression and accelerating molecular breeding.

We have sequenced a Japanese variety 'Reikou' with Illumina platform, and constructed subgenome-specific reference sequences by using DenovoMAGIC. A total of 62 (31 × 2 haplotypes) pseudomolecules were developed based on the linkage map in a total length of 1,125 Mb. By using the constructed pseudomolecules, we have performed RNA-Seq analysis in fruit color. Genomic selection for fruit hardiness was also performed with the four strawberry breeding stations across Japan. The conventional GS requires genome-wide genotyping for both the training and breeding populations. To decrease the cost and time for genotyping in the breeding population, we used Ensemble-based Genetic and Genomic Search (EGGS), which enable us to make a model with a lower number of DNA markers.

Genomic, genetic analysis and molecular breeding in polyploidy species is still difficult; however, the advance of NGS technologies as well as novel approaches for data analysis have made the challenge possible.

Session V

Decision Support Tools and Databases

Co-chairs

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Martin Luther University Halle-Wittenberg
Germany

Dr. BM Prasanna

Director-Global Maize Program &
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CIMMYT-Kenya
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Prof Dave Edwards
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Dave Edwards gained an Honours degree in agriculture from the University of Nottingham and a PhD from the Department of Plant Sciences, University of Cambridge. He has held positions within academia (Universities of Adelaide and Queensland, Australia; University of Cambridge, UK; and McGill University, Canada), government (Long Ashton Research Centre, UK; Department of Primary Industries, Victoria, Australia) and industry (ICI seeds, UK). In 2007 he moved to the University of Queensland, Australia, as an Associate Professor and was promoted to Professor in 2012. In January 2015 he moved his research group to the University of Western Australia, where he was Professor in Plant Genomics. His research interests include the structure and expression of plant genomes, and 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.

Genomics and bioinformatics requirements for future crop breeding

Dave Edwards

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The global population is predicted to reach more than nine billion by 2050, while at the same time, food production will become more challenging because of climate change. A new agricultural revolution, based on genomic knowledge and applied bioinformatics, is required to meet this demand for food security.

I will outline some of the recent advances in genomics, pangenomics and genome editing, and describe how these technologies are being applied to revolutionise the breeding of improved plant varieties, with greater yield and improved tolerance to the impacts of climate change.

Prof Mario Caccamo
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Mario Caccamo is head of Crop Bioinformatics at the National Institute of Agricultural Botany (NIAB) in Cambridge (UK) and holds an honorary professorship at the University of East Anglia. His current research interests are focused on the improvement of crops by using data-driven approaches. Previously, Professor Caccamo directed the Earlham Institute (formerly known as The Genome Analysis Centre) where he led the work to set up one of the largest European DNA sequencing and bioinformatics centres. Professor Caccamo completed a PhD in theoretical computer science at BRICS, University of Aarhus (Denmark) and an MSc in computer science in the University of Campinas (UNICAMP, Brazil). He has held postdoctoral and scientific roles at the Wellcome Trust Sanger Institute and the European Bioinformatics Institute during the early days of NGS technologies, contributing to the design and development of novel algorithmic approaches for DNA sequencing data analysis. Since April 2017 Professor Caccamo has been Managing Director of NIAB EMR.

Computational tools for better crops

Mario Caccamo

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Current annual yield increases in food crops will not meet the demands of a growing global population. Most crop yield gains in recent years have their sources in improved cropping techniques, fertilisation and irrigation. These strategies, however, are not sustainable in the medium and long term, and novel approaches are required to breed better-yielding and more-nutritious crops. The advent of inexpensive DNA-based genotyping tools has opened up new opportunities. The characterisation of genetic diversity in complex crop genomes is a key component in enabling the successful implementation of crop breeding. We are working on two Newton-funded projects that are focused on the characterisation of diversity for cereal crops. In a collaboration with the Agriculture Genetics Institute (Hanoi, Vietnam) we are working on Vietnamese rice native varieties that have been phenotyped for traits that are relevant to the challenges emerging from climate change, such as increasing soil salinity and pressure from novel diseases. The objective is to characterise the diversity present in 10% of the Vietnam rice seed bank to identify markers associated with traits of agronomical interest. The second project is a collaboration with the Seed of Discovery initiative at CIMMYT (Mexico) and is focused on the characterisation of the genetic diversity present in more than 150K wheat varieties. I will give an update on these two projects, focusing both on the results as well as the software infrastructure we are deploying to support high-throughput data analysis for these vast genomics datasets.

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David Marshall is a plant geneticist and bioinformatician with over 40 years' experience in the analysis of genetic diversity in wild and crop plant populations. Until recently, he was Head of Informatics and Computational Sciences at the James Hutton Institute (JHI) in Dundee, Scotland, and now works jointly between JHI and Scotland's Rural Colleges in Edinburgh (SRUC). His more recent focus has been on the discovery and utilisation of SNP variation in plants through the utilisation of modern high-throughput sequencing and genotyping technologies. His group has developed an international reputation for the development of visualisation tools (including Tablet, Flapjack, Curly-Whirly, Helium and the Germinate 3 data warehouse) for quality control of high-density data and the interrogation of large complex analyses. He works extensively with colleagues around the world, including several CGIAR centres, on a wide range of crop species.

Exploiting Comparative Genomics

David Marshall

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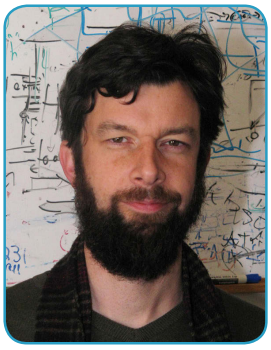
The availability of increasingly high quality genome sequence, diversity and expression data from an extensive range of monocot species is bringing exciting new opportunities to leverage this information. At one end of the spectrum, simply comparing gene models from a range of related species within a genus or family provide a logical framework to compare and often correct gene models derived from draft genome sequences. Phylogenetic analysis based on multiple species can also help to clarify potential functional roles for localised gene family expansion. Such comparative analyses can be greatly assisted and supported by systematic expression data across a range of species. Other useful components that can be deployed to help our analyses are the identification of major regions of synteny or the ancestral footprint of ancient genome duplications. These structural components can help to identify candidates for orthologous gene function or help understand the evolution towards sub-functionalisation.

The increasing diversity of sequenced genomes ensure that useful comparisons are not limited to a few major cereal genomes and can be made at various taxonomic level across the mono cotyledons.

Many examples will be given to illustrate the potential of these exciting developments and the software tools and procedures that can be utilised to maximise efficiency and utility. As many genomes are in essentially a draft state, an obligatory first step in inevitably the systematic correction of gene models. This is both enhanced and complicated by our growing understanding of the extent and importance of alternative splicing events in plants.



Mr Andrew Farmer
Bioinformatics Fellow,
National Center for Genome Resources,
2935 Rodeo Park Drive East,
Santa Fe, New Mexico 87505,
USA
E-mail: adf@ncgr.org

After graduating from St John's College in 1993, Mr Farmer joined the Theoretical Biology Group at Los Alamos National Laboratories to participate in the early development of sequence databases for HIV and other human pathogenic viruses, followed by an appointment at the Santa Fe Institute to explore viral sequence evolution using machine learning techniques. He joined the National Center for Genome Resources in 1996 and has remained there since, participating in a wide variety of projects including early work on systems for data management for the Human Genome Project, development of client-side software integration frameworks partnering with CGIAR centers, and playing a long-standing role on the USDA-supported Legume Information System. Mr Farmer's current projects focus on plant genomics with an emphasis on agricultural systems important to global food security through collaborations with public sector scientists and industry.

Unity through Diversity: Building a Legume Federation with Legume Information System and Friends

Andrew Farmer

National Center for Genome Resources, 2935 Rodeo Park Drive East, Santa Fe, New Mexico 87505, USA
E-mail: adf@ncgr.org

The rapid proliferation of genomic and genetic data for crop and model plant species since the advent of high-throughput sequencing and genotyping technologies has created rich opportunities for researchers seeking to address agriculturally relevant problems through the use of comparative techniques within and across diverse resources. However, providing integrated access to the disparate datasets generated by independent research groups remains a challenge.

We shall discuss ongoing work to address some of these issues through an open federation of groups managing information resources for legume genomics and breeding, each of which is focused on different subsets of the user community but all of whom have committed to strategies for shared management of data and to the adoption and development of common tools and protocols for interoperation.

Common scenarios of usage will demonstrate how we are currently approaching problems of integration across this diverse and economically important plant family, while featuring user interfaces developed to give intuitive federated access to diverse publically available annotated reference genomes, gene families, expression and diversity data including pangenomic resources.

These will serve as case studies in the development of new tools using open source frameworks such as Intermine and Chado/Tripal for the analysis and presentation of gene phylogenies, genome synteny, and studies linking genetic and phenotypic variation.

Panel Session

Genomics Applications Perspectives

Co-chairs

Prof. RB Singh
Chancellor,
Central Agricultural University,
Imphal
India

R.B. Singh is Chancellor, Central Agricultural University, Imphal, and past President, National Academy of Agricultural Sciences, India. Prof. Singh, Ph. D. in Genetics (NCSU, Raleigh, USA, 1964), possesses a career of leadership in improving agrarian livelihood, food, nutrition and ecological security, in cutting-edge research and technology development, in higher education and human resources development and in policy and programme formulation, execution and appraisal; each pursued in national, continental and global capacities. Prof. Singh had made important original contributions in the fields of Genetics, Plant Breeding and Biotechnology, guided doctoral research of 45 Ph.Ds. and authored over 300 research and policy papers and 12 books.

In recognition of his immense contribution to new knowledge, human resource capital and the science-led transformation of agriculture towards the alleviation of hunger and poverty in India and the Asia Pacific Region, Prof. Ram Badan Singh has been awarded the Padma Bhushan by the Hon'ble President of India – one of India's highest civilian honours that recognizes distinguished service of a high order to the Nation in any field, in 2003.

Prof. Eric Y. Danquah
Director,
West Africa Centre for Crop Improvement,
University of Ghana,
Ghana

Eric Yirenkyi Danquah is a Professor of Plant Genetics at the University of Ghana and a recipient of the University of Ghana Distinguished Award for Meritorious Service. He is the Founding Director of the West Africa Centre for Crop Improvement, University of Ghana. He is a Fellow of the Cambridge Commonwealth and Cambridge Philosophical Societies. He serves on the Technical Advisory Committee (TAC) of the AfricaYam Project at the IITA, Nigeria and is a member of the Advisory Board of the African Centre for Crop Improvement, University of KwaZulu-Natal, South Africa. He served on the Steering and Advisory Committee on the CGIAR Dryland Cereals and Grain Legumes, ICRISAT. He has several publications to his credit and has participated in international meetings the world over. He holds an MPhil degree (1987) in Plant Breeding and a PhD in Genetics (1993) from the University of Cambridge, UK.

Panelists

Dr. B Rajender
Ministry of Agriculture,
Cooperation and Farmers
Welfare
India

B. Rajender, Joint Secretary (Crops and Oilseeds), Ministry of Agriculture & Farmers Welfare, Government of India, is an Indian Administrative Officer of 1995 Batch of Bihar Cadre with 21 years of experience in various fields like Administration, Agriculture, Rural Development, Rural Infrastructure, Urban Development, Finance and Industry. He holds Bachelor's degree in Agriculture from Andhra Pradesh Agricultural University, Hyderabad and Master's and Doctorate in Plant Pathology from Indian Agricultural Research Institute, New Delhi. He has done special courses on rice breeding from IRRI, Philippines for two weeks and attended a workshop on management of irrigation for developing countries in Beijing, China for three weeks. Presently he is looking after National Food Security Mission dealing with rice, wheat and pulses, Seed Division dealing with administration of seed legislation and monitoring of availability of quality seeds production and distribution in the country and plant variety registration. and National Mission on Oilseeds and Oil Palm.

Dr. Paul Kimurto
Egerton University
Kenya

Paul Kimurto is the Director of Agro-Science Park and Associate Professor of Crop physiology (major) and plant Breeding (minor) at Egerton University, Faculty of Agriculture, Kenya. He holds a PhD in Crop Physiology/Breeding where he earned his PhD through Sandwich DAAD program between Egerton University & University of Potsdam (ATB), Germany. Prof Kimurto has over 15 yrs experience in academia and research. He is a professionally dryland research and drought stress physiology/breeding specialist with enormous experiences in dryland development and validation of breeding and variety development techniques and application of molecular breeding techniques. He has attended several International courses offered by ICRISAT, CIMMYT, Generation Challenge Program-GCP, International Atomic Energy Agency (IAEA), IFS, BECA/ILRI and Germany-DAAD in breeding, genetics, application of molecular breeding techniques, bio-saline and drought technology and seed systems. He has authored/co-authored several papers in many refereed journals. He has been involved in projects funded by several International donors like Gates Foundation, AGRA, USAID, ICRISAT and CIAT for research and development in Kenya.

Dr. Liao Boshou
Oil Crops Research Institute,
Chinese Academy of
Agricultural Sciences
China

Boshou Liao is the Director General of Oil Crops Research Institute of Chinese Academy of Agricultural Sciences (OCRI-CAAS). He graduated from Southwest Agricultural University in 1983 and then from Graduate School of CAAS in 1996. He has been working at OCRI-CAAS as the principal groundnut breeder since 1996 and released 12 groundnut cultivars. During 1995-1996, Boshou Liao worked in the University of Delaware of USA. He has been the Technical Coordinator of Groundnut Bacterial Wilt Working Group organized by ICRISAT since 1997. He is head of the CAAS-ICRISAT Joint Lab for Groundnut Aflatoxin Management. In 2007, Boshou Liao won the Doreen Mashler Award from ICRISAT for his contribution of promoting international cooperation for groundnut improvement.

Dr. Khaled Amiri
Khalifa Center for Genetic
Engineering and Biotechnology
UAE

Khaled Amiri is Associate Professor of Molecular Genetics in Biology Department at the UAE University. He obtained undergraduate education from the University of Colorado, Denver. He obtained his Ph.D. at University of Colorado, Health sciences Center. He studied the molecular genetics of catalytic RNA. In 1996, Dr. Amiri joined Biology Department at UAE University as a faculty member. Currently he is the director of Khalifa Center for Genetic Engineering and Biotechnology and the chair of Biology Department.

Dr. Khaled Amiri's research interest encompasses basic research on the role introns in biogenesis of mRNA, and genomic studies of desert plants. Dr. Amiri established the Unit for Genomic studies at the Biology Department, UAE University. The Unit is privileged with the state-of-art facilities to carry genomic, transcriptomic, and epigenetic analysis. Dr. Amiri published in a variety of peer-reviewed journals. He has numerous international collaboration. Also, Dr. Amiri has received numerous awards, organized scientific events, and participated in different scientific committees. He has also served on different boards (Dubai Autism Center, and DuBiotech.. etc.). He is currently involved in strategizing genomic research in the UAE and sustainable agriculture.

Dr. Chikelu Mba
Food and Agricultural Organization (FAO)
Italy

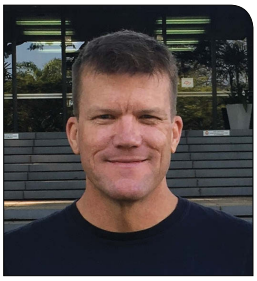
Chikelu Mba, a Plant Breeder Geneticist, Chike leads the Seeds and Plant Genetic Resources Team of the Plant Production and Protection Division of the Food and Agriculture Organization of the United Nations (FAO). The Team, made up of seven professional and four support staff members, is responsible for FAO's work on the conservation of plant genetic resources for food and agriculture; crop improvement and seed delivery systems.

Prior to joining FAO over seven years ago, Chike led the Plant Breeding and Genetics Laboratory of the Joint Division of FAO and the International Atomic Energy Agency (IAEA) for Nuclear Techniques in Food and Agriculture, Vienna and Seibersdorf, Austria. Previously, he was a cassava molecular geneticist and Coordinator of the Cassava Biotechnology Network for Latin America and the Caribbean at the International Centre for Tropical Agriculture (CIAT), Cali, Colombia.

Dr. Mba's career in agricultural research and development commenced in his native Nigeria where he worked for several years as Cassava Breeder Geneticist and Program Coordinator at the National Root Crops Research Institute (NRCRI), Umudike, Abia State, Nigeria. His duties at NRCRI, the largest root and tuber crops centre in Africa, included the development of well-adapted cassava varieties for the diverse agroecological zones of Nigeria and managing the institute's extensive in vitro and field cassava genebanks.

Chike, who serves on FAO's Interdepartmental Working Group on Biotechnologies, has published extensively on crop improvement-related themes.

He holds a PhD in Plant Breeding and Genetics; a Postgraduate Diploma in Education and a BSc in Botany – all from the University of Nigeria, Nsukka, Nigeria.



Dr. Mike Butterfield
CTC
Brazil

Mike Butterfield is the Manager of the sugarcane breeding program at CTC, Brazil – the largest private sugarcane research organization. Prior to CTC, he spent 6 years in Monsanto in sugarcane discovery breeding and enabling technologies, one year at ICRISAT as the Global Theme Leader for Biotechnology, and 15 years as a sugarcane breeder at the South African Sugarcane Research Institute. He is currently the secretary of the International Consortium for Sugarcane Biotechnology.

Dr. Victor Nwosu
MARS Inc.
USA

Victor Nwosu is currently a Senior Fellow – Peanut Sciences for Mars Wrigley Confectionery segment of Mars Incorporated. In his capacity as Senior Fellow, he manages peanut crop improvement and related projects in Argentina, Brazil, China, India, Nicaragua and the USA. He is an Executive Committee member of the International Peanut Genomic Initiative and of the Peanut Genome Consortium, and Member Board of Directors of Peanut Institute Foundation. He has dedicated most of his career to the global improvement of peanut crop.

He is a graduate of North Carolina State University, where he obtained his doctorate degree in 1995. Prior to joining Mars Wrigley Confectionery, Dr. Victor Nwosu was an Assistant Professor at Alabama A&M University. While at Alabama A&M University, he managed a Peanut CRSP funded project in collaboration with FUTO in Ghana. He is an author of five patents and sixteen reviewed journal articles.

Dr. Oscar Rierra-Lizarazu
Dow AgroSciennces
USA

Oscar Riera-Lizarazu is the North America (NA) Regional Crops' Technology Leader in the Agricultural Division of DowDupont, based in College Station, TX, USA. Prior to this assignment, Dr. Riera-Lizarazu has held various positions at Dow AgroSciences starting in 2013 as a Wheat Breeder and Station Leader and later becoming the Global Wheat and Sorghum Breeding Leader until 2017. Prior to joining Dow AgroSciences, Dr. Riera-Lizarazu had 16 years of national and international research experience on cereal genetics, cytogenetics, and breeding including director-level positions at the Int. Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, a tenured faculty position in Dept. of Crop and Soil Science at Oregon State University, USA, and research positions in non-profit institutions including the Int. Wheat and Maize Improvement Center (CIMMYT), Mexico, and the Bolivian Inst. of Agricultural Technology (IBTA), Bolivia.

Oscar Riera-Lizarazu received B.S. and M.S. degrees in Plant Science from the Utah State University and a Ph.D. in Plant Breeding and Genetics from the University of Minnesota, USA.

Closing Session

Dr. RS Paroda
Chairman
Trust for Advancement of Agricultural Sciences
India

Dr. Shobhana K Pattanayak
Secretary
Department of Agriculture, Cooperation and Farmers Welfare Ministry of Agriculture and Farmers Welfare, Govt. of India
India

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

Dr. Peter Carberry
Deputy Director General-Research
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
India

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

Poster Session

S.NO.	Presenter's Name	Title of Poster	E-mail	Poster ID
Theme I: Advances in Genomics				
1	Bellaire, Anke	Development and Metabolism — comparative High Resolution X-ray Computed Tomography (HRXCT) analysis of flower development combined with metabolomics reveals key points of developmental and metabolic regulation	anke.bellaire@univie.ac.at	CG1-P001
2	Boghireddy, Sailaja	Genome-wide analysis of long intergenic noncoding RNAs (lincRNAs) in contrasting heat stress responsive chickpea genotypes	b.sailaja@cgiar.org	CG1-P002
3	Chaturvedi, Palak	Pollen Proteomics: Evidence for developmental priming in abiotic stress defence	palak.chaturvedi@univie.ac.at	CG1-P003
4	Garg, Vanika	High-throughput sequencing approaches reveal complex roles of miRNAs and their targets in chickpea in response to Ascochyta blight	vanikag1@gmail.com	CG1-P004
5	Ghatak, Arindam	High-throughput quantitative proteogenomics approach in pearl millet to annotate new gene models	ghatak.arindam@yahoo.co.in	CG1-P005
6	Kudapa, Himabindu	The RNA-Seq-based gene expression atlas of a major food legume chickpea (*Cicer arietinum* L.)	k.himabindu@cgiar.org	CG1-P006
7	Kumar, Rakesh	A functional genomics approach to decipher strategic modification and regulatory mechanisms for drought-stress avoidance in groundnut	r.kumar@cgiar.org	CG1-P007
8	Kumar, Santosh	Genome-wide analysis of H3K4me3 mark in contrasting rice cultivars under drought stress	roy.santosh8@gmail.com	CG1-P008
9	Mallana Gowdra, Mallikarjuna	Genome-wide transcriptomic analysis under iron stress revealed candidate genes for kernel iron accumulation in maize (*Zea mays* L.)	MG.Mallikarjuna@icar.gov.in	CG1-P009
10	Pandey, Dev Mani	In silico characterisation of lipoxygenase and hydroperoxide lyase in peanut	dmpandey@bitmesra.ac.in	CG1-P010
11	Pazhamala, Lekha	Gene expression atlas of *Cajanus cajan* defines co-expressed gene clusters and a gene network critical for seed yield	l.pazhamala@cgiar.org	CG1-P011
12	Pazhamala, Lekha	Transcriptomic and cytological analyses with precise phenotyping characterises a pigeonpea environment-sensitive male sterile line, a pre-requisite for two line hybrid system	l.pazhamala@cgiar.org	CG1-P012
13	Savadi, Siddanna	Development of SSR markers from leaf rust (*Puccinia triticina*) transcriptome and their utility in genetic diversity and population structure analysis	siddannasavadi@gmail.com	CG1-P013
14	Vijayalakshmi, P	Identification of nitrogen use efficiency genes using genome-wide association studies and transcriptomics in pearl millet	V.Lakshmi@cgiar.org	CG1-P014
15	Sinha, Pallavi	Genome-wide epigenetic regulation in realising heterosis in pigeonpea (*Cajanus cajan* L.)	P.Sinha@cgiar.org	CG1-P015
16	Sinha, Pallavi	Transcriptome-wide gene expression atlas of groundnut (*Arachis hypogaea* L.)	P.Sinha@cgiar.org	CG1-P016
Theme II: Genome & Germplasm Diversity				
17	Ahmad, Zishan	Reintroduction and in vitro propagation of *Declapeis arayalpathra* — a critically endangered plant of Western Ghats, India	zishanahmad.rs@amu.ac.in	CG2-P001
18	Arora, Naveen	Evaluation or screening of the sorghum genotypes for expression of resistance against shoot fly (*Atherigona soccata* Rondani)	aroranaveen19@gmail.com	CG2-P002

S.NO.	Presenter's Name	Title of Poster	E-mail	Poster ID
19	Edirisingha, Iresha Kumari	Comparative analysis of leaf vein density in Sri Lankan traditional rice varieties	iedirisingha058@gmail.com	CG2-P003
20	Gupta, Rajeev	CINTRIN: Cambridge India Network for Translational Research in Nitrogen	g.rajeev@cgiar.org	CG2-P004
21	Karande, Satish Kumar	Genetic Divergence Analysis in Rice (*Oryza sativa* .L)	satishkarande_78@rediffmail.com	CG2-P005
22	Khan, Aamir W	Pangenome of Cicer species	a.khan@cgiar.org	CG2-P006
23	Naidu, Gopalakrishna	Yield-loss assessment among groundnut genotypes with differential response to iron deficiency chlorosis	gknaidugene@gmail.com	CG2-P007
24	Pandey, Sarita	Towards genetic dissection of nutritional traits in chickpea (*Cicer arietinum* L.)	p.sarita@cgiar.org	CG2-P008
25	Pandey, Arun K	Development of Enzyme-linked immunosorbent assay (ELISA) protocol for detection of Ara h 1, Ara h 2, Ara h 3, Ara h 6 and Ara h 8 allergens in peanut (*Arachis hypogaea* L.)	P.Arunkumar@cgiar.org	CG2-P009
26	Pratap, Aditya	Improvement in Indian mungbean breeding programme as revealed by morphological and microsatellite-based molecular analysis	Aditya.Pratap@icar.org.in	CG2-P010
27	Raizada, Avi	Development of e-SSR markers from transcriptome sequence of black gram [*Vigna mungo* (L.) Hepper]	raizadaavi165@gmail.com	CG2-P011
28	Rayaprolu, Laavanya	Genome-wide association study (GWAS) to identify genomic regions associated with candidate biofuel traits in sorghum	rayaprolulaavanya@gmail.com	CG2-P012
29	Romana, Kirandeep Kaur	Assessment of yield traits in diverse sorghum genotypes under different N regimes for N use efficiency improvement	K.Romana@cgiar.org	CG2-P013
30	Salgotra, Romesh	Characterisation of common bean (*Phaseolus vulgaris* L.) genotypes using trait-linked markers	rks_2959@rediffmail.com	CG2-P014
31	Soni, Pooja	Towards identification of genomic regions controlling pre-harvest aflatoxin contamination using multi-parent advanced generation intercross (MAGIC) population in groundnut	sneh.pooja000@gmail.com	CG2-P015
32	Taddi, Satyanarayana	Genome-wide association studies (GWAS) for shoot fly (*Atherigona soccata*) resistance in sorghum (*Sorghum bicolor*)	satya.bt09@gmail.com	CG2-P016
33	Tiwari, SP	Understanding the genetic variability for resistance against root lesion nematode and dry root rot fungi in germplasm lines of chickpea (*Cicer arietinum* L.).	tiwari_sp1234@rediffmail.com	CG2-P017
34	Vasanthi, RP	Development of high-yielding genotypes with resistance to drought and foliar diseases in groundnut (*Arachis hypogaea* L.)	vasanthi.rrs@gmail.com	CG2-P018
35	Zargar, Sajad M	Association mapping for identification of QTLs responsible for accumulation of iron and zinc, and proteomic analysis for identification of mineral stress responsive proteins in common bean (*Phaseolus vulgaris* L.).	smzargar@rediffmail.com	CG2-P019
36	Joshi, Priyanka	Genetically diverse genotypes of chickpea: a wealth and strength	priyanka.joshi95@yahoo.com	CG2-P020
37	Pattanashetti, Santosh K	Genetic variability for grain nutritional and productivity traits among selected pearl millet germplasm	S.Pattanashetti@cgiar.org	CG2-P021

S.NO.	Presenter's Name	Title of Poster	E-mail	Poster ID
Theme III: Sequencing-based trait mapping				
38	Barmukh, Rutwik	Towards fine mapping of 'QTL-hotspot' regions for drought tolerance in chickpea (*Cicer arietinum* L.)	rutwik.barmukh@gmail.com	CG3-P001
39	Chitikineni, Anu	Sequencing-based trait mapping of leaf spot resistance and the p rominent main stem using TILLING lines in groundnut (*Arachis hypogaea* L.)	a.chitikineni@cgiar.org	CG3-P002
40	Jain, Ankit	Genome-wide InDel marker resource for molecular breeding in chickpea	a.jain@cgiar.org	CG3-P003
41	Karadi, Ashwini	Identification of genomic regions conferring dry root rot resistance in chickpea (*Cicer arietinum* L.)	ash5557@gmail.com	CG3-P004
42	Kiranmayee, Usha	High-density linkage map and GWAS for flowering time identified new QTLs and putative candidate genes on sorghum chromosome SBI-10 (L) long arm	knskira@gmail.com	CG3-P005
43	Mahendrakar, Mahesh	In-silico identification of candidate gene for high grain iron and zinc in Pearl millet [*Pennisetum glaucum* (L.) R. Br.]	mahendrakar.mahesh@gmail.com	CG3-P006
44	Manchikatla, Praveen	Towards molecular mapping of root lesion nematode resistance in chickpea (*Cicer arietinum* L.)	praveen1211987@gmail.com	CG3-P007
45	Mani, Vetriventhan	Genome-wide association mapping for agronomic traits in foxtail millet	m.vetriventhan@cgiar.org	CG3-P008
46	Molla, Johiruddin	Sequencing-based trait mapping of EMS-induced mutants for 100 seed weight and seed colour in pigeonpea [*Cajanus cajan* (L.) Millsp]	johiruddinmolla@gmail.com	CG3-P009
47	Mondal, Suvendu	Fine mapping of a dominant rust resistance gene of cultivated groundnut revealed two R genes around the major Rust_QTL.	suvenduhere@yahoo.co.in	CG3-P010
48	Narkhede, Gopal	Mapping of fertility restorer loci in A1 cytoplasm of sorghum [*Sorghum bicolor* (L.) Moench]	gopnarkhede@gmail.com	CG3-P011
49	Pandey, Manish K	Towards fine mapping and cloning the genes for foliar disease resistance using next-generation sequencing approaches in groundnut	m.pandey@cgiar.org	CG3-P012
50	Ramasamy, Ellango	Response of tolerant and susceptible sorghum cultivar to drought stress: gene expression analysis	rellango@cgiar.org	CG3-P013
51	Sai Bindu, Karamthote	Identification of heat shock transcription factors in pearl millet	kcsaibindu88@gmail.com	CG3-P014
52	Thudi, Mahendar	Towards identification of candidate genes and development of markers for molecular breeding of early flowering in chickpea (*Cicer arietinum* L.)	t.mahendar@cgiar.org	CG3-P015
53	Yadav, Pooja	Identification of genes/genomic regions associated with cleistogamy and shrivelled seeds in pigeonpea (*Cajanus cajan* L.)	iampoojayadav@gmail.com	CG3-P016
54	Gangurde, Sunil	Genotyping-by-sequencing-based genetic mapping reveals higher epistatic interactions for resistance to stem rot disease in groundnut	sgangurde40@gmail.com	CG3-P017
Theme IV: Genomics-assisted breeding				
55	Bhat, Ramesh	Application of genomics in improving foliar disease resistance in peanut	bhatrs@uasd.in	CG4-P001
56	Chahota, Rakesh	Genomic tools for the improvement of horsegram (*Macrotyloma uniflorum*)	rkchahota@yahoo.com	CG4-P002

S.NO.	Presenter's Name	Title of Poster	E-mail	Poster ID
57	Chetukuri, Anuradha	Genetics of mungbean yellow mosaic virus resistance in blackgram [*Vigna mungo* (L.) Hepper].	anu.gene@gmail.com	CG4-P003
58	Jaganathan, Deepa	CRISPR/Cas9-based genome-editing approach for developing transgene-free salt tolerance rice varieties	deepajaganathan@mssrf.res.in	CG4-P004
59	Lata, Swaran	Assessment of distinctness, uniformity and stability of maize germplasm (*Zea mays* L.) based on morphological descriptors and molecular markers	slatasharama@gmail.com	CG4-P005
60	Manasa, KG	Improving Staygreen traits in farmer-preferred sorghum cultivars throughmarker-assisted backcross breeding	g.manasa@cgiar.org	CG4-P006
61	Nanayakkara, Dhanesha	A novel molecular marker for bacterial leaf blight resistance gene Xa21 in rice	dhanesha.nanayakkara@gmail.com	CG4-P007
62	Palchamy, Kadirvel	Towards marker-assisted breeding for higher productivity in safflower	kadirvel.palchamy@icar.gov.in	CG4-P008
63	Punna, Jayamma	Marker-assisted introgression of yield-enhancing genes to increase yield potential in rice	jayapunna@gmail.com	CG4-P009
64	Roorkiwal, Manish	Comparative analysis of different genotyping platforms for estimating genomic prediction in multi-environment trials of chickpea lines	m.roorkiwal@cgiar.org	CG4-P010
65	Saripalli, Gautam	Genome-wide association analysis under timely and late sown (terminal heat stress) conditions in wheat using GAPIT, SUPER and FarmCPU approaches	saripalligautam86@gmail.com	CG4-P011
66	Shasidhar, Yaduru	Molecular breeding for improving foliar disease resistance and oil quality in groundnut (*Arachis hypogaea* L.)	Y.Shasidhar@cgiar.org	CG4-P012
67	Somegowda, Vinutha	Identification of putative genomic regions for fodder quality traits in sorghum	vinuthaks.mysore@gmail.com	CG4-P013
68	Vijaya Kumar, KV	Identification of SNPs from amplicon sequencing of linked SSRs to post-flowering drought tolerance QTLs (Stg 3A and Stg 3B) in sorghum [*Sorghum bicolor* (L.) Moench]	k.vijaya@cgiar.org	CG4-P014
69	Mannur, DM	New life to chickpea variety Annigeri-1 by deployment of Fusarium wilt resistant loci through MABC	dmmannur@gmail.com	CG4-P015
Theme V: Decision support tools and databases				
70	Bera, Biswajit	In-silico analysis of existing/available genome sequences in tea	ntrf.india@gmail.com	CG5-P001
71	George, Suja	Leaf temperature, yield and genotype-specific patterns of gene expression in *Sorghum bicolor* under drought and salt stress	sujageorge@mssrf.res.in	CG5-P002
72	Mishra, Nilesh	Digital tools for knowledge sharing — a case of Tropical Legumes III project	m.nilesh@cgiar.org	CG5-P003
73	Nayidu, Naghabushana K	Study of ribosomal assembly genes in Arabidopsis	nagabushana@gmail.com	CG5-P004
74	Satbhai, Santosh	A leucine-rich repeat receptor-like kinase gene is a novel regulator of root growth under iron deficiency	ssatbhai@salk.edu	CG5-P005
75	Singh, Sadhana	Genome-wide identification of NAC family genes in chickpea (*Cicer arietinum* L.) and pigeonpea [*Cajanus cajan* (L.) Millsp.]	S.Sadhana@cgiar.org	CG5-P006
76	Singhal, Tripti	Identification of quantitative trait loci for grain iron and zinc content in pearl millet [*Pennisetum glaucum* (L.) R. Br.]	triptisinghal16@gmail.com	CG5-P007
77	Valluri, Vinod K	Cajanus Variation Database (CajanusVarDB): A genomic resource for advancing pigeonpea research	v.vinodkumar@cgiar.org	CG5-P008
78	Varshney, Rajeev K	Genomic Open-source Breeding Informatics Initiative (GOBII) for accelerating the rate of genetic gain	r.k.varshney@cgiar.org	CG5-P009
79	Bajaj, Prasad	Sequencing and Informatics facility at ICRISAT	p.bajaj@cgiar.org	CG5-P010

CG1-P001 | Development and metabolism – comparative High Resolution X-ray Computed Tomography (HRXCT) analysis of flower development combined with metabolomics reveals key points of developmental and metabolic regulation

Bellaire A[1], Ischebeck T[1], Staedler Y[2], Parameswaran S[3], Ito T[3], Schonenberger J[2], Weckwerth W[1*]

[1]Ecogenomics and Systems Biology, University of Vienna, Vienna, Austria
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The interrelationship of morphological development and metabolism is a poorly studied phenomenon. The main paradigm is that development is controlled by gene expression. However, it can be assumed that feedback sensing of the metabolic states within the plant tissue contributes significantly to the progress of morphogenesis.

The major aim of the present study is to link metabolism to early and late stages of flower and fruit development. A highly detailed picture of morphogenesis is achieved by non-invasive techniques such as micro-CT. This technique was used to quantify morphometric landmarks of early and late flower development in *Arabidopsis thaliana* and *Nicotiana tabacum*. The data were analysed by multivariate statistics and the ontogenetic trajectories are compared. The integration of metabolomic and morphometric data enabled the correlation of specific molecular signatures with the corresponding developmental morphotype, from the moment of floral initiation to anthesis, and further to silique formation and seed development in *Arabidopsis*. These signatures changed significantly during development indicating a pronounced metabolic reprogramming in the tissue.

Distinct sets of metabolites involved in these processes were identified and were linked to previous gene expression studies of flower development. A model of metabolic sensing during floral development is proposed (1).

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CG1-P002 | Genome-wide analysis of long intergenic noncoding RNAs (lincRNAs) in contrasting heat stress responsive chickpea genotypes

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Chickpea (*Cicer arietinum* L.) is an important legume crop, with high nutritional value. Exposure to high temperature during the vegetative and reproductive sta ges leads to limited crop productivity in chickpea. Owing to future climatic conditions, it is necessary to develop heat stress resilient chickpea varieties by understanding the gene regulation mechanism.

Besides the transcriptome and small noncoding RNAs, recent studies have been focusing on the long intergenic noncoding RNAs (lincRNAs) that play a role in the regulation of gene expression by acting as chromatin modifiers and miRNA sponges. In this context, to understand the regulatory role of lincRNAs in chickpea during heat stress, RNA-seq was performed on vegetative and reproductive tissues (roots and leaves) of three heat stress responsive chickpea (two tolerant — ICC 15614, ICC 1356 — and one sensitive — ICC 4567) genotypes in heat stress as well as control conditions. A total of 4577 lincRNAs and 153 differentially expressed genes were identified in root and leaf tissues at two different stages under heat stress. Further analysis on co-expression and lincRNAs-miRNAs interactions is in progress to identify the association of lincRNAs with the target mRNA transcripts and miRNAs.

In summary, this study provides a glimpse of lincRNAs and their role to unravel the complex regulatory mechanism underlying the heat stress response in chickpea.

CG1-P003 | Pollen Proteomics: Evidence for developmental priming in abiotic stress defence

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Pollen development is a well-programmed and crucial process that controls plant sexual reproduction and productivity. This process of development is highly sensitive to environmental changes such as temperature, drought and nutrition, and thus crucial in the era of global climate change and decreasing plant productivity under abiotic stress (1). Recently, we generated a first cell-specific reference-proteome of tomato pollen development, which includes microsporocytes, tetrads, microspores, polarised microspores and mature pollen (2). Each stage showed a specific reprogramming of the proteome. These responses in pollen development were termed "developmental priming", in contrast to "defence priming". Here, the hypothesis is that a genetic or epigenetic programme controls expression and translation of protective proteins such as Heat shock proteins and occurs already in the non-stressed state, to compensate for sudden changes in temperature during the maturation of the pollen (1, 2). Further, a novel approach was introduced for peptide quantification based on mass accuracy precursor alignment (MAPA), considering a target list of "proteotypic peptides" in the ecotype Hazera cv.3017 (3). This approach was exemplified by the comparison of control and heat-treated tomato pollen developmental stages (post meiotic and mature). In total, 51 unique proteins were identified that were potentially involved in heat defence mechanisms. Increased levels of heat-responsive proteins (such as HSPs, LEA, dehydration responsive family protein and thioredoxin/protein disulfide isomerase) might hint to the process of acquired thermotolerance (3). Further experiments will be performed to validate the hypothesis of developmental priming.

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CG1-P004 | High-throughput sequencing approaches reveal complex roles of miRNAs and their targets in chickpea in response to *Ascochyta blight*

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Ascochyta blight (AB), caused by the fungus *Ascochyta rabiei*, is one of the most devastating biotic stresses constraining chickpea growth and development. Recent studies have demonstrated the altered expression of miRNAs and their target genes in plants in response to fungal infections. In this study, we deployed RNA seq, small RNA (sRNA) seq and degradome seq to profile gene and miRNA expression in chickpea in response to *A. rabiei* infection. In total, 20 leaf tissue samples of five chickpea genotypes with contrasting phenotype for AB (C 214 and Pb 7 susceptible and ILC 3279, ICCV 05530, BC_3F_{6-} moderately resistant) stress were used. In the sRNA seq approach, ~532 million reads with an average of 26 million reads per sample were generated, leading to identification of 659 miRNAs.

The study identified differential expression patterns for several legumes specific and stress responsive (miR159, miR393) miRNAs. In the study, we observed that miRNAs respond to AB stress in a genotype, tissue and stage dependent manner. Degradome sequencing produced 52 million unique reads and identified mRNA targets for 306 miRNAs. Approximately 817 million high-quality reads from transcriptome profiling identified 10,626 constitutively expressed and 5,020 differentially expressed genes (DEGs) across various sample combinations. The DEGs identified were found to be related to transcription factors, chitinases, disease resistance and pathogenesis.

In summary, the study provides a framework for understanding molecular AB-chickpea interactions and offer candidate genes for development of improved chickpea cultivars with enhanced AB resistance.

CG1-P005 | High-throughput quantitative proteogenomics approach in pearl millet to annotate new gene models

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Proteogenomics is a new research field at the interface of proteomics and genomics. This approach facilitates the use of peptide MS to improve and refine genomic annotation.

Recently, we have applied this approach on newly sequenced pearl millet genome (1)**.** The annotated gene models and corresponding six-frame translated sequences were employed to identify new gene models (2, 3).The proteomic analysis was performed using pollen, stigma, ovary, root, seed and leaf tissues under control and drought stress conditions (4). The first preliminary data resulted in 9,212 peptides with unique sequence, of which 86.6% (7,979 peptides) match current gene models.

Further, a total of 1,233 peptides did not match gene models, indicating non-annotated regions. This proteogenomic annotation of pearl millet is continuously updated with an increasing number of identified proteins.

We also compared the genome and proteogenomic data of pearl millet with 545 functionally well-annotated heat and drought responsive genes of Arabidopsis and identified 40 proteins, indicating a high proportion of potentially stress-related proteins even under normal growth conditions. Remarkably, these proteins have shown a very diverse tissue-specific abundance, suggesting that many of the defence mechanisms corresponding to heat and drought are tissue-specific.

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CG1-P006 | The RNA-Seq-based gene expression atlas of a major food legume chickpea (*Cicer arietinum* L.)

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Chickpea (*Cicer arietinum* L.) is an important food legume and is an excellent source of protein, with a wide range of amino acids essential to the human diet. In addition, chickpea plants have root nodules with tremendous nitrogen-fixing ability. Plant growth/development are controlled by programmed expression of a suite of genes at the given time, stage and tissue.

To understand how the underlying genome sequence results in specific plant phenotypes at key developmental stages, information on gene expression patterns and their functions representing multiple tissues at important growth stages of plant is crucial. In this context, a comprehensive *Cicer arietinum* Gene Expression Atlas (CaGEA) was generated that provides a global view of gene expression in all major organs across the plant developmental stages covering the entire life cycle of chickpea.

The most drought-tolerant and widely used chickpea cultivar, ICC 4958, has been used to generate RNA-Seq data from 27 samples at five important developmental stages (germination, seedling, vegetative, reproductive and senescence) of the plant. From these samples, 27 cDNA libraries were generated and sequenced, resulting in a total of 816 million raw reads. Of these, 794 million filtered reads after QC were subjected for analysis. Gene expression patterns were analysed to better understand changes during different developmental stages. A total of 25,784 genes were identified to be transcriptionally active in one or more than one tissue, representing 91% of 28,269 predicted genes in the chickpea genome. CaGEA revealed 15,947 differentially expressed genes (≥2 folds) and, among these, 4,829 transcription factor genes were identified. In addition, 1,837 novel genes were found to be differentially expressed.

In summary, CaGEA is a valuable resource for gene discovery and functional characterisation to understand the systematic process of growth/development of chickpeas.

CG1-P007 | A functional genomics approach to decipher strategic modification and regulatory mechanisms for drought-stress avoidance in groundnut

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Groundnut (*Arachis hypogaea* L) is an important food legume of the tropical and subtropical world curently grown on more than 24 million hectares of land in about 120 countries. Although groundnut is mainly known for cooking oil and confectionary products, a fact few are aware of is its high nutritional value, including in proteins, antioxidants, vitamins and minerals.

Drought stress adversely affects groundnut production globally and reduces yield by more than 50%. In recent years, various functional genomics approaches, such as transcriptomics, proteomics and metabolomics, have gained huge attention because of their potential to unravel molecular events, including abiotic stresses. Drought tolerance is a complex trait and, to the best of our knowledge, no study dealing in all these approaches has been used for developing a better understanding of the legume. In this context, the present study is focused on enumerating the factors associated with the physiological changes and adaptation acquired by the drought-tolerant variety of groundnut, using transcriptomics, proteomics and metabolomics approaches.

To find the differences in pod development, this study will also analyse the peg composition changes of both the tolerant and the susceptible variety. Further, the metabolic and the proteome changes will be investigated in leaf and developing seeds of the tolerant and the susceptible variety during drought stress. Additionally, we will be examining the stomatal density in the leaves of the susceptible and tolerant variety to correlate with the transpiration water loss.

In summary, this study expects to add a new layer to the knowledge on the drought-stress mechanism in groundnut, and in turn will facilitate devising a strategy for developing a drought-tolerant groundnut variety, with more precision and speed.

CG1-P008 | Genome-wide analysis of H3K4me3 mark in contrasting rice cultivars under drought stress

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H3K4me3 modification is an active histone mark and positively correlates with gene expression ranging from plants to animals. In order to study the involvement of H3K4me3 mark in regulation of drought response, whole-genome ChIP-seq (Chromatin immunoprecipitation followed by high-throughput sequencing) was performed in two contrasting rice cultivars, N22 (drought tolerant) and IR64 (drought sensitive) at the heading stage in the flag leaf and spikelets tissue, for plants grown under control and drought conditions.

ChIP-seq tags generated were mapped on genome with the help of 'Bowtie2' software and, overall, more than 90% of the reads mapped and out of these 55-65% of the tags mapped uniquely. Associated peaks were called with the help of 'MACS' software and, on average, 15-30 thousands peaks were identified (p 1e-05). The number of identified peaks changed dynamically depending on growth conditions, tissue types as well as cultivar used. The average peak lengths ranged from 800 bp to 1100 bp depending on cultivar, tissue types as well as growth conditions. H3K4me3 histone mark was found to be associated with about 25% to 45% of total rice genes. Further analysis for peak genomic distribution showed that peaks were localised both in genic as well as intergenic loci in both cultivar.

However, most of the peaks were found to be enriched mostly within 1kb of the transcription start sites (TSSs) of genes and varied dynamically with growth conditions, tissue types as well as cultivar specific manner. Analysis of ChIP-seq and RNA seq data under similar conditions suggested that a distinct subset of genes were positively correlated with H3K4me3 mark.

This study clearly demonstrates the drought-mediated dynamism of the H3K4me3 histone mark in *indica* rice.

CG1-P009 | Genome-wide transcriptomic analysis under iron stress revealed candidate genes for kernel iron accumulation in maize (*Zea mays* L.)

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Deficiency of iron (Fe) causes micronutrient malnutrition or hidden hunger, affecting millions of people. Globally, one in four people are affected by Fe deficiency anaemia (IDA) with pregnant women and children at highest risk. The problem is severe in developing countries, where cereal-based diets predominate. Maize is the leading cereal crop in terms of production and one of the major sources of food and feed in developing countries of sub-Saharan Africa, South Asia and Latin America. To understand the genes and pathways associated with iron homeostasis, a genome-wide expression assay was performed with inbred line SKV616 in response to Fe stress.

A higher number of differentially expressed genes (DEGs) was found in the shoot as compared with root owing to the higher physiological demand for Fe. Several genes were differentially expressed in various pathways in response to Fe-stress treatment *viz*., genes of mugineic acid pathway, metal transporters, and phyto-hormone metabolism (auxin, cytokinin and ethylene).

Co-mapping of DEGs with previously identified QTLs for kernel iron concentration identified several candidate genes such as *OPT, nramp3* and *NAS*. *In-silico* analysis of major iron transporter gene families (*NRAMP, OPT, YSL* and *ZIP*) in maize revealed synteny with rice, barley, *Brachypodium* and foxtail millet. Phylogenetic analysis concluded that in Fe-transporters are conserved in the Poaceae lineage and evolved under positive or Darwinian selection.

The identified genes and pathways could be targeted to understand Fe stress tolerance in detail and to develop Fe-efficient and Fe-rich maize hybrids to fight Fe malnutrition and IDA.

CG1-P010 | *In silico* characterisation of lipoxygenase and hydroperoxide lyase in peanut

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Peanut (*Arachis hypogaea*) is a herbaceous legume that is grown worldwide for its seed and oil. The quality and yield of peanut are affected by various abiotic stresses. Many approaches have been taken into consideration to increase its shelf life, odour quality and seed quality. It is essential to understand gene regulation and corresponding metabolic pathways.

Peanut genome sequencing has been recently completed but the genes responsible for flavour and sensory attributes remain unidentified. Herein we aim to study the gene-encoded proteins such as lipoxygenase and hydroperoxide lyase because of their relation to flavour and odour. *In-silico* identification of chemical compound and enzymes was performed. Identification and their involvement in metabolic pathway was performed using KEGG pathway database. Phylogenetic tree analysis of enzymes was performed using MEGA v6.0. Identification of conserved domain, structure prediction and analysis of secondary structure as well as Ramachandran plot was also performed.

Obtained findings will be presented.

CG1-P011 | Gene expression atlas of *Cajanus cajan* defines co-expressed gene clusters and a gene network critical for seed yield

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Pigeonpea (*Cajanus cajan*) is an important grain legume of the semi-arid tropics, providing sustainable food and nutrition security in developing countries. Genome of this crop has been decoded to provide useful insights into the protein-coding regions, gene functions and clues to biological processes.

To complement the genome sequence information, a gene expression atlas of *Cajanus cajan* (CcGEA) using Asha genotype has been developed. Illumina HiSeq 2500 was used to generate 590.84 million paired-end RNA-Seq data from 30 tissues representing five developmental stages encompassing the complete lifecycle. As a result, a total of 28,793 genes have been identified with differential, specific, spatio-temporal and constitutive expression during various stages of development in different tissues. Genes clustered based on their co-expression identified four important clusters specific to aerial, underground, floral and senescing tissues. The Weighted Gene Co-expressed Network Analysis (WGCNA) provided a gene network composed of 28 genes specific to floral tissues, regulated by a developmental regulator SF3 and a sucrose-proton symporter. Analyses of these genes for *cis*-regulatory elements, splicing variants and expression in male sterile and fertile genotypes suggested their critical role in the development of normal pollens and seeds. Thus, the gene network has been implicated in seed production and yield.

This dataset provides a valuable resource for legume genomics for studying basal expression of genes when investigating mutants, identifying candidate genes for specific traits and for understanding the well-orchestrated growth and developmental process in this resilient crop.

CG1-P012 | Transcriptomic and cytological analyses with precise phenotyping characterises a pigeonpea environment-sensitive male sterile line, a pre-requisite for two line hybrid system

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Hybrid breeding has provided remarkable yield advantage to pigeonpea productivity in the semi-arid tropics. An alternative two-line hybrid technology is being explored for a less tedious and more cost-effective system in pigeonpea, for which an environment sensitive male sterile line (ESMS) is a pre-requisite.

An ESMS line has been characterised as a thermo-sensitive male sterile line (TSMS) precisely responding to day temperature. Temperatures higher than the threshold temperature (24°C) promoted male sterility while lower temperatures rendered them male fertile. Cytological studies revealed a post-meiotic defect, leading to undissociated tetrads in sterile plants possibly the most critical stage for fertility transition.

To understand the possible mechanism underlying fertility transition, transcriptome profiling of sterile and fertile anthers from five different developmental stages has been carried out using Illumina HiSeq 2500. Transcriptome analyses revealed that auxin homeostasis is important for regulating sugar transport and cell wall modification, which otherwise would alter signalling with disruption in nutrient flow, leading to microspore starvation in male-sterile plants.

The role of auxins has also been experimentally shown to have practical implications in reverting the male-sterile line, thus holds great promise for developing two-line hybrid system in pigeonpea.

CG1-P013 | Development of SSR markers from leaf rust (*Puccinia triticina*) transcriptome and their utility in genetic diversity and population structure analysis

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Leaf rust pathogen (*Puccinia triticina*) is a major biotic constraint for wheat production. Development of molecular markers facilitates understanding of the genetic variations in the populations and virulence trend in *P. triticina*. In the present study, novel SSR markers of *P. triticina* were developed using the transcriptome data. A total of 6809 (1.8%) SSRs were detected in *P. triticina* transcripts expressed during the wheat-leaf rust interactions.

Tri-nucleotide SSRs were the most abundant (52%) among the different SSR motifs detected. Abundance of class II SSRs was higher than class I SSRs in *P. triticina* transcripts. Twenty-eight (56%) of the 50 Pt-SSR primer pairs synthesised detected polymorphism in *P.triticina* pathotypes. The number of alleles per locus ranged from 2 to 12 with an average of 5.72. Polymorphic information content (PIC) ranged from 0.29 to 0.96 with an average of 0.69. Observed heterozygosity ranged from 0.10 to 0.48 with an average of 0.21. Pt-SSR7 marker could distinguish the pathotypes according to their virulence group. BLAST analysis and *in silico* effector prediction suggested that most of the Pt-SSR markers are associated with pathogenesis and have the potential to be functional markers in the leaf rust pathology.

Dendrogram analysis detected two clusters, and STRUCTURE analysis detected two subpopulations and an admixture population in the 48 *P. triticina* pathotypes that were assayed from Indian subcontinent. Pathotype Tr16 (0R0-7) is the most divergent among the leaf rust pathotypes.

Results of this study suggest that the newly developed Pt-SSRs will be useful in characterising and profiling the global diversity of *P. triticina*.

CG1-P014 | Identification of nitrogen use efficiency genes using genome-wide association studies and transcriptomics in pearl millet

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Pearl millet [*Penisetum glaucum* (L) R. Br.] is the sixth most important global cereal crop and widely grown under arid and semi-arid tropics. Pearl millet grain has relatively high nutritional value and is the main food source for 500 million of the poorest people living in major parts of Asia and Africa.

Nitrogen (N) is an important yield determent factor for crops. Its increased use in the past five decades has achieved significant yield improvement in crops, but has led to hazardous environmental repercussions. Under the CINTRIN project, we strive to identify nitrogen use efficient lines under low and high N_2 conditions for marginal and favourable ecologies, respectively.

A total of 400 pearl millet cultivars including the association mapping panel and parents of mapping populations were grown in the precision field of ICRISAT at three (0%, 50% and 100% of the recommended nitrogen doses) nitrogen levels in alpha lattice design with two replications during summer and the rainy seasons.

The trials were evaluated for different morphological (five traits), physiological (five traits), agronomic (five traits) and yield characters (six traits). Data obtained from the 400 pearl millet cultivars from the two seasons will be utilized for genome-wide association studies (GWAS).

Based on the genotypic performance under three nitrogen levels, nitrogen sensitive (NS) and nitrogen insensitive (NIS) pearl millet genotypes will be used for transcriptome studies to identify nitrogen use efficiency genes in pearl millet.

CG1-P015 | Genome-wide epigenetic regulation in realising heterosis in pigeonpea (*Cajanus cajan* L.)

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Epigenetic variations and the underlying genomes between hybrids and parental lines trigger global differential gene expression and have a potential role in heterosis. To investigate whether DNA methylation plays a role in heterosis, we compared at single-base-pair resolution the DNA methylome of two leading pigeonpea hybrids, ICPH 2671 and ICPH 2740, and their parental lines. Both hybrids displayed increased DNA methylation across their entire genomes, especially in transposable elements in comparison to their parents. Interestingly, increased methylation of the hybrid genomes predominantly occurred in regions that were differentially methylated in the two parents and covered by small RNAs, implying that the RNA directed DNA methylation (RdDM) pathway may direct DNA methylation in hybrids.

In addition, we found that genes belong to four major flowering pathways namely, the photoperiod, vernalisation, autonomous, gibberellin and SOC1 gene involved in genetic interactions of the four pathways were differentially methylated with altered gene expression. Moreover, growth vigor of F1 hybrids was compromised by treatment with 5-Aza-dC, an agent that demethylates DNA. Interestingly, two genes, CCA1 and TOC1, that were found to be reciprocally regulated in both hybrids were gradually downregulated in varying concentrations of 5-Aza-dC treated seedlings. We further investigated that the role of H3K4me3 variation between parental lines is positively correlated with gene expression, suggesting its trans-acting effects in hybrids.

Our data provide an overview of epigenetic marks and transcriptional modifications involved in heterosis for better understanding the molecular basis of heterosis in pigeonpea.

CG1-P016 | Transcriptome-wide gene expression atlas of groundnut (*Arachis hypogaea* L.)

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Peanut (*Arachis hypogaea* L.) is one of the leading legume crops and plays a significant role in ensuring nutritional food security in many developing countries in Asia and Africa. Recently, groundnut genome sequencing has provided a basis for the identification of genes and gene networks associated with economically important traits. We have provided molecular identities for 19 groundnut tissue types through RNA-sequencing and developed a global gene expression atlas (AhGEA) using ICGV 91114 genotype. RNA-sequencing of the selected 19 tissues, representing five developmental stages of groundnut from germination to senescence, generated 458.26 million paired-end reads.

Analyses of the global transcriptomes revealed many interesting features of dynamic patterns of gene expression across the tissues and stages. Specifically, we focus on identification of the transcriptional signatures that define the possible metabolic pathways involved in oil biosynthesis during seed development.

A large number of transcripts involved in oil biosynthesis were identified and found to participate in fatty acid synthesis. There were five possible metabolic pathways involved in the accumulation of oil during seed development. Further, we investigated the allergen-encoding transcripts and 12 isoallergens and variants encoded by 124 transcripts coming from both, A-genome (*Arachis duranensis*) and B-genome (*Arachis ipaensis*).

Taken together, the generated resource provides a reference for the groundnut exome and will facilitate transcriptome analysis as well as SNP discovery in groundnut.

CG2-P001 | Reintroduction and in vitro propagation of *Declapeis arayalpathra* — a critically endangered plant of Western Ghats, India

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The present studies describe a protocol for high-frequency in vitro propagation through nodal segments and shoot tips in *D. arayalpathra,* a critically endangered medicinal liana of the Western Ghats, India.

Nodal segments were more responsive than shoot tips in terms of shoot multiplication. Murashige and Skoog's (MS) basal medium, supplemented with 2.5 µM 6-benzyladenine (BA), was optimum for shoot induction through both the explants. Among different combinations of plant growth regulator (PGRs) and growth additive screened, MS medium supplemented with BA (2.5 µM) + indole-3-acetic acid (IAA) (0.25 µM) + adenine sulphate (ADS) (10.0 µM) induced a maximum of 9.0 shoots per nodal segment and 3.9 shoots per shoot tip with mean shoot length of 8.5 and 3.9 cm, respectively.

Half-strength MS medium supplemented with Naphthaleneacetic acid (NAA) (2.5 µM) was the best for in vitro root induction. After successful acclimatisation in Soilrite™, 92 % plantlets survived in field conditions.

Acclimatised plantlets were studied for chlorophyll and carotenoid content, net photosynthetic rate (P_N) and related attributes such as stomatal conductance (Gs) and transpiration rate during subsequent days of acclimatization. The rise and fall of different biochemical enzymes (SOD, CAT, APX and GR) were also studies during successful days of acclimatisation. Moreover, the effect of acclimatisation on the synthesis of 2-hydroxy-4-methoxy benzaldehyde (2H4MB) was also studied in relation to the biomass production.

Maximum fresh weight (2.8 gm/plant), dry weight (0.35 gm/plant) of roots and 2H4MB content (8.5 µg/ ml of root extract) were recorded after eight weeks of acclimatisation. The screening of in vitro raised plantlet root was also carried out by using GC-MS analysis, which witnessed more than 25 compounds. The regenerated plantlets were also screened for homogeneity by using RAPD and ISSR. The proposed protocol surely can be used for the conservation and commercial production of the plant.

CG2-P002 | Evaluation or screening of the sorghum genotypes for expression of resistance against shoot fly (*Atherigona soccata* Rondani)

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As a versatile cereal crop, sorghum is widely grown for food, feed, forage and fuel in semi-arid tropics. In the mixed crop-livestock systems, sorghum serves a good source of stover for the dairy and drought animals. Due to its quick growth, high yield and quality of biomass, sorghum is a good source of green fodder. Despite the high yield potential, the average sorghum grain and forage yields on farmers' field in India are quite low. This has been attributed to several biotic and abiotic stresses, of which insect pests are the most important constraint.

Sorghum is damaged by over 150 insect species, of which sorghum shoot fly is a major pest. Breeding for shoot fly resistance in sorghum is one of the most important factors governing the fodder/forage and grain yield. In the present study, 32 selected genotypes were evaluated for resistance to shoot fly under field conditions. The selected material consisted of a set of 10 restorer lines showing resistance/susceptibility to shoot fly and a set of 10 CMS lines, along with their respective maintainers and suitable check varieties. The evaluation is based on morphological traits and biochemical traits imparting resistance against shoot fly.

Additionally, genotyping by sequencing (GBS) based SNP analysis of these lines will provide information on extent of molecular diversity. The diversity revealed by GBS data would be used to validate the already identified QTLs with the molecular markers so that these can be efficiently used in breeding programmes.

CG2-P003 | Comparative analysis of leaf vein density in Sri Lankan traditional rice varieties

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Rice (*Oryza sativa* L.) is the staple food of over half of the world's population. Rice follows a C_3 photosynthetic pathway, which is less efficient, compared with the C_4 pathway. Previous research has reported the possibilities of a conversion from C_3 to C_4 pathways in rice. Early indications of such a conversion are expected to be evident in the leaf anatomy, where the leaf-vein density (LVD) would be increased, and Kranz anatomy be developed with time. While research is under way to develop rice varieties with increased LVD as an initial step towards developing C_4 rice, it is possible that varieties with high LVD could exist among the traditional germplasm.

In the present study, LVD (average vein length between two large longitudinal veins [LLV] and two small longitudinal veins [SLV], and the vein length per unit area [TLV]) of 11 Sri Lankan traditional rice varieties were analysed by performing a one-way ANOVA, and mean separation with Duncan's multiple range test in SAS v9. Among the tested varieties, the LVD parameters LLV, SLV and TLV were found to be significantly ($p<0.05$) different.

Based on the mean separation, the highest LLV was shown by *Thanthiribalan*, and the lowest was represented by seven varieties, including *Mahasuduwee*. The highest SLV was reported in *Wannidehanala* and the lowest was in Mahasuduwee. The highest TLV was reported in *Mahasuduwee* and the lowest in *Wannidehanala*. Therefore, *Mahasuduwee* carried a higher LVD, and it can be recommended as a potential variety for studying the C_3 to C_4 photosynthetic pathway conversion in rice.

CG2-P004 | CINTRIN: Cambridge India Network for Translational Research in Nitrogen

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The global demand for nitrogen (N) fertiliser for agricultural production, which already stands at ~110 million metric tons per year, is projected to increase to ~250 million metric tons by the year 2050. Because nitrate is very mobile in the soil, substantial amounts (>50% in some cases) of applied N is lost by leaching, run-off and de-nitrification. In addition to increase in cost of crop production, in the long run these processes of N loss not only pollute the ground water and adversely affect soil structure but also has detrimental effects on environment, such as increase in nitric oxide, ozone etc. Hence, developing crop varieties with improved efficiency for N absorption and utilisation will help mitigate these problems to some extent.

CINTRIN is a Virtual Joint Centers in Agricultural Nitrogen, delivered in partnership by the Newton Fund, BBSRC, and DBT. CINTRIN is a consortium of eight partners and led by ICRISAT and NIAB, with an overarching aim of improving not only the income and livelihood of farmers by reducing costs of inputs, but also to save the environment by minimising the negative impacts of excessive use of fertilisers. The natural variation for nitrogen use efficiency (NUE) will be studied in diverse germplasm of wheat, sorghum, pearl millet and foxtail millet. The findings will be applied to develop new breeding lines with enhanced NUE.

CINTRIN will also use model plants such as *Arabidopsis* and *Brachypodium* for basic research that will be translated into crops in future. In addition, CINTRIN will prime the long-term scientific relationship of ICRISAT and other Indian partners with those in the UK by exchange visits of scientists/students, scientific meetings, workshops and exchange of technologies.

CG2-P005 | Genetic divergence analysis in rice (*Oryza sativa*. L)

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Nature and magnitude of genetic divergence was assessed among 54 genotypes of rice using Mahalanobis D^2 statistic for 12 quantitative characters.

On the pooled basis over E1, E2 and E3, the 54 genotypes were grouped into eight clusters. The cluster III was the largest, involving 19 genotypes. The cluster IV included 15 genotypes, cluster I, II and VIII included three, 12 and two genotypes, respectively. The remaining three clusters (V, VI and VII) were solitary and included only one genotype.

The average intra-cluster variation ranged from 0.00 to 1.93. The highest intra-cluster distance was in cluster IV (D=1.93) followed by III (D=1.42) and II (D=1.12). The average inter-cluster distance was maximum between cluster V and VIII (D=10.02) followed by VI and VIII (D=9.72), while it was at a minimum between clusters V and VI (D=0.75). The intra-cluster means of various characters revealed that cluster VII ranked first in the performance of grain yield per plant (23.6 g), straw yield per plant (20.8 g), 1000 grain weight (32.1 g), spikelet fertility (94.9 %) and plant height (117 cm). The genotype No 05 was the only member of this cluster.

The per cent contribution of different characters towards genetic divergence ranged from 0.00 to 39.06 per cent.

CG2-P006 | Pangenome of *Cicer species*

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Chickpea serves as a crop of high nutritive value and is grown widely across the globe. The genome sequencing of chickpea revealed its architecture and genes associated with the traits of interest. Various resequencing efforts have been carried out, resulting in millions of SNPs and indels.

However, these efforts were not able to represent the complete genetic repertoire of chickpea because of narrow diversity present within the accessions used and the use of draft genome. The current genomics approaches are further limited by the use of a single reference genome, as one individual does not represent the entire genetic repertoire for a species. Pangenome is one such approach, which exploits the diversity of a species using many individuals. To fully utilise the potential and genetic composition of a species, its wild relatives need to be analysed using next-generation techniques. We have selected one accession each from eight annual wild species (*C. reticulatum, C. pinnatifidum, C. chorassanicum, C. judaicum, C. cuneatum, C. yamashitae, C. bijugum* and *C. echinospermum)* and the whole genome sequencing of these species has been completed using five libraries on Illumina HiSeq.

The *de novo* assemblies for these have been developed via the DeNovoMAGIC assembler. The genome size of these assemblies vary from 512.3 Mb to 927.0 Mb and N50 is in the range from 1.7 Mb to 16.3 Mb. These assemblies will be used to develop the pangenome for chickpea. The annotation of these species and the presence absence variations will establish core and dispensable genomes. The genes unique to these species can be validated and introgressed into cultivated ones to enhance productivity.

CG2-P007 | Yield-loss assessment among groundnut genotypes with differential response to iron deficiency chlorosis

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Iron deficiency chlorosis (IDC) is common in the groundnut crop grown on calcareous and alkaline soils, causing considerable reduction in pod yields in different parts of the world, such as India, China and Pakistan. To precisely assess yield loss due to IDC, a set of 11 groundnut genotypes with differential IDC response (resistant, moderately resistant and susceptible) were evaluated under split plot design in iron-deficient calcareous soils during rainy season of 2016. The experiment comprised iron-sprayed (two sprays with Fe-EDDHA at 20 and 40 days after sowing) and unsprayed conditions as main plots, while 11 genotypes with differential IDC response were sub-plots. Each treatment had a plot size of five rows of 3-metre length and was replicated thrice.

Under iron-sprayed condition, genotypic differences were not observed for IDC-related parameters such as visual chlorotic rating (VCR), SPAD chlorophyll meter reading (SCMR), chlorophyll and active iron (Fe^{2+}) content across five growth stages. However, under unsprayed conditions, IDC resistant and moderately resistant genotypes recorded low VCR scores, high SCMR, chlorophyll and active iron content compared with IDC susceptible genotypes.

Significant reduction for pod yield and its related parameters such as hundred seed weight, shelling per cent and haulm yield was observed among all genotypes under unsprayed condition. Wherein, IDC resistant/moderately resistant genotypes recorded less reduction pod yield (≤ 18 %) compared with IDC susceptible genotypes that showed higher reduction (25 to 50 %).

Hence, development of IDC tolerant groundnut cultivars would be a sustainable solution for iron deficient calcareous soils.

CG2-P008 | Towards genetic dissection of nutritional traits in chickpea (*Cicer arietinum* L.)

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Sufficient intake of nutrient-rich food is a prerequisite for humans to meet their metabolic requirements and for well-being. However, worldwide more than three billion people suffer from micronutrient malnutrition. Chickpea is a rich source of several nutrients such as protein, minerals and vitamins, and has the potential to provide a sustainable solution to nutritional security.

Taking into account the significance of this crop as a dietary component across a major global population of developing countries, it is important to understand the complex genetics of nutritional traits leading to their bio-fortification through genomics-based interventions. In this regard, Genome-Wide Association Studies (GWAS) have been initiated to identify the associated markers and understand the genetics of the nutritional traits. A chickpea reference set composed of 300 accessions representing diversity of the entire germplasm of the ICRISAT Genebank has been selected. This reference set is being evaluated for several nutrients such as minerals (Fe, Zn etc) and vitamins through inductively coupled plasma mass spectrometry (ICP-MS) and high-performance liquid chromatography (HPLC), respectively. These 300 lines have already been re-sequenced using the whole genome re-sequencing approach. The existing sequencing data are being aligned for SNP identification. Eventually, phenotypic data on nutritional traits will be used with the SNP data set. In summary, this study aims to provide in-depth understanding of genetic diversity in the chickpea reference set and significant marker-trait associations for nutritional traits that can be utilised, after validation, in molecular breeding for developing superior varieties with enhanced nutrient content.

CG2-P009 | Development of enzyme-linked immunosorbent assay (ELISA) protocol for detection of Ara h 1, Ara h 2, Ara h 3, Ara h 6 and Ara h 8 allergens in peanut (*Arachis hypogaea* L.)

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Peanut proteins can cause allergic reactions that can result in respiratory and circulatory effects in the body, sometimes leading to shock and death. An allergic reaction to peanut can be triggered by consuming even a single kernel or exposure to trace amounts (0.1 – 10 mg) of allergens. The determination of peanut allergen proteins by analytical methods and proper labelling of peanut-based food products can reduce the risk of severe reactions in the highly sensitised individuals. To start with, knowing the quantities of different allergens in peanut kernels (seeds) assumes significance. The genetic diversity available in peanut germplasm has not yet been fully explored and exploited because of the unavailability of easy-to-use protocols for screening large numbers of germplasm. In this context, the present study focused on developing individual protocols with appropriate dilutions of sample extracts in order to estimate five major allergens in peanut seeds precisely through ELISA-based methods. We optimised three different dilutions on the basis of the coefficient of variation (<20%) achieved in three technical triplicates for quantification of five major allergens, Ara h 1, Ara h 2, Ara h 3, Ara h 6 and Ara h 8. The standardised assays detected wide variation of allergen proteins in selected peanut genotypes for Ara h 1 (12.5–42733.87 µg/g), Ara h 2 (22.2–20600.3 µg/g), Ara h 3 (157.8–14556.4 µg/g), Ara h 6 (5767.6–42317.6 µg/g) and Ara h 8 (0.084–6.8 µg/g). The newly developed protocols can be used for screening allergen proteins on large germplasm in peanut seeds with high accuracy and precision.

CG2-P010 | Improvement in Indian mungbean breeding programme as revealed by morphological and microsatellite-based molecular analysis

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The systematic mungbean improvement programme in India started in 1967 after the inception of the All India Coordinated Pulses Improvement Programme, with yield improvement and disease resistance being the major objectives. The focus in the past 30 years changed to reduced maturity duration, non-twining and erect growth habit, non-droopy pods, synchronous maturity and determinacy in addition to yield-contributing traits.

The level of genetic diversity and population genetic structure of 41 elite lines of mungbean developed in the past 30 years were investigated using 80 mapped microsatellite loci. A total of 696 alleles were detected among the 41 lines at all loci with an average of 8.68 alleles per locus. The gene diversity (GD) values ranged from 0.93 and 0.05 with a mean of 0.68, and those of PIC ranged between 0.92 and 0.05, with mean of 0.66. Out of 80 markers, 51 were found highly polymorphic, with >0.60 PIC value and these were noticed as most informative. Throughmodel-based STRUCTURE analysis, three distinct genetic groups were identified.

The genetic grouping pattern distinguished the groups of elite lines developed in different periods and revealed that breeding programme led to a clear improvement in 100-seed weight, pod length, seeds per pod and reduced plant height in genotypes developed after the year 2000. The pattern was also supported by the factorial and UPGMA analysis. The identified 80 microsatellite loci located on all 11 linkage groups proved useful in detecting genetic variation and assessing progress in trait improvement in mungbean breeding.

CG2-P011 | Development of e-SSR markers from transcriptome sequence of black gram [*Vigna mungo* (L.) Hepper]

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Black gram is an important legume crop in Asia, grown primarily for its protein-rich seeds. The black gram breeding programme has lagged behind that of cereals and other legumes due to a narrow genetic base and a lack of genomic resources. There is a need to develop genomic resources for the improvement of the crop through molecular breeding, such as marker-assisted selection (MAS). Here, we developed e-SSR markers based on wild black gram, *Vigna mungo* var. *silvestris* transcriptome dataset (submission ID. SRR 5931432, SRX3091690 and study accession SRP115376) from NCBI. A total of 1621 SSR motifs were identified in transcriptome sequences and primers were designed for 1171 SSR motifs. A total of 50 primer-pairs flanking SSRs were randomly selected for screening in the four black gram genotypes: Trombay wild, RIL68, Nayagarh and LBG-17. Twenty-one primers got successfully amplified with an amplification rate of 42%. Eighteen primers were scored as polymorphic on 3% agarose gel. Fourteen SSR primers showed null alleles.

All 18 polymorphic SSR markers were further analysed in a panel of 27 black gram accessions. Polymorphic information content (PIC) value ranged from 0.14 to 0.76 with an average value of 0.49. Dendrogram generated based on e-SSR markers grouped all black gram genotypes into one major cluster and Trombay wild was represented as an OTU.

These e-SSR marker will have considerable utility for marker-assisted selection (MAS) and constitute important resources for genomic studies in black gram.

CG2-P012 | Genome-wide association study (GWAS) to identify genomic regions associated with candidate biofuel traits in sorghum

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Biofuels are gaining importance owing to increasing uncertainties in the supply of fossil fuels and the environmental pollution associated with their use. Sorghum [*Sorghum bicolor* (L.) Moench] is the fifth-largest cereal crop globally, and used as food, feed, fodder, fuel and fibre. Because of its high biomass production potential and wider adaptability, sorghum is among the preferred crops for lingo-cellulosic or second generation (2G) biofuel production. The objective of this study was to assess the extent of variability in sorghum minicore for agronomic and biofuel traits along with composition analysis to identify lines with high cellulose/hemicellulose and low lignin. The phenotypic and genotypic associations between biofuel and agronomic traits in sorghum mini-core collection comprising 242 germplasm accessions were evaluated for agronomic and candidate biofuel traits. GWAS was done using an association mapping panel of 242 minicore entries using approximately 290K SNPs. Some of the identified accessions can be directly used as feedstock for biofuel production, as donors in breeding programmes for improving the lines and also for understanding the genetics of stalk cell wall components in sorghum. The information of genomic regions controlling biofuel traits helps to enhance the breeding process for increased genetic gain.

CG2-P013 | Assessment of yield traits in diverse sorghum genotypes under different N regimes for N use efficiency improvement

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Crop production strategies that incorporate the reduced use of fertilisers while maintaining or increasing biomass and yields are desirable. Nitrogen (N), the most important nutrient element used in agriculture production systems, is prone to loss into the environment by leaching, denitrification and volatilisation, causing severe ecological damage. Thus increasing Nitrogen Use Efficiency (NUE) is an agronomic, economic and environmental priority for production systems to address ecological damages.

NUE in production systems are typically <50% (could be as low as 30%), indicating that 50 to 70% of applied N fertiliser is not used. Improving NUE will simultaneously increase profits for farmers by reducing input costs and ease environmental impacts of food production. Characterization of NUE and N use parameters will help breeders choose germplasm for further development.

At ICRISAT, 60 diverse sorghum genotypes that include parents of Back-Cross derived Nested Association Mapping (BC-NAM) populations and bi-parental mapping populations were field evaluated to identify high- and low-N responses with three N doses: 0% N, 50% N and 100% N of recommended nitrogen (90 kg per hectare) in alpha-lattice split plot design. The trial had three replications per treatment per genotype and planted with 15cm × 75cm spacing between plants and rows, respectively. Data recording for 14 diverse traits related to NUE was carried out.

The observed variation in yield trait(s) identified three promising genotypes *viz*., ICSV745, PVK801-P23 and IS 15428 across the three treatments.

CG2-P014 | Characterisation of common bean (*Phaseolus vulgaris* L.) genotypes using trait-linked markers

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Common bean (*Phaseolus vulgaris* L.) is one of the most important widely cultivated species in the Fabaceae (Leguminosae) family, which represents 50% of the grain legumes consumed worldwide (McClean *et al*., 2004). It has immense nutritional and medicinal importance because of the presence of substantial amount of proteins, carbohydrates, minerals, vitamins, flavonoids and other phenolic compounds, as well as the ability to combat several diseases including malignant diseases.

Owing to several advantages, it has grabbed the attention of researchers all over the world. However, it has been reported that the production in developing countries is high but the productivity is comparatively very low. Thus, increasing the yield of the crop is the major concern.

Here, we have selected the germplasm from different regions of Jammu and Kashmir, as it is known for its high quality and flavour. In order to evaluate diverse lines of common bean genotypes at the molecular level, functional markers pertaining to yield were employed. A total of 55 alleles were obtained from a set of 25 genic markers associated with yield and Power Marker software version 3.25 was used to estimate the discriminatory power of the markers. Assessment of genetic distances was performed by DARwin5 software and STRUCTURE software was further employed for population structure analysis. With three major sub-populations deduced, 96 genotypes were grouped into three major clusters. Sub-population I comprised 36.5% genotypes, sub-population II has 18.7% genotypes, sub-population III includes 27.1% whereas the rest of the 17.7% genotypes were considered to be the admixture.

Our findings further strengthen the use of SSR markers for characterisation of genotypes and can help to ameliorate the genetic basis of the common bean germplasm targeting yield attributing traits.

CG2-P015 | Towards identification of genomic regions controlling pre-harvest aflatoxin contamination using multi-parent advanced generation intercross (MAGIC) population in groundnut

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Aflatoxin contamination in groundnut is a serious problem that affects health and trade. There are three types of Aflatoxin-resistance mechanisms including *in vitro* seed colonisation resistance (IVSC), resistance to pre-harvest aflatoxin contamination (PAC) and resistance to aflatoxin production (AP).

To identify the genetic and genomic control of these three mechanisms, one multi-parent advanced generation intercross (MAGIC) population using eight genotypes has been developed. Among these eight parental lines, ICGV 88145, ICGV 12014, ICGV 89104 and ICG 51 possess resistance to IVSC; ICGV 91278 and 55-437 possess PAC resistance; and VRR 245 and U 4-7-5 possess resistance to AP. After making three rounds of crossing (28 two-way crosses, 14 four-way crosses and seven eight-way crosses), selected plants based on the genotyping data were either used for making further crosses or were selfed to generate large F_2 population.

The MAGIC population with ~2632 lines (F_6 generation) is planted in field during rainy 2017 for seed multiplication. This population will be used to generate phenotyping data on PAC and AP resistance for at least two seasons. In parallel, high density genotyping data will be generated using high-throughput 58K SNP array for developing a high-density genetic map.

Genotyping and phenotyping data will be used for conducting linkage, association and joint linkage-association mapping for capturing genome-wide small and large effect genetic factors controlling aflatoxin resistance.

CG2-P016 | Genome-wide association studies (GWAS) for shoot fly, *Atherigona soccata* resistance in sorghum (*sorghum bicolor*)

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Sorghum (*sorghum bicolor* L.), the world's fifth major cereal, and self-pollinated, diploid (2n = 2x = 20), with a small genome (730 Mbp), this makes the sorghum genome about 60% larger than that of rice, but only about 1/4 the size of the genomes of maize or human. It makes sorghum an attractive model for functional genomics of C4 grasses. It plays a key role in both food security and economies around the globe.

Shoot fly is a major insect pest of sorghum, damaging early crop growth, establishment and productivity. Host Plant Resistance is an efficient approach to minimising yield losses due to shoot fly infestation. A germplasm set of 102 lines was field evaluated for two years for Abaxial Trichome Density, Adaxial Trichome Density, Phenol, Protein, Cu, Fe, Zn, Mg, Nitrogen, LSP, DF, TSFDH, GS, Tannin and NBI traits known to be associated with shoot fly resistance. All traits revealed significant phenotypic variation and high heritability (>0.60) for individual and across seasons.

The STRUCTURE analysis provided the evidence for the presence of five subpopulations at K=5. A total of 198,992 SNPs were generated through GBS. We obtained 73,486 SNPs polymorphic with minor allele frequency (MAF) > 0.05.

Further Genome-Wide Association Studies (GWAS) identified a total of 54 SNPs across 15 traits significantly associated to traits imparting shoot fly resistance. Significant SNPs were annotated by SnpEff_ version_4.0. These marker trait associations can be used in sorghum improvement program for developing cultivars with enhanced resistance to shoot fly.

CG2-P017 | Understanding the genetic variability for resistance against root lesion nematode and dry root rot fungi in germplasm lines of chickpea (*Cicer arietinum* L.)

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Root-lesion nematode (RLN; *Pratylenchus thornei* Sher and Allen) is a migratory, endoparasitic commonly fed and reproduced in the cortical tissues of chickpea (*Cicer arietinum* L). Besides RLN, dry root rot (DRR), a fungal disease caused by *Rhizoctonia batatico-la,* is also an emerging disease leading to significant yield loses in chickpea. Understanding genetic variability at genome level and phenotypically will enable us to develop strategies for these important production constraints in chickpea. In our study, we systematically examined the extent of damage caused by RLN population, DRR independently as well as their combined effect. Initially, eight accessions (JG 62, ICC 17121.CR.L, ICC17123.CR, ICC 17124.CR, ICC 17163.CR, ICCV 05530, EC 556270.CR and ICCV 2) were examined. The infected plants remained stunted and exhibited bronzing with pale green leaves when the threshold level of damage was above 2 to 3 nematodes/gram (N/g) soil. Further, flowering and pod formation were affected drastically. Nevertheless, the seeds formed in the pods failed to germinate. The nematodes population increased in the presence of DRR infection, indicating the triggering effect in cohabitation nematodes and the fungus. The study revealed four- and more than seven-fold reproduction of *P. thornei* in JG 62 over ICCV 2 respectively, indicating JG 62 is susceptible to RLN and DRR while ICCV 2 is resistant. These lines are being genotyped using simple sequence repeat markers to understand the genetic diversity at genome level.

CG2-P018 | Development of high-yielding genotypes with resistance to drought and foliar diseases in groundnut (*Arachis hypogaea* L.)

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Groundnut crop is grown in 6.8 lakh ha in rainy and 0.85 lakh ha in post-rainy seasons in the state of Andhra Pradesh in India. Major area of 80% is rainy season where the crop is grown in soils of poor fertility and low water-holding capacity. In this situation, drought and foliar diseases are responsible for considerable reduction in yield and quality of the produce.

Hence, a breeding programme was initiated in 2008-09 and 2009-10 to develop resistant varieties to both drought and foliar diseases and about 36 crosses were made. In the rainy season of 2014, 98 advanced breeding lines (in F_6 and F_7 generations) selected from segregating generations of 36 crosses were evaluated in initial varietal trial, from which 47 lines were promoted to advanced varietal trial-I year and evaluated during 2015 rainy season. Out of these, 15 lines were promoted to advanced varietal trial-II year and evaluated during 2016 rainy season.

Five genotypes — TCGS 1653, TCGS 1694, TCGS 1609, TCGS 1696 and TCGS 1616 — recorded higher mean pod yields that ranged from 3050 $kgha^{-1}$ (TCGS 1653) to 2068 $kgha^{-1}$ (TCGS 1616) with yield advantage of 71 to 16% over Dharani (1781 $kgha^{-1}$). The line TCGS 1694, derived from Kadiri-6 × ICG (FDRS)79, showed moderate level of resistance to late leaf spot and rust besides its high mean pod yield of 2489 kg/ha and desirable pod and seed attributes. One more line, TCGS 1696 derived from ICG (FDRS) 79 × Tirupati 4, also showed moderate level of resistance to foliar diseases.

In the 2016 rainy season, three promising lines out of 15 lines evaluated had ICG (FDRS) 79 parentage and one had GPBD4 as one of the parents. Distinct advantage of foliar disease resistance along with resistance to drought has been observed in the material evaluated over three years.

CG2-P019 | Association mapping for identification of QTLs responsible for accumulation of iron and zinc, and proteomic analysis for identification of mineral stress responsive proteins in common bean (*Phaseolus vulgaris* L.).

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In our study, we have used the GWAS (genome-wide association study) approach and could identify 13 QTLs contributing to accumulation of Fe, Zn and protein in common bean seeds. Further, we tried to examine the impact of Fe deficiency and excess Zn on the leaf proteome of 15-day-old common bean seedlings (variety VLR-125) using gel-based proteomics (2-DE) in conjunction with MALDI-TOF/MS analysis.

Physiological and morphological parameters revealed that Fe deficiency and excess Zn had similar impact on chlorophyll content of shoots, shoot and root length and weight compared with the control condition. For proteomics analysis, selected proteins that were differentially expressed under Fe deficiency and excess Zn compared with control (basal MGRL medium) were studied in detail. A total of 46 proteins were found up-regulated and 26 proteins down-regulated in Fe deficiency compared with control. Nine proteins were observed up-regulated and six proteins were down-regulated in excess Zn condition compared with the control. Seven proteins were observed up-regulated and five proteins down-regulated under both Fe deficiency and excess Zn conditions, indicating a possibility of cross-talk under such conditions.

Based on cellular compartmentalisation, most of the identified proteins were found to be localised to the chloroplast and nucleus. These proteins were involved in various biological functions like carbohydrate metabolism, photosynthesis, defence and stress response, transport, cellular processes (replication, transcription and translation) and cellular respiration. Further in-depth proteome analysis is required to understand the cross-talk under Fe deficiency and excess Zn in common bean.

CG2-P020 | Genetically diverse genotypes of chickpea: A wealth and strength

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A total of 5,370 diverse chickpea genotypes, including 4,023 desi, 1,143 *kabuli* and 204 Intermediate type procured from India and abroad, were maintained at Sehore Research Center. These genotypes were characterised as different in plant growth habit (prostrate, spreading, semi-spreading, semi-erect and erect), flower colour (pink, white and blue), leaf colour (light green, dark green, yellowish, brown and dark brown), stem (with and without pigmentation), leaves (simple, multipinnate and compound), plant height (from 20cm to 80cm), seed shape (angular, owl's head and pea), and seed sizes from small to large with light to dark brown seed, green, black and pink seed coat colour.

The variations recorded included 35–90-day flowering period, 90–140-day maturity period, 1–18 primary branches, 1–44 secondary branches, 0–10 tertiary branches, 1–2 pods per peduncle, 30–90 g biomass and 5–38 g/plant seed yield. The selected genotypes may be utilised in chickpea crop improvement aimed at developing varieties with ideal plant type and desirable marketable traits for different agro ecological conditions.

CG2-P021 | Genetic variability for grain nutritional and productivity traits among selected pearl millet germplasm

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The success of a crop improvement programme largely depends on the availability of genetic variability for economically important traits in the germplasm. To ascertain the genetic variability, 126 selected pearl millet accessions, including three controls comprising released cultivars [ICTP 8203 (IP 17862), Raj 171 (IP 22281)] and large grain genepool [IP 22271], were preliminarily characterised for grain nutritional and productivity-related traits during rainy season of 2016. Enormous genetic variability was evident for grain nutritional traits such as protein (9.8-17.7%), Fe (15.3-107.2 mg kg^{-1}), and Zn (12.5-61.9 mg kg^{-1}); productivity-related traits such as days to 50% flowering (37-142 d), plant height (77-401 cm), panicle length (12.4-60 cm), panicle width (13.7-29.3 mm), panicle exertion (-13.8-15.4 cm), productive tillers (1-5.6), and 1000 seed weight (2.3-12.5 g).

Several superior accessions were identified for grain nutritional traits such as protein (36 acc.), Fe (15 acc.), Zn (34 acc.), and combined superiority for Fe, Zn and protein (15 acc.) when compared with best control (IP 17862). Significant positive correlations (r) were observed between traits such as Fe–Zn (0.80), Zn–protein (0.35), Fe–protein (0.26), Zn–panicle exertion (0.25), protein–productive tillers (0.21), while protein content had significant negative correlations with 1000 seed weight (-0.28) and plant height (-0.20). The most promising accessions identified were IP 14012 and IP 5800 for protein, while IP 10425 for Fe and Zn content.

Further studies are in progress to identify stable sources with combined superiority for grain nutritional and productivity related traits.

CG3-P001 | Towards fine mapping of '*QTL-hotspot*' regions for drought tolerance in chickpea (*Cicer arietinum* L.)

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The genetic refinement of drought tolerance is crucial for sustainable chickpea production in arid and semi-arid regions of the world. In our previous study, we identified a *'QTL-hotspot'* region on CaLG04 harbouring 12 QTLs for 12 drought-tolerance-related traits explaining up to 58.20% of phenotypic variation from the chickpea recombinant inbred line (RIL) population (ICC 4958 × ICC 1882). A genotyping-by-sequencing approach refined this region from 29 cM to 14 cM. Further, bin-mapping-based QTL analysis narrowed down the *'QTL-hotspot'* region into two smaller regions, viz. '*QTL-hotspot_a'* (139.22 kb) and *'QTL-hotspot_b'* (153.36 kb) on the Kabuli draft genome sequence. To further validate and identify more recombinations in these sub-regions, KASPar markers developed were used for screening fine mapping population, comprising 1,911 lines. The 19 F2:3 recombinant families identified were further phenotyped for 100 seed weight and other drought-related traits, which led to the identification of ~101 kb genomic regions within '*QTL-hotspot_a'*.

A whole genome re-sequencing (WGRS) study on 20 representative near isogenic lines (NILs) identified the presence of several single nucleotide polymorphisms, and small insertions and deletions (InDels) in important candidate genes. Phenotyping data on these lines will be used to associate variation in candidate genes with the traits. The selected candidate genes will be validated using TILLING (Targeting Induced Local Lesions IN Genomes) population. These approaches will enable us to uncover drought-tolerance mechanisms in chickpea.

CG3-P002 | Sequencing-based trait mapping of leaf spot resistance and the prominent main stem using TILLING lines in groundnut (*Arachis hypogaea* L.)

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Targeting Induced Local Lesions IN Genomes (TILLING) is a powerful reverse genetics approach for functional genomics studies. However, because of the availability of low-cost and high-throughput sequencing technology, it has become possible to sequence TILLING lines and identify SNPs associated with genes responsible for traits.

One TILLING population has been developed in the 'Tifrunner' genotype of groundnut, an economically important oilseed crop grown in tropical and warm temperate regions. The TILLING population has shown phenotypic variation for several traits, including resistance to leaf spots and the features of prominent main stem. A total of 25 lines, comprising of 16 susceptible and 9 resistant lines for leaf spots, and 11 lines with presence and 14 lines with absence of the prominent main stem from the TILLING population were sequenced on Illumina HiSeq 2500 and 745.8 Gb sequencing data was generated. These are being analysed to identify structural variations including SNPs and INDELs across the lines with Tifrunner.

Two mapping populations from these lines, T47-7 (resistant to leaf spots) x T33-3 (susceptible to leaf spots) and T90-1 (presence of stem) x T71-2 (absence of stem), have been developed. We plan to phenotype segregating progenies and sequence extreme bulks of segregating progenies for these traits. We anticipate identification of candidate genes and SNPs for these traits by deploying the BSA-Seq approach in groundnut in due course.

CG3-P003 | Genome-wide InDel marker resource for molecular breeding in chickpea

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Chickpea, an important crop component of subsistence farming, holds the key to meeting growing global food and nutritional demands. Deployment of molecular breeding approaches for successful crop improvement rely on availability of cost-effective marker resources. The narrow genetic base of chickpea results in low polymorphism rates of available markers systems such as SSRs, SNPs etc. With an objective of expanding the existing marker repertoire in chickpea, another popular marker system, 'InDels', was selected for the study. Available whole genome re-sequencing data on parental lines of inter-specific (ICC 4958 × PI 489777) and intra-specific (ICC 283× ICC 8261 and ICC 4958 × ICC 1882) mapping populations were used for InDel identification. Screening of data resulted in identification of 231,658 InDels. In order to develop PCR-based markers that can be resolved easily over gel, 8,307 InDels with ≥20 bp were filtered. Primer pairs could be designed for flanking region of 7,523 (90.56%) InDels. On average, markers appeared at a frequency of 1,038 InDels/LG with maximum number of markers on CaLG04 (1,952 InDels) and minimum being on CaLG08 (360 InDels). In total, primers pairs for 423 randomly selected InDels, spanning across all eight linkage groups, were used to validate the polymorphism on selected parental lines.

A high amplification rate of 80% was observed with most ranging from 46.06 to 58.01% polymorphism rate across parental lines of the mapping populations on 3% agarose gel. The InDel marker resource established here has broadened the existing repository of markers in chickpea, and will be useful for ongoing genetic and molecular breeding studies.

CG3-P004 | Identification of genomic regions conferring dry root rot resistance in chickpea (*Cicer arietinum* L.)

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Dry root rot (DRR; caused by *Rhizoctonia bataticola* (Taub.) Butler) is an emerging disease of chickpea (*Cicer arietinum* L.) that poses severe constraints to chickpea production in warm and arid regions. Development of resistant cultivars is the most economical, efficient and environmentally safe approach for managing DRR in chickpea. To identify the genomic regions conferring resistance to DRR, 185 Recombinant Inbred Lines (RILs) were developed from the cross between susceptible line BG 212 and ICCV 08305, a moderately resistant breeding line. The RIL population was phenotyped for DRR resistance using the paper towel method under a controlled environment at ICRISAT in 2016 and 2017. Genetic analysis revealed monogenic control of DRR resistance.

The RIL population was genotyped with a cost- effective SNP genotyping platform, comprising 50,590 high-quality non-redundant SNPs tiled on to Axiom® CicerSNP array. Of these, 13,110 highly polymorphic SNPs were used for genetic map construction. As a result, a high-density genetic map with 13,110 loci spanning 1,224.11 cM, with an average inter- marker distance of 0.09 cM, was developed. One QTL explaining 6.7% of phenotypic variation was identified on linkage group 8. The identified genomic region and the SNP markers linked will be further utilised for mining candidate genes involved in DRR resistance.

CG3-P005 | High-density linkage map and GWAS for flowering time identified new QTLs and putative candidate genes on sorghum chromosome SBI-10 (L) long arm

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Sorghum, a C_4 grass, is a failsafe source of food, feed, fuel, fibre and fodder. Flowering time (FT) is an important trait that afffects adaptation, reproduction and grain yield. An F_2 recombinant fine mapping population derived from introgression line cross RSG04008-6 × J2614-11 was utilised for identifying flowering time QTLs on sorghum chromosome SBI-10 (L) long arm.

Selective F_2 recombinants from the fine mapping population were Genotyping-By-Sequenced (GBSed) and a high-density map was constructed for SBI-10L. Flowering time was measured on the $F_{2:4}$ selective recombinants for two post-rainy seasons (2013 and 2014) under imposed water stress conditions. Six QTLs (out of which two QTLs had >10% phenotypic variation-PV) were identified for both the seasons and across-season analysis. Two QTLs were found to be overlapping, indicating possible strong association of this region with flowering time and presence of putative flowering time genes in the overlapping QTL region.

The PV values ranged from 3% to 12% with LOD values ranging from 2.5 to 5.0. QTL analysis and GWAS identified leucine rich repeat protein, AP2 transcription factors, squamosa-promoter binding protein, pentatricopeptide repeat protein, cytochrome P450 protein, type3 chlorophyll a/b binding protein, ankyrin repeat protein candidate genes in the QTL interval on SBI-10L.

These results may provide an insight for better understanding of genetic basis of flowering time gene (complex) on SBI-10L.

CG3-P006 | In-silico identification of candidate gene for high grain iron and zinc in pearl millet [*Pennisetum glaucum* (L) R Br]

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Nutritionally, pearl millet is superior to cereals such as rice, wheat, maize and sorghum. Some of the transition metals like iron (Fe) and zinc (Zn) are essential minerals required for normal growth and development of plants. Biofortification or increasing grain (Fe) and (Zn) by genetic means is one of the sustainable options for combating micronutrient-malnutrition.

In our present work we undertake expression studies of genes responsible for high Fe and Zn in pearl millet endosperm. Using the reference pearl millet genome, a total of 114 genes for high Fe and Zn from related crops, such as *Setaria italica, Zea mays, Oryza sativa, Brachypodium distachyon* and *Triticum aestivum*, were aligned using BLAST tool. A total of 29 genes covering seven chromosomes in pearl millet genome were identified.

Phylogenic analysis showed gene orthologs that were clustered with foxtail millet, maize and rice, representing a common ancestry. Promoter analysis revealed different *cis*-acting elements. Fe and Zn transport domains like DND, NLS, NES and AHA have been analysed for their sequence similarity and functional charectersation. Tissue-specific expression of high Fe and Zn in different tissues like flag leaf (emergence and panicle maturity stages), root (vegetative and grain maturity stages) and seed (mature embryo) are being studied using real-time PCR for locating putative candidate genes responsible for grain Fe and Zn content in pearl millet.

CG3-P007 | Towards molecular mapping of root lesion nematode resistance in chickpea (*Cicer arietinum* L.)

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Root lesion nematodes (RLN; caused by *Pratylenchus thornei*) are migratory nematodes that feed and reproduce within the chickpea root cortex, causing extensive necrosis of cells resulting in severe yield reductions in many chickpea-growing areas. Eradication of RLN from the infested fields is very difficult since it is present in a quiescent state in soil.

This study aims to understand the genetics of resistance to RLN and to identify genomic regions controlling RLN resistance in chickpea. Based on the extensive screening for RLN resistance at Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV) Jabalpur, a highly susceptible genotype JG 74 (yielding 1.94 q/ha at 483.33 *P. thornei* /200 cm^3 soil) was selected to cross with three RLN-resistant genotypes — JGK 3 (yielding 7.99 q/ha at 492.33 *P. thornei* /200 cm^3 soil), JG 16 (yielding 8.33 q/ha at 333.33 *P. thornei* /200 cm^3 soil) and JG 63 (yielding 7.28 q/ha at 344.43 *P. thornei* /200 cm^3 soil) during July 2017 at ICRISAT. The resulting F_1 seeds were planted during the crop season 2017-18.

True F_1s will be identified and advanced to develop the F_2 mapping population. F_2 individuals will be genotyped with 50,590 SNPs using Axiom® CicerSNP array. The F_3 progenies will be phenotyped for RLN resistance in field plots infested with RLN at JNKVV-Jabalpur. QTL analysis will be done to identify the genomic regions controlling RLN resistance.

The SNP markers closely linked to RLN resistance genes will accelerate the development of new resistant cultivars by reducing the need for laborious and expensive resistance phenotyping.

CG3-P008 | Genome-wide association mapping for agronomic traits in foxtail millet

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Foxtail millet (*Setaria italica* (L.) P. Beauv.) is an important small millet, cultivated in Asia, Europe, North America, Australia and North Africa for grains or forage, and an essential food for human consumption in China, India, Korea and Japan.

A large diversity available in germplasm collections provides opportunities to mine sequence variations associated with phenotypes of interest. Here we conducted a genome-wide association study (GWAS) for agronomic traits using data on foxtail millet core collection (155 accessions) evaluated with four control cultivars during three rainy seasons at Patancheru, India.

The residual maximum likelihood analysis indicated that variance due to genotype, year, and their interactions, were significant for all the traits investigated. The phenotypic values for individual years and pooled analyses were used for GWAS.

We found several SNPs associated with each trait; however, only nine of them were found to be associated in at least two of three years and combined of three years: four SNPs for days 50% flowering, three SNPs for inflorescence length and one SNP locus each for peduncle length and weight of panicle. These SNPs explained 4 to 14% of phenotypic variation for each trait. Four of them are located in genes which were likely to be involved in the expression of the traits. These regions must still be validated, but assuming they hold up, their favorable alleles and/or allele combinations could be useful for target improvement of foxtail millet.

CG3-P009 | Sequencing-based trait mapping of EMS-induced mutants for 100 seed weight and seed colour in pigeonpea (*Cajanus cajan* (L.) Millsp)

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Pigeonpea [*Cajanus cajan* (L.) Millsp] is the sixth most important legume crop grown predominantly in the tropical and sub-tropical regions of the world. It is the main source of protein for more than a billion people.

In pigeonpea, 100 seed weight and seed colour are the traits preferred for enhanced market value. 100 seed weight has a critical role in milling and in determining the price that farmers obtain from traders. White seeded pigeonpea varieties are preferred in several states of India and many other countries where de-hulling facilities are not available and whole seeds are consumed. In the same direction, finding of genomic regions linked to 100 seed weight and seed colour can facilitate pigeonpea breeding for varietal development.

Thus, 536 ethyl methane sulfonate induced mutant lines of two high yielding genotypes *viz.* ICPL 87119 (99 lines) and ICP 8863 (437 lines) was phenotyped for seed color and 100 seed weight. Further crossing is initiated between wild-type parent and mutant lines. F_1 obtained from the same will be selfed to produce segregating the F_2 generation, from which DNA will be isolated for high-density genotyping. The genotyping and phenotyping data will be used for finding genomic regions associated with the target traits following MutMap approach.

Identified genomic regions will be helpful in deploying genomic-assisted breeding for target traits in pigeonpea.

CG3-P010 | Fine mapping of a dominant rust resistance gene of cultivated groundnut revealed two R genes around the major Rust_QTL

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Disease resistance in plants is manifested by the specific interaction between R gene product in plants and its cognate avirulence gene product (AVR) in the pathogen.

Puccinia arachidis causes rust disease in groundnut and inflicts photosynthetic damages to the plants. Till now, no experimental evidence is known for the action of R gene in groundnut for rust resistance. After the successful sequencing of *Arachis duranensis* and *A. ipaensis* by IPGI, a fine mapping approach towards the development of closely linked markers and mapping of rust resistance gene was undertaken at BARC, Mumbai.

Phenotyping of a RIL population (VG 9514 x TAG 24) at five environments for field rust score and subsequent QTL analysis has identified a 1.25 cM map-interval that harboured a consensus major Rust_QTL in A03 linkage group/chromosome. This Rust_QTL is flanked by two SSR markers, FRS72 and SSR_GO340445. Both the markers clearly identified the rust-resistant genotype from a collection of 95 groundnut genotypes. This 1.25 cM map interval contained 0.33 Mbp in the physical map of *A. duranensis* and had a TIR-NB-LRR category R-gene (*Aradu.Z87JB*) and three glucan endo-1,3 β glucosidase genes (*Aradu.RKA6M, Aradu.IWV86* and *Aradu.VG51Q*). Another resistance gene analogue was also found in the vicinity of mapped Rust_QTL. The sequence between SSR marker RS47 and FRS49 contain a LRR-PK which is equivalent to RHG4 in soybean.

Probably, the protein kinase (PK) domain in *Ah*RHG4 acts as decoy for the cognate AVR from *Puccinia arachidis* and helps the TIR-NB-LRR R-protein to initiate a controlled programme cell death in resistant groundnut plants.

CG3-P011 | Mapping of fertility restorer loci in A_1 cytoplasm of sorghum [*Sorghum bicolor* (L.) Moench]

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Sorghum originated from Ethiopia and became an important cereal crop in sub-Saharan Africa and South Asia after a long period of domestication and selective breeding. The plant trait of cytoplasmically-inherited male sterility (CGMS) and its suppression by nuclear restorer-of-fertility (*Rf*) genes can be viewed as a genetic arms race between the mitochondrial and nuclear genomes.

Most nuclear *Rf* genes have been shown to encode P-type pentatricopeptide repeat proteins (PPRs). We designed this study to: i) identify SNP-Trait Association for fertility restoration (*Rf*) genes; and ii) identify putative SNPs for designing assays for efficient screening of breeding population. The experimental material consisted of F_2 and backcross (BC) population developed by crossing Random Inbred Line (RIL) individuals with male sterile line (296A).

In this study we propose to identify genomic location of *Rf* loci by their association to molecular markers. The *Rf* gene containing regions will be identified using F_2 and BC population with Genotyping-by-sequencing (GBS) based SNP markers covering the entire sorghum genome.

CG3-P012 | Towards fine mapping and cloning the genes for foliar disease resistance using next-generation sequencing approaches in groundnut

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Next-generation sequencing technologies have evolved rapidly in the past decade, helping researchers to explore much deeper into the genomes. Of the several biotic stresses that pose serious damage to groundnut (*Arachis hypogaea*) production worldwide, two foliar fungal diseases, namely rust and late leaf spot (LLS), mostly co-occur, causing yield loss of up to 50% in addition to deterioration of fodder quality. The high level of resistance to both the diseases have been detected in interspecific derivatives of *A. cardenasii* and been deployed in breeding programmes in developing resistant varieties. The microsatellite and single nucleotide polymorphism markers (through genotyping-by-sequencing) based genetic mapping identified one major quantitative trait locus (QTL) explaining 87% phenotypic variance (PV) for rust and 69% for LLS resistance on A03, while 44% PV on A02 pseudomolecule use the recombinant inbred line population (TAG 24 × GPBD 4). Further deployment of whole genome re-sequencing based approach, referred as 'QTL-seq', in the same population confirmed co-localisation of genomic regions for both the diseases between 131.60-134.66 Mb on the pseudomolecule A03. This genomic region harbours several genes and so far no causal resistance genes could be located, perhaps due to lack of recombination in the population in the QTL regions. Nevertheless, the diagnostic markers have been successfully developed for the disease and were deployed successfully in developing molecular breeding products possessing enhanced resistance to rust and LLS.

In order to pinpoint resistance genes, near isogenic lines and a large F_2 population are being developed for further fine mapping these two QTL regions. Further fine mapping will provide information on resistance genes and facilitate development and deployment of functional markers in breeding new groundnut varieties with enhanced disease resistance, using different molecular approaches such as marker-assisted backcrossing and genome editing.

CG3-P013 | Response of tolerant and susceptible sorghum cultivar to drought stress: gene expression analysis

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Drought is a multidimensional stress with high recurrence in semi-arid tropics that causes changes in the physiological, morphological, biochemical and molecular traits. However, sorghum has innate resistance mechanisms to tolerate drought, but only few studies to comprehend these mechanisms have been performed. To address these missing links, we conducted a transcriptome experiment in contrasting sorghum genotypes (IS 18542 and IS 23143) that revealed specific genes set expressed in leaf and root tissue in different level of drought conditions.

The standard RNA-seq analysis packages were used to enlist the transcripts differentially expressed in both mild (0.5 fraction of transpirable soil water-*FTSW*) and severe (0.25 FTSW) stress conditions. Fragment Per Kilobase of transcript per Million mapped reads (*FPKM)* of Differentially Expressed Genes (*DEGs)* involved in plant hormone signal transduction pathway in roots between tolerance (IS 18542) and susceptible (IS 23143) lines were identified. Apart from the known mechanisms like maintaining cell homeostasis in water-deficit conditions, increasing anti-oxidant function, antagonistic regulation of sulphur metabolism, other important pathways such as signal transduction in cell protection and interactive signal in different tissues are identified in RNA-seq data. A functional characterisation of the genes and pathways identified could lead to new targets for the enhancement of plant stress response in different tissue, which will be particularly important in the face of climate change and the increasing prevalence of these abiotic stress. Results in relation to tissue specific, stress level specific and interaction specific DEGs along with putative functional SNPs are described in detail.

CG3-P014 | Identification of heat shock transcription factors in pearl millet

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Due to their sessile nature, plants are always subjected to biotic and abiotic stresses that reduce the crop productivity worldwide. Abiotic stresses include salt, drought, high temperature, cold etc. High temperature and drought have adverse effects on water relations and photosynthesis, and result in substantial crop reduction. Heat shock transcription factors (HSFs) transcriptionally regulate heat shock proteins (*HSP)* genes that in turn regulate the heat-stress response. HSPs act as molecular chaperones, preventing aggregation and denaturation of proteins.

The study of the HSF gene family is important for understanding the mechanism by which pearl millet responds to stress. The availability of the pearl millet genome sequence has provided an opportunity for the identification and study of heat shock transcription factors. The present study aimed to characterise the heat shock transcription factor genes in pearl millet. Comparative studies of the 250 HSFs from closely related genera such as *Setaria italica, Zea mays, Oryza sativa, Brachypodium distachyon, Sorghum vulgare* and *Triticum aestivum* using BLAST alignment tool against pearl millet genome was conducted. It revealed a total of 66 genes coding for different HSPs and HSFs. Out of these, 17 genes coding for HSPs (e.g. pgl_GLEAN_1000686 etc) have been identified in pearl millet. Chromosome and subcellular localisation, DNA binding domain (DBD), trans-membrane helices (THMM) and protein sequences were also analysed *in-silico.*

Further expression analysis of the identified genes in tissue samples such as root, stem, leaf and panicle (subjected to heat stress) is being analysed using real time-PCR for detecting putative candidate genes for heat stress in pearl millet.

CG3-P015 | Towards identification of candidate genes and development of markers for molecular breeding of early flowering in chickpea (*Cicer arietinum* L.)

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Chickpea (*Cicer arietinum* L.) is a cool-season legume crop cultivated mostly on residual soil moisture in semi-arid regions. Recently, a large shift in chickpea areas from cooler, long-season environments to warmer, short-season environments has increased yield losses due to terminal drought and heat stresses.

Earliness in both flowering time and maturity are important for adaptation of chickpea to short-season environments, as it helps the crop to escape these stresses. With an aim of identifying candidate genes and develop markers for early flowering and enhanced seed size, 25 morphologically distinct mutant lines in the genetic background of ICC 4958 were selected based on phenotyping of 3,200 M_3 TILLING lines (targeted induced local lesions in genome). Forty-two simple sequence repeat markers evenly distributed on chickpea genome were used to identify genetically similar mutant. A mutant line (ICC 4859-M3-2828) phenotypically distinct for flowering and seed size and possessing >95% similarity to wild type (ICC 4958) was selected and crossed with ICC 4958 during April 2017 to generate F_1. The true hybrids are being used for generating MutMap population that segregates for early flowering and enhanced seed size.

By using next-generation sequencing technologies, casual SNPs and candidate genes for these traits will be identified using MutMap. The identified SNPs will be used for developing markers for use in molecular breeding programmes.

CG3-P016 | Identification of genes/genomic regions associated with cleistogamy and shrivelled seeds in pigeonpea (*Cajanus cajan* L.)

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Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the major grain legume crops in the tropical and sub-tropical regions of the world. Its open or semi-cleistogamous flowers promote natural out-crossing. However, the open pollination behaviour causes genetic deterioration in purity of seeds in varieties.

In this direction, introgression of cleistogamy or self-pollination behaviour in pure-line varieties can be a genetic tool to maintain purity of elite lines. In pigeonpea, a mutant line ICPL 99010 has been identified as a cleistogamous line. However, cleistogamy has been found linked with shrivelled seeds, which hamper generation advancement and trait improvement. Therefore, efforts have been initiated to identify the molecular markers/genes/genomic regions associated with cleistogamy and shriveled seeds.

Thus, a recombinant inbred line (RIL) population developed by the crossing of parents ICPL 99010 (cleisto flowers) and ICP 5529 (open flowers) has been phenotyped for cleistogamy and shrivelled seeds. In parallel, high-density genotyping of RILs was performed using SNP array (Axiom®CajanusSNP Array) with 56 K SNPs.

Trait phenotyping data and SNP genotyping data will be analysed to identify genes and genomic regions associated with the target traits. Identified genes/genomic regions for cleistogamy/shrivelled seeds will be helpful in selection of lines with self-pollinating behaviour and acceptable seed size.

CG3-P017 | Genotyping-by-sequencing-based genetic mapping reveals higher epistatic interactions for resistance to stem rot disease in groundnut

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Groundnut is an important global crop commodity and serves as a major source of cooking oil, diverse confectionery preparations and livestock feed. Stem rot disease caused by *Sclerotium rolfsii* is the most devastating disease of groundnut and can cause crop damage completely; that is, 100% yield loss.

Genomic-assisted breeding (GAB) has potential for accelerated development of stem rot resistance varieties in a short period with more precision. In this context, linkage analysis and quantitative trait locus (QTL) mapping for resistance to stem rot disease was performed in a bi-parental recombinant inbred line population developed from TG37A (susceptible) x NRCG-CS85 (resistant), comprising 270 individuals.

Genotyping-by-sequencing (GBS) approach was deployed to generate SNP genotyping data leading to development of a genetic map with 585 SNP loci spanning distance of 2430 cM. QTL analysis using multi-season phenotyping and genotyping data could not detect any main-effect QTLs but identified 44 epistatic QTLs with phenotypic variation explained, ranging from 14.32% to 67.95%. Large number interactions indicate the complexity of genetic architecture of resistance to stem rot disease.

The identified genomic regions and linked markers will further facilitate candidate gene discovery and marker development to deploy GAB for developing stem rot disease resistance groundnut varieties.

CG4-P001 | Application of genomics in improving foliar disease resistance in peanut

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Peanut, an important food and oilseed crop, suffers considerable yield loss due to fungal foliar diseases such as late leaf spot (LLS) and rust. In the past, though concentrated efforts were made using conventional breeding, they have not been very successful in combining disease resistance, high productivity and desirable pod and kernel features, due to various genetic factors. Application of genomics has the potential to complement the breeding programme and address some of the genetic factors.

Here, we report on the development of genomic resources, their utilisation in breeding for LLS and rust resistance. A large number of mapping populations (RILs, ILs/AB-QTL and epi-RILs), mutant resources and heterogeneous inbred family (HIF)-derived near isogenic lines (NILs) were developed for mapping and validation. In total, 2,957 AhTE, 500 CAPS and 5,36,072 SNP markers were developed using genome-wide analysis of 33 diverse genotypes, and they were validated in the lab. Genetic/linkage maps were constructed and the QTLs were mapped for foliar disease resistance and other taxonomic and productivity traits. A few trait-specific genes were also identified. These genomic resources were employed for marker-assisted backcrossing (MABC) in JL 24 and TMV 2 to improve foliar disease resistance.

The selected superior backcross lines with high productivity and resistance to LLS and rust are undergoing multi-location trial for variety development and commercial release.

CG4-P002 | Genomic tools for the improvement of horsegram (*Macrotyloma uniflorum*)

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Horsegram (*Macrotyloma uniflorum*) is an orphan legume but provides protein supplement for the large vegetarian populace of the Indian sub-continent and is also grown as a fodder crop in some other semi-arid regions of the world. A self-pollinated diploid plant (2n=20) has been originated in Africa, since there is no molecular breeding programme in horsegram as it lacks the genomic information and the absence of the linkage map.

Therefore the present study was initiated with the objectives of developing genomic resources in this resource-poor legume. The study was started with the identification of 97 translational SSRs markers from the related well-characterised model legumes. NCBI's databases of horsegram were explored to develop 63EST SSRs and 27IPLs. Transcriptome analysis of two horsegram lines helped us to develop 3410 genic SSRs (Bhardwaj etal 2013).

Hiseq Illumina sequencing data were used to mine genomic SSRs and developed the 5456 novel genomic SSRs (Chahota et al 2017). The newly developed genic and genomic SSR were employed to determine the genetic diversity and population structure of Indian germplasm, which reveled the presence of two gene pools in this crop (Vikas et al 2015). This resulted in the development of a core set of 125 lines that are being used in genome wide association studies. The RIL mapping population of 190 individuals was analysed using SSRs, a framework linkage map was constructed and important QTLs of various traits were indentified.

A popular cultivar HPK4 was used for a whole genome sequencing project that is enabling us to identify 36105 genes in this crop (Hirakawa et al 2017).

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CG4-P003 | Genetics of mungbean yellow mosaic virus resistance in blackgram (*Vigna mungo* (L.) Hepper).

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Blackgram is one of the most highly profitable pulse crops, and is cultivated in almost all parts of India. Besides different constraints, viral diseases, mainly yellow mosaic virus disease, is the prime hazard with massive economic losses, especially in the Indian subcontinent. The Yellow Mosaic disease (YMD) caused by Mungbean Yellow Mosaic Virus (MYMV) is one of the most damaging diseases of blackgram.

Genetics of resistance to YMV was studied in the F_2 population of a cross LBG 759 (Susceptible parent) × T9 (Resistant parent). Goodness of fit test (chi square test) relevant to test the deviation of observed ratio to Mendelian segregation ratio for MYMV in the segregating population suited well with 1:3 (Resistance: Susceptible). It indicates a typical monogenic recessive gene is governing resistance and susceptibility reaction against MYMV in blackgram.

The population was screened with micro-satellite markers to assess the polymorphism. Only about 15% of the SSR markers were found to be polymorphic.

CG4-P004 | CRISPR/Cas9-based genome editing approach for developing transgene-free salt tolerance rice varieties

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Rice, a staple crop of South-East Asia, is highly sensitive to salinity and usually does not grow in soils with high electrical conductivity (EC). Developing saline-tolerant rice is one of the key priorities of agriculture. Recently, studies on plants have revealed an important role for miRNAs in plant abiotic stress tolerance. Hence, taking the advantage of well-characterised miRNAs for salinity and recently developed CRISPR/Cas9 genome editing tools, we attempt to knock out miRNAs that are negative regulators during various stress conditions, namely miR393 and miR396 to develop transgene-free salt tolerant rice genotypes. Guide RNAs (gRNA) for the respective miRNAs were designed and cloned into a CRISPR-Cas9 binary vector suitable for rice transformation. Rice protoplasts isolated from rice *indica* variety will be used to test the functionality of the CRISPR miRNA constructs prior to transformation into two saline-sensitive genotypes (IR64 and ASD 16). These two genotypes have been selected as they are most widely grown and resistant to blast, flood and pest. Positive mutant lines will be identified through genotyping followed by whole genome re-sequencing. Physiological characterisation will be carried out for the selected mutant rice lines for salinity tolerance. In addition, diversity of these miRNAs among wild rice genotypes is also being examined.

CG4-P005 | Assesment of distinctness, uniformity and stability of maize germplasm (*Zea mays* L.) based on morphological descriptors and molecular markers

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Characterisation and evaluation of maize germplasm is a necessary first step to facilitating breeding efforts. A major challenge facing those involved in the testing of new plant varieties for Distinctness, Uniformity and Stability (DUS) is the need to compare them against all those of "common knowledge".

A set of 33 exotic germplasm lines of the International Maize and Wheat Improvement Centre (CIMMYT) including three checks, namely Bajaura Makka, Girija and Jaisinghpur Local of CSK HPKV Palampur, were used to compare how morphological characterisation and SSR molecular marker described variety relationships.

All the exotic germplasm were confirmed distinct on the basis of morphological and molecular markers.

The results revealed that, among the 33 germplasm lines, non-hierarchical Euclidean cluster analysis germplasm lines were grouped into nine clusters.

Among them, cluster IV, V, VI, VIII and IX were monogenotypic whereas the rest were polygenotypic based on genetic divergence, and EC444416 had the distinguishable character of absence of anthocyanin colouration of brace roots.

Based on polymorphism exhibited by SSR markers, dendrogram was constructed using Jaccard's similarity coefficient using the UPGMA method of NTSYS-PC package (version 2.02), and the germplasm lines were grouped into two major clusters with a genetic similarity of 35 per cent. Two clusters separated local germplasm into two groups.

The result showed that molecular markers also exposed useful genetic diversity and the visual displays appeared to disperse the lines somewhat more evenly over the plot than the morphological methods, suggesting that the maize germplasm collection is a rich source of material with adequate variation for future use in breeding programmes.

CG4-P006 | Improving stay-green traits in farmer-preferred sorghum cultivars through marker-assisted backcross breeding

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Stay-green (delayed senescence) is a well-characterised post-flowering drought-tolerance response against terminal drought in sorghum. Traits contributing to this complex mechanism had been mapped to six major stable QTLs: Stg1, Stg2, Stg3A, Stg3B, StgC and Stg4. Among them, Stg3A and Stg3B were found to be most important drought-tolerant QTLs.

Field evaluated introgression lines (ILs) in R16 background are being used to transfer the QTLs to elite/farmer-preferred varieties, *viz*., Parbhani Moti, CRS1, M35-1 and Phule vasudha through Marker-Assisted Backcrossing (MABC) program. F1s were generated in all combinations of donor-recurrent and confirmed with 12 polymorphic SSRs, and true F1s were backcrossed for three successful generations to produce BC_3F_1 families.

Simultaneously, BC_1F_1 were selfed consecutively for three generations to obtain $BC_1F_{3:4}$ lines. In total 55 families were forwarded to generate $BC_3F_{2:3}$ and 312 lines of $BC_1F_{3:4}$ were selected with target QTL using 49 polymorphic and 3 dominant SSRs. A total of 139 SNPs falling in the QTL region were identified and designed, using the available GBS data between the ILs and their parents. Parental polymorphism for 139 SNPs resulted in the amplification of 105 SNPs (75%) and among them 69 SNPs were (50%) polymorphic.

Families of $BC_3F_{2:3}$ and $BC_1F_{3:4}$ will be screened with these polymorphic SNPs for their segregation in future generations. Genotypes with good recovery and better performance in terminal drought condition will be sent for field evaluation.

CG4-P007 | A novel molecular marker for bacterial leaf blight resistance gene *Xa21* in rice

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Rice (*Oryza sativa* L.) is a widely cultivated cereal, and it is the staple food in many Asian countries. Among the rice diseases, bacterial leaf blight (BLB) caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) has caused devastative economic losses, both in terms of yield and quality. The *Xa21* mapped to the rice chromosome 11 is known to convey resistance against BLB by involving plant pathogen recognition and response. The *Xa21* is known to express the highest durable resistance against BLB.

In the current study, a diagnostic molecular marker was developed and validated for *Oryza sativa* subsp. *indica* to be used in marker-assisted selection in rice improvement programmes. The *Xa21* sequences of 47 Sri Lankan rice varieties and Nipponbare (*japonica* reference variety) was retrieved from a public database, and the aligned sequence revealed many insertions and deletions (INDELs) and single nucleotide polymorphisms in its exon. Eleven previously published makers were anchored on to the sequence alignment and none of them amplified over the major INDEL (19 bp) detected at the exon. A new high resolution melting (HRM)-based molecular marker (*ABP0001*) was designed targeting the said INDEL. The length polymorphism amplified by *ABP0001* was capable of distinguishing the resistant variety IRBB 60 from the susceptible advanced breeding line Ld 99-12-38, and diagnostically genotyped BLB resistant BC_3F_2 progeny lines of IRBB 60/Ld 99-12-38.

The newly designed marker can be assayed on agarose gel, and as a high-throughput marker using HRM. The marker is efficient compared to the previously used markers for accurately genotyping *Xa21*.

CG4-P008 | Towards marker-assisted breeding for higher productivity in safflower

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Safflower (*Carthamus tinctorius* L.) is a traditional oilseed crop of India, primarily known for its healthy cooking oil, containing more than 80% of polyunsaturated fatty acid (PUFA), the highest among edible oils. India is among the major producers of safflower in the world. Though it is a valuable crop, the cultivation is rapidly decreasing in India due to low productivity (~800 kg/ha); low oil content and susceptibility to biotic stresses are some major concerns. Global germplasm collection of safflower represents an excellent variability for agronomic traits.

Exotic germplasm sources with high oil content (~40%), high oleic acid content (~80%) and aphid resistance have been identified, which are being harnessed for breeding cultivars. Molecular markers and genomics tools have the potential to expedite breeding efforts in safflower. Safflower has relatively poor genomic resources and efforts are under way to improve it.

Designing of high-throughput DNA markers and development of high resolution genetic linkage map are in progress. Using a bi-parental mapping population (F_2), a skeleton SSR linkage map has been developed. Mapping of QTLs associated with oil content and aphid resistance in RIL populations are in progress.

A cost-effective KASP assay has been designed for high oleic trait based on a mutation in the candidate gene, *fatty acid desaturase 2-1* (*FAD2-1*) of safflower, which is routinely used in marker-assisted selection.

CG4-P009 | Marker-assisted introgression of yield-enhancing genes to increase yield potential in rice

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Recently, several candidate gene loci for yield improvement have been identified. In the present study, the locus controlling grain number per panicle (*Gn1a*) located on Chromosome 1, locus controlling panicle size and branching (*OsSPL14*) located on Chromosome 8, and the locus strong culm (*SCM2*) located on Chromosome 6 are being utilised for improving the grain number, culm strength and yield of the elite, high-yielding, bacterial blight resistant, fine-grain type rice variety, Samba Mahsuri (ISM), through marker-assisted backcross breeding.

Breeding lines of Swarna possessing *Gn1a* + *SCM2* + *OsSPL14,* while PCR-based co-dominant markers specific for the yield-enhancing genes and the bacterial blight resistance genes, *Xa21, xa13* and *xa5,* were utilised for targeted transfer of the genes into ISM background.

The F_1s developed by crossing the Swarna introgression line and ISM were analysed for their heterozygozity using the gene-specific co-dominant markers and true F_1s were crossed with ISM to develop BC_1F_1s. They were then screened with the gene-specific markers through foreground selection and with a set of 80 parental polymorphic SSR markers through background selection to identify the best, positive BC_1F_1 plant with maximum recovery of ISM genome (~ 77 % recurrent parent genome recovery). It was then crossed with ISM to generate BC_2F_1s.

A single, best, positive BC_2F_1 plant homozygous for the bacterial blight resistance genes and heterozygous for the target yield enhancing genes possessing ~ 85% recovery of the recurrent parent genome has been identified and advanced for backcrossing (i.e. for developing BC_3F_1s) and selfing (for developing BC_2F_2).

Some of the BC_1F_2 plants, when grown under field conditions, were observed to be highly resistant to bacterial blight and possessed significantly longer panicles, with a higher number of grains compared with ISM and had a strong stem.

CG4-P010 | Comparative analysis of different genotyping platforms for estimating genomic prediction in multi-environment trials of chickpea lines

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Genomic selection (GS) is a popular cost- and time-effective molecular breeding approach that aid in precise selection of superior lines using genome-wide marker data prior to field phenotyping. Inclusion of G×E interactions enhances the precision of assessing the predictive ability that aids in selection of lines across the environments. Phenotyping data on 320 elite chickpea breeding lines for eight traits, for three seasons under different water regimes at two locations, were recorded.

Genotyping of the elite breeding lines was carried out using two different platforms *viz.* DArTseq (1.6K) and Genotyping-by-Sequencing (GBS; 89K SNPs). Further to assess the impact of environment, lines, and other interactions, 13 different models were fitted. In order to mimic a real scenario that breeder encounters on field, three different cross-validation (CV) schemes were used to assess the prediction accuracies (CV2: incomplete field trials; CV1: newly developed lines; and CV0: new environments). DArTseq was found performing better than GBS platform consistently among main effect models, and main effect models with genomic random effect of the line with informed interaction and models with naïve and informed interactions. Models based on GBS genotyping data, were found to produce the lowest prediction accuracies among most of the interaction models. It was either DArTseq (in most cases) or GBS combined with DArTseq accounted for highest prediction accuracies.

However, further improvement in existing GS model and deployment of other advanced genotyping platform, as well as combination of the same with other genotyping platforms, may further improve prediction accuracies.

CG4-P011 | Genome-wide association analysis under timely and late sown (terminal heat stress) conditions in wheat using GAPIT, SUPER and FarmCPU approaches

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GWAS for terminal heat tolerance was carried out following three different approaches, using genotypic data on ~17000 SNPs and phenotypic data on 13 traits related to heat tolerance, on spring wheat reference set (SWRS) consisting of 287 lines. This association panel was raised at Meerut (2012-13) under timely (TS) and late sown (LS, terminal heat stress) conditions. All the traits displayed normal distribution. A decline in the average trait values was noticed under terminal heat stress conditions.

A total of 3984 MTAs (1988 in LS and 1996 in TS) were detected using GAPIT, although after FDR, only a single MTA for flag leaf rolling was found to be significant. Using the SUPER approach, after FDR, 2004 MTAs (1468 in LS and 536 in TS) were identified for 13 traits. Themaximum number of MTAs (2872, 1200 in LS and 1672 in TS) was identified following the FarmCPU approach after Bonferrni correction. Out of these MTAs, a maximum of 145 MTAs for grain number per spike (TS conditions) and minimum of 139 MTAs for 1000-grain weight (LS condition) were identified. Candidates genes underlying the MTAs were also identified. These included genes for chlorophyll A-B binding protein domain, transcription factor MADS box, histone acetylase, pentatricopeptide repeat, NAC domain, ncRNA and F-box domain involved in grain yield and related traits.

Similar analysis is in progress for data recorded in two more environments. The MTAs/candidates genes identified in this study will prove useful in molecular breeding for terminal heat tolerance.

CG4-P012 | Molecular breeding for improving foliar disease resistance and oil quality in groundnut (*Arachis hypogaea* L.)

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Foliar diseases such as late leaf spot (LLS) caused by *Cercosporidium personatum*, and rust caused by *Puccinia arachidis*, lead to yield loss of up to 50–70% along with adverse effects on the quality of the produce.

Further, improving the oil quality has emerged as the demand-driven research activity due to benefits associated with human health and increasing shelf life of the products. In this context, we deployed the marker-assisted backcrossing (MABC) approach to improve foliar disease resistance (FDR) and oil quality in three popular varieties, namely GJG9, GG20 and GJGHPS1 of Gujarat, the leading state in groundnut production in India. With the help of linked markers, we have introgressed desired alleles of the genomic regions conferring resistance to rust and LLS from the parent GPBD4 while FAD mutant alleles from SunOleic 95R. As a result, 2nd and 3rd backcrosses homozygous lines were confirmed for introgressed traits; FDR and high oleic acid. 58K SNP array-based high density genotyping identified lines with genome recovery up to 94% for FDR and 92% for high oleic acid. Promising introgression lines with FDR and high oleic acid will be used for multilocation testing for further evaluation and release.

CG4-P013 | Identification of putative genomic regions for fodder quality traits in sorghum

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Genome-wide association study (GWAS) provides a powerful tool for crop improvement and has resulted in identification of several important genomic regions in sorghum for traits such as grain quality, agronomic traits, numerous biotic and abiotic stress and biofuel traits, but GWAS has not been performed for fodder quality traits under water contrasting conditions.

Management practices to improve fodder yield and quality may not be suitable in semi-arid tropics, due to unpredictable environments and high drought incidence. Thus genetic improvement using biotechnological tools is the best approach to enhancing fodder quality. Recombinant Inbred Line (RIL) and the germplasm reference set are good sources of base materials to identify regions of the genome that co-segregate with a given trait, considering the diversity of the population.

Hence, sorghum RIL population based on cross ICSV1x ICSV 700 and germplasm reference set (150 accessions) were evaluated under drought and control conditions in a replicated trial of alpha lattice design, with three and two replications for RIL population and germplasm reference set, respectively. The agronomic data were recorded on days to 50% flowering, fresh and dry biomass weight, panicle weight, grain yield and test weight. The biomass for fodder quality assessment was performed using near infrared spectroscopy (NIRS), which records traits such as nitrogen, acid and neutral detergent fibre, acid detergent lignin, *in vitro* organic matter digestibility (IVOMD).

The phenotyping data along with the genotyping data (marker SNP) will be analysed to identify the genomic regions for high fodder quality.

CG4-P014 | Identification of SNPs from amplicon sequencing of linked SSRs to post-flowering drought tolerance QTLs (*Stg 3A* and *Stg 3B*) in sorghum [*Sorghum bicolor* (L.) Moench]

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Sorghum is one of the major food, fodder and fuel crops of dryland regions. Sorghum carries out C_4 photosynthesis with a specialized Kranz anatomy for efficient carbon fixation, which makes it a cereal crop well-adapted to environments with high temperature and water limitation, and emerged as a model crop species for tropical grass genomics. Among several QTL detected, six major QTLs, namely *StgC* (on SBI-01), *Stg1* (on SBI-03), *Stg2* (on SBI-03), *Stg3A* and *Stg3B* (on SBI-02) and *Stg4* (on SBI-05), were consistent across genetic and environment backgrounds and accounted for 53.5% phenotypic variance. In this study we focused on *Stg3A* and *Stg3B* QTLs present between 56Mbp to 72Mbp regions on chromosome SBI-02 for identification of SNPs between contrasting genotypes. About 12 SSR markers (six markers for *Stg3A* and six for *Stg3B*) were utilised for the generation of amplicons on Phule Vasudha, Parbhani Moti, CRS-1, M35-1, R-16 (recurrents) and B-35, K-260, K-359*w* (donors). All the 96 amplicons from the eight genotypes (five recurrent and three donors) were subjected for sequencing. The consistent SNPs were called by comparing all the reads of respective genotypes with reference genome sequence using CLC workbench. There were 16 SNPs consistently detected across recurrent and donors. Further validation of these SNPs with KASPer assay on diverse set of germplasm will hasten the efficiency of marker assay for post-flowering drought tolerance in breeding application.

CG4-P015 | New life to chickpea variety Annigeri-1 by deployment of *Fusarium* wilt-resistant loci through MABC

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Fusarium wilt is one of the major constraints and development of resistant cultivars plays an important role in chickpea breeding for sustainable production. *Fusarium* wilt is considered the "Yellow plague of chickpea" and is caused by *Fusarium oxysporum* f. sp. *ciceris*.

The present study attempted to introgress *Fusarium* wilt resistance race 4 (*foc4*) from WR-315 to an elite chickpea cultivar Annigeri-1 through Marker Assisted Backcrossing (MABC). The F1s derived from Annigeri-1 × WR-315 cross was backcrossed to Annigeri-1 to generate BC_1F_1 and continued to BC_3F_1.

Selection of backcross progenies was made using *Fusarium* wilt-resistance linked markers (TA96, TA27 and TR19) for foreground selection (FGS). Thirty-eight polymorphic simple sequence repeats (SSR) markers were used for background selection (BGS) in early generations (BC_1F_1 to BC_2F_1 and BC_3F_1) for recurrent parent genome recovery (RPGR).

Use of MABC strategy could successfully recover 91% to 94% RPGR. After three rounds of selfing, selection and field evaluation in wilt sick plot, three BC_3F_4 MABC lines with 91% to 94% of RPGR resistant to *Fusarium* wilt race 4 (*foc4*) were identified.

These lines will be evaluated for yield and yield attributing traits in large-scale trials.

The best performing and promising lines with desired traits will be identified for further evaluation.

CG5-P001 | In-silico analysis of existing/available genome sequences in tea

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With the availability of next-generation sequencing technologies, extraordinary progress has been made in the field of sequencing of plant genomes. Genome sequence of nearly 50 plant species have been published now and the rate at which plant genomes are being decoded is steadily increasing. With the availability of data in such huge scale, there is an immediate requirement of powerful computational pipelines that will aid in analysis of genomes, studies on the regulation of gene expression, large-scale informative marker analyses and accumulation of this information in curative databases.

In view of the above, we have carried out some work in three different perspectives: i) generation of software and tools that will help in downstream processing of large-scale genome-sequencing data ii) *In-silico* analysis from available data on agriculturally and economically important genes related to different traits, and iii) maintaining these data in a structured database.

Use of bioinformatics tools for effective analysis of genome assembly and annotation work has become a major task and challenge towards the genomics-assisted tea breeding programme. No matter how much genomic information and resources are available, its use and application will have little impact on crop improvement, without a robust strategy.

We have designed two software pipelines, one for gene ontology (GO) enrichment analysis in a large-scale genome sequence and another is related to identification and analysis of intrinsically disordered proteins (IDPs) in plant genomes. Studies are being carried out to analyse the evolutionary and functional roles of these proteins in plant genomes. It is of high interest to observe the correlation of this study with the analysis of gene-specific DNA markers. The genes, proteins and functionally significant classes from already available genome sequences are stored in a user-friendly database that will help in future research.

This paper aims to highlight the development of a molecular-breeding strategy based on available genomic recourses and outcome of whole genome sequencing of tea in order to expedite tea improvement work integrating the involvement and contribution of dry laboratory (Bioinformatics), and validation of work in both the wet laboratory and field activities.

CG5-P002 | Leaf temperature, yield and genotype specific patterns of gene expression in *Sorghum bicolor* under drought and salt stress

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Abiotic stresses are one of the major causes of agriculture productivity losses and understanding stress-response mechanisms in plants is crucial in improving productivity under stress conditions. *Sorghum bicolor* L. Moench, an important crop, is an excellent model for unravelling plant stress responses because of reported variability in stress tolerance among varieties.

We compared the transcriptomic changes in sorghum genotypes varying in leaf temperature and grain yield under drought and salt stress. High genotype-specific patterns of differential gene expression under stress conditions were observed. Genotypes maintaining high grain yield showed the fewest changes and those maintaining low grain yield showed most changes in the transcriptome. The study revealed that different molecular mechanisms regulate leaf temperature under salt and drought stresses and was successful in identifying genes contributing to differences in leaf temperature under salt/drought stress conditions. Considerable yield specific gene expression was observed under stress conditions. Genes involved in 'microtubule based movement/microtubule motor activity', 'cell wall biogenesis/degradation/organization', 'nucleosome/chromatin organisation', 'cell cycle/cell division' and 'DNA replication' were found to be downregulated in low-yielding genotypes compared with high-yielding genotypes — indicating reduced transcription, cell division, cell differentiation and DNA replication in low-yielding genotypes.

This study is the first to report differential downregulation of core histone genes under stress conditions in low-yielding genotypes compared with high-yielding genotypes, and points towards the pivotal role of these genes in regulating yield.

CG5-P003 | Digital tools for knowledge sharing — a case of Tropical Legumes III Project

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Access to information is needed in every field of life, and agriculture in no exception. Limited access to information can be considered as one of the key factors constraining smallholder farmers' productivity and growth.

In recent times, development partners are putting emphasis on making data and information public. Implementing partners are urged to be more vocal and active in knowledge sharing of the resources generated from project activities. As these resources are generated using public investment, they are international public goods (IPGs) and should be accessible by the global community including scientists, researcher, students, farmers and others.

In this paper, authors present different tools and platforms (Tropical Legumes III website — with 165,375 hits since April 2017 from more than 171 countries; Social media channels — Facebook: 704 followers; Twitter: 426 followers; SlideShare: 91 resources, and Flickr: 524 photographs) used by Tropical Legumes III project to share its activities and stories from the field.

CG5-P004 | Study of ribosomal assembly genes in Arabidopsis

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Ribosomes are the biological nano-machines responsible for translation of mRNAs into proteins. Assembly of ribosomes is thought to be evolutionarily conserved among eukaryotes. While much of our current knowledge on ribosome assembly comes from studies in *Saccharomyces cerevisiae*, there is little information on the process in plants.

Of the ~120 genes involved in ribosomal assembly in yeast, most are present in multiple copies in the Arabidopsis genome; for example, *S. cerevisiae* NOG1 protein sequence shows 63%, 59% and 48% similarity to *Arabidopsis thaliana* NOG1-1 (AT1G50920), *At*NOG1-2 (AT1G10300) and *At*NOG1-3 (AT1G80770), respectively; *Sc*PRP43 has 77% similarity with both *At*PRP43-1 (AT3G62310) and *At*PRP43-2 (AT2G47250); *Sc*NOC2 has 47 and 45% similarity to *At*NOC1-1 (AT2G18220) and *At*NOC1-2(AT3G55510), respectively; and *Sc*HAS1 is 71% and 72% similar to *At*HAS1-1 (AT3G18600) and *At*HAS1-2(AT5G65900). *Sc*NOP7 has one ortholog in Arabidopsis *At*-NOP7 (AT5G14520) that is 55% similar to *Sc*NOP7.

Each *A. thaliana* gene family is differentially expressed at different stages of the Arabidopsis life cycle; *At*NOP7 is expressed highest at the bolting stage, while *At*NOG1-1 is expressed the highest at senescence. *At*NOP7-GFP and *At*NOG1-1-GFP both localise to the nucleus.

Initial screening of SALK T-DNA insertion lines for *AtNOP7* and *AtNOG1-1* do not present any observable mutant phenotype; however, future over-expression and pyramiding of all copies of each gene family will help identify individual gene and family gene functions in plant ribosome assembly.

CG5-P005 | A Leucine-Rich Repeat Receptor-Like Kinase gene is a novel regulator of root growth under iron deficiency

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Iron (Fe) is an important mineral micronutrient for plants and animals. Low availability of Fe significantly limits crop yield in many parts of the world and consequently has serious impacts on human nutrition. Due to limited bio-availability of Fe, plants have evolved into sophisticated adaptive alterations of their developmental programme to optimise Fe acquisition and homeostasis. In particular, modifications of root architecture that are caused by the adjustment of root growth traits are a key for the survival of plants on Fe-deficient soils. Understanding the genetic and molecular bases for these root growth responses will not only answer fundamental biological questions, but also have important implications for plant breeding or genetic engineering.

We used a diverse panel of 232 natural accessions of Arabidopsis to identify novel genes and regulatory systems that quantitatively regulate root growth responses to Fe deficiency. Using GWA mapping to identify common variants that associate with altered root growth responses to Fe-deficiency, we identified a candidate gene from the Leucine-Rich Repeat Receptor-Like Kinase (LRR-RLK) family of genes (from hereon called *LRR-RLK3*). Loss of function as well as overexpressor line analysis revealed that *LRR-RLK3* and its natural alleles regulate root growth rate in response to the absence of Fe in the growth medium. At the cellular level, LRR-RLK3 protein abundance is rapidly regulated by external Fe levels. On the transcriptional level *LRR-RLK3* function is important for regulation of *IRT1*, the primary Fe uptake transporter in roots. Overall, we have identified a novel player and molecular mechanisms that adjust root growth rate and iron homeostasis to altered Fe levels.

CG5-P006 | Genome-wide identification of NAC family genes in chickpea (*Cicer arietinum* L.) and pigeonpea [*Cajanus cajan* (L.) Millsp.]

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NAC is one of the largest transcription factor (TF) families in plants, with more than 100 genes per species. The acronym NAC owes its origin to three different genes (*NAM*, *ATAF*, *CUC*) into which the NAC domain was first reported. NAC TFs p lay an important role in plant development, senescence, morphogenesis and abiotic stress responses. Recently, NAC TFs have attracted interest in utilising NAC genes for development of stress-tolerant varieties, especially for drought and salinity.

In this context, we aim to identify and characterise candidate NAC family genes in chickpea for potential use in chickpea improvement. A total of 73 NAC genes were identified from the chickpea genome using similarity and Hidden Markov Model (HMM) search, of which 62 could be mapped to pseudomolecules. The length of these proteins ranged from 106 to 624 amino acids. A similar approach was used to identify NAC genes in another legume crop, pigeonpea, in which 88 NAC genes were identified. Phylogenetic analysis of these identified NAC genes in chickpea, pigeonpea, *Arabidopsis* and rice (*Oryza sativa*) enabled us to predict several putative stress-related NAC genes in chickpea and pigeonpea.

Subsequently, these putative stress-related NAC genes will be further studied for their expression profiles in response to drought stress using real-time quantitative PCR in different tissues of chickpea and pigeonpea.

CG5-P007 | Identification of quantitative trait loci for grain iron and zinc content in pearl millet [*Pennisetum glaucum* (L.) R. Br.]

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Pearl millet is one of the crops with many nutritional properties and essential micronutrients like iron and zinc. Large numbers of genes are involved in the expression of these micronutrients but information on genomic regions is very limited. Hence, the present study was carried out, to identify the region of genomes responsible for high expression of iron and zinc involving 215 recombinant inbred lines (RILs) derived from the cross of PPMI 683 and PPMI 627. The grains of the RILs were evaluated for iron and zinc content using AAS during three consecutive years (2014, 2015, and 2016) at IARI, New Delhi. RILs were genotyped with 288 SSR markers and 142 markers that were found polymorphic used for QTL mapping. The total length of the map was 4796.6 cM, with an average marker interval of 33.7 cM.

QTL for grain iron content for three years (2014, 2015, and 2016) was detected on chromosome 3 with an LOD score of 2.5 and a recombination frequency threshold of 0.5, which explained 9.59%, 8.30%, 7.26% phenotypic variation, respectively.

Additionally, two QTL for grain zinc content at year 2015 and one QTL at year 2016 were also detected on chromosome 6 and chromosome 7 with LOD score of 2.5 and phenotypic variance 6.81%, 9.28% and 6.44%, respectively. One more QTL for iron at chromosome 7 for the year 2014 was also indentified that explained 25.64% phenotypic variation. The QTLs detected can be used to enhance the grain iron and zinc content in pearl millet.

CG5-P008 | Cajanus Variation Database (CajanusVarDB): A genomic resource for advancing pigeonpea research

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Decoding of the pigeonpea genome coupled with reduction in sequencing costs have provided the much needed push to genomics research. Single nucleotide polymorphism (SNP)/insertion or deletion (InDels) markers serve as an invaluable resource and are considerably used in the breeding programs. The large multitude of markers serves as a challenge as well as an opportunity to develop reliable bioinformatics application targeted for the end users. Resequencing of the pigeonpea 396 accessions has resulted in discovery of 8.55 millions SNPs and InDels located on 11 pseudomolecules of pigeonpea. The huge number of variations cannot be queried with excel or text files.

Here we present a database, entitled as CajanusVarDB, which would be freely accessible. The repository is developed to facilitate the user with an easy interface for the selection of variations on the genome using their search criteria. The database helps the user to browse for all the information linked to SNP-ID (s) or the SNPs present in the genic regions. The user can also search for all the variations present within a specific region.

Similarly, the user can look for the SNPs/InDels between two genotypes along a combination of multiple search criteria. For example, 'non-synonymous' and 'disease resistance' will fetch the SNPs linked to disease resistance and codon change.

The database also contains the information for the pigeonpea genes orthologous with genes of arabidopsis, soybean, chickpea and groundnut. The genome browser helps in visualization of the various genomic tracks and alignment of the data for each accession along the genome. The information present in this database can be used to develop markers associated with important traits. The database is expected to accelerate the genomics assisted breeding in pigeonpea for its improvement.

CG5-P009 | Genomic Open-source Breeding Informatics Initiative (GOBII) for accelerating the rate of genetic gain

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Genomic Open-source Breeding Informatics Initiative (GOBII) is the first large-scale public-sector effort to systematically apply high-density genotypic information to the breeding of staple crops in the developing world. GOBII involves a multi-disciplinary team from Cornell University, CIMMYT, IRRI and ICRISAT, with a focus on five crops including rice, wheat, maize, sorghum and chickpea. GOBII database has been developed and is being improved continuously improved with more advanced features.

As part of GOBII, to deploy the genomic information in breeding programs, ICRISAT has set up the GOBII platform at ICRISAT on 128 core and 512 GB RAM dedicated clusters with over 40 TB of storage space. Chickpea and Sorghum genomic data are uploaded through the GOBII data loaders. In addition, GOBII is also focusing on developing user-friendly tools for deploying genomic information for crop improvement. The GOBII version of Flapjack has been developed and is being used for making selections for marker-assisted backcrossing (MABC) crosses and the Galaxy pipeline is being standardised and used for initiating GS for deploying genomic selection (GS). In addition to GOBII, HTPG is focusing on providing low-cost high-density genotyping. The GOBII team at ICRISAT is working with HTPG so that GOBII can host the data generated as part of HTPG. Programmers at ICRISAT also working for developing the APIs for GOBII to link GOBII with various breeding management systems and HTPG.

n summary, GOBII is working closely to develop open-source computational infrastructure and analysis capabilities, enabling the implementation of genomic and marker-assisted selection as part of routine breeding programs.

CG5-P010 | Sequencing and Informatics facility at ICRISAT

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In this era of Next Generation Sequencing (NGS), the high cost of setting up sequencing and computational facilities (despite lowering operation costs) acts as a barrier for research community, especially to those belonging to developing countries, to exploit the benefits of technology. At the Sequencing and Informatics Facility under the Centre of Excellence in Genomics (CEG), ICRISAT has years of experience and expert technical know-how in various sequencing approaches such as whole genome sequencing, whole transcriptome, RNA-Seq, small RNA profiling, genotyping-by-sequencing (GBS), ChIP-Seq, detection of DNA methylation (Meth-Seq) etc, along with expertise in techniques.

We are equipped with instruments such as Illumina HiSeq 2500, Illumina MiSeq, 3730xl DNA Analyzer, BioRobotics MicroGrid, Liquid Handling and Automation systems, which has enabled us to generate a huge amount of data, ranging from few gigabases to multiple terabases. To complement this setup, we have a dedicated high-performance computational facility with 408 cores, 6TB RAM and 540TB storage to take care of computations and memory-hungry analysis pipelines.

These tasks are performed by a team of well-informed computational biologists who extract meaningful information from the enormous data generated by these systems. The core aim of this established centre is to empower and strengthen researchers and biologists who are inadequately equipped and cannot afford such facilities, by providing these services at a minimal cost-to-cost basis. This will further help in sharing knowledge and increase utilisation of our facilities, which in turn will further bring down costs by factoring economies of scale, benefitting all stakeholders in the process. Our team has developed various genomics tools and databases, which are freely available and also facilitates training courses to help researchers from various backgrounds to understand their unique datasets. In brief, we are a friendly collaborative platform to researchers that enables breaking higher glass ceilings in genomics-assisted breeding and crop improvement.

1st CEG Alumni Meet

1st CEG Alumni Meet

(Current CEG Team & Alumni only)

ICRISAT, Hyderabad, India

December 9, 2017

Programme

Saturday, December 9, 2017	***Venue: Fred Bentley Conference Hall (Bld 212)***	
09:00 – 09:30 hrs	**Inaugural Session**	
09:00 – 09:05 hrs	Welcome	**Rajeev Varshney** Research Program Director – Genetic Gains, *ICRISAT*
09:05 – 09:20 hrs	Inaugural Address	**David Bergvinson** Director General, *ICRISAT*
09:20 – 09:30 hrs	Opening Remarks	**Peter Carberry** Deputy Director General – Research, *ICRISAT*
09:30 – 10:00 hrs	*Tea/Coffee Break*	
10:00 – 12:00 hrs	**Session I: Sharing Research Experience for Enhanced Collaboration** **Co-Chairs: Manish Pandey, *ICRISAT, India*** **Manish Roorkiwal, *ICRISAT, India***	
10:00 – 10:15 hrs	Understanding common bean domestication and QTLs/gene discovery for key nutritional traits in common bean from North-Western Himalayas	**Reyazul Rouf Mir** *Sher-e-Kashmir University of Agricultural Sciences & Technology of Kashmir (SKUAST-K), India*
10:15 – 10:30 hrs	Practical haplotype graph to genotype from randomly generated sequences to aid in genomic selection	**Punna Ramu** *Cornell University, USA*
10:30 – 10:45 hrs	Towards utilisation of genomic resources in groundnut crop improvement at UAS Dharwad	**Spurthi Nayak** *University of Agricultural Sciences – Dharwad, India*
10:45 – 11:00 hrs	Towards understanding the spikelet formation in barley through developmental mutants	**Ravi Koppolu** *Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany*
11:00 – 11:15 hrs	Genomics approaches for salt stress tolerance in chickpea	**Mayank Kaashyap** *RMIT University, Australia*
11:15 – 11:30 hrs	Performance of Hybrid wheat in India	**Manish Vishwakarma** *Borlaug Institute for South Asia – CIMMYT, India*
11:30 – 11:45 hrs	Breeding process and genotyping platform: a commercial perspective	**Pawan Khera** *Mahindra Agri Solutions Ltd., India*
11:45 – 12:00 hrs	Genomics-enabled breeding to develop new generation of climate-smart elite rice varieties	**Vikas Singh** *International Rice Research Institute -South Asia Hub, India*
12:00 – 13:00 hrs	*Lunch*	

13:00 – 15:30 hrs	**Session II: Sharing Research Experience for Enhanced Collaboration** **Co-Chairs: Rachit Saxena, *ICRISAT, India*** **Mahendar Thudi, *ICRISAT, India***	
13:00 – 13:15 hrs	Genomics - based exploitation of wheat genetic resources for plant breeding	**Sandip Kale** *The Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Germany*
13:15 – 13:30 hrs	CRISPR/Cas9 based genome editing approach for developing transgene-free salt tolerance rice varieties	**Deepa Jaganathan** *M S Swaminathan Research Foundation (MSSRF), India*
13:30 – 13:45 hrs	Tissue-specific proteome analysis of drought stress response in pearl millet	**Arindam Ghatak** *University of Vienna, Austria*
13:45 – 14:00 hrs	Pollen proteomics: evidence for developmental priming in abiotic stress defense	**Palak Chaturvedi** *University of Vienna, Austria*
14:00 – 14:15 hrs	Challenges and opportunities in livestock genomics: Indian perspective	**Sarwar Azam** *National Institute of Animal Biotechnology (NIAB), India*
14:15 – 14:30 hrs	Eco-friendly approaches for plant disease management	**Ashish Kumar** *Jawaharlal Nehru Krishi Vishwavidyalaya (JNKVV), India*
14:30 – 14:45 hrs	Teaching interrelated units in Biotechnology	**Abirami Ramalingam** *Swinburne University of Technology, Australia*
14:45 – 15:00 hrs	Genome-wide epigenetic regulation in realizing heterosis in pigeonpea	**Pallavi Sinha** *ICRISAT, India*
15:00 – 15:30 hrs	*Tea/Coffee Break*	
15:00 – 15:30 hrs	**Session III: Closing Session** **Co-Chairs: Rajeev Varshney, ICRISAT, India** **Rajeev Gupta, ICRISAT, India**	
15:00 – 15:10 hrs	Any other business (Formation of CEG Alumni Association)	**Manish Pandey & Rachit Saxena** *SAT, India*
15:10 – 15:20 hrs	CEG Alumni on social media	**Anu Chitikineni, Himabindu Kudapa & Nilesh Mishra** *ICRISAT, India*
15:20 – 15:25 hrs	Concluding Remarks	**Rajeev Varshney** *ICRISAT, India*
15:25 – 15:30 hrs	Vote of Thanks	**Rajeev Gupta** *ICRISAT, India*
19:00 – 21:00 hrs	*Dinner*	

Understanding common bean domestication and QTLs/gene discovery for key nutritional traits in common bean from North-Western Himalayas

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Common bean is one of the most important grain legume crops grown worldwide. The hilly regions of the states of Jammu and Kashmir are famous for producing high-quality, tasty and highly flavoured beans. In order to characterise this huge diversity and trace the origin of common bean available in Jammu and Kashmir, systematic efforts were made for the first time in collection, evaluation and characterisation using *Phaseolin locus* (*Phs*) assays and sequencing of Internal Transcriber Sapcer (ITS) region.

A set of 429 common bean lines were initially collected/procured and, based on clustering analysis, a diverse set of 96 lines was selected. The PCR assay for *phaseolin locus* led to the characterisation of 96 lines into Meso-american and Andean types. The core set of 96 lines was genotyped using genome-wide 91 SSR markers and by the genotyping-by-sequencing (GBS) approach. The genotypic data thus generated was used with trait data for Anthracnose resistance, nutritional traits like seed Zn, Fe, protein content, starch content, phenol content and soluble sugars. Study of population structure revealed two sub-populations in our core set conferring to two gene pools: Mesoamerica and Andes. The information of population structure matrix, trait phenotypic data and marker genotypic data was together used in the software program TASSEL, and significant/major/stable marker-trait associations (MTAs) were identified.

The significant and major MTAs identified during the present study will prove useful for enhancing nutritional quality in local common bean landraces of Jammu and Kashmir.

Practical haplotype graph to genotype from randomly generated sequences to aid in genomic selection

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With improved sequencing technologies, genotyping costs are declining very rapidly. This facilitates the genotyping of all available samples to include them in the genomic selection (GS) process to enhance the genetic grain in each cycle of crop breeding programmes. The major limiting factor to deploying this is, "how fast could we could genotype all progenies and turn around the data in time to make the selections and crosses?"

To address this question, we have developed and evaluated three high-through-put, cheap and robust genotyping technologies: rAmpSeq (target repeat regions), Nextera, and iTruSeq (random priming) methods. Even though sequencing costs have dropped tremendously, and numerous technologies are becoming available, the bioinformatics challenge has increased to process sequencing data. To tackle this, we have developed a practical haplotype graph (PHG)-based approach to genotype from randomly generated sequences from any region of the genome. PHG is a trellis-graph-based representation of the gene regions (anchors) and the intergenic regions (inter anchors) that represent diversity across and between species, create custom genome for alignment, calling rare alleles, imputation and data compression. Randomly generated sequences from a given taxa are aligned to consensus sequences in PHG to identify the haplotype node at a given anchor. All the anchors for a taxon are processed through the Hidden Markov Model (HMM) to identify the haplotype path through the genome. Path information is used to identify the variants (SNPs).

Low-cost sequencing technologies, coupled with PHG facilitate in genotyping of large number of samples to increase the size of training population in GS models, increases selection intensity and helps in increasing prediction accuracy.

Towards utilisation of genomic resources in groundnut crop improvement at UAS Dharwad

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Cultivated groundnut is a nutrient-rich commercial crop that is being grown in more than 100 countries in the world. It is appraised for its cooking oil, protein-rich food and fodder. Losses in productivity of the crop are attributed to several biotic and abiotic stresses. For effective improvement of cultivars with increased disease resistance and tolerance to abiotic stresses in groundnut, there is a need for intervention with recently advancing genomic tools.

At the University of Agricultural Sciences, Dharwad, the groundnut breeders have developed several improved cultivars that are resistant to foliar diseases like late leaf spot and rust, cultivars with high oleic content where the modern genomic tools have been utilised. There is scope to tether modern genomic tools like GWAS, transcriptomics, metabolomics and interactomics with conventional breeding for cultivar improvement. As a new faculty at the department, I am focusing my research on abiotic stress tolerance and improving the quality for confectionery usage of groundnut. In collaboration with ICRISAT, an initiative has already been taken to dissect candidate genes for heat tolerance through next-generation sequencing based methods.

We are also in the process of establishing a bioinformatics facility to conduct small to medium scale computational analysis. Besides research, we are teaching the post-graduate students the advances in biotechnology with special focus on genomics.

Towards understanding the spikelet formation in barley through developmental mutants

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The spike inflorescence is a characteristic feature of grass tribe Triticeae, which comprises economically important species such as wheat, barley, rye and Triticale. Within the spike inflorescences of Triticeae species, spikelets are born on the nodes of a spike axis called rachis. Thus the spikelets form the building blocks of spike inflorescence. The number of spikelets per rachis node varies from one to many within the Triticeae species. Interestingly, barley spikes show a unique pattern of spikelet development by producing three spikelets per rachis node. Through our work we intend to understand the genetics of this unique process by studying developmental mutants showing perturbations in this process. Towards this, we have genetically characterised and cloned the gene underlying the mutant *Six-rowed spike 4* (*vrs4*), which shows more than three spikelets per rachis node. The other developmental mutants, such as *multiflorus 2* (*mul2)* and *rattail* (*rtt*), which show abnormalities in barley spikelet/floret development, are currently being studied for their genetics. The outcomes from these studies will be briefly presented in the talk.

Genomics approaches for salt stress tolerance in chickpea (*Cicer arietinum* L.)

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Salinity is a major constraint for the second-most-important grain legume, chickpea, because of intrinsic salt sensitivity. Chickpea exhibits large genetic variation with some improvement in salt tolerance over the years. However, it still needs to be improved further for sustainable crop production. RNA-Sequencing is a revolutionary tool that allows comprehensive transcriptome profiling to identify genes/alleles associated with stress tolerance/sensitivity. This study comprehensively analysed gene expression in JG 11 and ICCV 2 genotypes that were identified as salt tolerant and salt sensitive, respectively, upon extensive multilocation field trials. RNA-Sequencing of root and flower tissues of the tolerant and the sensitive genotypes resulted in the identification of 5,075 differentially expressed genes (DEGs) in response to the salt stress. A suite of important genes involved in cell wall modification and root morphogenesis such as XHTs, casparian strip membrane proteins and pollen tube development that could potentially confer salt tolerance were identified.

Apart from understanding the coding landscapes of the transcriptome, emerging evidence now suggests that long non-coding RNAs (lncRNAs) may have a potential role in regulating the functional RNA in response to abiotic stress. To understand this and extensively characterise low and rarely expressed long non-coding RNAs in chickpea, RNA-Sequencing libraries from flower tissues of salt tolerant (JG11) and salt sensitive (ICCV2) genotypes were sequenced to nearly 1,167 million reads with an average of 50 million reads per sample. In total, 7,364 lncRNAs were identified in response to salt stress. The comparative homology analysis across six plant model species including *Arabidosis*, *Medicago*, *Glycine*, *Phaseolus*, *Oryza* and *Vitis* revealed 2,345 lncRNAs specific to chickpea. A total of 178 lncRNAs were differentially expressed among the genotypes with a higher number being differentially expressed in the tolerant genotype during the salt stress. The gene set enrichment analysis showed that these lncRNAs were significantly involved in epigenetic gene regulation and therefore may play an important role in post-transcriptional RNA modification and mRNA cleavage. The functional annotation of both, coding and non-coding transcripts, genes suggests that they may be the potential options to be utilised for improving chickpea crop improvement in terms of salt tolerance.

Performance of hybrid wheat in India

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Wheat is one of the main sources of food for more than 4.5 billion people in the world. It supplies them with about 20% of the daily protein and calories they need. So far, the production is meeting the demand, but if the trend continues, there will be problem in the future — demand could affect the return rate and could lead to food scarcity. The world population has been predicted to reach 9.8 billion in 2050, which will increase the demand for wheat by up to 60%.

To meet this requirement, annual wheat yields must increase by 1.6% from the current level of below 1%. After the quantum yield jump during the Green Revolution, wheat has not achieved tremendous yield; overthe past decade it has slowed down and threatened the food security of the developing world. With wheat, we have depended solely on line breeding, which has limitations due to a lack of diversity in germplasm, technology adoption and performance at the farmer's field. Hybrid technology might be a promising approach that could exploit the heterosis to achieve higher yields without any genetic manipulation and substantially enhanced inputs. In this study, we summarise the performance of 737 hybrids evaluated during the 2013 to 2017 crop seasons in multiple locations in India. Best Linear Unbiased Estimate (BLUE) values were used to obtain mid-parent, high-parent and commercial heterosis of the hybrids. Results have demonstrated great potential of hybrid wheat in India.

Genomics-enabled breeding to develop new generation of climate-smart elite rice varieties

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The increasing frequency of climate extremes such as water-deficit stress, high temperature and altered soil properties, along with higher incidence of pests and diseases, is posing a serious threat to rice farming. Crop scientists have started improving the existing crops for traits providing tolerance to various stresses through a genomics-enabled breeding approach to face this challenge.

The present study aims to improve four high-yielding elite rice varieties (Swarna-Sub1, Lalat, Sahbhagi dhan, Naveen) for various biotic (blast-*Pi9*, bacterial leaf blight-*Xa4, xa5, xa13, Xa21*, gall midge-*Gm4, Gm8* and brown plant hopper- *Bph3, Bph17*) and abiotic stresses (drought- *qDTY1.1, qDTY2.2, qDTY3.1, qDTY4.1, qDTY12.1,* and cold- *qCTS4a, qCTS11*). Two approaches — namely, backcross first and assembled first — were used to improve the target varieties. As a result, 10 improved lines in the genetic background of Swarna-Sub1 with 11 genes combinations (*Pi9, Xa4, xa5, xa13, Xa21, Bph3, Bph17, Gm4, Gm8, qDTY1.1, qDTY3.1*), 12 lines in the genetic background of Lalat with six genes combinations (*Pi9, xa5, Xa21, qDTY1.1, qDTY3.1, qDTY12.1*), eight improved lines in the genetic background of Sahbhagi dhan with six genes combinations (*Pi9, Xa21, qDTY1.1, qDTY3.1, qCTS4a, qCTS11*) and 17 lines in the genetic background of Naveen with six genes combinations (*Pi9, Gm8, Xa21, qDTY1.1, qDTY2.2, qDTY4.1*).

Genetic interaction of introgressed genomic loci is being studied in different generations and different genetic backgrounds, as it has shown significant tradeoffs on various agronomic traits. The identified improved lines in different genetic backgrounds will be tested in TPEs for possible release for commercial cultivation. Authors are thankful to the Department of Biotechnology, GOI, for funding various projects to IRRI-SA Hub.

Resequencing barley germplasm

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Genetic resources stored in ex situ collections imply great value for breeding since they could represent a reservoir of allelic diversity not yet exploited in modern breeding. This is specifically of interest in the context of improving or maintaining crop yields in changing environments and climates. The Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK) is hosting a large ex-situ collection of around 22K wheat accessions. The Genebank 2.0 project aims to explore this untapped treasure of diversity. Initially, a set of 9,700 winter wheat accessions collected from 70 different countries has been selected. The majority of accessions were from European countries wherein 37% were from West Europe while 21% were from East Europe. Further, 50% of selected accessions were plant cultivars while 30% were landraces and research materials, hybrid, mutant, etc. type cover the rest 20%. Genotyping data has been generated from ~3K accessions using genotyping-by-sequencing (GBS) approach. On average, 2.5 million reads have been obtained for each accession, resulting in identification of 80,941 SNPs. As expected, the majority of the SNPs were from telomeric regions indicating the efficiency of GBS to capture un- or low-methylated regions. Population structure analysis identified three distinct sub-populations corresponding to their origin. Similarly, diversity studies clearly separated Asian accessions from European accessions. The genotypic information will be helpful for developing high-yielding, disease-resistant wheat varieties through various breeding approaches.

Tissue-specific proteome analysis of drought-stress response in pearl millet

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Pearl millet [*Pennisetum glaucum* (L.) R.Br] is an important cereal crop in the world after rice, wheat, maize and sorghum (1). A recently completed draft genome dissects and provides a characteristic adaptation of pearl millet to dry environments (2). The molecular mechanisms of drought-stress tolerance in pearl millet remain elusive at the proteome level. We have used a shotgun proteomics approach to investigate protein signatures from different tissues under drought and control conditions (1). Drought-stressed plants showed significant changes in stomatal conductance and increased root growth compared with the control plants. Root, leaf, and seed tissues were harvested and 2281 proteins were identified and quantified in total. Leaf tissue showed the largest number of significant changes (120), followed by roots (25) and seeds (10). Increased levels of root proteins involved in cell wall, lipid, secondary and signalling metabolism and the concomitantly observed increased root length point to an impaired shoot-root communication under drought stress. The harvest index (HI) showed a significant reduction in drought stress. Considering the importance of pearl millet as a stress-tolerant food crop, this study provides a first reference data set for drought-stress proteome and related drought-responsive proteins (DRP's) in pearl millet (1). Future investigation will be based on the comparative proteomics study of wheat and pearl millet under drought stress and to identify the key proteins that play an important role in drought tolerance/adaptive mechanism of the individual cultivar.

References

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Pollen Proteomics: Evidence for developmental priming in abiotic stress defence

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Pollen development is a well programmed and crucial process that controls plant sexual reproduction and productivity. This process of development is highly sensitive to environmental changes such as temperature, drought and nutrition, and thus crucial in the era of global climate change and decreasing plant productivity under abiotic stress. Recently, we have generated a first cell-specific reference-proteome of tomato pollen development, which includes microsporocytes, tetrads, microspores, polarised microspores, and mature pollen. Each stage showed a specific reprogramming of the proteome. These specific responses in pollen development were termed "developmental priming", in contrast to "defence priming". Here, the hypothesis is that a genetic or epigenetic programme controls expression and translation of protective proteins such as Heat shock proteins and occurs already in the non-stressed state, to compensate for sudden changes in temperature during the maturation of the pollen. Further, a novel approach was introduced for peptide quantification based on mass accuracy precursor alignment (MAPA), considering a target list of "proteotypic peptides" in the ecotype Hazera cv.3017. This approach was exemplified by the comparison of control and heat-treated tomato pollen developmental stages (post-meiotic and mature). In total, 51 unique proteins were identified that were potentially involved in heat defence mechanisms. Increased levels of heat-responsive proteins (such as HSPs, LEA, dehydration responsive family protein and thioredoxin/protein disulfide isomerase) might hint at the process of acquired thermotolerance. Further experiments will be performed to validate the hypothesis of developmental priming and elucidate ethylene-mediated pollen thermotolerance in developing pollen grains using the proteomics approach.

Challenges and opportunities in livestock genomics: Indian perspective

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India has largest repertoire of livestock in the world. The livestock sector contributes about 25% of total agriculture production and 4% to the country's GDP. Two-thirds of the rural community are directly dependent on the livestock sector for their livelihoods. We have the largest cattle population in the world, with 40 recognised breeds. Among these, a few cattle breeds and pure lines of various indigenous breeds are declining drastically in recent decades because of factors such as cross-breeding with exotic breeds, uncontrolled breeding between indigenous breeds, negligence due to less productivity, and so on.

To characterise the pure line, we will sequence 20 individuals (preferably males) from each of the five indigenous breeds (Gir, Sahiwal, Red Sindhi, Tharparkar, Kankrej) of cattle well known for milk production. The sequencing data will be analysed to extract Single Nucleotide Polymorphisms (SNPs) across the breeds. SNPs will be prioritised from the NGS data and a High-Definition (HD) SNP chip will be developed for indigenous cattle. The HD SNP chip will further be used to genotype 50 individuals from each of the 40 indigenous breeds.

This would reveal the genetic architecture and genetic relationships across all the indigenous cattle breeds. The study will be helpful in conserving indigenous breeds and will provide a platform to deploy a genomic selection strategy to enhance milk production.

Eco-friendly approaches for plant disease management

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Fungal pathogens play a major role in the development of diseases in many important field and horticulture crops, resulting in severe plant yield losses. Intensified use of fungicides has resulted in the accumulation of toxic compounds, potentially hazardous to humans and the environment, and also in the build-up of resistance of the pathogens. In order to tackle these national and global problems, effective alternatives to chemical control are being employed. Use of biological control agents is a nature-friendly approach that uses specific microorganisms that interfere with plant pathogens and pests to overcome the problems caused by chemical methods of plant protection.

Fungi in the genus *Trichoderma* are among the most promising biocontrol agents against plant pathogenic fungi. *Trichoderma* being a soil fungus, its growth, multiplication and eventually its biocontrol potential is highly affected by various soil physical, chemical and biological properties. Therefore, it becomes important that the selected strain should have the ability to compete with the native microflora, establish itself successfully in the crop rhizhoshere/spermosphere, and should have a wide array of mechanisms to inhibit several pathogens. Given these considerations, it is expected that the best method for obtaining a potential biocontrol agent might be to isolate *Trichoderma* strains originally from those areas where they are actually expected to function later as a biocontrol agent and where they are already growing under conditions of temperature, moisture etc. similar to those found in nature.

Keeping this in mind, a repository of 40 isolates of *Trichoderma* has been developed from Madhya Pradesh and tested against different plant pathogens under *in-vitro* conditions using confrontation assay. Further, selected isolates have been tested for their plant growth promotion activity in green houses and field conditions. It was observed that some selected isolates were not only the potential antagonists but also better plant growth promoting agent.

Teaching interrelated units in biotechnology

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As a sessional academic at Swinburne University of Technology and RMIT University in Melbourne, Australia, I teach interrelated units in Biotechnology programmes for undergraduate and postgraduate student cohorts. The student groups are diverse, comprising Australians, as well as people from other countries, such as China, India, Iran, etc. The units that I am engaged in encompass Scientific Research Methods, Bioinformatics, Biochemistry, Advance Topics in Biotechnology, and Research Projects.

By engaging with a diversity of students through lectures, supervision and training, the teaching and learning experience has been extremely rewarding. Of late, I have been involved with teaching in a leading foreign institution, through one of Swinburne University of Technology's many international partnership programmes.

While my current work in academia mostly involves teaching and learning, I continue to be involved with research through article publications and research grant applications. More recently, I completed a Graduate Certificate programme in Teaching and Learning for Higher Education. As an alumnus of the Centre of Excellence in Genomics, ICRISAT, my research training experience as a Post-Doctoral Research and Visiting Scientist has been a tremendous influence on shaping my career as an academic, where I continue to inspire students on crop improvement programmes through multiple, state-of-the-art platforms.

A Journey of 10 Years

A memorable journey of 10 years: Fostering genomics research towards scientific excellence and partnership

Background

The Center of Excellence in Genomics (CEG) of ICRISAT (ceg.icrisat.org) will complete its first 10 years in December 2017. The genesis of CEG goes back to a grant entitled 'Centre of Excellence for High-throughput Allele Determination for Molecular Breeding' under the Center of Excellence (CoE) scheme of the Department of Biotechnology (DBT), Government of India given to ICRISAT mainly to provide genotyping services for SSR and DArT markers and training to NARS researchers in 2007. The Center of Excellence (CoE) was subsequently institutionalised by ICRISAT as a research, service and training centre, with three major modules : (i) Applied Genomics & Molecular Breeding, (ii) Sequencing and Genotyping Services, and (ii) Capacity Building. CEG serves as a cost-effective genomics platforms for scientists and research staff from different Themes/Research Programmes of ICRISAT as well as NARS partners. The CEG has 184 collaborators from 35 countries in six continents.

In 2007, the availability of genomic resources was very limited in ICRISAT mandate crops. Therefore, CEG scientists, in collaboration with researchers from ICRISAT and national/international organisations, initiated efforts to develop large-scale molecular markers, transcript sequence data, genetic, transcript and physical maps, cost-effective and high-throughput marker genotyping platforms, as well as decoding genome sequences of ICRISAT mandate crops. While analysing the sequence, a number of computational genomics tools and databases were developed. Furthermore, in collaboration with scientists/staff from ICRISAT and partners from Asia and Africa, the genomics research was translated successfully into developing superior lines in several ICRISAT mandate crops. In terms of service, CEG was offering initially SSR and DArT genotyping services and then subsequently SNP and sequencing services at cost-to-cost basis. To empower the research and breeding community, CEG organised several training courses, many national and international workshops/symposia/conferences, and hosted several research scholars/post-docs/visiting scientists. The CEG has been visited by a number of high-profile personalities from science, politics, and donor and government organisations. CEG scientists, together with colleagues from ICRISAT and outside, have been successful in mobilising more than US$96 million and published 353 scientific articles, including nine in *Nature* journals, with 12,000 citations. This article highlights some key achievements from the CEG as a collaborative team effort.

Assembling reference genomes

The unprecedented evolution in next-generation sequencing (NGS) technologies has made it possible to develop high-quality genome assemblies in crop plants, including complex and large-sized genomes. CEG has also evolved simultaneously and together with its partners deployed NGS technologies in developing high-quality reference genomes for pigeonpea (*Nature Biotechnology* 2012, 30:83–89), chickpea (*Nature Biotechnology* 2013, 31:240–246), groundnut (*Proc Natl Acad Sci USA* 2016, 113:6785–6790 and *Nature Genetics* 2016, 48:438–446) and pearl millet (*Nature Biotechnology* 2017, 35: 969-976 **(Figure 1).** Genome sequence for sorghum was made available by the US community (*Nature* 2009, 457:551–556). Availability of draft genome assemblies as mentioned above would not have been possible without extensive collaboration of CEG with highly reputed researchers and institutes across the globe. For example, the CEG led the genome sequencing consortia/initiatives such as the International Initiative on Pigeonpea Genomics (IIPG), the International Chickpea Genome Sequence Consortium (ICGSC) and the International Pearl Millet Genome Sequence Consortium (IPMGSC). CEG also co-led the Diploid Progenitor Peanut A-genome Sequencing Consortium (DPPAGSC) for progenitor species of cultivated groundnut — *Arachis duranensis* (A-genome) — and also played a key role internationally in the International Peanut Genome Initiative (IPGI) to sequence the genome of the *A. duranensis* (A-genome) and *A. ipaensis* (B-genome) species.

In addition to these genomes, the CEG scientists also helped and extended collaboration to several partners to sequence genomes of some other plant species such as adzuki bean (*Vigna angularis*) (*Proc Natl Acad Sci USA* 2016, 112:3213–13218; *Scientific Reports* 2015 5:8069), mungbean (*Vigna radiata*) (*Nature Communications* 2014, 5:5443), sesame (*Sesamum indicum)* (*Genome Biology* 2014, 15:R 39 1-13) and longan (*Dimocarpus longan*) (*GigaScience* 2017, doi: 10.1093/gigascience/gix023).

In summary, CEG scientists have led/contributed in sequencing of 11 crop genomes, which is unprecedented in the CGIAR system to which ICRISAT belongs.

Re-sequencing of diverse germplasm collections

A single genome of a crop does not represent the total sequence content/variation in that species. Therefore, re-sequencing of diverse germplasm is necessary for harnessing the benefits of the above-mentioned genome sequencing efforts and germplasm collections. In this context, CEG has taken several initiatives to sequence diverse germplasm accessions of the ICRISAT mandate crops. These initiatives include: (a) 35 chickpea genotypes representing parental lines of 16 mapping populations (*BMC Pant Biology* 2016, 16(1):10), (b) 129 chickpea varieties comprising 88 *desi* and 41 *kabuli* types released in 14 countries across the globe (*Scientific Reports* 2016, 6: 38636), (c) chickpea reference set comprising 300 genotypes including 293 cultivated and seven wild accessions (unpublished), (d) 'The 3000 Chickpea Genome Sequencing Initiative', (e) 20 pigeonpea parental genotypes of mapping populations, (f) 292 genotypes of the pigeonpea reference set (*Nature Genetics* 2017, 49:1082–1088), (g) 104 parental lines of pigeonpea hybrids (cytoplasmic male sterile lines, maintainers and restorers), (h) 34 groundnut accessions i.e., 23 tetraploid (*A. hypogaea*) and 11 diploid species accessions (*Scientific Reports* 2017, 7:40577; *Molecular Plant* 2017, 10:309–322), (i) 292 accessions including mini-core set in sorghum, (j) 345 accessions of the world association mapping panel, called the pearl millet inbred germplasm association panel (PMiGAP),

38 parental lines of mapping populations, 580 B- and R- lines, and 31 wild species accession (*Nature Biotechnology* 2017, 35: 969-976.

Developing cost-effective and high-throughput genotyping platforms

Of all the genomic resources, reference genome and genetic markers are the most important for accelerating trait mapping and molecular breeding. The availability of marker resources facilitated development and deployment through different suitable platforms over the past decade. The journey for these crops started with genotyping using meagre SSRs through PCR and agarose gels in 2007 to today's sequencing- and array-based high-throughput, high-density SNP genotyping in almost all the ICRISAT mandate crops **(Table 1)**. Continuous efforts were made by CEG to develop low-cost and high-throughput genotyping platforms to deploy markers in trait mapping and breeding.

In this context, ICRISAT collaborated with DArT Pty Ltd, Australia, and developed diversity arrays technology (DArT) arrays with 15,360 features for all the three legumes (chickpea, pigeonpea and groundnut) (*Plant Science* 2016, 242: 98–107). Similarly, Kompetitive Allele Specific PCR (KASP) assays were developed in all three legumes, with 2,005 SNPs in chickpea (*Plant Biotechnology Journal* 2012, 10:716–732), 1,616 SNPs in pigeonpea (*DNA Research* 2012, 19:449–461) and 90 SNPs in groundnut (*Plant Genome* 2013, 6:3). In addition, Golden-Gate assays with 768 SNPs and VeraCode assays with 96 SNPs in chickpea and 48 SNPs in pigeonpea were also developed (*The Plant Genome* 2013, 6:2).

Further, to generate high-density genotyping data in the three legume crops, most recently high-density SNP arrays have been developed in chickpea (*Plant Biotechnology Journal* 2017, doi:10.1111/pbi.12836), groundnut (*Scientific Reports* 2017, 7:40577) and pigeonpea (unpublished). In addition to the above marker-based genotyping platforms, sequencing-based genotyping platforms and approaches such as genotyping by sequencing, skim sequencing and whole genome resequencing have been optimised in almost all the ICRISAT mandate crops (*Plant Science* 2016, 242 : 98–107).

Efficient and cost-effective genotyping services through CEG played an important role in brainstorming for establishing a high-throughput genotyping platform (HTPG) in the CGIAR system. The HPTG platform, led by ICRISAT and developed in collaboration with the Intertek Group PLC and funded by the Bill & Melinda Gates Foundation, has made it possible to avail genotyping services for 10 SNPs at US$1.5–2.0 per sample including the costs of DNA extraction. The HTPG platform at present is an important component in the Excellence in Breeding platform (EiB) of CGIAR (excellenceinbreeding.org).

Trait mapping

By using developed genomic resources, genotyping platforms and working in collaboration with breeders, physiologists, pathologists, entomologists, microbiologists, genetic resource and pre-breeding specialists from ICRISAT and other collaborating institutes, CEG has been successful in mapping 20 to 50 traits in the ICRISAT mandate crops. The list of mapped traits have been provided in **Figures 2 to 6.**

It is important to mention here that mapped traits do not essentially mean that diagnostic markers are available for all these traits. In fact, in terms diagnostic markers, they are available for a limited number of traits so far.

Efforts need to be accelerated to map desired traits in a cost-effective and faster manner.

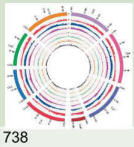
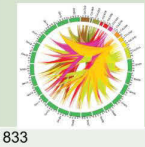
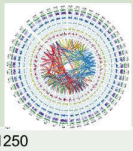
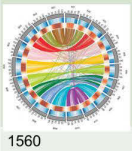
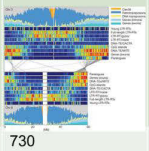
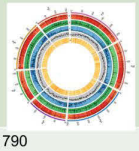
Features	Chickpea	Pigeonpea	Groundnut	Groundnut	Groundnut	Sorghum	Pearl Millet
Scientific name	***Cicer arietinum***	***Cajanus cajan***	***Arachis duranensis***	***Arachis duranensis***	***Arachis ipaensis***	***Sorghum bicolor***	***Pennisetum glaucum***
Chromosome no.	2n=2x=16	2n = 2x = 22	2n = 2x = 20	2n = 2x = 20	2n = 2x = 20	2n = 2x = 20	2n = 2x = 14
Genotype sequenced	CDC Frontier	ICPL 87119 (Asha)	PI475845	V14167	K30076	BTx623	Tift $23D_2B_1$-P1-P5
Reference	Varshney et al. (2013)	Varshney et al. (2012)	Chen et al 2016	Bertioli et al. 2016	Bertioli et al. 2016	Paterson et al. (2009)	Varshney et al. (2017)
Circular representation of Genome assembly							
Genome size (Mb)	738	833	1250	1250	1560	730	1790
Assembly size (Mb)	532	606	1051	1211	1512	679	1760
No of gene models	28,269	48,680	50,324	36,734	41,840	34,496	38,579
No of genes annotated	28,255	46,750	-	-	-	27,640	38,542
No of scaffolds	7,163	137,542	8,173	635,392	759,499	679	25,241
N50	40 Mb	516 Kb	650 Kb	948 Kb	5343 Kb	35 Kb	18.18 Kb
Longest scaffold	59.46 Mb	48.97 Mb	5.3 Mb	8.5 Mb	21.2 Mb	-	4.8 Mb
GC content	30.78 %	32.80 %	31.79 %	-	-	-	47.90 %

Figure 1: Sequencing of reference genomes of ICRISAT mandate crops

TABLE 1. ADVANCES IN THE GENOMIC RESOURCES DURING THE LAST DECADE FROM 2007 TO 2017 IN THE ICRISAT MANDATE CROPS

Features	Chickpea		Pigeonpea		Groundnut		Sorghum		Pearl Millet	
	2007	2017	2007	2017	2007	2017	2007	2017	2007	2017
Molecular markers										
SSR markers	++	+++	+	+++	+	+++	+++	++++	+	+++
SNP markers	No	+++	No	+++	No	++	++	++++	No	++++
DArT markers	No	+++	No	+++	No	+++	No	+++	No	+
Diagnostic markers	No	+++	No	+++	No	+++	No	+++	No	+++
Maps										
Genetic maps	+	+++	No	+++	+	+++	++	+++	+	+++
Physical maps	No	+	No	No	No	+				
Assembly										
Genome	No	+++	No	+++	No	++	No	+++	No	+++
Transcriptome	No	+++	No	+++	No	+++	No	++	No	++
Marker genotyping platforms										
KASP assays	No	+++	No	+++	No	++	No	++	No	++
GoldenGate	No	++	No	++	No	++	No	++		++
SNP arrays	No	+++	No	+++	No	+++	No	No	No	No
Trait mapping										
Biotic stress	+	+++	No	+++	+	++	++	+++	+	++
Abiotic stress	+	+++	No	++	No	+	+	+++	+	++
Other traits	+	+++	No	++	+	+++	+	++	+	+++
Molecular breeding products										
Superior lines	No	+++	No	No	No	+++	+	++	+	++

+ limited, ++ optimum, +++ abundant, ++++ highly abundant, No- non availability

Figure 2: Molecular mapping of 50 traits in chickpea

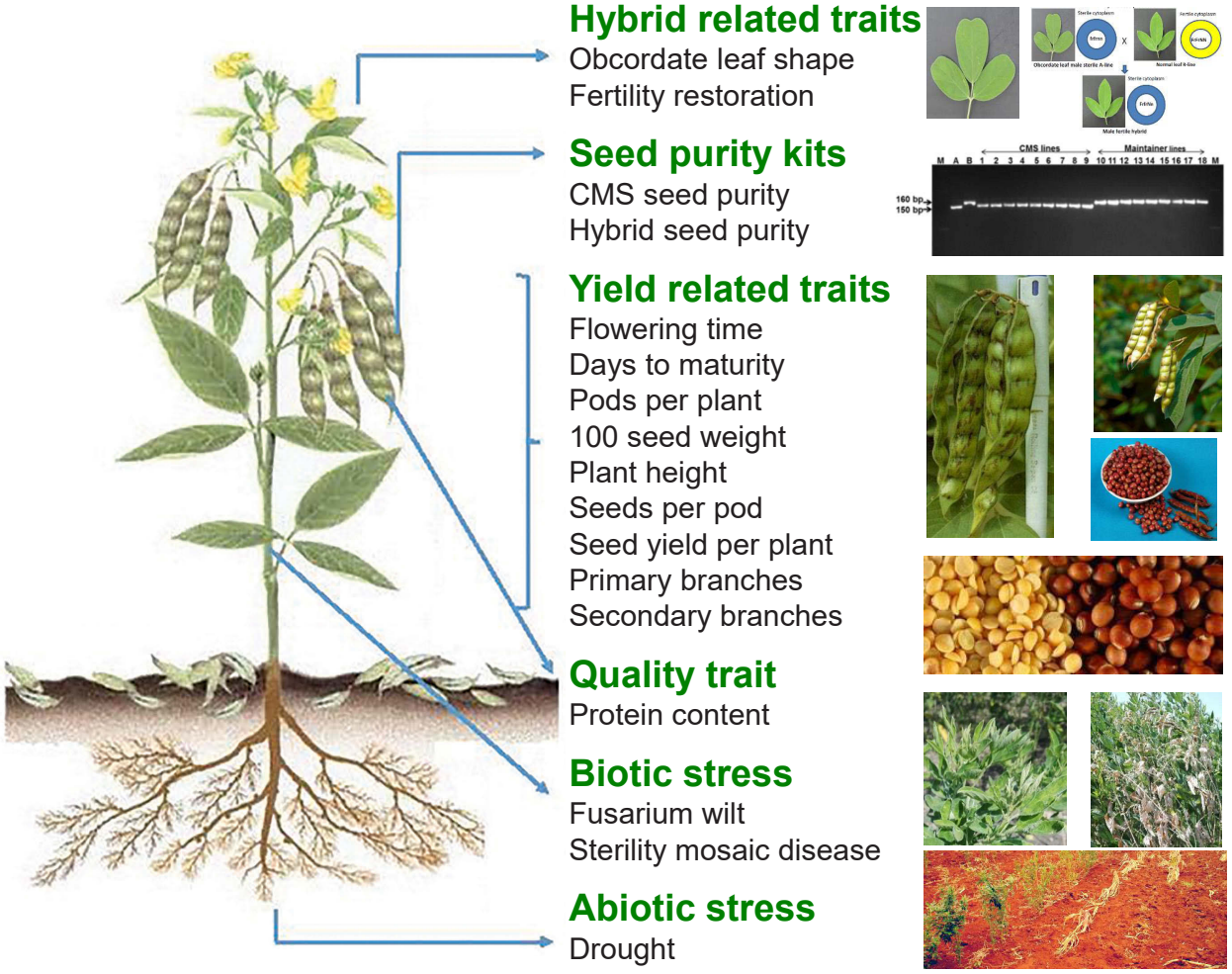


Figure 3: Molecular mapping of ca. 20 traits in pigeonpea

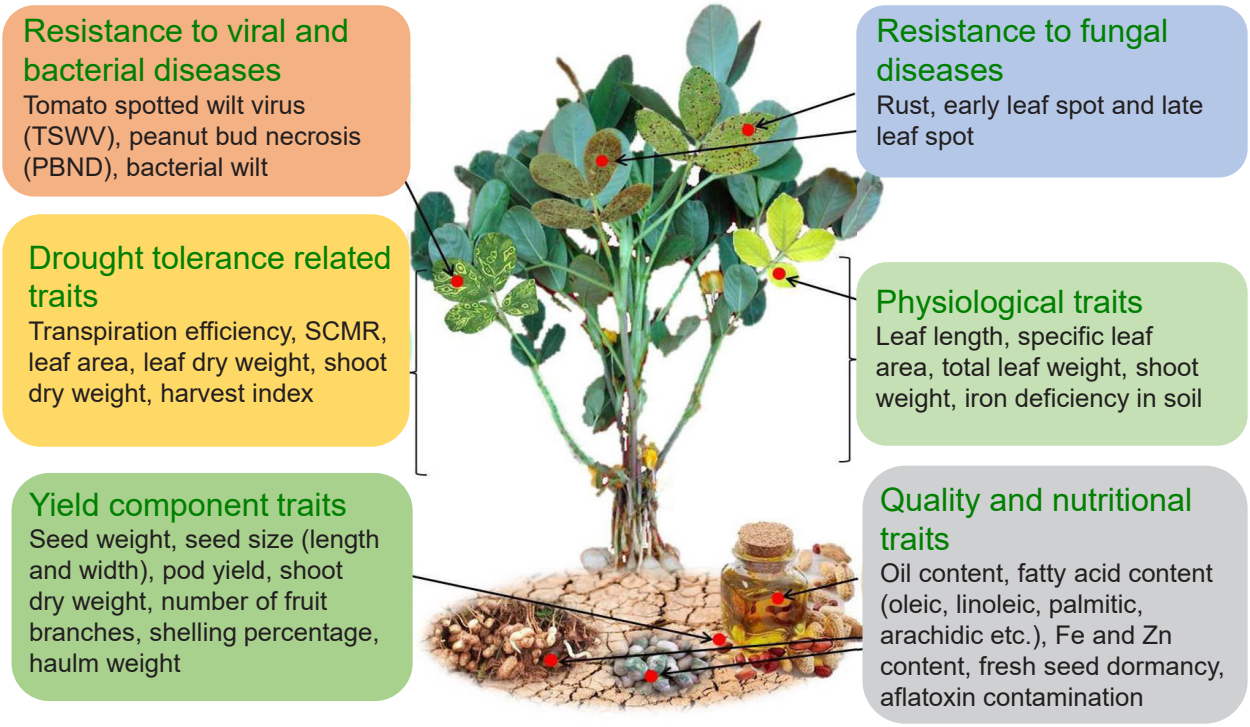


Figure 4: Molecular mapping of ca. 40 traits in groundnut

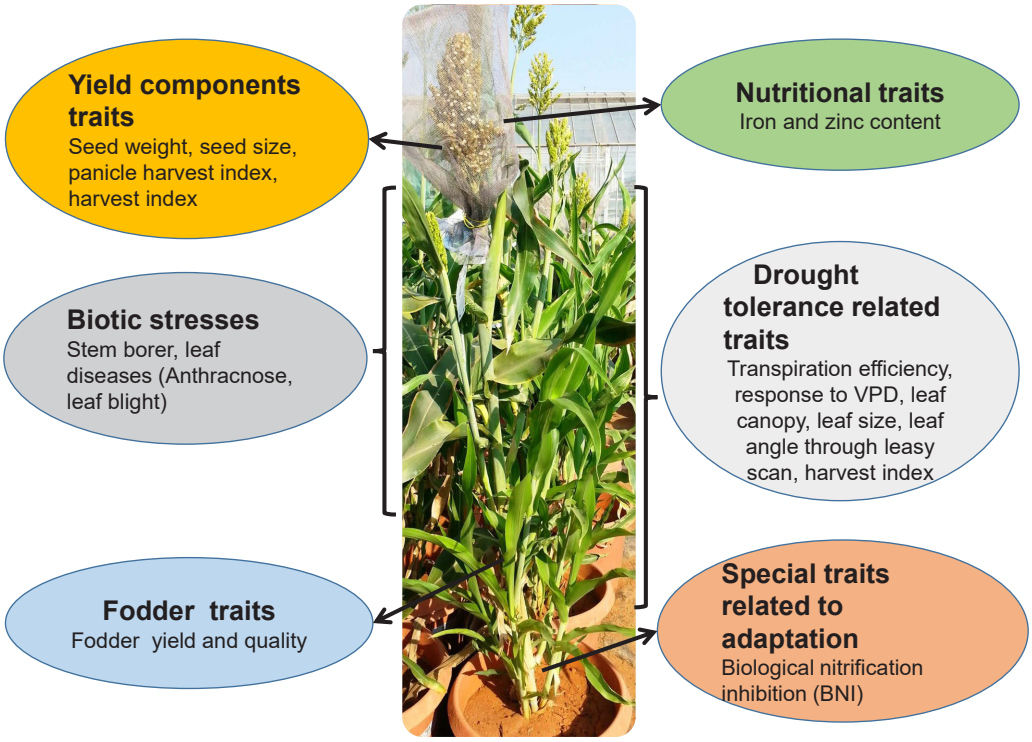


Figure 5: Molecular mapping of ca. 20 traits in sorghum

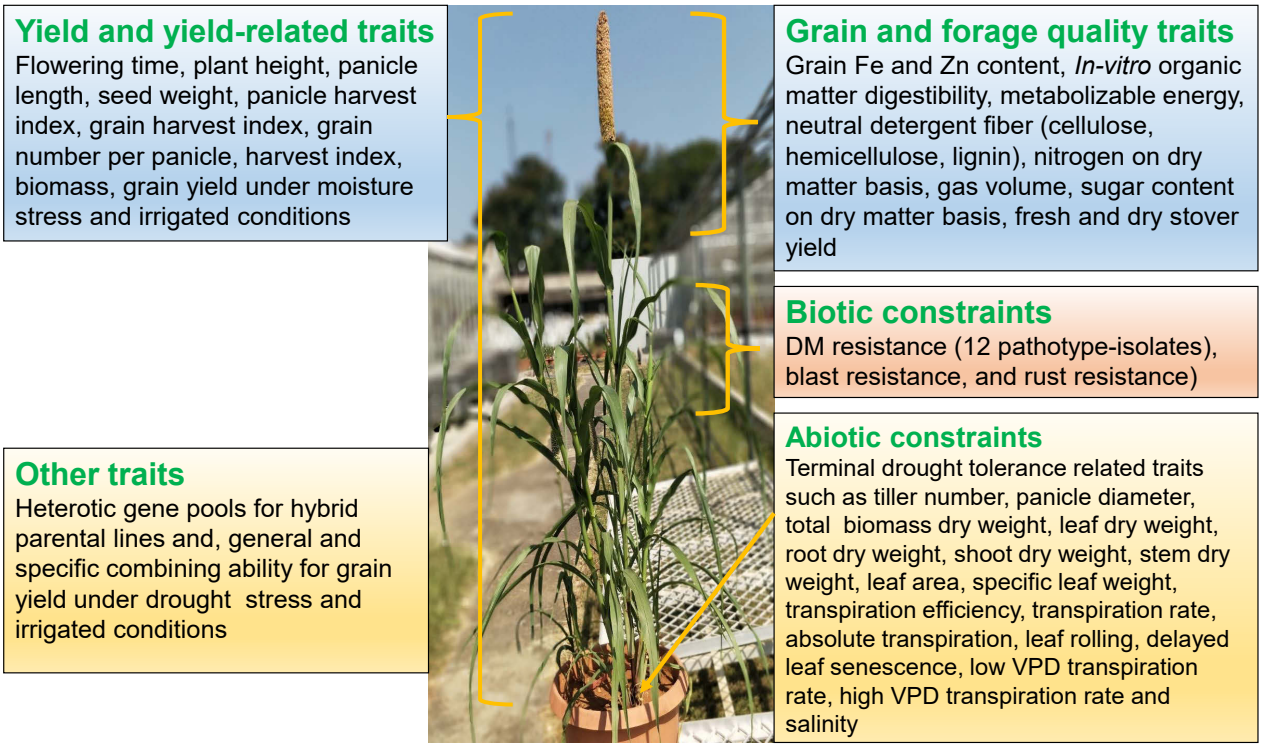


Figure 6: Molecular mapping of ca. 40 traits in pearl millet

Translating genomics research in product development

Molecular markers associated with different breeding traits were deployed in several breeding programmes in ICRISAT as well as collaborating national programmes in India and Africa. As a result of extensive collaboration with colleagues, several superior lines have been developed for a number of traits in almost all mandate crops (Table 2). CEG has now initiated some efforts in the area of deployment of genomic selection in crop improvement programmes.

Understanding function of genes and pathways

Identification of the genes and pathways responsible for various abiotic and biotic stresses is essential for devising strategies for crop improvement with more precision and high efficiency **(Figure 7)**. As early as 2007/2008, expressed sequencing tags (ESTs)-based transcriptome analysis was conducted for defining transcriptome assemblies and identifying candidate genes for drought and salinity stress in chickpea (*BMC Genomics* 2009, 10:523), fusarium wilt (FW) and sterility mosaic disease (SMD) in pigeonpea (*BMC Plant Biology* 2010, 10:45). However, in recent years, NGS-based transcriptome analysis has been used in groundnut to identify resistance mechanisms for late leaf spot, in vitro seed colonisation (*Scientific Reports* 2017, 7: 9659), pre-harvest aflatoxin contamination and aflatoxin production. Furthermore, in the absence of genome sequences, transcriptome assemblies were developed in chickpea (*Plant Biotech Journal* 2011, 9:922-931, *PLoS One* 2014, 9(1): e86039) and pigeonpea (*Molecular Plants* 2012, 5: 1020-1028) using transcript sequencing data generated from different platforms (Sanger, FLX/454 and Illumina). The development of the gene expression atlas in pigeonpea has also been completed (*Journal of Experimental Botany* 2017, doi: 10.1093/jxb/erx010) while development of gene expression atlas is underway in chickpea and groundnut.

In pearl millet, the whole genome sequence of the downy mildew pathogen (*Biotechnology Report* 2017, doi: 10.1016/j.btre.2017.07.006) was attempted to understand the gene expression of important defence enzymes, PR-proteins and HRGPs in pearl millet for mounting systemic immunity against the downy mildew pathogen (*Scientific Reports* 2017, 7:43991). Similarly, in collaboration with pathologists at ICRISAT and CSIRO, draft genome assembly was developed for *Fusarium oxysporum* f sp. ciceris (Foc-38-1) (*BMC Genomics* 201617:191). Furthermore, genome-wide transcriptome profiling of *Foc* conidial germination in collaboration with pathologists showed that *Foc* have large sets of germination-related genes and families of genes encoding secreted effectors, cell wall/pectin-degrading enzymes, metabolism-related enzymes, transporters and peptidases. We found that metabolism-related enzymes are up-regulated at an early point whereas most transporters and secondary metabolites important for tissue colonisation and pathogenicity are up-regulated later (*Scientific Reports* 2016 17;6:37353).

TABLE 2: SOME EXAMPLES OF TRANSLATING GENOME INFORMATION IN CROP IMPROVEMENT

Crop / Improved genotypes	Trait (s) improved	Current status of improved lines	Reference
Chickpea			
JG 11 and ICCV 10	Drought tolerance	Superior lines are in multi-location trials for evaluation and release	*The Plant Genome* 2013, 6:3
C 214	Fusarium wilt and Ascochyta blight resistance	Superior lines are in multi-location trials for evaluation and release	*The Plant Genome* 2014, 7:1
Groundnut			
ICGV 91114, JL 24 and TAG 24	Leaf rust resistance	Superior lines are in multi-location trials for evaluation and release	*Theor Appl Genet* 2014, 127:1771-1781
ICGV 06110, ICGV 06142 and ICGV 06420	Oil quality (high oleic acid)	Superior lines are in multi-location trials for evaluation and release	*Plant Science* 2015, 242:203-213
DH 86, ICGV 87846, ICGV 00350, ICGV 03128, ICGV 05155 and ICGV 00351	Resistance to leaf rust and late leaf spot; oil quality (high oleic acid)	Introgression lines (BC_3F_2 generation) during rainy 2017 season	Unpublished
GJG 9, GG20 and GJGHPS1	Resistance to leaf rust and late leaf spot; oil quality (high oleic acid)	Pyramided lines (F_3 generation) during rainy 2017 season	Unpublished
Pigeonpea			
ICPH 2671 and ICPH 3438	Hybrid purity	SSR-based hybrid seed testing purity kits developed	*BMC Plant Biol* 2011, 11:56; *Mol Breed* 2010, 26:371-380
ICPA 2039 and ICPB 2039	CMS seed purity	Gene-based markers for seed purity analysis of A_4CMS seeds developed	*BMC Genomics* 2009, 10:523
Sorghum			
M 35-1, Phule Vasudha, CRS1, Parbhani Moti, SPV 2217, BJV44, SVD806, GS23, GS16, GRS1 (DSV5)	Post-flowering drought tolerance (stay-green trait) and shoot fly resistance	Introgression lines at (BC_3F_2:F_3 generation) for field evaluation during post-rainy 2017	Unpublished
IS 8813, IS 13256, IS 23120, IS 18542	Low lignin	Introgression lines at (BC_3F_2:F_3 generation) for field evaluation during post-rainy 2017	Unpublished
Pearl millet			
H 77/833-2, J 2340 and ICMB 93333	Resistance to downy mildew and drought tolerance	The test cross hybrids (HHB 67 Improved and GHB 538 Improved) in multi-location trials for evaluation and release while introgression lines (BC_3F_3) for ICMB 93333 developed and the test cross hybrids tested.	AICRP-PM Annual Report, 2016-17
ICMB 95222 and Pollen parent of popular hybrid 9444	Blast resistance	QTL introgression lines (BC_3F_3 and BC_4F_3) and the test cross hybrids (HHB 146 Improved and Bayer-9444) are being tested	Unpublished

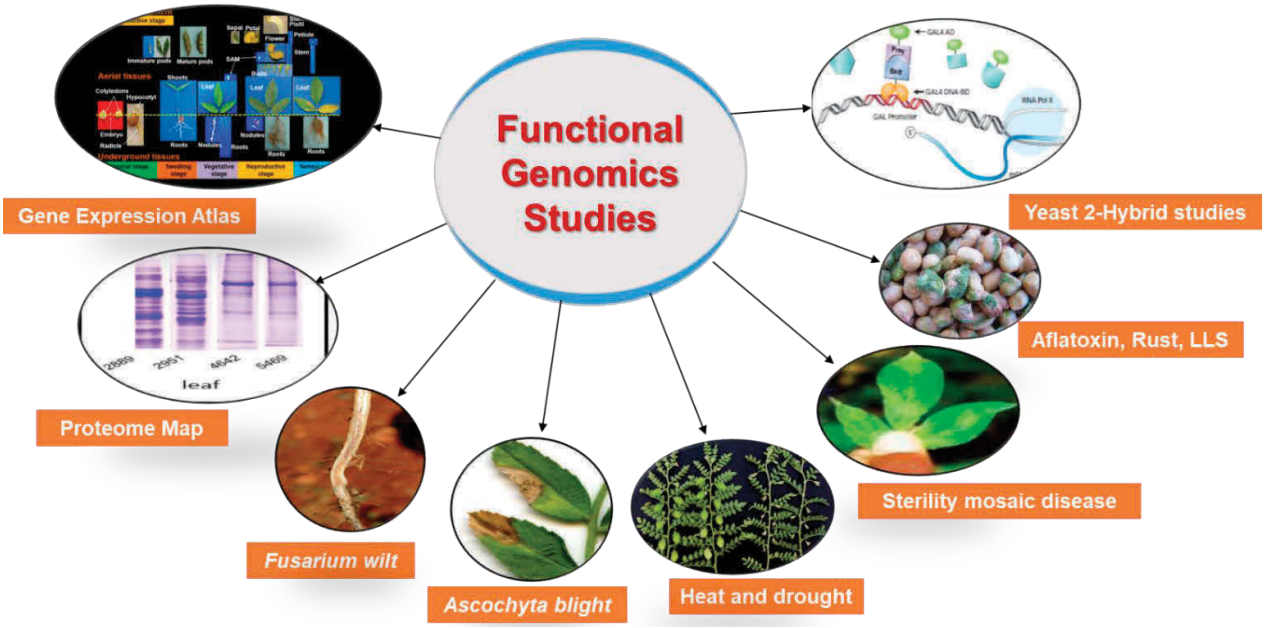


Figure 7: Functional genomics approaches being used at CEG for better understanding of traits and trait mechanisms

Sequencing and genotyping services

With an objective to enhance the adoption of molecular markers, CEG started to provide genotyping services for SSR and DArT markers at cost-to-cost basis as early as in 2008. Subsequently, CEG also offered SNP genotyping services using the BeadXpress and the KASPar marker system. It is important to mention here that CEG has generated more than 3.5 million datapoints for SSRs in the past 10 years **(Figure 8)**.

With the establishment of NGS platforms in 2012, CEG started to offer sequencing services that include sequencing-based genotyping, whole-genome re-sequencing, skim sequencing, transcriptome profiling, etc. As a result, the SSR and DArT genotyping services in recent years have declined and from 2013, more services have been provided in NGS data generation. For instance, around 45.9 Tbp sequence data have been generated during the past five years **(Figure 9)**.

In summary, over the past 10 years, genotyping and sequencing services have been provided for 34 crops and 40 organisations from 14 different countries across the globe.

Conferences and knowledge dissemination

With the aim of disseminating scientific knowledge and keeping the scientific community in Asia and Africa up to date with recent advances in genomics and molecular breeding, CEG has organised the following conferences/workshops/symposia:

- InterDrought-V, February, 21-25, 2017 (http://ceg.icrisat.org/idv/). IDV was attended by more than 900 delegates from 55 countries
- 5th International conference on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI-V), February 18-20, 2015 (http://ceg.icrisat.org/v-nggibci/). NGGIBCI-V was attended by more than 300 delegates from 31 countries
- 4th international workshop on Next Generation Genomics and Integrated Breeding for Crop Improvement (NGGIBCI-IV), February 19-21, 2014 (http://ceg.icrisat.org/NGGIBCI/). NGGIBCI-IV was attended by more than 150 delegates from 20 countries
- International Conference on Legume Genetics and Genomics (ICLGG)-VI, October 2-7, 2012 (http://ceg.icrisat.org/VI-ICLGG/). ICLGG-VI was attended by more than 500 delegates from 44 countries
- 3rd International workshop on next generation sequencing data analysis & modern breeding approaches, August 29-31, 2012 (http://ceg.icrisat.org/3-ngs.html)
- 2nd International workshop on Next Generation Sequencing (NGS) Data Analysis, July 21-23, 2009 (http://ceg.icrisat.org/2-ngs.html)
- 1st International workshop on Next Generation Sequencing (NGS) Data Analysis, July 21-23, 2009 (http://ceg.icrisat.org/1-ngs.html)
- 2nd National Workshop on Marker-Assisted Selection in Crop Improvement, October 27-29, 2010
- Advances in Arachis through Genomics and Biotechnology (AAGB-2009), October 19 - 22, 2009 at ICRISAT-Mali
- Advances in Arachis through Genomics and Biotechnology (AAGB-2008), November 4-8, 2008 at ICRISAT, India

High-profile visits to CEG

A number of high-profile delegates such as Mr Bill Gates (Co-Chair of the Bill & Melinda Gates Foundation), Shri Radha Mohan Singh (Union Minister of Agriculture and Farmers Welfare, Government of India), Shri Krishna Byregowda (Minister of Agriculture, Government of Karnataka), Shri Pocharam Srinivas

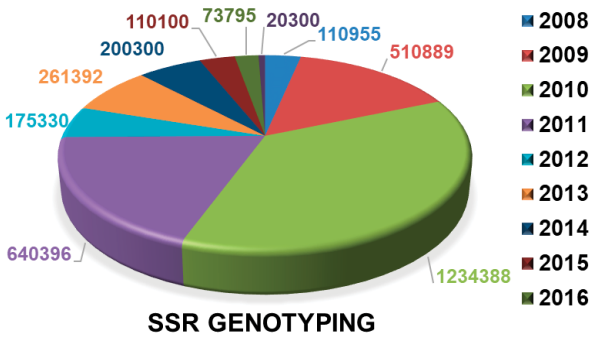


Figure 8: More than 3.5 million datapoints generated by CEG in the past eight years

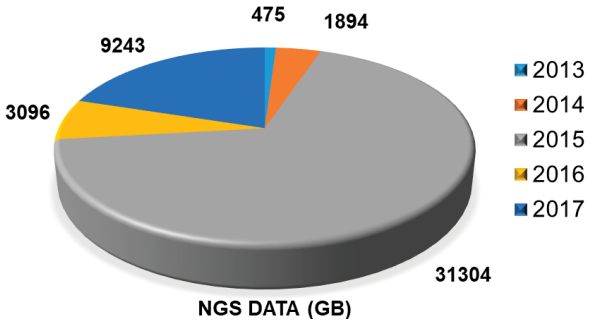


Figure 9: More than 45.9 Tbp sequencing data generated by CEG in the past five years

Reddy (Minister of Agriculture, Government of Telangana), Prof MS Swaminathan (Father of Green Revolution in India), Dr Raj Shah (President, Rockfeller Foundation), Dr Rob Bertram (Chief Scientist, USAID's Bureau for Food Security), Prof Ed Southern (Chair, Kirkhouse Trust), Prof Howard Yana Shapiro (Chief Agricultural Officer, MARS Inc) and Dr. Frank Rijsberman (the then CEO, CGIAR Consortium) have visited and interacted with scientists/staff of CEG.

A number of Secretaries from the Government of India including Shri SK Pattanayak and Shri AK Bahuguna; different Directors General of Indian Council of Agricultural Research such as Dr Trilochan Mohapatra, Dr S Ayappan and Dr Mangla Rai; and Vice Chancellors/President of various universities from India, Africa, USA, Europe, China have visited CEG. In addition, CEG has had the privilege of being visited by delegations from several funding/international agencies, such as the Bill & Melinda Gates Foundation, the World Bank, CGIAR, International Science and Partnership Council of CGIAR, US Agency for International Development, Biotechnology and Biological Sciences Research Council (BBSRC), Ministry of Agriculture, Ministry of Science & Technology of Government of India.

CEG in the media

CEG scientists have been prominent and highly featured in the print as well as electronic media for their high-impact research. News stories from CEG have been published in many leading

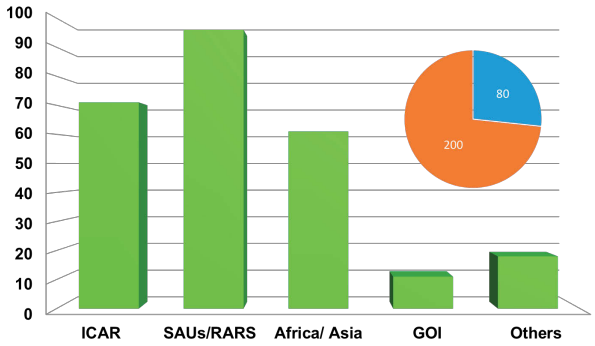


Figure 10: Distribution of scientists from different types of organisations. Indian scientists have been classified under ICAR, SAUs/RARS, GoI and others, while scientists from non-Indian organisations have been grouped under Africa/Asia categories.

newspapers/magazines/websites in various languages in India and abroad. These include *Asian Scientist*, *Bio1000*, *Biospectrum*, *Business Mirror*, *Business Standard*, *CNBC*, *CNN-IBN*, *CGIAR Consortium*, *Daji World*, *Deccan Herald*, *DNA India*, *Dainik Bhaskar*, *Dainik Jagran*, *Down to Earth*, *Economic Times*, *FnB NewsFarming ahead*, *Food Navagator*, *French Tribune*, *Genome Engineering*, *Genome Web*, *IBN Live*, *International Business Times*, *ISAAA.org*, *Mumbai Mirror*, *NDTV*, *New Agriculturist*, *PHY Org*, *Rural Marketing*, *SciDevNet*, *Science Daily*, *Science News Line*, *The Businessline*, *The Hindustan*, *The Japan Times*, *The Indian Express*, *The Times of India*, *The Hindu*, *Telegraph India*, *Thomson Reuters*, *TV18*, *Weekly Times Now*. News stories or interviews about CEG work have also been covered in several radio and TV channels in India and other countries. CEG has a good presence on social media on Facebook (https://www.facebook.com/coeingenomics/), Twitter (@coeingenomics) and others

Summary

As evident from the above, the CEG has completed 10 glorious years of excellence in science and development and partnership.

While working in collaboration with scientists from different Themes/Programmes/Regions of ICRISAT and its partners representing 184 institutes from 35 countries, CEG has emerged as a high-quality science, service and training centre at international level. While genome sequences have been assembled for 11 crops, 20–50 traits have been mapped in ICRISAT mandate crops. A number of superior lines have been developed through molecular breeding and many of them are in advanced stage of multi-location trials in India and other countries.

CEG scientists and their collaborators have been successful in mobilising more than US$96 million and publishing 353 papers in 113 journals (including nine papers in *Nature* journals) with a cumulative impact factor of 1,374. Scientific contribution of CEG scientists has been recognised by several national and international agencies, and have been honoured with a number of awards/honours/fellowships.

CEG has generated 3.5 million SSR datapoints and 50 Tbp sequence data. About 300 scientists, through formal training courses and 200 scientists as a Visiting Scientists, Post-docs, PhD and Master degree students, have been trained at CEG.

Many of them are successful leaders in plant science research and crop improvement in India and abroad.

CEG has organised around 10 international conferences/symposia/workshops over the past 10 years. CEG has also had high-profile personalities as its visitors.

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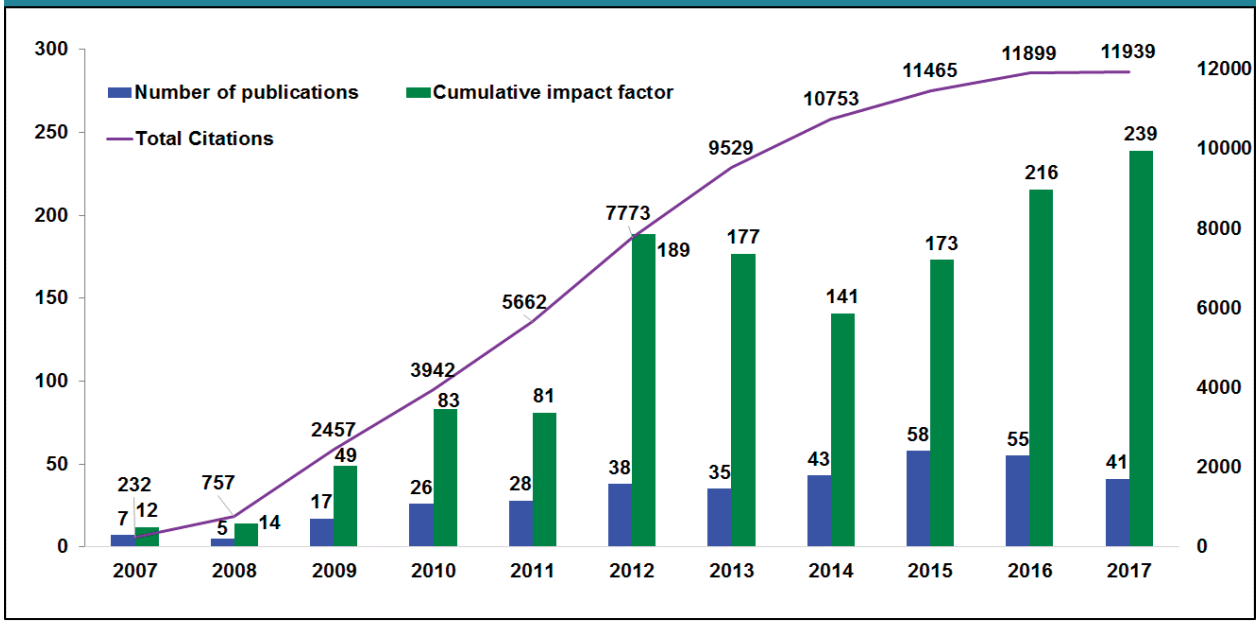
Publications

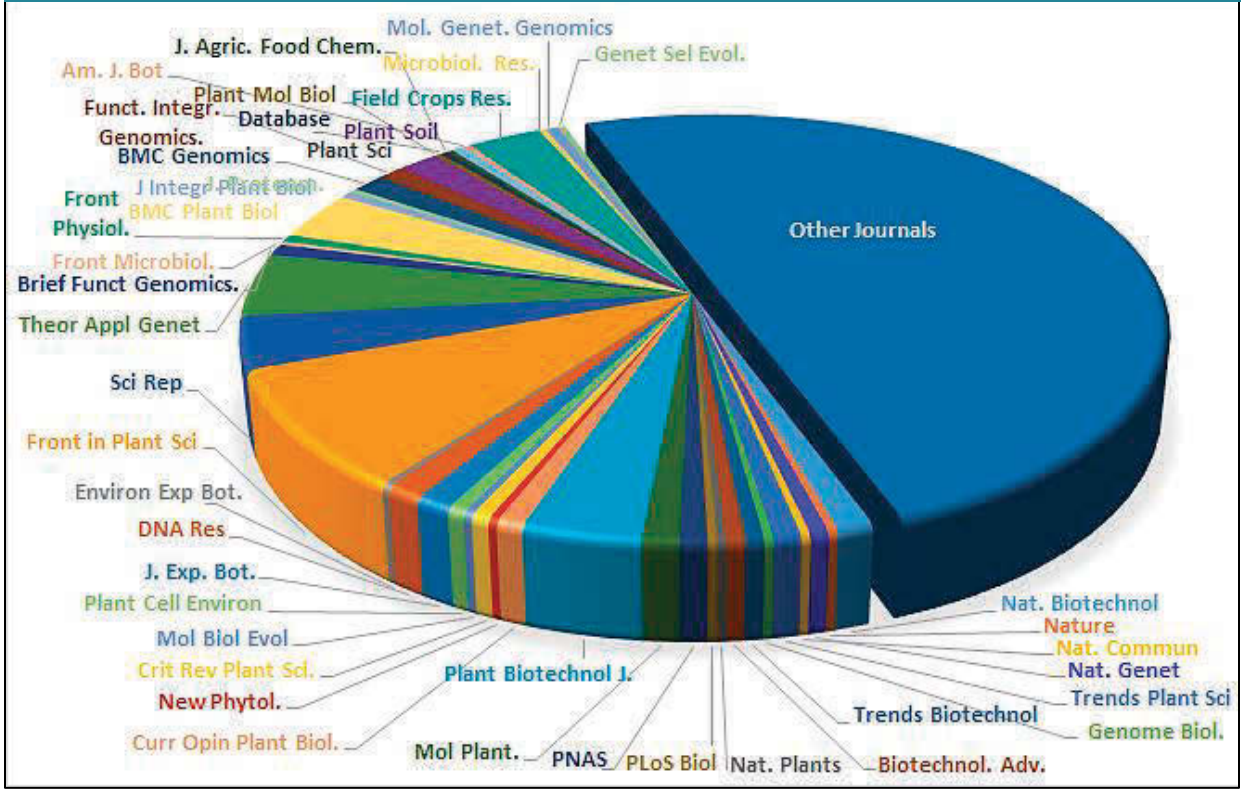
PUBLICATIONS IN DIFFERENT JOURNALS				
S. No.	**Journal Name**	**No**	**Impact Factor**	**Total Impact Factors**
1	*Nature Biotechnology*	4	41.7	166.67
2	*Nature*	1	40.1	40.14
3	*Nature Genetics*	2	28.0	55.92
4	*Nature Communications*	1	12.1	12.12
5	*Trends in Plant Science*	3	11.9	35.73
6	*Genome Biology*	1	11.9	11.91
7	*Trends in Biotechnology*	2	11.1	22.25
8	*Biotechnology Advances*	2	10.6	21.19
9	*Nature Plants*	1	10.3	10.30
10	*PLOS Biology*	1	9.8	9.80
11	*Proceedings of National Academy of Sciences*	3	9.7	28.98
12	*Molecular Plant*	4	8.8	35.31
13	*Plant Biotechnology Journal*	13	7.4	96.76
14	*Current Opinion in Plant Biology*	3	7.4	22.07
15	*New Phytologist*	1	7.3	7.33
16	*Critical Reviews in Plant Sciences*	2	6.8	13.65
17	*Molecular Biology and Evolution*	1	6.2	6.20
18	*Plant Cell and Environment*	2	6.2	12.35
19	*Journal of Experimental Botany*	4	5.8	23.32
20	*DNA Research*	4	5.4	21.62
21	*Environmental and Experimental Botany*	1	4.4	4.37
22	*Frontiers in Plant Science*	32	4.3	137.54
23	*Scientific Reports*	14	4.3	59.63
24	*Theoretical and Applied Genetics*	17	4.1	70.24
25	*Briefings in Functional Genomics*	3	4.1	12.29
26	*Frontiers in Microbiology*	1	4.1	4.08
27	*Frontiers in Physiology*	2	4.1	8.27
28	*BMC Plant Biology*	13	4.0	51.53
29	*Journal of Integrative Plant Biology*	2	4.0	7.92
30	*Journal of Proteomics*	1	3.9	3.91
31	*BMC Genomics*	5	3.7	18.65
32	*Functional & Integrative Genomics*	4	3.5	13.98

33	*Plant Science*	6	3.4	20.62
34	*Plant Molecular Biology*	1	3.4	3.36
35	*Database*	1	3.3	3.29
36	*Journal Of Agricultural And Food Chemistry*	1	3.2	3.15
37	*Plant and Soil*	2	3.1	6.10
38	*American Journal of Botany*	1	3.1	3.05
39	*Field Crops Research*	11	3.0	33.53
40	*Microbiological Research*	1	3.0	3.04
41	*Molecular Genetics and Genomics*	2	3.0	5.96
42	*Genetics Selection Evolution*	1	3.0	2.96
43	Other journals including *G3*, *PLOS ONE*, *The Plant Genome*, *Molecular Breeding*, *BMC Bioinformatics*, *Functional Plant Biology*, *Crop Science*, *Euphytica & Plant Breeding*	176		243.25
Total		353	407.8	1374.34

TRENDS IN DIFFERENT PARAMETERS IN PUBLICATIONS



DISTRIBUTION OF PUBLICATIONS IN DIFFERENT JOURNALS



COMPLETE LIST OF PUBLICATIONS FROM CEG AND ITS COLLABORATORS

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5. Genome-wide SNP genotyping resolves signatures of selection and tetrasomic recombination in peanut. *Molecular Plant* 10: 309-322.
6. Indel-seq: a fast forward genetics approach for identification of trait associated putative candidate genomic regions and its application in pigeon pea (*Cajanus cajan*). *Plant Biotechnology Journal* 15: 906–914.
7. Development and evaluation of high-density Axiom® *CicerSNP* Array for high-resolution genetic mapping and breeding applications in chickpea. *Plant Biotechnology Journal* doi:10.1111/pbi.12836
8. QTL-seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (*Arachis hypogaea* L.). *Plant Biotechnology Journal* 15: 927–941.
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339. Novel set of groundnut SSRs for genetic diversity and interspecific transferability. *International Journal of Integrative Biology* 7: 100-106.
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344. Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut (*Arachis hypogaea*). *BMC Plant Biology* 8: 55.
345. Chickpea improvement: Role of wild species and genetic markers. *Biotechnology and Genetic Engineering Reviews* 25: 267-314.
346. Potential for using morphological, biochemical, and molecular markers for resistance to insect pests in grain legumes. *Journal of Food Legumes* 21: 211-217.

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349. Quantitative trait loci for grain yield in pearl millet under variable post flowering moisture conditions. *Crop Science* 47: 969-980.
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Grants/Projects

LIST OF KEY GRANTS FROM CEG AND THEIR COLLABORATORS

	Funding Agency	Project Title	Grant duration	Grant value in US$ '000	Scientist/PI responsible
1	Syngenta Foundation	Enhancement of the set of microsatellite (SSR) markers for improving pearl millet breeding efficiency in Africa and Asia	2006–2007	70	RK Varshney
2	ICAR, India	Pigeonpea genomics initiative under the Indo US Agricultural Knowledge Initiative (AKI)	2006–2008	307	RK Varshney
3	NFBSRA, India	Gene-based genetic maps and molecular markers for abiotic stress tolerance in cultivated groundnut	2006–2008	95	RK Varshney
4	The SM Sehgal Foundation, India	Exploiting gene synteny to improve stem borer resistance mapping in sorghum	2006–2009	150	CT Hash/ SP Deshpande
5	BBSRC – SARID	Unravelling the molecular genetic basis of striga resistance in cereals: Integrating Quantitative Trait Loci (QTL) and genomic approaches	2006–2010	80	SP Deshpande
6	DBT, India	Centre of excellence for high-throughput allele determination for molecular breeding	2006–2011	1,016	RK Varshney / CT Hash
7	BMGF through CP – Generation	Comparative genomics for gene discovery in the generation challenge programme	2007	42	RK Varshney
8	BMGF through CP – Generation	Comparative genomics for gene discovery	2007	22	RK Varshney
9	Bioversity International	Genotyping groundnut germplasm from Foundation PROINPA using SSR	2007	7	RK Varshney
10	NFBSRA, India	Evaluating candidate genes towards Eenhancement of drought tolerance in chickpea (*Cicer arietinum*)	2007–2008	70	RK Varshney
11	IISc, Bangalore, India	DBT Research Associate	2007–2008	7	NL Raju
12	BMGF through CP – Generation	Improving tropical legume productivity for marginal environments in Sub-Saharan Africa – Phase I	2007–2010	2,903	David Hoisington/ RK Varshney / V Vadez

13	BMGF through CP – Generation	Comparative genomics for gene discovery in the generation challenge programme	2007–2010	565	RK Varshney
14	ACIAR, Australia	Improving postrainy sorghum varieties to meet the growing grain and fodder demand in India	2007–2013	768	SP Deshpande
15	DBT, India	Construction of the transcript map and development of functional markers for chickpea	2008–2011	108	RK Varshney
16	BBSRC– DFID	Integrating genomics and mapping approaches to improve pearl millet productivity in drought prone regions of Africa and Asia"	2008–2013	200	CT Hash
17	BMGF through CP – Generation	Marker assisted back crossing (MABC) for drought tolerance in chickpea students for analysis of drought tolerance in chickpea (TLI – Kenyan Student)	2009–2010	50	RK Varshney
18	BMGF through CP – Generation	Commissioned research projects 2009	2009–2012	1,079	CT Hash/ HD Upadhyaya/ B Haussmann/ E Rattunde/ PM Gaur/ M Blummel/ S Senthilvel/ RK Varshney/ M Butterfiled
19	DBT, India	Deployment of molecular markers in chickpea breeding for developing superior cultivars with enhanced disease resistance	2009–2014	340	RK Varshney
20	NSF, USA (UC-Davis)	"BREAD" Overcoming the domestication bottleneck for symbiotic nitrogen fixation in legumes	2010–2011	234	RK Varshney
21	BMGF (through CIMMYT) – CP – Generation	Commissioned research projects 2010	2010–2011	82	RK Varshney
22	CP Generation	Discovery and development of alleles contributing to sorghum drought tolerance	2010–2013	680	CT Hash/SP Deshpande

23	BMGF (through CIMMYT) – CP – Generation	Challenge Initiatives Projects – 2010	2010–2014	1,915	E Rattune/ BIG Haussmann/ RK Varshney
24	BMGF (through CIMMYT) – CP – Generation	Improving tropical legume productivity for marginal environments in Sub-Saharan Africa and South Asia – Phase II	2010–2014	3,351	RK Varshney/ V Vadez
25	IISC, Bangalore, India	DBT Research Associateship	2011	4	Ashish Kumar
26	BMGF (through CIMMYT) – CP – Generation	Development of an SNP platform for molecular breeding in elite material of chickpea	2011	8	RK Varshney
27	JIRCAS, Japan	Seed multiplication of sorghum mapping	2011–2012	16	CT Hash/ SP Deshpande
28	ILRI	Delivering new sorghum millet innovations for food security and improving livelihoods in Eastern Africa	2011–2013	204	S deVilliers/ SP Deshpande
29	IGSTC	Biotechnological approaches to improve chickpea crop productivity for farming community and industry	2011–2014	118	RK Varshney/ M Thudi
30	BMGF through CP – Generation	Commissioned research projects 2011	2011–2014	729	RK Varshney/ PM Gaur/ TM Shah
31	BMGF	Improving the livelihoods of smallholder farmers in drought-prone areas of Sub-Saharan Africa and India through enhanced grain legume production and productivity – tropical legumes II, phase 2	2011–2014	21,000	CLL Gowda/ RK Varshney
32	BMGF through CP – Generation	Harnessing the potential of MAGIC population for gene discovery and breeding applications in chickpea	2011–2014	430	RK Varshney/ PM Gaur
33	JIRCAS, Japan	Development of genetic markers for sorgoleone (a BNI component) release capacity in sorghum	2012–2013	22	CT Hash/ SP Deshpande
34	BMGF through CP – Generation	Developing and implementing the genomic component of the IBP	2012–2014	244	RK Varshney
35	USAID – India	Pigeonpea improvement using molecular breeding	2012–2015	2,180	RK Varshney

36	DBT, India	Genomics-assisted accelerated product development of high-yielding pigeonpea hybrids	2012–2015	550	RK Varshney/ RK Saxena
37	DST, India	Genomic approaches for stress-tolerant chickpea	2012–2014	989	RK Varshney/ M Roorkiwal
38	Uniliver Industries Pvt Ltd	Unlocking health benefits of pearl millet: Identifying factors for starch digestibility, and slowly digestable starch (SDS) using a world inbred germplasm association panel	2012–2016	103	SD Mazumdar/ RK Srivastava
39	BBSRC-DFID-BMGF-DBT-SCPRID	Smart cereals for management of stem borers in staple cereals in Africa	2012–2016	624	SP Deshpande/ Damaris Odeny
40	DST, India	Innovation in science pursuit for inspired research (INSPIRE)	2012–2017	152	H Kudapa
41	BMGF	A high-quality reference genome sequence of pearl millet (*Pennisetum glaucum* L.) for accelerated breeding of improved cultivars	2013–2014	2,200	RK Varshney
42	DBT, India	DBT Junior Research Fellow	2013–2014	2	Shashidhar Y
43	BMGF through CP – Generation	Integrating GUI for genomic selection in IBP tool box.	2013–2014	210	RK Varshney/ A Rathore
44	Peanut Foundation	Genome-wide association studies (GWAS) to identify markers associated with target trails for peanut breeding using diverse global germplasm collections	2013–2014	67	RK Varshney
45	PMIL	Translational genomics to reduce pre-harvest aflatoxin contamination of peanut	2013–2017	372	RK Varshney
46	ACIAR	Improving postrainy sorghum varieties to meet the growing grain and fodder demand in India: Phase II	2013–2017	592	SP Deshpande
47	MARS CHOCOLATE, USA	Improving short duration/drought tolerant peanut genotypes for oil quality and disease resistance through marker-assisted gene/QTL pyramiding approach	2013–2018	1,000	RK Varshney
48	USAID	Global hunger and food security research strategy: climate resilience, nutrition and policy – feed the future innovation lab for climate-resilient sorghum	2013–2018	1,786	S Deshpande

49	The University of Georgia Research Foundation Inc	Global hunger and food security research strategy: cimate resilience, nutrition and policy – feed the future innovation lab for climate-resilient sorghum	2013–2018	1,786	SP Deshpande
50	USAID – FTF	Feed the future innovation lab for climate-resilient sorghum	2013–2018	4,990	SP Deshpande
51	BMGF through CP Generation	Tropical legumes 1 workstream continuation	2014	690	RK Varshney/V Vadez
52	BMGF through CP Generation	Re-sequencing of multi-parent advanced generation inter-cross (MAGIC) lines of chickpea (*Cicer arietinum*)	2014	145	RK Varshney/ PM Gaur
53	BMGF through CP Generation	Collaboration and establishment of a regional hub of the integrated breeding platform	2014–2016	200	RK Varshney
54	ICARDA	Chickpea genome sequencing and analysis	2014–2016	292	RK Varshney/ Anu Chitikineni
55	DAC & FW, India	Utilising chickpea genome sequence for crop improvement	2014–2017	2,015	RK Varshney
56	DBT, India	Biofertilisation and bioirrigation for sustainable mixed cropping of pigeonpea and finger millet (BIOFI)	2014–2017	70	RK Varshney
57	Bayer BioScience Pvt Ltd	Marker-assisted recurrent selection (MARS) directed foliar blast resistance transfer in an elite pearl millet pollen parent	2014–2017	156	RK Srivastava
58	DST-SERB, India	Tracking breeding – induced genomic genome changes in pigeonpea (*Cajanus Cajan* L. Millsp.)	2014–2017	26	RK Saxena
59	Cornell University, USA	Delivering high-density genomics breeder's tools	2014–2019	2,899	RK Varshney & S Grando
60	BMGF through CP Generation	Support for fifth international conference on next-generation genomics and integrated breeding for crop improvement	2015	50	RK Varshney
61	IFPRI	Understanding molecular Defence mechanism and identification of candidate genes for resistance to aspergillus infection and aflatoxin contamination in groundnut	2015–2016	50	SN Nayak

62	BMGF through CP Generation	Shared industrial-scale low-density SNP genotyping for CGIAR and partner breeding programmes serving SSA and SA	2015–2017	3,998	RK Varshney
63	Govt of Karnataka, India	Genomics-assisted breeding for high-yielding and climate-resilient pigeonpea varieties/hybrids and promotion of best suitable cultivars for food and nutritional security in Karnataka state in India	2015–2017	148	RK Saxena
64	BMGF	Improving livelihoods for smallholder farmers: enhanced grain legume productivity and production in Sub-Saharan Africa and South Asia	2015–2019	24,000	RK Varshney and colleagues
65	DST, India	Understanding the drought-tolerance mechanism in chickpea using epigenetics (INSPIRE)	2015–2020	131	M Roorkiwal
66	USAID	Support to participate legume researchers from developing countries and wider dissemination of pigeonpea genome projects in InterDrought Conference, 21-26 Feb 2017	2016–2017	77	RK Varshney
67	CSIR, India	Identification of genes in QTL-hotspot region for drought tolerance in chickpea (*Cicer arietinum* L)	2016–2017	6	RK Varshney
68	DST, India	Unravelling the effect of elevated carbon-dioxide mediated abiotic stress in chickpea transcriptome	2016–2019	47	P Palit
69	DBT, India	Genome wide analysis of high temperature responsive minas and their target regulation in tolerant and sensitive cultivars of chickpea (*Cicer arietinum* L.)	2016–2017	18	Sailaja Prasad
70	Govt of Karnataka, India	Harnessing the power of genetics and genomics for enhancing rabi sorghum productivity in Karnataka state	2016–2018	252	S Deshpande
71	Govt of Karnataka, India	Improving popular groundnut varieties for foliar disease resistance and high oblate trait using genomics-assisted breeding approach and multi-location testing of MABC Lines for varietal release in Karnataka	2016–2018	279	M Pandey

72	Govt of Karnataka, India	Development of climate resilient chickpea varieties using genomics assisted breeding approaches and promotion of best suitable cultivars for food and nutritional security in Karnataka	2016–2018	226	M Thudi
73	ICAR – ICRISAT	Development of genetic and genomic resources of finger millet and its application in crop improvement	2016–2018	40	SP Deshpande, R Gupta/ RK Varshney et al.
74	Govt of Karnataka, India	Harnessing the power of genetics and genomics for enhancing rabi sorghum productivity in Karnataka State	2016–2018	261	SP Deshpande
75	Govt of Karnataka, India	Integrated genomics-assisted breeding for efficient development of superior finger millet varieties for Karnataka	2016–2019	1,400	S P Deshpande
76	Mars Chocolate, USA	Identification of markers and genomic regions associated with aflatoxin resistance in peanut	2016–2019	750	RK Varshney/ M Pandey
77	DBT, India	Cambridge-India network for translational research in nitrogen	2016–2019	482	R Gupta
78	Govt of Karnataka, India	Integrated genomics-assisted breeding for efficient development of superior finger millet varieties for Karnataka	2016–2019	1,428	S Deshpande
79	BRRI, Bangladesh	To facilitate procurement deployment and training on various automation data collection solutions	2017	155	Enghwa NG
80	Global Innovation & Technology Alliance, India	Development of pearl millet hybrid seeds and novel food products: An affordable resource in the prevention of Type 2 diabetes in India	2017–2019	77	RK Srivastava
81	SERB, India	A functional genomics approach to decipher strategic modification and regulatory mechanisms involved in drought stress avoidance in groundnut	2017–2019	31	Rakesh Kumar
82	DAC&FW, India	Delivering more produce and income to farmers through enhancing genetic gains for chickpea and pigeonpea	2017–2020	1,375	RK Varshney and colleagues
83	DST – SERB, India	Identification of candidate genes and development of markers for molecular breeding of early flowering in chickpea (*Cicer arietinum* L.)	2017–2020	54	M Thudi

84	DST – SERB, India	Genome-wide association studies for nutritional traits in chickpea using the reference set	2017–2019	31	S Pandey
85	DBT-Bio-CARe, India	Genome-wide epigenetic profiling of pigeonpea parental lines and thereof derived hybrids for understanding molecular basis of heterosis	2017–2020	19	P Sinha
86	DST – Women Scientist Scheme – A	Integrated 'omics' approach for combating fusarium wilt and sterility mosaic disease, two most dreaded diseases of pigeonpea (*Cajanus cajan*)	2017–2020	46	PT Lekha
87	DST – SERB, India	Genetic characterisation of shoot fly-resistant and drought-tolerant traits, and their expression profiling to identify putative candidate genes on sorghum chromosome SBI-10 long arm	2017–2019	31	KNS Usha Kiranmayee

Collaborators/Partners

AFRICA

Institut de l'Environnement et de Recherches Agricoles, Burkina Faso

University of Ouagadougou, Burkina Faso

Field Crops Research Institute, Egypt

Ethiopian Institute of Agricultural Research, Ethiopia

CSIR - Savanna Agricultural Research Institute, Ghana

West Africa Centre for Crop Improvement, Ghana

Biosciences eastern and central Africa, Kenya

Egerton University, Kenya

International Centre of Insect Physiology and Ecology, Kenya

Kenya Agricultural Research Institute, Kenya

Maseno University, Kenya

Moi University, Kenya

The World Agroforestry Centre (ICRAF), Kenya

National Smallholder Farmers' Association of Malawi, Malawi

Institut d'Economie Rurale, Mali

Université Abdou Moumouni, Niger

Agricultural Research Council of Nigeria, Nigeria

Institute for Agricultural Research, Nigeria

International Institute of Tropical Agriculture, Nigeria

National Centre for Genetic Resources and Biotechnology, Nigeria

Institut Sénégalais de Recherches Agricoles, Senegal

West and Central African Council for Agricultural Research and Development, Senegal

Agriculture research Corporation, Sudan

University of Khartoum, Sudan

Agricultural Research Institute-Uyole, Tanzania

Maruku Agricultural Research Institute (MARI), Tanzania

Naliendele Agricultural Research Institute, Tanzania

Selian Agricultural Research Institute, Tanzania

Sokoine University of Agriculture (DAEA), Tanzania

Association for Strengthening Agricultural Research in Eastern and Central Africa, Uganda

Makerere University College of Agricultural and Environmental Sciences (CAES), Uganda

National Crops Resources Research Institute, Uganda

National Semi Arid Resources Research Institute (NaSARRI), Uganda

ASIA

Beijing Genomics Institute, China

Fujian Agricultural and Forestry University, China

Guangdong Academy of Agricultural Sciences, China

Henan Academy of Agricultural Sciences, China

Jiangsu Academy of Agricultural Sciences, China

Oil Crops Research Institute, China

Shandong Academy of Agricultural Sciences, China

Shandong Peanut Research Institute, China

Zhejiang Academy of Agricultural Sciences, China

Acharya N. G. Ranga Agricultural University, India

Banaras Hindu University, India

Bayer BioScience Pvt. Ltd., India

Bioseed Research India Pvt. Ltd., India

Centre for Cellular and Molecular Platforms, India

Chaudhary Charan Singh Haryana Agricultural University, India

Chaudhary Charan Singh University, India

CSIR - Centre for Cellular and Molecular Biology, India

Department of Agriculture Cooperation & Farmers Welfare, India

Department of Biotechnology, India

Department of Science & Technology, India

Dr. Panjabrao Deshmukh Krishi Vidyapeeth, India

Government of Karnataka, India

Hemchandracharya North Gujarat University, India

Hindustan Unilever Limited, India

Indian Council of Agricultural Research, India

ICAR—Central Arid Zone Research Institute, India

ICAR - Directorate of Groundnut Research, India

ICAR - Indian Agricultural Research Institute, India

ICAR- National Bureau of Plant Genetic Resources, India

ICAR - Indian Institute of Millets Research, India

ICAR - Indian Institute of Oilseeds Research, India

ICAR - Indian Institute of Pulses Research, India

ICAR - National Research Centre on Plant Biotechnology, India

Indo-German Science & Technology Centre, India

Institute of Bioinformatics and Applied Biotechnology, India

Jawaharlal Nehru Krishi Vishwa Vidyalaya, India

Jawaharlal Nehru Technological University, India

Junagadh Agricultural University, India

KisanHub, India

Krishidhan Seeds Pvt. Ltd., India

Mahatma Phule Krishi Vidyapeeth, India

National Centre for Biological Sciences, India

National Institute of Plant Genome Research, India

Osmania University, India

Premas Biotech, India

Professor Jayashankar Telangana State Agricultural University, India

Punjab Agricultural University, India

Rajasthan Agricultural Research Institute, India

Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, India

Sher-e-Kashmir University of Agricultural Sciences and Technology, India

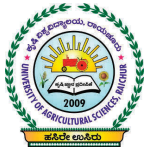
Sri Karan Narendra Agriculture University, India

Swami Keshwanand Rajasthan Agricultural University, India

Tamil Nadu Agricultural University, India

University of Agricultural Sciences Bangalore, India

University of Agricultural Sciences Dharwad, India



University of Agricultural Sciences Raichur, India

University of Delhi, India

University of Hyderabad, India

University of Mysore, India

Vasantrao Naik Marathwada Krishi Vidyapeeth, India

Visva-Bharati, India

Hokkaido University, Japan

Japan International Research Center for Agricultural Sciences, Japan

Kazusa DNA Research Institute, Japan

National Institute of Agrobiological Sciences, Japan

University of Tokyo, Japan

International Center for Agricultural Research in the Dry Areas, Lebanon

International Rice Research Institute, Philippines

Macrogen, South Korea

Seoul National University, South Korea

Field Crops Research and Development Institute, Sri Lanka

World Vegetable Center (AVRDC), Taiwan

AUSTRALIA

Australian Centre for International Agricultural Research, Australia

Australia Centre For Plant Functional Genomics Pty Ltd, Australia

Commonwealth Scientific and Industrial Research Organization, Australia

Curtin University, Australia

Grains Research and Development Corporation, Australia

Pulse Breeding Australia, Australia

Queensland Alliance For Agriculture and Food Innovation, Australia

Royal Melbourne Institute of Technology, Australia

South Australian Research And development Institute, Australia

The University of Adelaide, Australia

The University of Melbourne, Australia

The University of Western Australia, Australia

The University of Sydney, Australia

EUROPE

Universität Wien, Austria

Institute of Experimental Botany AS CR, Czech Republic

Centre de coopération internationale en recherche agronomique pour le développement, France

Institut de recherche pour le développement, France

Université de Montpellier, France

GenXPro GmbH, Germany

Goethe Universität, Germany

Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Germany

Forschungszentrum Jülich, Germany

Julius Kühn-Institut, Germany

Universität Hohenheim, Germany

National University of Ireland Galway, Ireland

Università di Bologna, Italy

Universidad de Córdoba, Spain

Syngenta Foundation for Sustainable Agriculture, Switzerland

Aberystwyth University, UK

Agricultural Development and Advisory Service, UK

Biotechnology and Biological Sciences Research Council, UK

Durham University, UK

Earlham Institute (TGAC), UK

Institute of Grassland and Environmental Research, UK

John Innes Centre, UK

Newton-Bhabha Fund, UK

Rothamsted Research, Harpenden, UK

The James Hutton Institute, UK

The National Institute of Agricultural Botany, UK

The Sainsbury Laboratory - Norwich, UK

The Sainsbury Laboratory Cambridge University , UK

Unilever, UK

University of Cambridge, UK

University of Sheffield, UK

NORTH AMERICA

NRC Industrial Research Assistance Program, Canada

University of Saskatchewan, Canada

Centro Internacional de Mejoramiento de Maíz y Trigo, Mexico

Generation Challenge Programme, Mexico

Baylor College of Medicine, USA

Bill & Melinda Gates Foundation, USA

Boyce Thompson Institute, USA

Cornell University, USA

Florida International University, USA

Illumina, USA

Iowa State University, USA

MARS Chocolate Inc, USA

Monsanto, USA

National Center for Genome Resources, USA

National Science Foundation, USA

NRGene, USA

New Mexico State University, USA

Purdue University, USA

The Peanut Foundation, USA

The University of Arizona, USA

The University of Oklahoma, USA

Tuskegee University, USA

UC Davis, USA

UC Riverside, USA

United States Agency for International Development, USA

United States Department of Agriculture, USA

University of Florida, USA

University of Georgia, USA

University of Minnesota, USA

University of Missouri, USA

University of Pennsylvania, USA

Virginia Tech College of Agriculture and Life Sciences, USA

South America

Empresa Brasileira de Pesquisa Agropecuária, Brazil

International Center for Tropical Agriculture, Colombia

Universidade de Brasília, Brazil

Awards and Honours

KEY AWARDS/HONOURS RECEIVED BY CEG TEAM MEMBERS

	Awards	Awarding Agency	Year	Recipient
1	IPGI Leadership Award	The International Peanut Genome Initiative	2017	Rajeev K Varshney
2	Elected Fellow	Telangana Academy of Sciences	2017	Mahendar Thudi
3	Associateship	National Academy of Agricultural Sciences (NAAS)	2017	Manish K Pandey
4	NAAS Young Scientist Award	National Academy of Agricultural Sciences (NAAS)	2017	Rachit K Saxena
5	INSA Medal for Young Scientist	Indian National Science Academy (INSA)	2017	Vikas Singh
6	Highly Cited and Most Influential Researcher	Thomson Reuters	2017	Rajeev K Varshney
7	Member	National Academy of Sciences (NASI), India	2017	Manish K Pandey
8	Jawaharlal Nehru Award for PG Outstanding Doctoral Thesis Research	Indian Council of Agricultural Research (ICAR)	2017	Sailaja Boghireddy
9	WOS-A Award	Department of Science and Technology, Ministry of Science and Technology, India	2017	Lekha Pazhamala
10	Bioclues Innovation Research Development (BIRD)	BIOinformatics CLUb for Experimenting Scientists	2017	Vanika Garg
11	Elected Fellow	German National Academy of Sciences Leopoldina	2016	Rajeev K Varshney
12	Elected Fellow	The World Academy of Sciences (TWAS)	2016	Rajeev K Varshney
13	Elected Fellow	American Association for the Advancement of Sciences	2016	Rajeev K Varshney
14	Highly Cited and Most Influential Researcher	Thomson Reuters	2016	Rajeev K Varshney
15	Qilu Friendship Award	The People's Republic of China (Shandong Province)	2016	Rajeev K Varshney
16	Doreen Margaret Mashler Award	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	2016	Rajeev K Varshney
17	Elected Fellow	Indian Society of Genetics and Plant Breeding	2016	Rajeev K Varshney

18	Bio-CARe Award	Department of Biotechnology, Ministry of Science and Technology, India	2016	Pallavi Sinha
19	Bio-CARe Award	Department of Biotechnology, Ministry of Science and Technology, India	2016	Spurthi Nayak
20	WOS-A Award	Department of Science and Technology, Ministry of Science and Technology, India	2016	Paramita Palit
21	Shanti Swarup Bhatnagar Prize	Council of Scientific & Industrial Research (CSIR)	2015	Rajeev K Varshney
22	Elected Fellow	Crop Science Society of America (CSSA)	2015	Rajeev K Varshney
23	Elected Fellow	The National Academy of Sciences, India (NASI)	2015	Rajeev K Varshney
24	Highly Cited and Most Influential Researcher	Thomson Reuters	2015	Rajeev K Varshney
25	INSA – Young Scientist Medal	Indian National Science Academy (INSA)	2015	Himabindu Kudapa
26	NASI – Young Scientist Platinum Jubilee Award	The National Academy of Sciences, India (NASI)	2015	Himabindu Kudapa
27	Elected Fellow	Association of Biotechnology & Pharmacy (ABAP)	2015	Rajeev K Varshney
28	Senior Scientist Award	Association of Biotechnology & Pharmacy (ABAP), India	2015	Rajeev K Varshney
29	Young Scientist Award	Dr KV Rao Scientific Society	2015	Deepa Jaganathan
30	Elected Fellow	Akademi of Sciences for Andhra Pradesh and Telangana	2014	Rajeev K Varshney
31	Highly Cited and Most Influential Researcher	Thomson Reuters	2014	Rajeev K Varshney
32	Elected Fellow	Indian National Science Academy (INSA)	2013	Rajeev K Varshney
33	The Greater Good Initiative Award	Illumina Inc	2013	Rajeev K Varshney
34	Young Crop Scientist Award	Crop Science Society of America (CSSA)	2013	Rajeev K Varshney
35	Promising Young Scientist Award	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	2013	Rachit K Saxena
36	INSA – Young Scientist Medal	Indian National Science Academy (INSA)	2012	Rachit K Saxena

37	Bioclues Innovation Research Development (BIRD) – special mention	BIOinformatics CLUb for Experimenting Scientists	2011	Sarwar Azam
38	Elected Fellow	National Academy of Agricultural Sciences (NAAS)	2010	Rajeev K Varshney
39	First NASI-Scopus Young Scientist Award in Agriculture	National Academy of Sciences, India and Elsevier South Asia	2010	Rajeev K Varshney
40	Associate Fellow	National Academy of Agricultural Sciences (NAAS)	2008	Rajeev K Varshney
41	INSA – Young Scientist Medal	Indian National Science Academy (INSA)	2008	Rajeev K Varshney
42	Promising Young Scientist Platinum Jubilee Award	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	2008	Rajeev K Varshney
43	Young Scientist Platinum Jubilee Award	National Academy of Sciences (NASI), India	2007	Rajeev K Varshney
44	Promising Young Scientist Platinum Jubilee Award	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	2007	Rajeev K Varshney

Best Wishes
&
Congratulatory Messages

M.S. SWAMINATHAN RESEARCH FOUNDATION

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

Message

Agriculture sustainability is the major challenge in the present scenario due to the depletion of natural resources. Basic ecological grounds like land, water and biodiversity are in depleting stage due to rise in population pressure. Major food crops productivity reached to the inertiastate owing to the influence of diverse factors such as insufficient land, depletion of ground water level and changing climate. So as to accomplish the global food security there is a prerequisite to improve the crop productivity by adapting the climate smart agriculture and by growing alternate climate-smart crops.

Green revolution has played a vital role in bringing the self-sufficiency through the yield improvement in countries like India. Integrating ecology with technology is the better approach towards an 'evergreen revolution'. Modern breeding tools like next generation sequencing (NGS) technologies can play a decisive role in crop improvement programs. Next-generation genomics supported by technological advances in different disciplines of agriculture including agronomy will offer science-based agricultural innovations to develop nutrition-rich crops to exterminate hunger.

The ICRISAT's Center of Excellence in Genomics (CEG) is a lead genomics center not only at national level but international level which has been engaged in both upstream science of genomics as well as its integration in applied aspects of breeding. I always feel happy to hear the news of sequencing of a new crop and high impact factor journal papers from the CEG almost every year. I would like to congratulate Rajeev Varshney, the Director of CEG as well as Dr David Bergvinson, Director General, ICRISAT and the team of the dedicated scientists and staff to make spectacular progress in genome science and breeding.

I am also happy to note that ICRISAT is organizing 6th Next generation Genomics and Integrated Breeding for Crop Improvement (VI NGGIBCI) conference on Crop Genomics: Present and Future to celebrate the 10th Anniversary of CEG. Though I planned to come to participate in this conference, due to some prior engagements, I have not been able to make it. Nevertheless, I extend my congratulations to the organizers and wish the conference a great success.

M S Swaminathan

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InangLupa Movement

Vision: An inclusive, science-based, resilient and market-oriented Philippine agriculture

Greetings from the InangLupa Movement, Inc!

I feel very happy to note about the 10th Anniversary of the Center of Excellence in Genomics (CEG) that we established in 2007. Ever since its inception, the CEG has been engaged in three different areas: (a) high-quality genome science and molecular breeding, (b) strengthening the capacity of NARS partners through training scientists in adopting molecular breeding, and (c) providing high throughput, cost-effective sequencing and genotyping services. Though I have seen CEG growing from its birth up to 8 years, I have been following research from CEG through social media for last 2 years.

It is really wonderful to see CEG as a big tree from the seed which we sowed in 2007. I have always been hearing good stories about CEG's work across the globe. I must appreciate the efforts of Rajeev, the dynamic young scientist, whose leadership in science led the scientific community blessed with the genome sequences of poor man crops like pigeonpea, chickpea, groundnut and pearl millet.

On the occasion of celebrating the 10th anniversary of CEG at ICRISAT, I would like to congratulate Team CEG and Team ICRISAT!

God bless us all!

Sincerely,

WILLIAM D. DAR
President, InangLupa Movement, Inc.
Former Director General, ICRISAT (2000-2014)

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P. K. GUPTA *FNASc, FASc, FNAAS, FNA*
Hony Emeritus Professor & INSA Honorary Scientist, Department of Genetics and Plant Breeding, Ch. Charan Singh University, Meerut- 250 004, India, Resi.: F-119, Shastri Nagar, Meerut-250 004; Telefax : (0121) 2768195 (Lab.), 2762505 (Resi.);e-mail: pkgupta36@gmail.com

A Message

It is a matter of both pleasure and pride for me to write a few words about the Centre of Excellence in Genomics (CEG) at ICRISAT, which is completing its 10 glorious years under the dynamic leadership of Dr Rajeev Varshney, who incidentally received his initial formal training with me as his teacher and mentor for his PhD degree. Fortunately, I have been a regular visitor to CEG as a guest faculty in training courses, and also as a participant in several conferences that CEG organized during the last 10 years. This provided me an opportunity to follow-up and have first-hand knowledge about the progress of CEG and the research output of the team led by Rajeev Varshney. The leadership provided by Rajeev has been outstanding and phenomenal indeed in terms of the output of research conducted by his team at ICRISAT and the services provided by CEG to many other centers in India both for basic and applied research in the field of Plant Genomics and Crop Improvement. The facilities availed and the data generated through this Centre not only led to the publication of a series of research papers in journals, which happen to be the best in the world, but also led to the development of superior pre-bred material in several legume crops, which should lead in future to the development of many popular cultivars for commercial cultivation. The facilities of the Centre have also been utilized for providing training to several hundred scientists at the international level in the field of genomics and molecular breeding. All this would have never been possible without the extreme hard-work, which Rajeev has put in for this to happen. I consider it a great good fortune for the country and the CGIAR system to have recruited Rajeev Varshney to work as a scientist at ICRISAT in the year 2005, when he returned from Germany after having spent five fruitful and productive years of his post-doctoral research career there. The outstanding research output of Rajeev Varshney and his team at ICRISAT both in terms quantity and quality has been amazing and is a reason for envy not only for many of us in India, but even for some of the most outstanding scientists abroad in the area of genomics and crop improvement. This also brought Rajeev many recognitions too many to be listed. He was elected to the Fellowships of not only almost all national academies, but also those of several societies and Academies abroad, at a relatively young age. He was also selected for the prestigious Shanti Swarup Bhatnagar Award for the year 2016, which any outstanding scientist in the country would aspire for. It is a matter of pride for us at Meerut to have had Rajeev as an alumnus of our institute, to which Rajeev brought fame and glory.

In view of the above, I would like to congratulate Rajeev Varshney and the outstanding team of his colleagues and students, which made all the above possible.

Wishing Rajeev and his team all the best for the future!

Pkgupta

(P K Gupta) 3.11.2017

P. K. Gupta
Hony. Emeritus Professor & INSA Sr. Scientist
Department of Genetics & Plant Breeding
Ch. Charan Singh University
Meerut 250 004 (U.P.)

Prof.E.A.Siddiq
FNA.FNASc., FNAAS,
Senior Scientist, NASI Platinum Jubilee Fellowship
Hon. Professor (Biotechnology) Professor Jayashankar Telangana State Agricultural University
Adjunct Faculty, Centre For DNA Fingerprinting and Diagnostics
Former National Professor (ICAR) & Deputy Director General (CS) ICAR

MESSAGE

I am happy that the Center of Excellence in Genomics (CEG) at ICRISAT is celebrating its 10th Anniversary on December 7, 2017. My hearty congratulations on its reaching this milestone of enviable achievements. I compliment the excellent work done by the Center along with its partners in developing high quality genomic resources and rationally utilizing them for directed improvement of millets and pulses. I am confident that the knowledge generated from their efforts would greatly help in accelerating continued improvement of these otherwise highly nutritious crops to the advantage of people in the semi arid world in general and rain-deficit India in particular, CEG scientists under the dynamic leadership of Dr. Rajeev Varshney in particular deserve huge round of congratulations for accomplishing what was once considered a challenge for breeders.

(E.A.SIDDIQ)

Institute of Biotechnology
Professor Jayashankar Telangana State Agricultural University
Rajendranagar, Hyderabad-500 030

Nov.16, 2017

Dear Dr. Varshney,

First of all, please allow me, and on behalf of all your colleagues and friends in BG-China, to extend my cordial congratulations on the opening of at the 10th Anniversary of the Center of Excellence in Genomics (CEG) at ICRISAT.

I am so sorry that I would miss the opportunity to join you and all other colleagues, however, I am so pleased to note about all the great achievements by CEG, and have witnessed its growing up to be a globally influential Center in genomics.

BGI-Shenzhen has been a pioneering partner with the CEG since its beginning. We are so happy that BGI-China and ICRISAT together with several other partners have been successful to sequence the genomes of several important crops and publish quite a few papers in the internationally peer-reviewed journals such as Nature. These genome sequences pave a way for deploying molecular breeding in the ICRISAT mandate crops.

While CEG is celebrating its 10th Anniversary, the BGI-Shenzhen congratulates CEG and ICRISAT on its great achievements, and will like to cherish 10 years of glorious partnership.

While talking and interacting with Rajeev, I am very optimistic that the CEG will be reaching to the new heights in coming years. Our sincere congratulations to Dr. Varshney, CEG team, ICRISAT and all the best for the future!

Sincerely,

Huanming Yang, Ph.D.
Chairman of the Board
BGI-China, Shenzhen

I have watched CEG evolve from small beginnings into one of the world's leading genomic centres, a success based on a foundation of excellent science and close partnerships with similar institutes around the world. The research has always been aimed at giving the plant breeder, the farmer and many others the tools needed to fulfil ICRISAT's unique role in helping the small farmers of the tropical drylands. There is one other critical factor that has contributed to this success and that is the ability, skills and motivation to help the small farmer shown by the leadership and members of CEG.

TEAM CEG enjoy this anniversary — you have earned it!

Nigel Poole
ICRISAT Ambassador of Goodwill
ICRISAT Board Member and Chair 2008–2014

Congratulations, Rajeev and team CEG on a remarkable 10 years of achievement. You have delivered high-quality research that is both well published and delivering to ICRISAT's mission of eradicating hunger, poverty and reducing malnutrition. The next 10 years will see even greater benefits from CEG's world-leading research on ICRISAT crops. Thanks, to all who have worked in CEG, for all the hard work over the past 10 years and I look forward to the great research to come in the future.

Peter Carberry
(Recipient of Australian Medal of Agricultural Science, the Officier de l'Ordre National du Burkina Faso, and the Advance Global Australian Food & Agriculture Award; Fellow of the Australian Academy of Technological Sciences and Engineering, and the Australian Institute of Agricultural Science and Technology)
Deputy Director General – Research, ICRISAT, India

First of all, my hearty congratulations on the completion of 10 successful years by the Center of Excellence in Genomics (CEG) at ICRISAT. These years have been very productive. It has changed the legume research scenario not only in India but also at the international level. I have great admiration for the commitment of Dr Rajeev Varshney for steering the CEG programme towards Indian and international agriculture and building the much needed capacity of our young scientists.

As chairman of the Trust for Advancement of Agricultural Sciences (TAAS), and as former Executive Secretary of the Asia Pacific Association of Agricultural Research Institutions (APAARI), I have been interacting regularly with CEG and the ICRISAT scientists. It is indeed high time now to replicate such success at other institutions so that genomics and upstream research can be integrated in various crop-improvement programmes both in India and elsewhere.

Kudos to team CEG!!!

R S Paroda
(Recipient of Norman Borlaug Award, Rafi Ahmed Kidwai Award, Padma Bhushan)
Chairman, Trust for Advancement of Agricultural Sciences
Former Director General, Indian Council of Agricultural Research
Former Member and Chair, ICRISAT Governing Board

I am very glad to learn that the Center of Excellence in Genomics (CEG) at ICRISAT is celebrating its 10th anniversary. CEG-ICRISAT has contributed profoundly in deploying next-generation genomics technologies for gene discovery and molecular breeding. I would like to convey my heartiest congratulations to CEG-ICRISAT and its director, Rajeev Varshney, for making significant progress in the area of genome biology and modern breeding. I feel confident that the CEG will continue to make outstanding contributions and help solve next-generation problems of crop improvement.

With my warm regards and best wishes,

Gurdev S Khush
(Recipient of the World Food Prize, the Japan Prize, the Wolf Prize, the Borlaug Award and Padma Shri, Member US National Academy of Sciences & Fellow of Royal Society)
Professor, University of California, USA

I congratulate Rajeev Varshney and his team from the Center of Excellence in Genomics (CEG) at ICRISAT on the occasion of their 10th anniversary. I have had an opportunity to visit CEG and was impressed with the state-of art-facility, with all its modern sequencing and genotyping machines and computational genomics facilities. I have been following the research CEG has been making and without any doubt this is just impressive. The most important thing is that they have not just decoded the genome sequence but have also used this information in breeding programmes and have also created a new generation of scientists in the area of molecular breeding. I commend the leadership and staff for all their achievements, and wish them all the best!

Ronald L Philipps
(Recipient of the Wolf Prize and CSSA Presidential Award, Member US National Academy of Sciences)
Regents Professor Emeritus, University of Minnesota, USA
Former President, Crop Science Society of America (CSSA)
Former Chief Scientist, USDA, USA

It is wonderful to see the celebration of the 10th Anniversary of the Center of Excellence in Genomics (CEG) at ICRISAT. I have witnessed the establishment and the breathtaking evolution of CEG from its inception in 2007. Having been the mentor of Rajeev for the past 17 years, I feel very pleased to see the excellent outputs from the CEG — be it genome sequencing, trait mapping, functional genomics, computational genomics or molecular breeding.

Under the leadership of Rajeev, CEG has become an international beacon for crop plant research over the past 10 years. Conferences organised by the Center regularly attract the best researchers from all over the world.

Seeing the outstanding scientific contributions and successes over the past 10 years, I am looking forward to the many more exciting results that will emerge from the CEG in the coming years! Congratulations to Rajeev and his colleagues and collaborators in CEG on the fantastic successes of the past, and many more years of great achievements!

Andreas Graner
(Recipient of the Gregor Mendel Innovation Award and Kurt von Ruemker Award, and Member, Germany National Academy of Sciences)
Managing Director, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany

It is indeed a great pleasure for me to learn about the celebration of the 10th anniversary of the Center of Excellence in Genomics (CEG) at ICRISAT. Rajeev Varshney is known to me from the time when he and colleagues established the CEG at ICRISAT. I have always admired the energy, partnership and leadership of Rajeev that has made it possible for the CEG to make huge achievements during past 10 years in the area of genomics and molecular breeding. CEG is known for their contribution in converting so-called orphan legume crops to genomic resources-rich crops. I don't think that there can be any other better way to celebrate these achievements other than organising this wonderful congress.

Congratulations CEG and ICRISAT for all your achievements, and wish you all the best for a successful conference!

Jeff Ehlers
(Recipient of the TMAC Award for Meritorious Achievement)
Programme Officer, Bill & Melinda Gates Foundation, USA

Many congratulations, Rajeev and the CEG team, for successfully completing 10 years. While collaborating with many CEG/ICRISAT scientists, I have seen tremendous progress in genomics research and molecular breeding aspects, especially in grain legumes, from the CEG during past 10 years. No doubt that this has been possible only because of the hard work and dedication of scientists and staff of CEG, and strong leadership from ICRISAT! We look forward to seeing many more exciting research outcomes from genetics, breeding and crop improvement activities of CEG in the years to come! Congratulations and all the best!

Kadambot Siddique
(Recipient of Queen's Birthday Honours Award with Member of the Order of Australia, Fellow of Australian Academy of Technological Sciences and Engineering and Australian Agricultural Institute, and UN FAO Special Ambassador for the International Year of Pulses)
Hackett Professor of Agriculture Chair and Director
The University of Western Australia, Australia

There has been a paradigm shift in crop genomics research during the past few years, driven largely by DNA sequencing and simultaneous improvements in computational methods. Here, we have an example of the Center of Excellence in Genomics (CEG) at ICRISAT. CEG, while working with their partners, have brought this paradigm shift firmly into the realm of so-called orphan crops. Many genome sequences, many traits mapped and many molecular breeding lines! It is inspiring! Many many congratulations to CEG and Rajeev Varshney for his scientific contributions.

Asis Datta
(Recipient of Padma Shree, Padma Bhushna, GD Birla Award, Shanti Swarup Bhatnagar Prize, TWAS Prize, Goyal Prize, Ranbaxy Award)
Distinguished Emeritus Scientist, National Institute of Plant Genome Research, India
Former Vice Chancellor, Jawaharlal Nehru University
Former Director, National Institute of Plant Genome Research

Congratulations on 10 years of superb science at ICRISAT's Center of Excellence in Genomics (CEG)! ICRISAT and CEG work on the some of the world's most important and understudied crops in the world. CEG has led the way in cracking open the secrets of their genomes to breeders, geneticists and the public globally. The next decade will see this knowledge applied globally!

Edward Buckler
(Recipient of NAS Prize in Food and Agriculture Sciences, CS CSSA Presidential Award, Member US National Academy of Sciences)
Research Geneticist, USDA-ARS/Cornell University, USA

Wow! It is amazing to note that the ICRISAT's Center of Excellence in Genomics (CEG) is completing its 10 years. Time really flies! I remember the days when Rajeev Varshney used to work with Generation Challenge Program (GCP) as its Sub Programme Leader for Genomics and we used to discuss advancing genomics research in CGIAR mandate crops, especially so-called orphan crops. CEG, in collaboration with GCP and other partners with the shared vision, worked together and developed large-scale genomic resources, mapped a number of traits and developed better lines through molecular breeding. CEG's efforts and progress made during the past 10 years have been commendable and probably unparalleled by any other genomics centre. I would like to congratulate Rajeev, CEG and ICRISAT for all these great achievements and wish them all the best for the years to come!

Jean-Marcel Ribaut
Director, Integrated Breeding Platform
Formerly Director, Generation Challenge Program (CGIAR)

I want to congratulate ICRISAT and all CEG staff on the CEG's 10th anniversary. As one of the founding fathers, and having committed my career to using modern molecular tools in plant genetics and breeding, it's great to see that the work we started has continued and had great impact around the world. Great credit is due to all CEG scientists, students and support staff, along with all at ICRISAT, not only in genomic research, but also in training and capacity building. Many around the world have, and hopefully many more will, benefit from the results of the group and the training they have received. I look forward to attending the CEG10 Symposium and wish continued success to the team in promoting the use of genomics in plant research and breeding.

Dave Hoisington
Programme Director, Peanut Mycotoxin & Innovation Laboratory (USAID)
Senior Research Scientist, University of Georgia, Athens
Formerly Deputy Director General – Research, Global Theme Leader – Biotechnology, ICRISAT

It is with great pleasure that I send this message on the 10th anniversary. It is wonderful to participate in the celebrations of the Center of Excellence in Genomics (CEG) at ICRISAT-Patancheru. The CEG was established by ICRISAT Management in 2007 to strengthen research in the area of genomics and related research. I have been closely associated with Dr Rajeev Varshney and other CEG scientists and staff in my various capacities, including Deputy Director General-Research, Research Programme Director- Grain Legumes, and Global Theme Leader- Crop Improvement. Looking back, I consider that ICRISAT Management made a wise decision to establish CEG as an entity to encourage and support genomics research. I am highly impressed with the scientific outputs generated in the past decade. CEG has excelled by publishing several quality papers in reputed international journals, including Nature. I am also aware of the success stories of CEG in translating genome sequence information via genomics-assisted breeding programmes at ICRISAT and in the breeding programmes of national partners. CEG has imparted training to a large number of scientists globally in genomics and genomics-assisted breeding, and is successful in developing a big network. CEG staff have also generated a huge amount of funding to support research at ICRISAT and partners. All these things have been possible only because of the hard work and dedication of Rajeev and his team. As part of the leadership team from ICRISAT, we provided our full support to CEG to excel and they did us proud. I am sure that CEG will be delivering many more outputs and outcomes in the years to come!

Congratulations CEG and all the best for your future endeavours!

CL Laxmipathi Gowda
(Recipient of Sano Tozaburo Special Prize, International Crop Science Award)
Co-Founder, GRSV Consulting Services, India
Former Deputy Director General – Research, Research Program Director, Grain Legumes, ICRISAT

Being a team member of the Center of Excellence in Genomics (CEG) during my tenure as Global Theme Leader, Biotechnology at ICRISAT, I am very pleased to be part of the celebrations of the 10th anniversary of CEG. The advances in genomics and molecular breeding made by CEG in the past 10 years are impressive and important. Knowledge generated by CEG has provided effective methods and tools to harness the genetic diversity present in germplasm collections and genebanks, for enhancing yields and disease resistance in a number of crops. In addition, a large number of scientists have been trained, providing the base for future advancement. The significant progress on all fronts made by CEG is inspiring and we wish to see such achievements continue to grow in the years to come. Congratulations, Rajeev and team CEG, and all the best!

Mike Butterfield
Manager, Genetic Technologies and Hybridisation
CTC – Centro de Tecnologies and Hybridisation, Brazil
Formerly Global Theme Leader – Biotechnology, ICRISAT

During my time at ICRISAT, as the Global Theme Leader for Biotechnology and later as the Research Programme Director for Dryland Cereals, I was actively involved with activities at the Center of Excellence in Genomics (CEG), and had close interactions with team members. The CEG has had many successes, including important contributions towards advancements in science. The development of large-scale genomic resources and their use of genomics-assisted breeding are clear examples. In addition, the CEG has been an effective platform for the development of next-generation scientists through the training of many graduate students (MS and PhD), post-doctoral associates, and visiting scientists. To many newcomers, the CEG was the first initial steps toward transitioning into scientists. I obviously remember this time fondly and I would like to take this opportunity now to extend my appreciation to Rajeev Varshney and each and every member of team CEG, and especially felicitate them on their 10th anniversary. I wish you all the best now and in the future.

Oscar Riera-Lizarazu
Global Breeding Leader for Wheat, Dow AgroSciences, USA
Former Global Theme Leader – Biotechnology, Research Program Director – Dryland Cereals, ICRISAT

MESSAGES FROM CEG-ALUMNI

Gaurav Agarwal, Postdoc Fellow, University of Georgia, USA

"ICRISAT (CEG) has been a great work place. It gave me enormous exposure and confidence by having to work with people from different stream and backgrounds. CEG has been one lively, dynamic lab. It taught me not only to learn about new areas in biology but also gave me that sense of being competitive and the ability to work in team. Overall, CEG has been great launching pad in my career and the exposure has added to my personality and scientific aptitude."

Sarwar Azam, Scientist - B, NIAB, India

"CEG: A center which makes an ordinary scientist extra ordinary by scaling his approaches, vision and knowledge. I was lucky to be part of this center."

Ramana Kumari Basava, Research Associate, ICAR – IIRR, India

"I had a very good learning experience during my stay at ICRISAT and I very much liked the work environment and helpful colleagues. Wishing CEG to celebrate many more anniversaries."

Abhishek Bohra, Scientist , ICAR – IIPR, India

"A three-year stay there allowed me to get acquainted with the latest developments in plant science, particularly "-omics" science and the efficient use of modern techniques and tools. It helped in bringing a radical change in my approach towards science. I really feel honoured to be a part of CEG fraternity. I express my gratitude towards Dr Rajeev K Varshney and colleagues/friends who played key roles in enhancing my potential and shaping my career."

Siva K Chamarthi, Molecular Breeder, IITA, Nigeria

"Congratulations to all CEG team for great success of CEG. I am the one who worked with Dr Varshney as a first postdoc. Later on, so many people were added to CEG and they all nourish CEG as of now. We were very much happy with great leadership of Dr Varshney and the way he nurtured us to face the world challenges are great. I still remember our old days when we worked day and night. That hard work made me today to stand in this competitive world. On the other hand, there are few ups and downs I faced in my career and that made me confident. I overcame those hurdles by your support and I am thankful to you. Sometimes I remember and felt that I missed your mentorship and CEG team. My heartfelt congratulations to you and CEG team to achieve more and more success in the future."

Sarvamangala Cholin, Assistant Professor, UHS - Bagalkot, India

"Great learning and work culture, excellent professional guidance and opportunity to learn under expertise wider exposure on area of research 24/7 Lab and informatics facility (Wet lab and dry Lab)."

Preethi Dauthal, Assistant Professor, Marwadi University, India

"I have learned a lot working with CEG/ICRISAT during 2009-10. I got to have a great time there and learned many new skills. Under the guidance of Dr Rajeev Varshney, I learned more than I could have ever expected. Thanks to you, best of luck in the next stage of your career. I wish research at CEG/ICRISAT continues to flourish and attain new heights under your mentorship."

Mansee Govil, Teacher, Sacred Heart Convent School, India

"I joined the team in 2010. I would like to show my profound gratitude for the experience that I have gained from CEG and especially Dr Rajeev K Varshney. His leadership and words of encouragement mean a lot to me. I'm very grateful for the opportunities he had given me. Thank you once again for all his time and effort! My best wishes to Dr Varshney and the whole CEG team..."

GD Heda, Professor of Biology, Mississippi University for Women, USA

"I was very fortunate to be able to spend my sabbatical break (August-December 2015) at CEG. Prior to this visit, the only time that I visited the ICRISAT campus was in early 80s, as a Ph.D. student (of Prof GM Reddy, Osmania University) to do some library work. I was so impressed with the campus and its facilities that I wanted to pursue my career at ICRISAT if stayed in India. But soon after completing my PhD, I left for the USA in 1983. When the opportunity arose to identify an institution for my sabbatical, I chose ICRISAT. My student days dream of working at ICRISAT was made possible by you by hosting me at the campus. I must say that my stay of five months at ICRISAT was one of the most memorable and joyful events of my life. The professional atmosphere and the quality of life remained the same in this scenic campus as I had witnessed as a student back in 1980s. My sabbatical time at ICRISAT allowed me to rejuvenate my professional links with more than a dozen institutions in India that are now allowing me to establish a "study abroad to India" programme of our university, and also allowing me to prepare my application for a US Fulbright Scholar programme."

Deepa Jaganathan, Postdoc Fellow, MSSRF, India

"Oh dear campus, missing you is a daring thing which I have to attempt now!

Mornings walks, Watching sunshine through tree branches, Listening the songs of unknown birds,

Everyday reports to Ganesha, Night walks and counting of countless stars, Endless chats during small walk up to gate, Mango rains on hot summer, Bold walks to lab at midnights, Sunday cycling, big lake walking, collecting peacock feathers, Fear of snakes still bare foot walking on lawns!

Oh dear campus, missing you is a daring thing which I have to attempt now!"

Mohammed Javed, Research Scholar, Pondicherry University, India

"Center of Excellence in Genomics conducts high-quality research in applied genomics, developing innovative concepts for the study of plant biology. Visionary leadership and strong management make it more advanced and make it easy for better understanding of the plant sciences."

Mayank Kaashyap, Researcher, RMIT University, Australia

"I find myself among those fortunate research students who got an opportunity to work in an international research environment. I got to learn the work ethic that helped me to shape my career and work at any research organisation. I wish the legacy continues and I will always be indebted to the place and to my mentor, Dr Rajeev Varshney."

Seetha Kannan, Home maker, Hyderabad, India

"The launching pad for all aspiring young scientists, technicians and students and a centre that facilitates young minds to learn cutting-edge technology and to establish contacts/networks in India and abroad."

Krishna M Katta, Senior Scientist, AgGenome Labs Pvt Ltd, India

"CEG had been a fantastic work environment, with a good team of breeders, statisticians and computational scientists. In fact, I got introduced to the area of computational molecular breeding at ICRISAT, and I thank CEG and Rajeev especially for providing me with an opportunity to work in ICRISAT."

Pawan Khera, Biotechnologist, Mahindra Agri Solutions Ltd, India

"I am proud to be part of Rajeev sir's group, CEG/ICRISAT — the skills, competitiveness, growth and exposure provided are invaluable and cannot be expressed in words. My suggestion to the present members are to work hard, be mentally strong, come out of your comfort zone and strive for excellence. Best wishes to CEG and may it reach greater heights in future."

Dong Hyun Kim, Researcher, Korean Institute – iPET, Korea

"It was great privilege to have worked at ICRISAT for three years. I learned the process from the beginning of R&D (to determine institute missions) to the appliance of R&D, and also about Indian culture. The experiences at ICRISAT helped me get my position. I hope all ICRISAT staff, especially CEG members, success in everything.

Ravi Koppolu, Postdoc Fellow, IPK, Germany

"ICRISAT, especially the Center of Excellence in Genomics (CEG), was instrumental in shaping my early-stage research career. CEG offered me a genuine international research lab atmosphere, where I had the possibility to learn and apply various genetic and genomic technologies that in turn immensely helped me to successfully conduct my PhD at IPK. I always feel privileged and proud that I had the opportunity to work under the able guidance of Dr Rajeev Varshney, and thank you sir, for positively influencing my research career."

Ashish Kumar, Scientist, JNKVV – Rewa, India

"I want to thank Dr Rajeev Varshney and the whole CEG team for giving me the opportunity to serve. I gained valuable insight into legume genomics because Dr Varshney gave me the opportunity to work on a variety of projects. Dr Varshney and his staff were extremely welcoming and helpful, and offered me terrific career advice during my stay. In addition to my enthusiasm, I was brought to the position of strong writing skills, assertiveness, and the ability to encourage others to work cooperatively with the team. I look forward to be associated with CEG once again in future. Until then, good luck!"

Naresh Kumar, Scientist, ICAR - IARI, India

"It's been overall a learning experience. I appreciate the time spent at CEG, with professional highs and lows, hours of white-coated lab work during day and nights, Monday meetings by Dr Varshney, while hundreds of memories full of mind-boggling scientific discussion with fellows and fraternity definitely improved the quality and quantum of knowledge. Great fellows and managers! I am grateful to one and all who have been part of my life at ICRISAT. I wish for the grand success of the symposium. Once again, thanks a lot."

Vinay Kumar, Assistant Director, Export Inspection Agency, India

"If we talk about crop genomics, it would be incomplete without the contribution of CEG, ICRISAT for their mandate crops. CEG team was leading in pigeonpea and chickpea genome sequencing and also actively contributed in groundnut genome sequencing. I wish both CEG and ICRISAT every success in the future."

MG Mallikarjuna, Scientist, ICAR - IARI, India

"A wonderful place where the science of genomics is at its peak under the excellent leadership."

Reyazul Rouf Mir, Assistant Professor, SKUAST – Kashmir, India

"My first appointment after PhD and working under the supervision of dynamic leader, Dr Rajeev Kumar Varshney, is something I will always remember. We are proud that we were associated with a prestigious research group led by a prestigious leader. We hope CEG will continuously make headway in conducting cutting-edge research in future, helping to feed the poor farmers/sections of society."

S Muniswamy, Scientist, ARS – Gulbarga, India

"I sincerely thank ICRISAT for providing me with the opportunity to work with international collaboration in many projects. I completed my PhD in molecular work at CEG under the supervision of Dr Rajeev K Varshney, as a visiting fellow in 2013. I am very much thankful to each and every staff member of CEG/ICRISAT, especially Dr Varshney, and his team for giving me an excellent opportunity to work with them. My best wishes to the excellent team of CEG."

Gnanesh Nanjappa, DST Ramanujan Fellow, CSRTI, India

"For me, life at CEG/ICRISAT has been breath-taking and enriching. The environment not only helped me in imbibing knowledge but also in developing my overall personality, fuelling me with confidence. My sincere thanks to Dr Rajeev Varshney and all the CEG family for their support and altruism. They have played a very crucial role in shaping me and I carry beautiful memories of this place and will always cherish them. Thank you, CEG, for making my journey so pleasant. It is indeed, a place that inspires to do noble deeds."

Jalaja Naravula, Assistant Professor, Vignan University, India

"At ICRISAT, we worked in a team of about 35 members in CEG. In future I wish the team work to be maintained at CEG. It was really a good experience with my guide. I learnt so much from him and he is the inseparable person and everyone will learn something from Dr Rajeev for their life journey."

Spurthi Nayak, Assistant Professor, UAS – Dharwad, India

"The turning point in my life was to get into ICRISAT for my PhD. As a student, I got every opportunity to excel in academics and had great support from my mentor, Dr Rajeev Varshney. Proud to be among the first set of students he supervised. Interactions with great scientists and students across the world were possible during my eight years at ICRISAT. This is the time to remember and celebrate, the occasion of the 10th anniversary of CEG and the 45th anniversary of ICRISAT. My sincere best wishes to the team at CEG and ICRISAT."

Kishan Patel, Research Scholar, ICRISAT, India

"CEG/ICRISAT is the best in the world, and I wish to continue to work with CEG."

Jaya Punna, Research Scholar, PJTSAU, India

"It was a wonderful opportunity for me in life to work with Stalwart of Genomics Dr Rajeev K Varshney and his great team."

Ramu Punna, Postdoc Fellow, Cornell University, USA

"I feel it is like my home lab and my scientific career is travelled through CEG. CEG is the best place to learn basic genomic technologies in agriculture. We are proud of CEG for releasing drought tolerant and biotic stress resistant varieties through genomic tools. Good luck CEG."

Mani Ramakrishnan, Associate Professor, Presidency University, India

"I wish ICRISAT for a great success in implementing more and more innovative ideas for the welfare of farmers and the world grain revolution. My Best Regards to Dr Rajeev Varshney and the Entire Team."

Basavarajappa H Ramappa, Assistant Professor, UHS - Bagalkot, India

"World-class environment & had wonderful working and learning experience at ICRISAT. Wonderful hands on experience center with experienced team of CEG, I learnt lot about genomics with great mentor Dr Rajeev K Varshney, we wish the center should reach greater heights and world-class nodal center for genomics."

P Janaki Ramayya, Senior Scientific Officer, IRRI, India

"Even though I worked for a short period of time, I feel very proud to work in such a world renowned plant genomics laboratory of CEG, ICRISAT. I learned many new techniques related to Molecular Breeding of crop plants at CEG, ICRISAT, Patancheru and very much thankful to Dr Rajeev K Varshney for giving me that opportunity."

Pradeep Ruperao, Researcher, NIAB, UK

"My experience at ICRISAT-CEG was not only making a research progress but also it was an opportunity to learn from experts, interacting and sharing ideas with people from various discipline. In the past 10 years, CEG has done a significant progress from developing genetic molecular markers to decoding the genetic code of orphan crops. I congratulate CEG team for making efficient progress. This symposium would be an excellent platform for plant biologists to decide how to proceed with future sequencing, proteomics, and functional genomics; and I wish this will pave the way for sustainable crop development."

Arun Sama, Senior Scientist, Tierra Seed Science Pvt Ltd, India

"As is well known to many, CEG/ICRISAT is a great Research Organization which is helping millions of farmers in India and Africa. All the best to CEG & ICRISAT"

Senthilvel Senapathy, Senior Scientist, ICAR - IIOR, India

"The most happening place and an ideal hub for learning and knowledge sharing."

Ranjan Shaw, Senior Research Fellow, ICAR - IIOR, India

"Being a part of CEG was the one of best part of my career. I got the opportunity to learn a lot of things in one of the best laboratory. I wish all success for CEG in coming days."

S Sheelamary, Scientist, ICAR - SBI, India

"It's an unforgettable place in the early professional career. Had a very good opportunity to interact with the scientists of abroad and colleagues of different states of India and countries of the world. I had a chance to interact with Dr Rajeev, who is such a wonderful dynamic personality. The way he taught the genomics is incomparable. I wish the institute should flourish more and more in the future. Thanks to DR RAJEEV."

Muneendra K Singh, Breeder, Limagrain, India

"We wish God for success of center of excellence in genomics as globally."

Manish Vishwakarma, Assistant Breeder, BISA – CIMMYT, India

"It gives me immense pleasure to express my feeling about the Institute and people where I started my professional research career. I am very fortunate that I got the opportunity to work with the eminent class of lead scientists and cream workers. In my three-year research expedition at CEG, ICRISAT, I learned a lot that would never ever last in my research career. I wish the glory and leadership of CEG, ICRISAT never end."

M Yamanura, Technical Assistant, UAS - Dharwad, India

"I started my career as Research associate with ICRISAT collaborated project entitled "Taking Pigeonpea hybrids to the door steps of the farmers" from 10.10.2008 to 06.08. 2011 and as Senior Research Fellow under USAID funded project "Pigeonpea Improvement Using Molecular Breeding" from 1.6.2013 to 17.08.2015. I completed my PhD molecular work at CEG under the supervision of Dr Rajeev K Varshney as visiting fellow from 10 to 30 October, 2013. I am very thankful to each and every staff member of CEG/ICRISAT for giving me a wonderful opportunity to work with them since from starting to till date."

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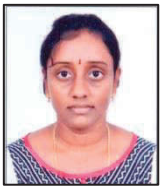

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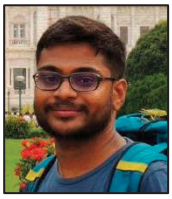

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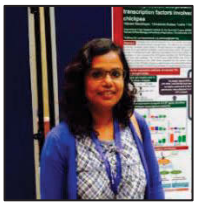

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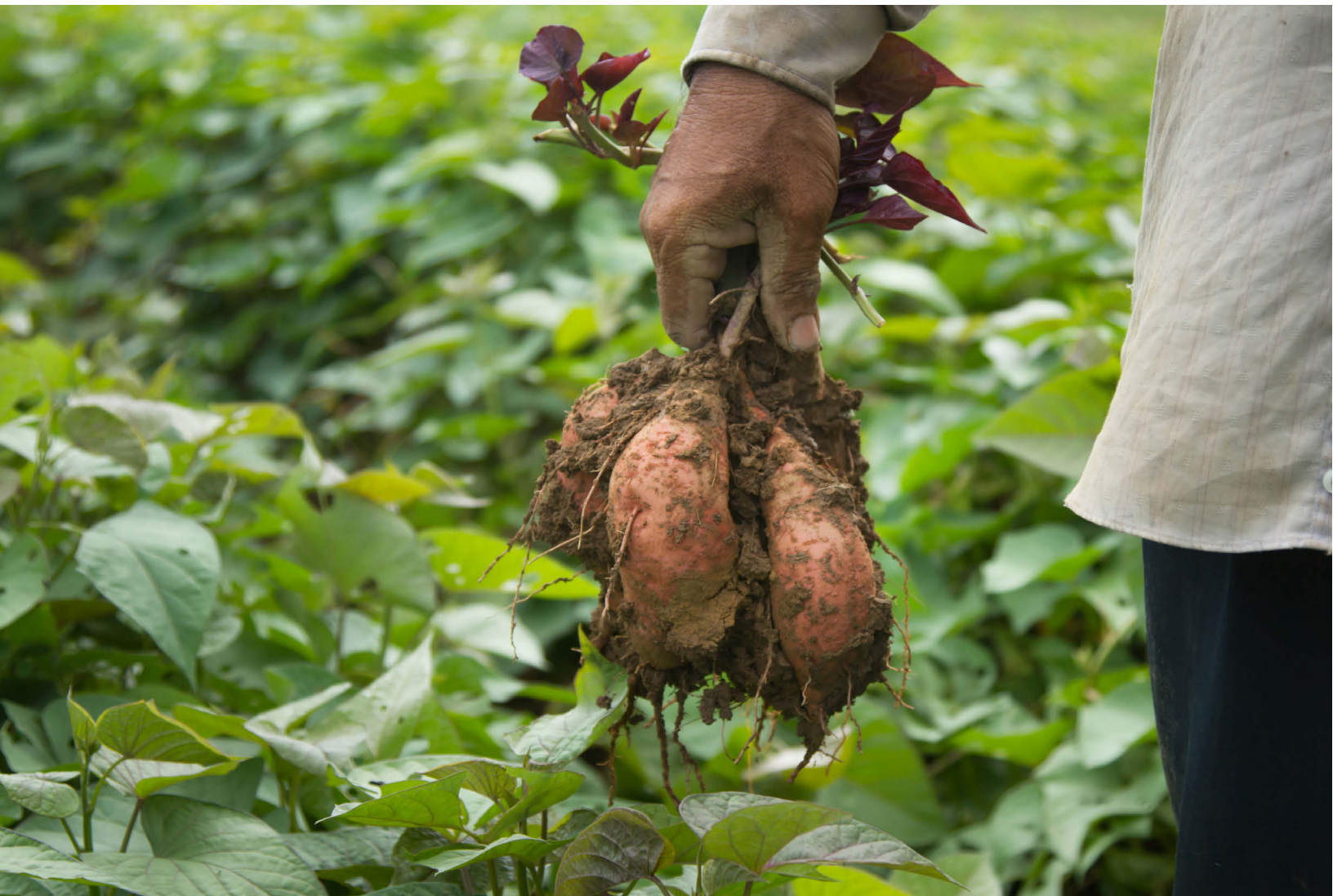

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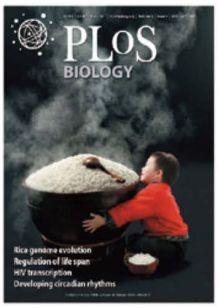
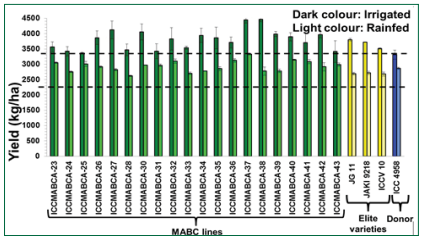


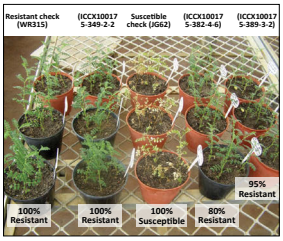
Research Impacts in Field

1. Improved lines with enhanced yield in chickpea

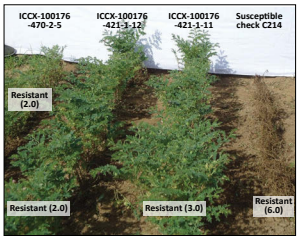


12% higher yield under rainfed and 24% higher yield under irrigated condition

2. Improved lines with disease resistance in chickpea

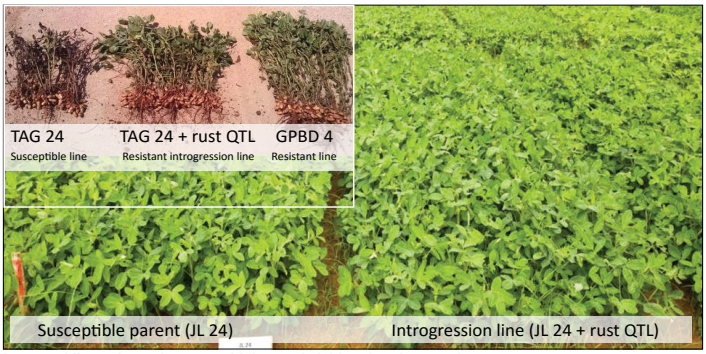


Ascochyta blight resistant line



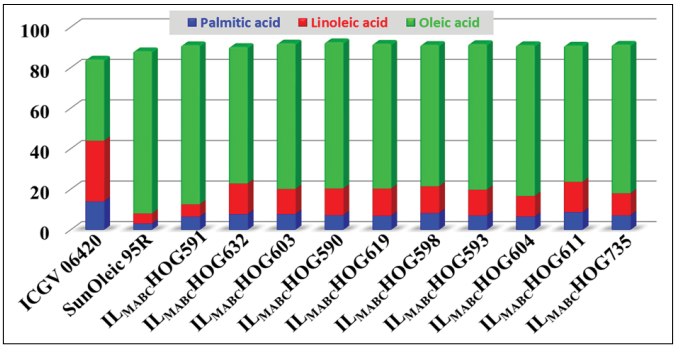
Fusarium wilt resistant line

3. Improved lines for foliar disease (rust and late leaf spot) resistance in groundnut



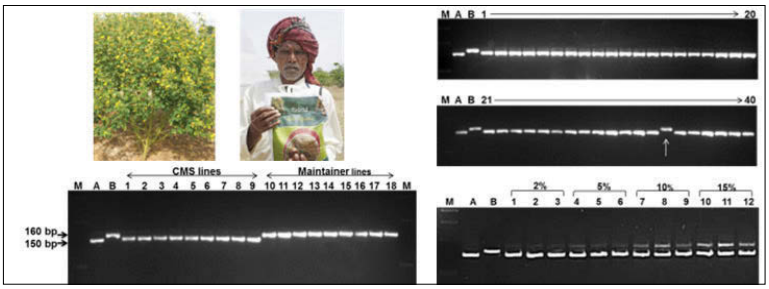
Improved lines showed 56-96% higher pod yield and early maturity

4. Improved lines for high oleic acid in groundnut

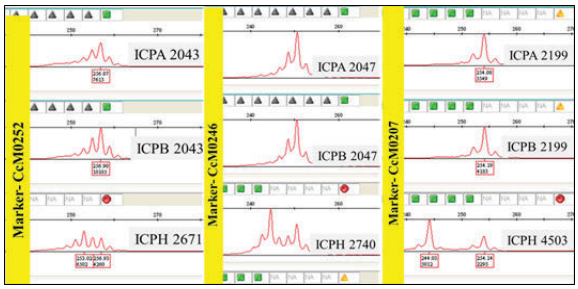


Improved lines upto 80% oleic acid

5. Efficient hybrid breeding in pigeonpea



Marker-assisted male sterile lines testing



Markers for hybrid purity testing

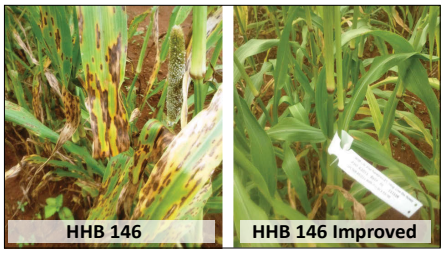
6. Improved lines for downy mildew resistance (DMR) in pearl millet

IHHB 67 Improved-Second cycle

7. Improved lines for high grain Fe & Zn density and DMR in pearl millet

Double QTL intogression line

8. Improved lines for blast resistance in pearl millet



863B- LG4 blast resistant introgression line

9. Improved lines for striga resistance in sorghum

10. Improved lines for drought tolerance in sorghum

11. Improved lines for Shoot fly resistance in sorghum

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