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.

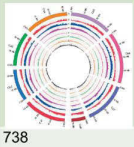
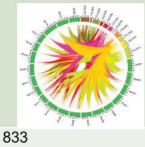
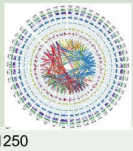
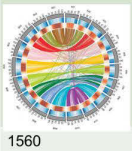
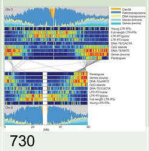
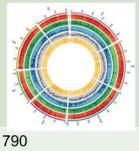
Features	Chickpea	Pigeonpea	Groundnut	Groundnut	Groundnut	Sorghum	Pearl Millet
Scientific name	***Cicer arietinum***	***Cajanus cajan***	***Arachis duranensis***	***Arachis duranensis***	***Arachis ipaensis***	***Sorghum bicolor***	***Pennisetum glaucum***
Chromosome no.	2n=2x=16	2n = 2x = 22	2n = 2x = 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

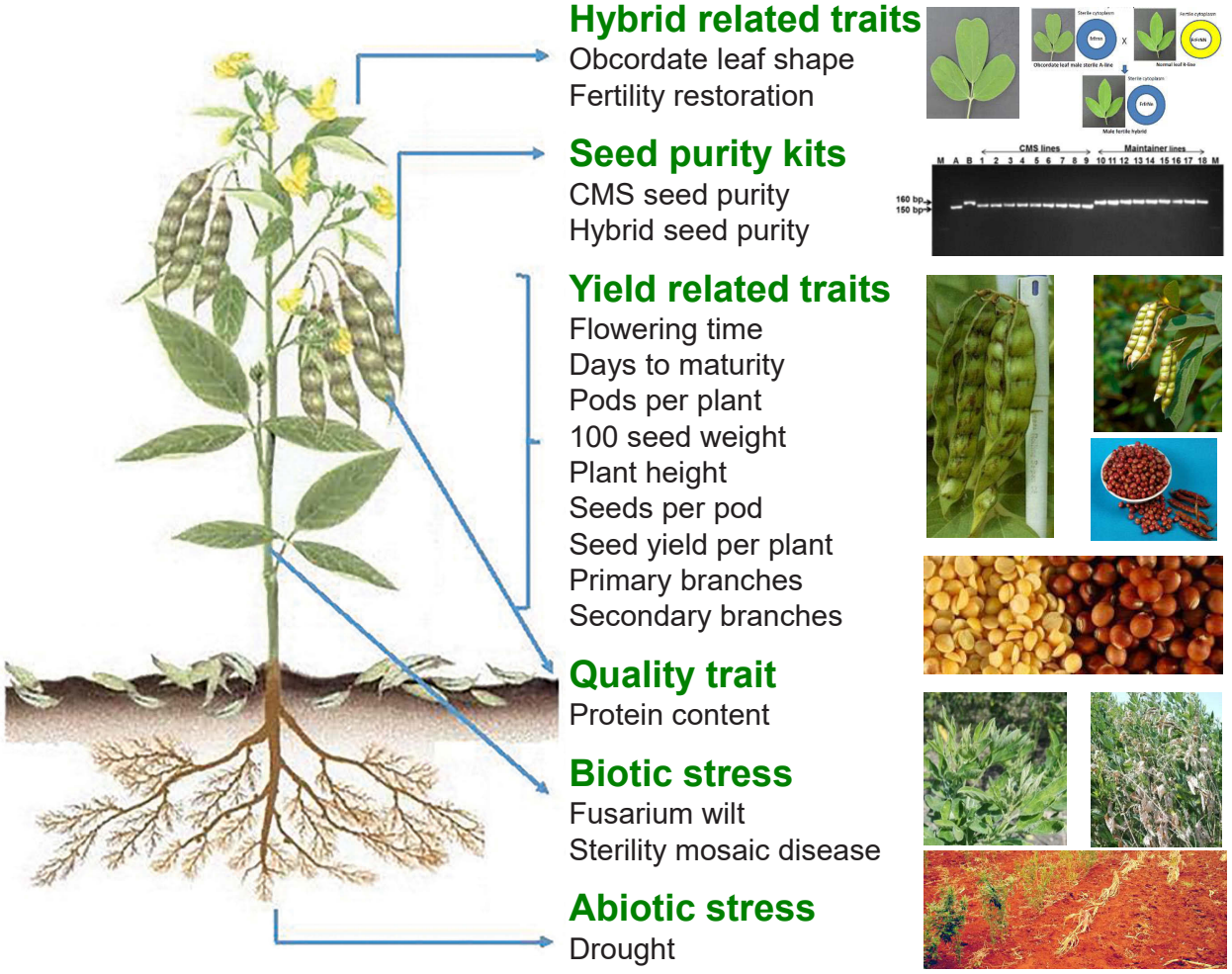


Figure 3: Molecular mapping of ca. 20 traits in pigeonpea

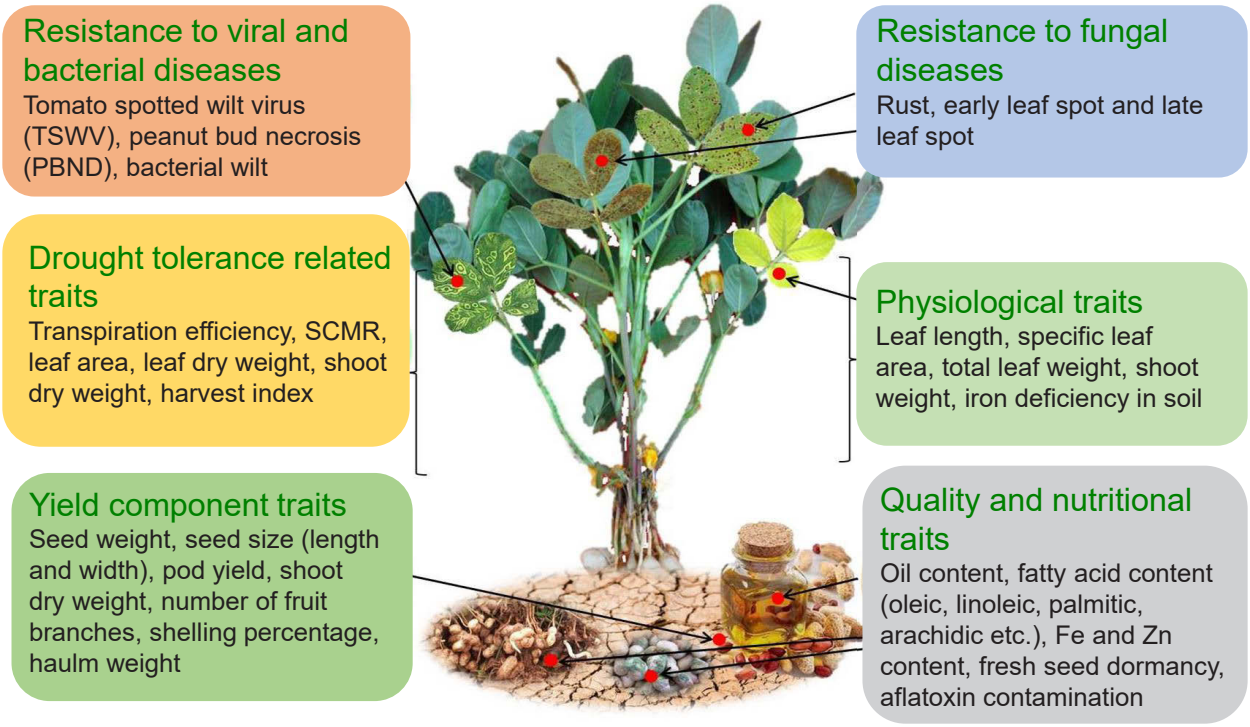


Figure 4: Molecular mapping of ca. 40 traits in groundnut

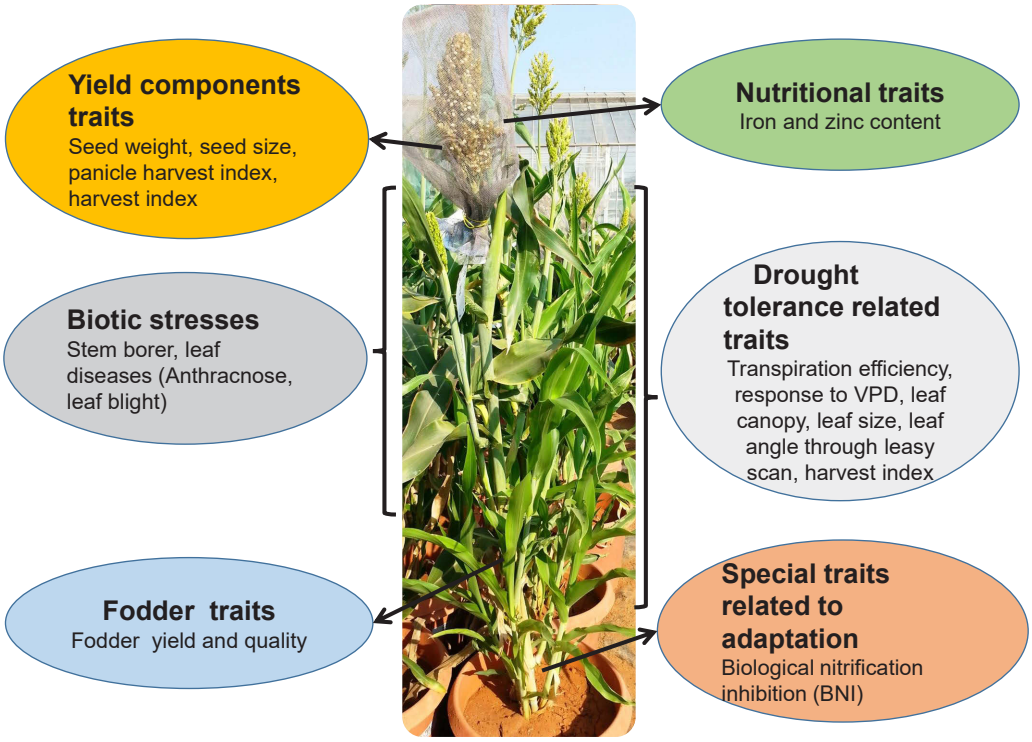


Figure 5: Molecular mapping of ca. 20 traits in sorghum

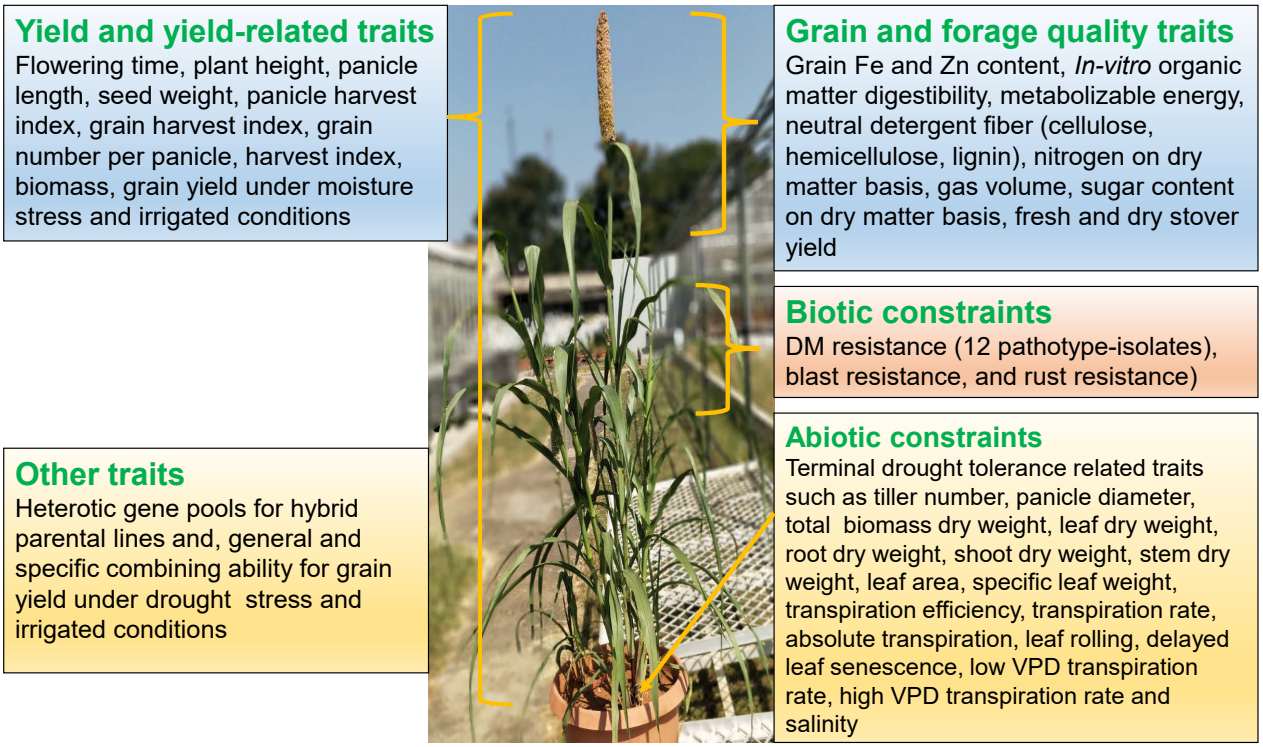


Figure 6: Molecular mapping of ca. 40 traits in pearl millet

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

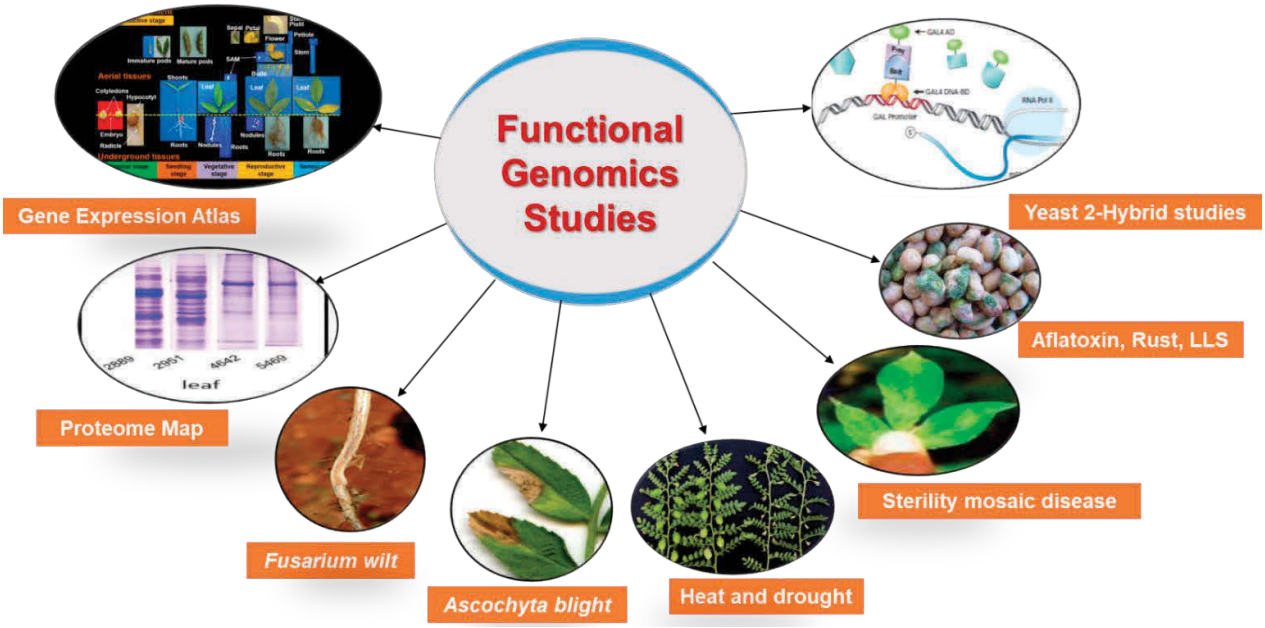


Figure 7: Functional genomics approaches being used at CEG for better understanding of traits and trait mechanisms

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

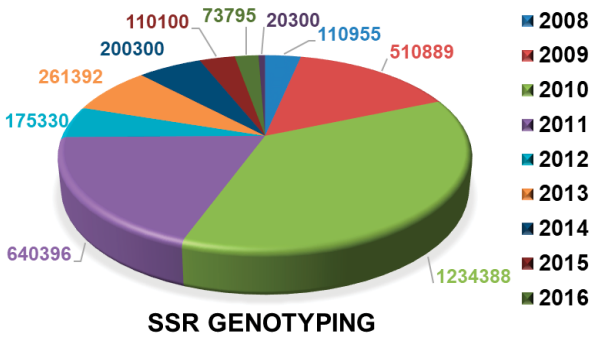


Figure 8: More than 3.5 million datapoints generated by CEG in the past eight years

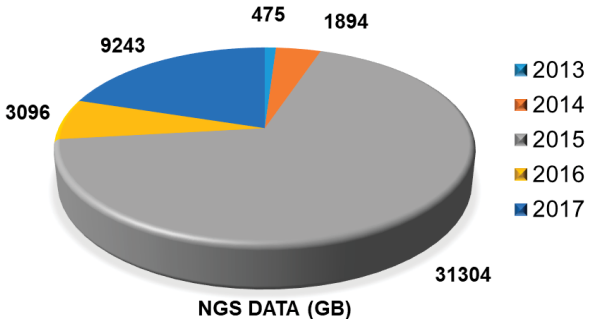


Figure 9: More than 45.9 Tbp sequencing data generated by CEG in the past five years

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

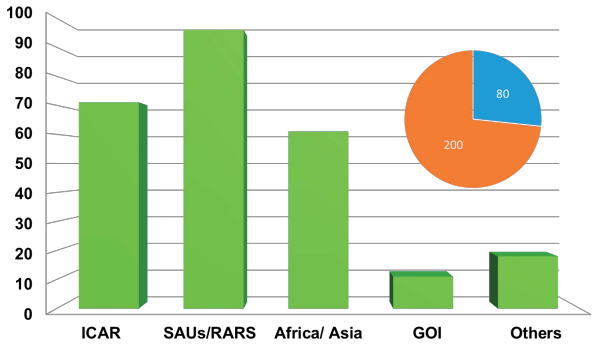


Figure 10: Distribution of scientists from different types of organisations. Indian scientists have been classified under ICAR, SAUs/RARS, GoI and others, while scientists from non-Indian organisations have been grouped under Africa/Asia categories.

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.

Acknowledgements

Team CEG is grateful to all their colleagues and collaborators at ICRISAT and all collaborating institutes from around the world for their collaboration in generating high-quality science and development of improved lines. Team CEG is grateful to Dr Nigel Kirby (Chair) and all members of the Governing Board, Dr David Bergvinson (Director General), Dr Peter Carberry (Deputy Director General) and the Management and Research Committee for all their support.

Thanks are also due to all previous Governing Board members (Dr Simon Best, Dr Nigel Poole, Dr Chandra Madramootoo, Dr Mangla Rai, Dr S Ayappan, Dr Jeff Bennetzen, Dr Debby Delmer, Shri Ashish Bahuguna among others) and the senior Management of ICRISAT (Dr William Dar, Dr Dyno Keatinge, Dr David Hoisington, Dr CLL Gowda, Dr Mike Butterfield, Dr Oscar Rierra-Lizarazu and Dr Stefania Grando) for all their support and collaboration.

Finally, Team CEG is grateful to all donors (that are included as partners/collaborators) for their generous financial support and strategic guidance, without which CEG's 10-year journey would not have been a memorable one.

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