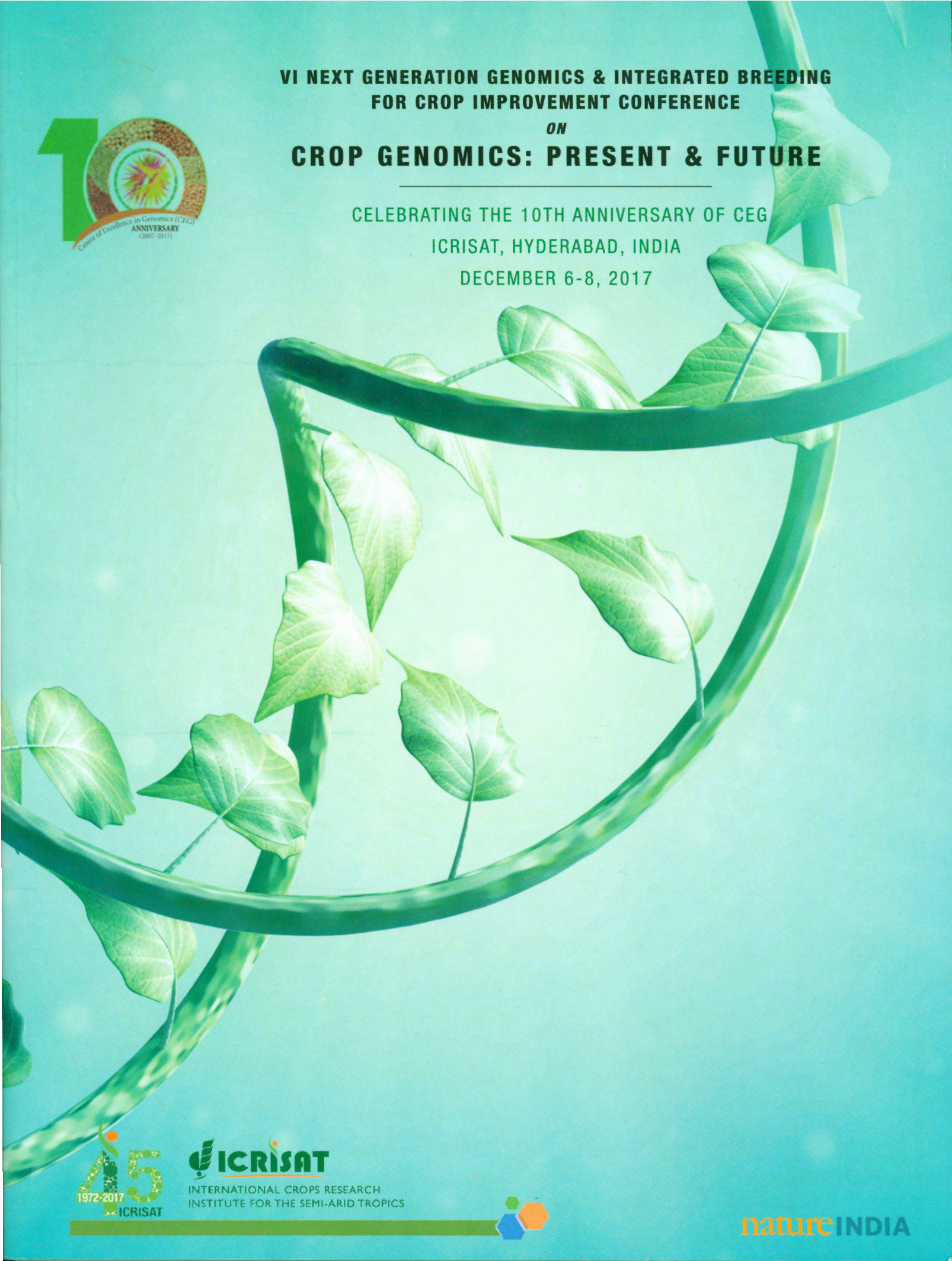

VI NEXT GENERATION GENOMICS & INTEGRATED BREEDING FOR CROP IMPROVEMENT CONFERENCE

ON

CROP GENOMICS: PRESENT & FUTURE

CELEBRATING THE 10TH ANNIVERSARY OF CEG

ICRISAT, HYDERABAD, INDIA

DECEMBER 6-8, 2017

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

45 1972-2017 ICRISAT

ICRISAT
INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS

nature INDIA

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

SS Karande*, BL Thaware and SG Bhave

DBSKKV, Dapoli – 415 712, Maharashtra, India
*E-mail: satishkarande_78@rediffmail.com

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*

Aamir W Khan[1,2], Manish Roorkiwal[1], Mahendar Thudi[1], Anu Chitikineni[1], Hari D Upadhyaya[1], Henry T Nguyen[3], David Edwards[2], Rajeev K Varshney[1,2,*]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, India
[2]The University of Western Australia, Crawley, Australia
[3]University of Missouri, Columbia, USA
*E-mail: r.k.varshney@cgiar.org

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.