



**VI NEXT GENERATION GENOMICS & INTEGRATED BREEDING
FOR CROP IMPROVEMENT CONFERENCE**

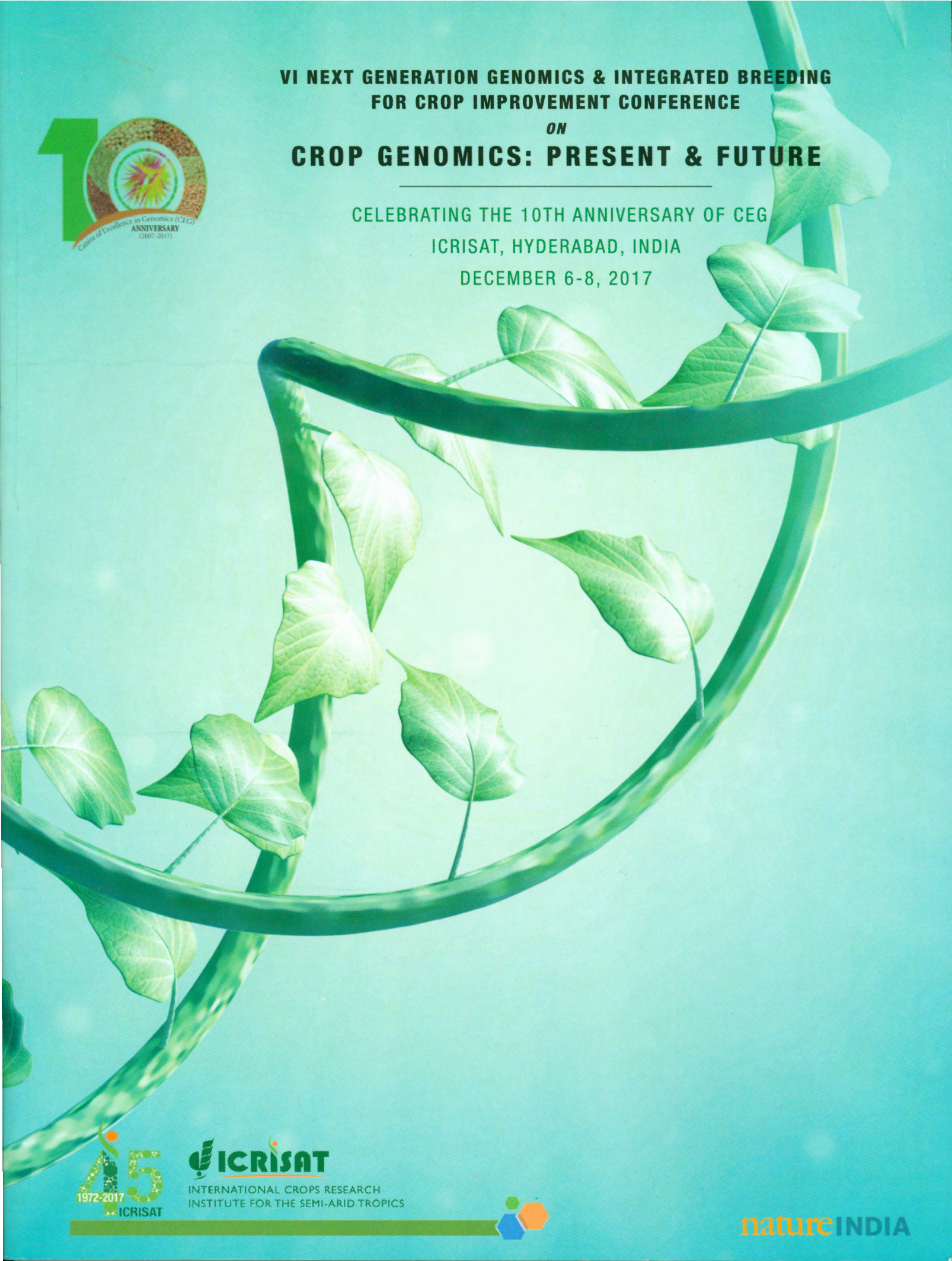
ON

CROP GENOMICS: PRESENT & FUTURE

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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 map-

ping 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.

