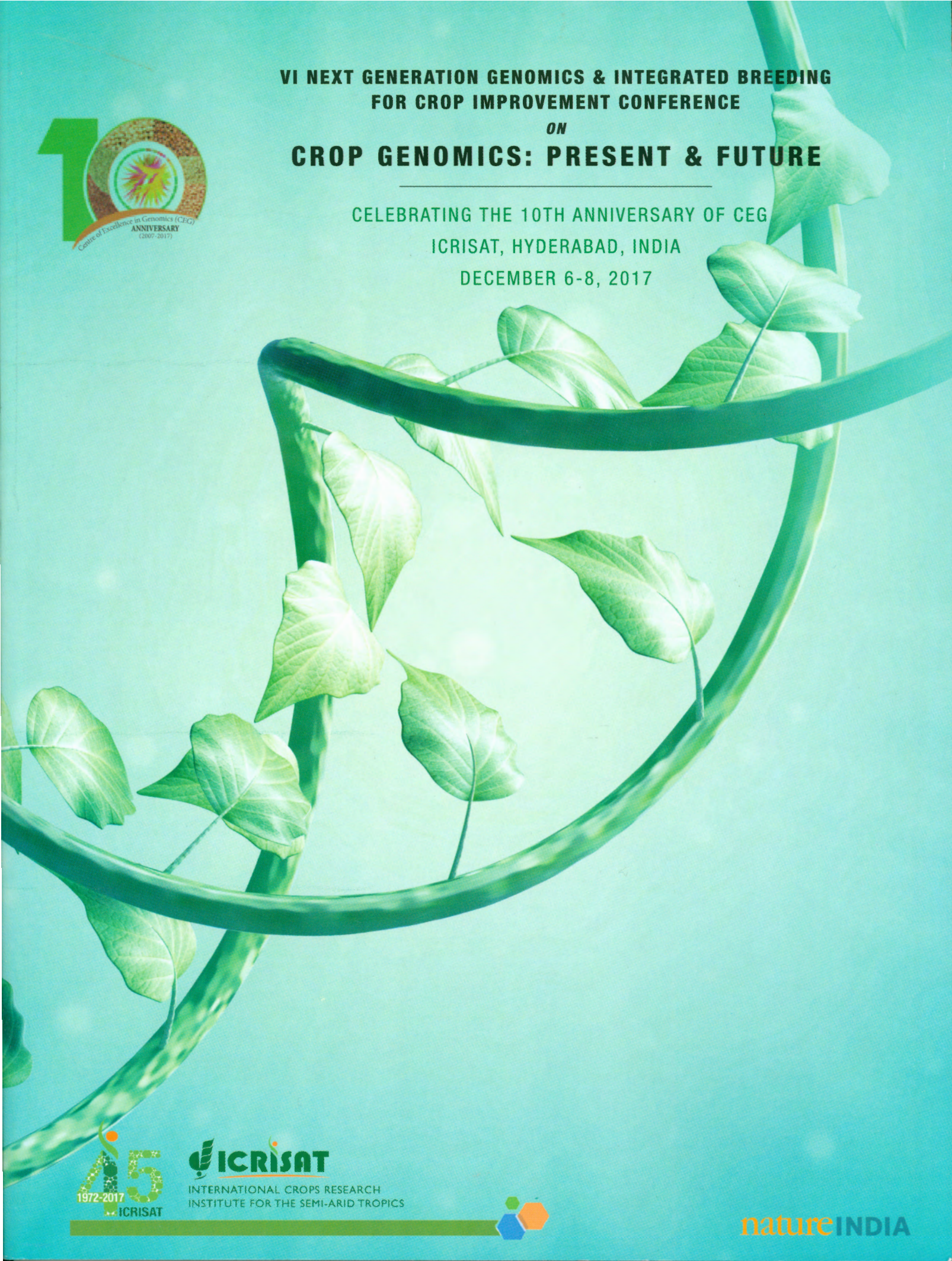

VI NEXT GENERATION GENOMICS & INTEGRATED BREEDING FOR CROP IMPROVEMENT CONFERENCE

ON

CROP GENOMICS: PRESENT & FUTURE

CELEBRATING THE 10TH ANNIVERSARY OF CEG

ICRISAT, HYDERABAD, INDIA

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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.