

VI NEXT GENERATION GENOMICS & INTEGRATED BREEDING FOR CROP IMPROVEMENT CONFERENCE

## CROP GENOMICS: PRESENT & FUTURE

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## 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 sig-

nificant 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.

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