

## P0562

**Title:** Fine genetic mapping of combined shoot fly resistance (SFR) and stay green (STG) traits on sorghum chromosome SBI-10.

K N S Usha kiranmayee<sup>1,2</sup>, H C Sharma<sup>1</sup>, P B KaviKishore<sup>2</sup>, P Ramu<sup>4</sup>, S Sivasubramani<sup>1</sup>, R S Munghate<sup>1</sup>, S Sakhale<sup>1</sup>, C T Hash<sup>3</sup>, Santosh P Deshpande<sup>1\*</sup>

Corresponding author: [s.deshpande@cgiar.org](mailto:s.deshpande@cgiar.org)\*

<sup>1</sup> International Crop Research Institute for the Semi-Arid Tropics, Patancheru PO, Hyderabad, India

<sup>2</sup> Department of Genetics, Osmania University, Hyderabad, India

<sup>3</sup> International Crop Research Institute for the Semi-Arid Tropics, Niamey, Niger

<sup>4</sup> Cornell university, Ithaca, New York, United States

Sorghum is fifth most important C<sub>4</sub> cereal crop used as food, feed, fodder, fuel and a “fail safe” source in semi-arid tropics of the world. Susceptibility to shoot fly and terminal drought stress are major constraints of sorghum production in this region. At ICRISAT-HQ, Patancheru, QTLs imparting shoot fly resistance (SFR) from donor IS18551 and drought tolerance from E36-1 have already been introgressed and validated in different genetic backgrounds. QTLs for glossiness and trichome density on sorghum chromosome SBI-10 associated with SFR QTL in the genetic background of BTx623 overlaps with stay-green QTL from E36-1 in genetic background of R16. A Total of 1931 F<sub>2</sub> population derived from cross involving introgression line with SFR QTL (J2614) and stay green QTL (RSG04008) were genotyped by eight polymorphic SSRs at target region and 182 double recombinants were selected. Recombinants with homozygous favorable alleles in all possible combinations were selected and skim-sequenced using Genotyping-by-sequencing (GBS) method to get scorable polymorphic SNPs across target region. Selected 182 double recombinants were evaluated for trichome density, glossiness and terminal drought tolerance for two seasons. On the basis of genotyping and phenotyping data, we will select 5-10 recombinants having all favorable alleles at all three QTLs to produce required segregating population. Individuals of the population will then be genotyped to identify the desired triple-homozygotes, which will be selfed to generate multiple resistant variety which can be used by farmers directly and for breeders as a donor for “3-gene-cassette”.