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## Abstract Book



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## T6PP061:

### Fine mapping of Stg3B genomic region in Sorghum

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Sorghum (*Sorghum bicolor* L.) is the fifth most important cereal crop, cultivated in arid and semi-arid regions of the world. Staygreen trait in sorghum is a post-flowering drought stress tolerant phenomenon. There are six stg QTL's (stg1, stg2, stg3A, stg3B, stgC and stg4) that have been identified so far. Stg3B is mapped on chromosome 2 and is one of the most important QTLs for Staygreen trait. Large QTL interval in Stg3B and lack of polymorphic markers have impacted the recurrent parent recovery under Marker-assisted Backcrossing (MABC) programs. The current study was set up with the objective of fine mapping the Stg3B QTL region. Crosses were made between sorghum genotypes K359W (Staygreen) and R16 (non-Staygreen). True F1 hybrids were identified using SSR marker, Xtxp-211. The confirmed F1's were selfed to obtain segregating F2 population. Around 1200 F2 plants were phenotyped for plant height, days to flowering, SPAD at flowering, SPAD at maturity, days to maturity and seed yield. At seedling stage, the leaves were collected for genotyping purpose. The F<sub>2</sub>'s were advanced to F<sub>3</sub> generation by selfing as per single seed descent method. The F<sub>3</sub>'s of around 200 individuals along with parents and few standard checks were sown in the field as per alpha lattice design in two replications and screened under well-watered and water stress conditions. Further marker development was done by designing KASP markers for SNPs identified in the Stg3B region. Preliminary results indicate more recombinants in the region with the potential that additional SNP markers can be identified for future MABC.

## T6PP062:

### Phenotyping of chickpea germplasm resources to unleash the disease resistance potentials

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Chickpea (*Cicer arietinum* L.) is a major food pulse crop which serves as an important source of dietary proteins especially for Indian population. Apart from this, chickpea also carries out biological nitrogen fixation, reducing dependence on nitrogen fertilizers. However, increased frequency of climate extremes interrupts the chickpea cultivation, this often leads to moisture stress towards the end of the cropping season and more prone to biotic and abiotic stress. Therefore, a total of 3567 chickpea accession (~ 2800 composite core collection and remaining core collection developed from phenotyping and genotyping characterization) have been screened for chickpea Fusarium wilt (FW), Dry root rot (DRR), Ascochyta blight (AB) and Botrytis gray mould (BGM) disease under field and controlled environmental conditions. During 2021-22 cropping season 900 accessions were evaluated at ICRISAT FW sick field, found 11 resistant accessions (< 10 rating) and these resistant lines were subjected reconfirmation in the current cropping season with another 900 lines. In addition to this, 700 accessions evaluated for DRR under controlled condition by using paper towel technique, found 40 accession as resistant with rating of ≤3 rating on 1-9 scale. Further, 3500 and 1700 accessions were screened for BGM and AM diseases under controlled environment condition. At total, 32 and 35 accession lines were found to be moderately resistant with ≤5 and ≤4 rating on 1-9 scale. The levels of resistance in these lines will be confirmed again to identify stable multiple disease accession which can be used for chickpea resistant breeding.