

# International Conference on Innovations to Transform Drylands

21–23 February 2023  
ICRISAT, Hyderabad, India

## Abstract Book



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## T6PP099:

### Molecular diversity in *A. glabrata* and prebreeding for introgressing novel resistance for stem rot and late leaf spot in cultivated groundnut

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The perennial *Arachis glabrata* belongs to Rhizomatosea section with tetraploid (R2; 2n=40) genomes and is mostly known for forage, ornamental or soil conservation crop. The genotyping of 77 accessions of *A. glabrata* using Thermofisher's Agriseq assay containing 5000 genome-wide SNPs showed significant diversity. In parallel, significant phenotyping diversity was observed upon phenotyping these accessions for two most important diseases of the groundnut namely stem rot and late leaf spot. Among LLS and stem rot resistant sources, several accessions showed immune reaction but most of them possessed thick and rubber like leaf structure and thicker stem structure which might have served as physical barrier for these pathogens. Promising resistance sources were identified for LLS resistance (ICG 8161, ICG 8165, ICG 8166, ICG 8185, and ICG 8965) and stem rot resistance (ICG 8185, ICG 8167, ICG 8175 and ICG 8924) for potential use in pre-breeding. Interestingly, accession ICG 8168 has demonstrated resistance for both the diseases along with leaf structure similar to cultivated groundnut, therefore, we have initiated pre-breeding research for the introgression of resistance segments into elite background of high oleic genotype ICGV181008. Further research is required to understand the genetics and molecular mechanism of these resistance sources in addition to intensifying efforts in introgressing these segments in the genetic background of elite varieties.

## T6PP100:

### Genetic variation in *CaTIFY4b* improves adaptation to terminal drought conditions in chickpea

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Chickpea (*Cicer arietinum*) is a major cool-season legume crop typically cultivated on residual soil moisture during the post-rainy season, and it is often exposed to a late-season water deficit towards the end of the crop cycle. Identifying the genetic components underlying adaptation to terminal drought stress is important for improving chickpea productivity. Here, we present the fine mapping and functional characterization of "QTL-hotspot", a genomic region on linkage group 04 (CaLG04) in chickpea that harbours major-effect quantitative trait loci (QTLs) for key drought-adaptive traits. We report that a non-synonymous mutation in the plant-specific transcription factor *CaTIFY4b* regulates seed weight and organ size, and contributes to drought adaptation in chickpea. Ectopic expression of *CaTIFY4b* in the model legume *Medicago truncatula* increased root growth and architecture under water deficit. Gene expression analysis indicated that *CaTIFY4b* might control organ size under drought in chickpea by regulating the expression of GRF-INTERACTING FACTOR1 (GIF1), a transcriptional co-activator of Growth-Regulating Factors. Phenotypic characterization of chickpea homozygous lines linked *CaTIFY4b* to the regulation of key physiological parameters, including pre-anthesis water use, transpiration efficiency, root architecture, and canopy development, enabling high yield performance under rainfed field conditions. Taken together, our study offers new insights into the role of *CaTIFY4b* and diverse molecular and physiological mechanisms underpinning chickpea growth and production under terminal drought scenarios.