

IDT9-041 | Fine mapping studies identified a 113 kb region within “QTL-hotspot_a” for seed weight and drought related traits in chickpea

Kale SM¹, Jaganathan D^{1,2}, Roorkiwal M¹, Thudi M¹, Purushothaman R¹, Praveenkumar M^{1,2}, Krishnamurthy L¹, P B Kavi Kishor², Gaur P¹, Varshney RK^{1,3,*}

¹International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, 502324, Telangana, India.

²Osmania University, Hyderabad, 500007, Telangana, India.

³The University of Western Australia, Crawley, 6009, Australia.

*E-mail: r.k.varshney@cgiar.org

A “QTL-hotspot” region of 7 Mb size for drought component traits was identified on CaLG04, using a recombinant inbred line (RIL) population (ICC 4958 × ICC 1882) in chickpea. Further, skim-based genotyping by sequencing (GBS) approach with large SNP markers delimited the “QTL-hotspot” region into two sub-regions; viz, “QTL-hotspot_a” of 139.22 kb and “QTL-hotspot_b” of 153.36 kb, on the *kabuli* draft genome sequence. In order to validate and identify more recombinations in the sub-regions for further refinement, a fine mapping population with 1,911 lines was developed. Flanking markers of the two “QTL-hotspot” sub-regions were converted to KASPar assays and used to screen the fine mapping population consisting of 1,911 lines. As a result, 19 F_{2,3}

recombinant families were identified. These families were phenotyped for seed weight and other drought-related traits. Comparison of genotype and phenotype data identified a genomic region of ~113 Kb size within “QTL-hotspot_a” responsible for 100 seed weight (100SDW) and other drought-related traits in chickpea. Subsequently, a syntenic study between the refined “QTL-hotspot” region and desi genome identified a 2 Mb region on Ca_LG_4 pseudomolecule. Whole genome re-sequencing (WGRS) analysis of selected lines from each recombinant family identified several non-synonymous and InDel mutations within important candidate genes. Functional validation of these genes will help decipher the mechanism of drought stress tolerance in chickpea.

IDT9-042 | High throughput phenotyping and advanced genotyping reveals QTLs for plant vigor and water saving traits in a “QTL-hotspot”: New opportunities for enhancing drought tolerance in chickpea

Sivasakthi K^{1,2}, Thudi M¹, Tharanya M^{1,2}, Kale SM¹, Kholová J¹, Halime MH¹, Jaganathan D¹, Baddam R¹, Thirunalasundari T², Gaur PM¹, Varshney RK¹, Vadez V^{1*}

¹International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru 502 324, Hyderabad, Telangana, India

²Bharathidasan University, Tiruchirappalli 620 024, Tamilnadu, India

*E-mail: v.vadez@cgiar.org

Terminal drought stress leads to substantial yield losses in chickpea (*Cicer arietinum* L.). Water conservation at vegetative growth (canopy conductivity and canopy size and development) allow plants to increase soil water extraction during grain filling and are hypothesised to help chickpea adaptation to water limited environments. Plant vigour and water saving traits were phenotyped in 232 recombinant inbred lines (RILs), derived from a cross between ICC4958 and ICC1882, at 28 days after sowing under well water conditions using a high throughput phenotyping platform. Different density genetic maps (241-SSR-Low density, 1007-SSR+SNPs-High density and 1557-SNPs-Ultra high density) were used for QTLs identification. Several major QTLs (M-QTLs) for plant vigour traits (3D-leaf area, shoot biomass, plant height and growth related traits) were identified

on CaLG04, and co-mapped with previously identified and fine mapped major drought tolerance QTL-hotspot region on CaLG04 (~300Kb). The canopy conductance trait (e.g Transpiration rate) had a M-QTL mapped on CaLG03 using ultra-high density bin markers. Plant vigour traits on CaLG04 and canopy conductance related traits on CaLG03 provide opportunity to manipulate these loci to tailor recombinants having lower transpiration rate and high plant vigour. This ideotype might be enhancing the water stress adaptation in chickpea. To test this hypothesis, a subset of 40 RILs contrasting for vigour and water use traits was tested in lysimeters and field under different water stress treatments. High vigour low water use lines had higher seed yield under severe water stress treatments than high vigour and high water use lines, validating the hypothesis.