Chickpea breeding for water-limited environments

Pooran M Gaur[1]*, Srinivasan Samineni[1], Mahendar Thudi[1], Sobhan B Sajja[1], Sushil K Chaturvedi[2], Veera Jayalakshmi[3], Anita Babbar[4], M Yasin[5], DM Mannur[6], AG Vijaykumar[7], Rajeev K Varshney[1], GP Dixit[2]

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Patancheru, Hyderabad 502 324, India
[2]ICAR-Indian Institute of Pulses Research (IIPR), Kanpur 208 024, India
[3]ANGRAU Regional Agricultural Research Station, Nandyal518 502, AP, India
[4]Jawarharlal Nehru KrishiVishwaVidyalaya (JNKVV), Jabalpur 482 004, India
[5]RVSKVV-RAK College of Agriculture, Sehore 466 001, Madhya Pradesh, India
[6]UAS-Raichur Agricultural Research Station, Gulbarga 585 101, Karnataka, India
[7]UAS-Dharwad Regional Agricultural Research Station, Bijapur 586 101, Karnataka, India
*E-mail: p.gaur@cgiar.org

Chickpea (*Cicer arietinum* L.) is a dry season food legume and is largely grown on residual soil moisture after the rainy season. The crop often experiences moisture stress towards the end of the crop season (terminal drought). The crop may also face heat stress at the reproductive stage, if sowing is delayed. The increasing climate variability, reflected in wide fluctuations in temperatures and rainfall, is further aggravating risks of terminal drought and heat stresses to chickpea crop, particularly in the semi-arid tropics (SAT). The genetic approaches being used for managing terminal drought and heat stresses include development of varieties with early maturity and enhanced tolerance to these stresses. Excellent progress has been made in the development of early maturing varieties with high yield potential, which helped in bringing additional area under cultivation and enhancing productivity of chickpea in short-season SAT environments. Several varieties with improved drought tolerance have been developed by the classical approach of selecting for grain yield under moisture stress conditions. Similarly, selection for pod set in the crop, subjected to reproductive stage heat stress by delayed planting, has helped in development of heat-tolerant varieties. A genomic region called "QTL-hot spot", which controls a number of drought tolerance traits including root traits, has been introgressed into several popular cultivars using marker-assisted backcrossing (MABC); and introgression lines giving significantly higher yield than the popular cultivars under moisture stress conditions have been identified. Multi-parent advanced generation inter-cross (MAGIC) approach has been found promising in enhancing genetic recombination and developing lines with enhanced tolerance to terminal drought and heat stresses. Integrated breeding approaches involving, particularly, genomic tools, precision phenotyping, and rapid generation turnover techniques, have improved efficiency of chickpea breeding programs in developing varieties better adapted to water limited environments.

Wheat (*Triticum aestivum* L.) genotypes present high variability of stem carbohydrates and differences in the expression of genes regulating fructan metabolism under contrasting water regimes

del Pozo A[1]*, Yáñez A[2], Tapia G[3], Guerra F[4]

[1]Centro Mejoramiento y Fenómica, Facultad de Ciencias Agrarias, Universidad de Talca, Talca, Chile.
[2]Departamento de Ciencias Agrarias, Facultad de Ciencias Agrarias y Forestales, Universidad Católica del Maule, Curicó, Chile
[3]CRI-Quilamapu, Instituto de Investigaciones Agropecuarias, Chillán, Chile
[4]Instituto de Ciencias Biológicas, Universidad de Talca, Casilla 747, Talca, Chile
*E-mail: adelpozo@utalca.cl

The genetic and physiological mechanisms underlying the relationship between water-soluble carbohydrates (WSC) and water stress tolerance were investigated. The genotypic variability of stem weight, stem water-soluble carbohydrate content, grain yield (GY) and other agronomical traits was evaluated in a large collection of 384 wheat genotypes grown in field conditions under water stress, mild water stress and fully irrigated. Also, the dynamics of the main WSCs in stems, and the expression of genes involved in fructan metabolism were evaluated in water stress tolerant and susceptible genotypes, grown in a glasshouse under water stress (WS; 50% field capacity from heading) and fully irrigated (FI; 100% field capacity) conditions. The WSC content at anthesis presented a negative correlation with spikes per square meter, but a positive correlation with kernel per spike and grain weight. Consequently, the relationships between WSC content with GY were low or not significant in the three water regimes. In the glasshouse, the stress-tolerant genotype exhibited higher concentrations of WSCs, glucose, fructose and fructan in the stems, compared to FI. In addition, the stress-tolerant genotype exhibited higher up-regulation of the fructan 1-fructosyltransferase B (1-FFTB) and fructan 1-exohydrolase w2 (1-FEHw2) genes, whereas the susceptible cultivar presented an up-regulation of the fructan 6-fructosyltransferase (6-SFT) and fructan 1-exohydrolase w3 (1-FEHw3) genes. Our results indicated clear differences in the pattern of WSC accumulation and the expression of genes regulating fructan metabolism between the tolerant and susceptible genotypes.