

## IDT6-027 | Drought priming induces thermo-tolerance to post-anthesis high-temperature in offspring of winter wheat

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High temperature stress is a worldwide environmental constraint on crop production. Exposure of plants to a stress event could induce tolerance in them and even in their offspring to subsequent stresses. This study was to test the hypothesis that drought priming of parent plants could trigger a cross tolerance to high-temperature stress in their offspring. Winter wheat plants were used and were firstly subjected to a drought stress during grain filling, and their offspring were exposed to a post-anthesis high-temperature stress. Grain yield, photosynthesis, anti-oxidation, and proteomic profile in wheat flag leaves of the offspring were determined. The results showed a less yield loss in the next

generation of the wheat plants that had received drought priming, which could be ascribed to the improved photosynthesis because of the up-regulated expression of proteins involved in the light reaction and in the Calvin cycle, and to the enhanced anti-oxidation capacity as exemplified by the decreased contents of MDA and H<sub>2</sub>O<sub>2</sub> because of the improved activities of SOD and POD. In addition, the proteomic analysis suggested that the enhanced thermo-tolerance could also be attributed to the more robust signal perception and transduction, better maintenance of protein structures, up-regulation of sucrose synthesis and accumulation of heat shock proteins.

## IDT6-028 | Identification of genomic regions associated with the yield and related traits in pigeonpea (*Cajanus cajan* L. Millsp.)

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Pigeonpea [*Cajanus cajan* (L) Millsp.] is an important multi-use shrub legume of the tropics, sub-tropics and warmer regions of the world, growing between 30°N and 35°S latitude. The goal of this study was to identify genomic regions associated with yield and related traits in three newly developed F2 mapping populations of pigeonpea; AL 201 × ICPL 20325, ICP 5529 × ICP 7035 and ICP 8863 × ICPL 87119. Genotyping by Sequencing (GBS) platform was used for genetic analysis and linkage analysis was performed using JoinMap version 4. Quantitative Trait Linkage (QTL) analysis of eight yield and yield-related traits were performed using single marker analysis (SMA) employing composite interval (CIM) using stepwise regres-

sion linear model. A total of 42 QTLs were detected, with 5 in AL 201 × ICPL 20325, 7 in ICP 5529 × ICP 7035 and 30 in ICP 8863 × ICPL 87119. Individual QTLs ranged from 1-4 per trait and the phenotypic value explained (PVE%) ranged between 10.35 -16.27% in AL 201× ICPL 20325, 10.44 -17.9 in ICP 5529 × ICP7035 and 10.71-89.12% in ICP 8863 × ICPL 87119. The detected QTLs were co-localized within the same genomic regions, indicating the presence of pleiotropic effect or close genetic linkage. For further fine mapping and use in marker assisted transfer, validation for the accuracy and consistency of the identified QTLs in several, independent and diverse mapping populations transfer is crucial.