

IDT3-020 | Vegetative growth and water use characterization of a maize introgression library

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Previous work showed that a maize introgression library (IL) derived from the cross between Gaspé Flint (an early flowering Canadian landrace) and B73 (the reference maize line) segregated for phenology as well for seminal root architecture (SRA) traits. In this experiment, the IL was evaluated in the high-throughput phenotyping platform PhenoArch (INRA, Montpellier), a platform for large-scale automated imagery and evapotranspiration measurements of potted plants in controlled environment. Biomass accumulation for each plant was estimated by software- and model-assisted imaging analysis. Each pot was weighed daily allowing for the accurate estimation of evapotranspiration. The maize IL lines were tested under well-watered (WW) and water-deficit (WD) conditions (soil water potential

> -0.05 and ~ -0.4 MPa, respectively). The following traits were investigated: biomass accumulation, daily water use, water use efficiency, specific transpiration, early vigor and phyllochron. Significant genetic effects were detected for all traits ($P < 0.05$, Dunnett test) in WW and WD. Stepwise QTL analysis enabled us to identify the chromosomal regions underlying the phenotypic segregation for all the measured traits on chr. 1, 2, 3, 4, 7, 8 and 9 in both well-watered and water-deficit conditions. A number of QTLs for phenology and RSA traits affected vegetative growth and WUE. The data collected using the platform PhenoArch will contribute to the comprehensive multi-trait phenotypic characterization of the IL. The most interesting IL lines and corresponding QTLs are considered for fine mapping and QTL cloning

IDT3-021 | The whole-plant response to soil water availability as a mean for drought-resistance phenotyping

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Soil water deficit is a major environmental stress that majorly affects plants development and functioning. Despite the enormous efforts that have been invested, the fast and accurate phenotyping to abiotic stress remains a bottleneck in efforts to enhance yields in water-limited environments. The rates of soil water withdrawal and plant transpiration are related in a non-linear manner as enhanced soil water extraction at higher transpiration rates decreases soil water availability (SWA) that decreases the transpiration rate. Since SWA availability depends in a dynamic manner on soil water energetic status, VPD, and transpiration rate, the rate of convergence of this loop, enables one to phenotype plant drought resistance. A novel high throughput experimental platform for simultaneous and continuous non-invasive monitoring of water relations in the soil-plant-atmos-

phere continuum of numerous plants has been used to measure the response profile for each plant in the array to gradually varying SWA. Three probes for each pot in the array and a specially designed algorithm enable detailed water-relations characterization of whole-plant transpiration, biomass gain, stomatal conductance and root flux. They also enable a quantitative determination of plant water-use efficiency and relative water content at high resolution under varying soil and atmospheric conditions. Results for that were grown in a semi-commercial greenhouse during winter and summer months will be presented. The individual response of 65 introgression lines of a wild tomato species (*Solanum pennellii*) crossed with cultivated tomato (*S. lycopersicum*) to SWA gradual decrease was investigated. The investigation output will be presented and discussed.