

HIGH-THROUGHPUT PHENOTYPING OF A MAIZE INTROGRESSION LIBRARY AND DURUM WHEAT NEAR-ISOGENIC LINES UNDER WATER DEFICIT CONDITIONS

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A maize Introgression Library (IL) of 73 lines derived from the cross between Gaspé Flint (an early line) and B73 used as donor and recurrent genotypes, respectively (Salvi et al., 2011), and four pairs of durum wheat near-isogenic lines (NILs) for a major yield QTL (*Qyld.idw-3B*; Maccaferri et al., 2008) were tested in the high-throughput phenotyping platform PhenoArch (INRA, Montpellier), a greenhouse platform allowing for large-scale automated imagery and evapotranspiration measurements. Through image analysis and using suitable models, it has been possible to estimate biomass accumulation and leaf area expansion for each plant. Phyllochron and additional morpho-physiological features were measured.

The maize IL lines were tested under well-watered and water-deficit conditions (soil water potential > -1 and ~ -4 Bar, respectively) while the wheat NILs were subjected to three levels of drought stress: no stress (soil water potential > -1 Bar), mild stress (soil water potential of $-5/-8$ Bar) and severe stress (soil water potential ~ -13 Bar).

Data analysis is underway. The analysis of the results will allow us to test: a) how previously characterized loci known to constitutively regulate vegetative growth affect growth plasticity under different water regimes; b) for the presence of (i) growth-related genes/QTLs previously identified by means of meta-QTL analysis and (ii) novel loci affecting the plasticity of vegetative growth in response to drought stress.