

CAWaS

Cotton adaptation to water stress: Genetic and morpho-physiological determinism of drought stress response during the vegetative phase of cultivated cotton (*Gossypium hirsutum* L.)

ABSTRACT

Cotton cultivation is essentially rain fed, and irregular rainfall patterns expose cotton farmers to adverse effects on crop yields and fiber quality. A better understanding of the morphological and genetic basis of drought tolerance in cotton and the identification of reliable agro-physiological traits relevant for use in plant breeding would aid in improving the efficiency of breeding for this complex trait.

Keywords : Root, Cotton, Water deficit, QTL, Phenotyping, Plant, Phenotyping, Architecture, Ecophysio

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Project leader : Marc Giband

Project leader's institution : CIRAD

Project leader's RU : AGAP

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Funding : Labex

GOAL

The project aims at characterizing the variability in the root development and plantlet growth parameters in response to water stress during the vegetative phase in cultivated cotton (*G. hirsutum* L.) genotypes. The phenotypic data, combined with large-scale SNP-based genotypic data, will allow to gain insights into the genetic bases of root and plantlet growth, development and adaptation to water stress in cotton, and to identify molecular markers associated with favorable alleles. Put together, the information gained will allow to generate knowledge and tools useful for breeding programs aimed at improving cotton productivity in drought-prone areas.

RESULTS

A panel composed of 270 accessions of Upland cotton (*G. hirsutum* L.) varieties and breeding lines was phenotyped on the high-throughput phenotyping platform PhenoArch under contrasting water regimes. The panel displayed significant variability with respect to the genotypes' responses to low water availability, and less susceptible accessions were identified. Adaptive traits, such as increased Water Use Efficiency (WUE) under low water availability could be responsible for the increased tolerance to water stress. Carbon Isotope Discrimination (CID) was shown to be an easy to measure proxy for WUE. The panel was also characterized for Root System Architecture (RSA) traits using the PhenoRoots platform, a purposely developed root phenotyping system. Five RSA ideotypes were described. Important RSA traits,

such as root density, maximum root depth, and explored area showed medium to high heritability. The 270 accessions were genotyped using a 63K SNP chip, and close to 22000 high-quality polymorphic markers were identified after filtering. Genome-Wide Association Studies (GWAS) identified 22 QTLs for RSA traits, and 125 QTLs for above-ground traits (2 water regimes). Molecular markers associated to major QTLs related to tolerance to low water availability in cotton were identified.

PERSPECTIVES

Field experiments, in which a subset of the genotypes will be grown under contrasting water regimes, will be conducted in Brazil during the 2019-2020 season to validate the results of the project. Markers associated to major QTLs will be validated by genotyping and phenotyping additional cotton accessions. Crosses are under way to develop plant populations with increased tolerance to low water availability.