

### Differential gene response to decreasing water soil content during early developmental phases

#### Explanation and Purpose

Water availability during early vegetative stage is a major determinant of plant biomass yield, also for a drought resistant species like *Sorghum bicolor* (Moench). Investigations on the gene response to decreasing water availability are needed to advance the knowledge on the mechanisms and processes related to drought stress tolerance.

Genes involved in drought response were identified using a high density microarray containing all available sorghum TC sequences, as well as several rice and maize TC sequences known to be involved in water deficit response. The microarray analysis revealed that the response to drought started between 3.65 and 4.14pF, when plant transpiration sharply decreased. Until 3.65 pF value most of the differentially expressed genes were down-regulated, indicating that the early response at the beginning of water stress consists in a reduction of some metabolic functions (sugar and aminoacid metabolism).

#### Exploitation Strategy

These results provide further insight in the complex metabolic pathway triggered by drought stress. The genes that are differentially expressed and located in drought tolerance QTLs (for example stay-green traits) could be used as molecular marker for the drought tolerance trait. Furthermore, the same genes could be important tools to screen different sorghum varieties directly in the laboratories. In this easy and fast way, waste of time and water (required for the field trials) could be avoided.

#### Further Research

The microarray results are a snapshot of the functional status of young sorghum leaves under drought stress. Further research activities are needed to better characterize the differentially expressed genes as real drought tolerance traits and to identify molecular markers for drought tolerance.

For these reasons, additional studies of phenotypization will be performed in different sorghum varieties to better understand the connection between genetics and plant physiology at the beginning of water stress.

#### Impact of Exploitation

Publication: **L. Pasini, M. Bergonti, A. Fracasso, A. Marocco, S. Amaducci**. Microarray analysis of differentially expressed mRNAs and miRNAs in young leaves of sorghum under dry-down conditions, Journal of Plant Physiology, in press.

### Sweet Sorghum: an alternative energy crop



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