

Global gene expression profiling of contrasting *Gossypium* sp. for deciphering highly stage specific genes and metabolic pathways governing drought tolerance

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An improvement of our knowledge on gene composition and expression is essential to investigate the molecular basis of drought tolerant to define the gene pool involved in cross talk to different pathways at biochemical levels and molecular levels for the survival of plants during drought condition. The availability of complete genome sequences and large sets of expressed sequence tags (ESTs) from several plants has recently triggered the development of efficient and informative methods for large-scale and genome-wide analysis of genetic variation and gene expression patterns. As Cultivated Cotton *Gossypium Spp.* are the world's most important fiber plants. The deposition of > 90% cellulose in the cotton fiber secondary wall makes this unique cell powerful for understanding cellulose biogenesis, a process with great importance in nature and industry. We carried out Microarray hybridization of contrasting *Gossypium herbaceum* germplasms using **Affymetrix cotton chip**. 2 germplasm of *Gossypium herbaceum* were used for this study 454 pyrosequencing

was used to enrich the very few sequence data currently available for the cotton species and to identify genes involved to survive the plants during drought condition. Affymetrix microarray Cotton chip was used to compare gene expression pattern in tolerant and sensitive genotype of *G. herbaceum*. Statistical data analysis was performed using Array assist 5.5, R Packages and SAS using criteria of p value ≤ 0.05 and fold change ≥ 2.0 . In parallel we also performed deep **transcriptome sequencing** of two germplasms (out of five selected) with contrasting drought tolerance using **Roche's 454-GSFLX genome sequencer**. Our efforts on microarray and transcriptome sequencing with very strong statistical analysis lead to discovery of many differentially unique (germplasm specific) and novel genes, metabolic pathways, and enriched enzyme activities probably responsible for drought tolerance in *Gossypium.spp.* The good statistical results related to drought tolerance in *Gossypium herbaceum* will be presented.

Biography

I am a Senior Research Scholar (PhD student) in NBRI, in the area of Bioinformatics (Cotton Genomics). I have 3 international publication till yet and 2 are communicated in Plant Physiology.