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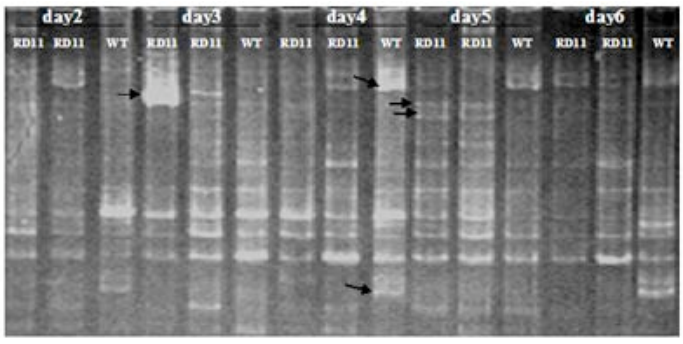
1. A master switch to tackle drought stress

In SATrends issues 62 (Jan 2006) and 75 (Feb 2007), we reported that when the *DREB1A* gene driven by the promoter of a stress-inducible gene, *rd29A*, was genetically introduced into groundnuts, it not only improved the transpiration efficiency, but also induced a positive root response under water stress conditions. Here we report that the expression of DREB1A transcription factor also manifests in a differential gene expression under drought stress, thereby, acting as a master switch to counter the effects of drought.



A cDNA profile obtained from the leaf samples of transgenic groundnut expressing rd29A::DREB1A during day 2 to 6 of the dry down cycle. Arrows indicate the differentially expressed cDNAs in transgenic plant, when compared with non-transgenic plant. Straight arrows indicate newly expressed, and downward arrows indicate down regulated cDNAs.

The total RNA from the leaves of five selected transgenic events expressing the *DREB1A* gene under stress were subjected to differential display of transcripts for comparing the expression profiles of transgenic and wild type groundnut plants under water stress. This enabled the detection of gene transcripts that were expressed in response to the stress. A total of 51 differentially expressed transcripts were identified, where 35 transcripts were newly expressed, 11 were up-regulated, and five were down-regulated. Analysis of the partial sequences of 40 cDNAs indicated that most were from abiotic stress responsive genes (SRGs) that could be classified broadly in four groups as follows:

- cDNAs showing similarity with drought responsive *Arachis* cDNAs.
- cDNAs showing similarity with expressed sequenced tags (ESTs) responding to biotic and abiotic stresses that may be from regulatory genes.
- cDNAs showing similarity with mitochondrial genes involved in alternative respiratory pathways that have been postulated to play a key role in plant stress responses.
- cDNAs showing low level of sequence similarity with stress responsive ESTs which might be considered novel stress inducible genes.

Nevertheless, only 17 cDNA clones showed a strong similarity with the published ESTs, thereby indicating that a majority of these may be novel. This would indicate that the expression of *DREB1A* in transgenic plants might influence the expression of these genes either directly or indirectly. Further analysis of the transcript levels may provide insights into the regulatory pathways of these genes.

Analysis of the newly expressed genes indicate that their products might function co-operatively to protect the cells from dehydration and may also play an important role in plant adaptive mechanisms under water stress conditions. Cloning and characterization of full-length cDNAs and promoter regions of the genomic sequences corresponding to the stress-regulated clones could provide further insights into the mechanism of expression of an individual gene, as well as its potential role in stress response. Future activities would involve the identification and functional analysis of these transcripts for use in both genetic engineering as well as marker-assisted selection for plant breeding.

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2. Spotlight on hybrid seed production

Seven years ago ICRISAT and the Institute d'Economie Rural (IER) in Mali started developing the first Guinea-race male-sterile female parent lines of sorghum. Since then, new hybrid sorghums based on Guinea-race germplasm are being developed to achieve higher grain productivity while maintaining the grain quality and adaptive traits of the Guinea-race sorghums primarily grown by farmers in West Africa. Hybrids produced on these female parents have now been tested in multi-location and multi-year trials. Results show that these new hybrids provide a 31% yield increase over the best local variety, averaged over all hybrids and environments in