



Category: Plant Genomics

Transcriptome profiling and identification of differentially expressed transcripts in response to mid season drought in groundnut *Arachis hypogaea* L

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Abstract

Drought is one of the major constraints in groundnut and its inheritance is governed by many genes with small effects operating in a coordinated manner. To this end, a total of eleven genotypes viz., ICGV 07070, ICGV 07132, TCGS 1398, TCGS 1073, TCGS 1157, TCGS 1173, MLTG 4, Narayani, Tirupati 1, Kadiri 6 and Kadiri 9 were screened in pot culture for moisture stress tolerance. Among the eleven genotypes, TCGS 1157 and MLTG 4 genotypes were more tolerant and Narayani and Kadiri 6 were highly sensitive to moisture stress. To unravel the molecular mechanisms conditioning drought tolerance, transcriptome was profiled cDNA-RAPD in these contrasting genotypes submitted to midseason moisture stress (50-80 DAS) and compared with respective well-watered control in field conditions. cDNA-RAPD profiles were developed with 35 RAPD markers in three regimes of moisture stress i.e., 60, 70 and 80 DAS. The transcript profile data revealed that drought stress induces the expression of many drought responsive transcripts and prolonged moisture stress has enormous impact on gene expression pattern. In the 35 cDNA- RAPD profiles analysed, a total of 823 transcripts were differentially expressed of which 523 transcripts exhibited qualitative difference (switched on: 263 transcripts, switched off: 260 transcripts) and 300 transcripts displayed quantitative differences (up regulated: 122 transcripts, down regulated: 178 transcripts). In the initial stages of moisture stress (10 to 20 days) many novel transcripts were activated along with modulation of gene expression (both up and down regulation) in comparison with well-watered control genotypes. The novel transcripts triggered by moisture stress will play a major role in stress perception, signal transduction, and synthesis of regulators and different compounds associated with drought tolerance mechanism. Under prolonged drought stress (30 days), the expression of novel transcripts were reduced by 30% and the up and down regulated transcripts was increased by 15%. Two moisture stress responsive transcripts were identified with OPA2 (750 bp) and OPA4 (450) markers. They were expressed only under drought stress in resistant genotypes (TCGS1157 and MLTG4) and absent susceptible genotypes and also in well-watered control of all the four genotypes three moisture stress regimes. Further characterization of these transcripts by sequencing will greatly help in understanding nature of the genes and the mechanism by which groundnut plants respond to drought stress. After validation, these two markers can be routinely employed for selection of drought tolerant germplasm lines.

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