

Transcriptome analysis in response to gradual water deficit in *Arachis* wild relatives

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Abstract

Peanut (cultivated tetraploid *Arachis hypogaea*) is an important food legume widely cultivated mainly in Asia, Africa and the Americas although its productivity is limited in drought-prone areas; therefore the development of drought-resistant varieties is a priority. Peanut has a narrow genetic diversity and is reproductively isolated from its wild diploid relatives due to ploidy differences. In contrast to peanut, wild relatives have higher genetic diversity and show adaptation to a range of environments thus constituting a rich source of allele diversity for resistance to biotic and tolerance to abiotic stresses. In this study, the transcriptomes of two wild diploids, *A. duranensis* and *A. magna*, representatives of the AA and BB peanut component genomes respectively, were analyzed under gradual water deficit. Two SSH libraries produced from roots of *A. magna* generated 759 Sanger ESTs with 249 Unigenes, whilst from *A. duranensis* roots, 380,601 Roche/454 reads resulted in 12,792 Unigenes. Forty-six Unigenes were selected as drought-related candidates for validation by RT-qPCR by *in silico* analysis of all libraries. A total of 18 candidate genes showed significantly different levels of expression in stressed plants, confirming their involvement in drought response. To date, this is the first report on global gene expression profile of wild *Arachis* species submitted to an abiotic stress. Data produced in this study is a valuable resource for gene identification, characterization of new alleles and development of molecular markers in *Arachis*.