A transcriptional approach for identifying genes related to drought stress

Notes

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Stress-responsive mechanisms triggered in plants under drought stress affect plant growth and cause serious limitation to crop productivity. Due to its high genetic diversity and adaptation to a range of environments, wild relatives of peanut constitute a rich source of allele diversity for resistance to biotic and abiotic stresses. Based on previous data and as a first step to identify drought-responsive genes in *Arachis*, the wild specie *A. magna*, accession KG30097, was selected as it showed high adaptability to water stress conditions. The transcriptome of *A. magna* leaves submitted to gradual water stress was analyzed. Subtractive libraries were constructed with cDNA from leaf tissues of stressed and well-watered control plants. Subtractive hybridization was performed in both directions: cDNA from stressed plants was used as driver and afterwards as tester, allowing for the enrichment of genes either induced or inhibited during water stress. *In silico* analysis revealed 759 reads, which were grouped into 249 clusters, with a novelty index of 32,8%. Several up and downregulated genes were identified exclusively in stressed or control conditions. The expression profile of some differentially regulated genes was validated by real time PCR, using cDNA from roots and leafs of stressed and control plants. Glycine descarboxilase, metallothionein-like protein, drought stress responsive protein, and two unknown proteins were shown to be up-regulated and the gene coding for a disease responsive protein was down-regulated. The information produced in this study is a valuable resource for gene identification, characterization of new wild alleles, and development of molecular markers.

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