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Large scale transcriptome analysis of wild peanut (*Arachis duranensis*) under gradual water stress

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Cultivated peanut, *Arachis hypogaea,* is one of the most widely grown grain legumes in the world due to its high energy value. However, most of domesticated species are susceptible to biotic and abiotic stresses, resulting in production losses. Unlike, wild species are sources of alleles related to disease resistance and adaptation to different environments, which are desirable traits of economic importance. In particular, the wild species, *A. duranensis* (access K7988), has a high adaptability to water stress conditions. The aim of this study is to identify gene expression regulation in *A. duranensis* plants subjected to gradual water stress and its control irrigated plants. Leaves and roots were collected at five different points of stress, when changes were observed in the pattern of plant transpiration, and after 30 minutes and 72 hours of rehydration. Total RNA was extracted and a pool was formed for each treatment, using equal amounts of total RNA from individuals in each collection point and for each tissue. Two cDNA libraries were constructed from total RNA purified from these pools and sequenced by pyrosequencing large scale technology 454 (GS-FLX Titanium Fragment Series Kits, Roche Applied Science). A total of 380,601 reads (average size of 390pb) was generated and 21,710 Unigenes were obtained after clustering and assembly. The most differentially expressed candidate genes related to abiotic stress were selected for validation through RT-qPCR and their relative RNA expression patterns determined. All information generated here will be important for the characterization of new wild alleles, gene discovery and development of molecular markers.

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