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### A Survey of Physiological and Genetic Responses of *Arachis* Species to Water Deficit

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Wild *Arachis* species show a wide variability of agronomic traits and are potential sources of alleles for breeding programs aiming plants with better performance under environmental stress conditions. This work aimed at characterizing physiological and genetic mechanisms of *Arachis* species in response to water deficit (WD). The physiological parameters herein evaluated for four wild species of *Arachis* and cultivated peanut were leaf relative water content; gas exchange; electrolytic leakage and content of malondialdehyde, photosynthetic pigments and proline in plants kept in pots with 20, 45 and 75% of water capacity, for five days, in a controlled environment greenhouse. Results of gas exchange, chlorophyll fluorescence and pigment contents pointed to a non-stomatic photosynthesis limitation, negatively related to the increase of cell membrane damage in all species analyzed. Transcription factors (TF) were identified and those putatively related to WD responses were selected through *in silico* analyses of predicted proteomes of *A. duranensis* and *A. ipaensis* genes and predicted amino acid sequences generated from preliminary RNA sequencing data for *A. hypogaea* and *A. stenosperma* submitted to drought stress. The conservation of the TF family types and frequencies indicates that the regulatory pathways might be shared by these species. Furthermore, analyses of predicted orthologues of drought-responsive genes revealed the conservation of TF regulatory pathways among *Arachis* spp. and *Arabidopsis*. The expression modulation of eight of these TF genes were different among the *Arachis* spp., whenever water was limited in soil, suggesting variances in transcriptional regulation of TF genes, which might lead to diverse acclimatization mechanisms to drought stress in *Arachis* spp.

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