Evaluating Peanut Seed and Leaf Proteome for Use in Drought Tolerance Screening.

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In peanut, water stress (WS) significantly lowers plant resistance to Aspergillus flavus infection leading to aflatoxin contamination of peanut seed. One of the strategies adopted to decrease the risk of aflatoxin contamination in peanut is to identify and develop drought-tolerant peanut genotypes through molecular breeding. Objective of this research was to study changes in leaf and seed proteome of drought-tolerant (DT) and drought-susceptible (DS) peanut genotypes due to WS for evaluating the possibility of using leaf proteome as a biochemical marker for determining drought tolerance. Over twenty peanut genotypes with diverse drought-tolerance characteristics collected from ICRISAT and ANGR Agricultural University, India were used in this study. Peanut plants growing in pot culture under greenhouse conditions were subjected to WS for 0 to 28 days. Seeds and leaves were collected from irrigated (control) and water stressed plants and analyzed by 2-DE. Differentially expressed proteins were identified using MALDI-TOF Mass Spectrometry. Peanut seed proteome showed that in DT genotypes expression of methionine-rich proteins was either maintained or up-regulated while they were significantly suppressed in DS genotypes when subjected to WS. Likewise, in leaf tissue of DT genotypes several photosynthesis and defense related proteins were over expressed due to WS while these proteins were either partially or completely suppressed in DS genotypes. In addition, four new proteins were induced following WS in drought-tolerant cv. Vemana. We have identified these proteins as serine/threonine protein phosphate PP1, glycine betaine, peroxidase 43 and SNF1 protein kinase which plays a role as defense. These data showed that the proteomic responses of both seed and leaf tissue of DT or DS genotypes are similar and hence, either tissue can be used for evaluating drought-tolerance characteristics of peanut germplasm.

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