

Water Stress Induced Differential Gene Expression in Peanut.

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Aflatoxin contamination is one of the main factors affecting peanut seed quality. Drought is known to persuade aflatoxin contamination causing *A. flavus* infestation and aflatoxin production. One of the strategies to decrease the risk of aflatoxin contamination is to develop drought-tolerant peanut genotypes. In this study, we initiated quantitative analysis to identify the differentially expressed cDNA transcripts associated with drought stress in peanut genotypes, and to understand the molecular mechanism of water stress. Peanut plants (50 d old), growing in pot culture under greenhouse conditions were subjected to water stress. Following the stress, leaves were collected and total RNA was isolated and analyzed to determine progressive changes in transcript profiles. We generated differential expression profiles of cDNA transcripts in drought-tolerant and drought-susceptible genotypes employing Differential Display RT-PCR. Out of 24 primer pairs tested, 11 primers resolved a total of 52 transcripts- (>1 Kb: 2 up-regulated and 30 down-regulated). Three primer pairs showed up-regulated transcripts, five primers showed down-regulated transcripts, while three other primer combinations showed both up- and down-regulated transcripts. Short stress period (<3 d) did not show any changes in the transcript profile. In drought-tolerant genotypes, fewer transcripts were affected compared to drought-susceptible genotypes due to water stress. Drought-tolerant genotypes showed up-regulation of transcripts continually up to 14 d stress, period indicating their association with the tolerance. Whereas, in drought-susceptible genotypes, these transcripts were up-regulated only during the initial periods of stress but prolonged stress appears to suppress these transcripts. These data suggests that drought-tolerant genotypes were able to continue their normal metabolic process by maintaining gene expression while drought-susceptible genotypes failed to withstand the drought stress due to loss or reduction of gene expression. The water stress responsive transcripts are being sequenced and characterized to determine their function. Supported by USAID/PCRSP # FAM 51.