

## Gene Expression in the Interaction between *Aspergillus* and an Aflatoxin-Resistant Peanut Germplasm

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This study explores the seed-*Aspergillus* interaction that leads to aflatoxin accumulation. Gene expression changes in peanut seeds and *Aspergillus flavus* at early hours of infection, as well as seed viability and aflatoxin accumulation after 72 h were evaluated. A simultaneous RNA sequencing approach was used to capture both seed and pathogen specific transcripts. The experiments were performed on two aflatoxin-resistant genotypes of the wild diploid species *Arachis cardenasii* Krapov. & W.C. Greg. and on a cultivated peanut variety, which accumulates aflatoxin when incubated with *A. flavus*. For each experiment, gene expression analysis and identification of differentially expressed genes was based on paired-end sequence reads of two biological replicates. Differentially regulated transcripts detected in the resistant seeds of *A. cardenasii*, but not in the cultivated peanut variety, encode genes involved in phytoalexin biosynthesis, including stilbenes and isoflavonoids. Mapping of reads to the aflatoxin biosynthesis (AB) gene cluster, in the two aflatoxin-resistant diploid peanuts exposed to *Aspergillus*, showed no expression of genes within a region of the AB cluster proximal to the sugar metabolism flanking area; the opposite was observed in the cultivated peanut genotype. Additional studies are in progress to identify modules of co-expressed genes associated with the observed transcriptional responses. This research is part of a joint effort to study peanut-*Aspergillus* interactions to advance aflatoxin-resistant germplasms.