DNA Markers for Resistance to Post-harvest Aflatoxin Accumulation in Peanut (*Arachis hypogaea* L.).

Aflatoxins are toxic and carcinogenic secondary metabolites produced by *Aspergillus flavus* Link ex. Fries and *A. parasiticus* Speare, soil-borne fungi that colonize agricultural commodities. Pre- and post-harvest contamination of peanut by aflatoxin is a major problem worldwide, causing profit loss for the peanut industry and raising serious human and animal health concerns. Peanut genotypes with resistance to colonization by *Aspergillus* species or to aflatoxin accumulation should be part of an integrated aflatoxin management program. Aflatoxin content is expensive to measure and exhibits high environmental variation, thus, the use of molecular markers tightly linked to aflatoxin resistance genes would improve selection efficiency. Tetraploid (2n=4x=40) lines derived from an interspecific hybrid between the diploid (2n=2x=20) wild peanut species *A. cardenasii*, a species on whose seeds *Aspergillus* species do not grow well and will not produce high levels of aflatoxin, and the *Aspergillus*-susceptible tetraploid (2n=4x=40) *A. hypogaea* that showed variation in their ability to support aflatoxin production were previously screened for AFLP polymorphisms. At the 5% significance level, 34, 39, and 34 markers were found to be significantly associated with reduced aflatoxin B1, aflatoxin B2, and total aflatoxin, respectively. The goal of this study was to evaluate these markers in two segregating F$_2$ populations derived from NC GP WS 2, the *cardenasii*-derived line exhibiting the lowest levels of aflatoxin production. The aflatoxin assay used to phenotype the F$_2$ plants was a destructive one, therefore, embryos were removed from the cotyledons and regenerated via tissue culture in order to maintain the lines for generation advancement. The populations were genotyped using 39 AFLP markers associated with reduced aflatoxin accumulation in NC GP WS 2. Genotypic and phenotypic data produced in these tests was analyzed in order to identify markers linked to reduced aflatoxin accumulation. Linked markers can be used in the future to improve the efficiency of selection when transferring the low aflatoxin production of the interspecific lines into elite peanut breeding materials.