

Public Abstract

First Name:Dana

Middle Name:Lynn

Last Name:Bush

Adviser's First Name:Georgia

Adviser's Last Name:Davis

Co-Adviser's First Name:

Co-Adviser's Last Name:

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Department:Agronomy

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Title:The Role of Genetic and Phenotypic Diversity in Maize and its Effect on Aflatoxin Accumulation by the Fungus *Aspergillus Flavus*

The fungus *Aspergillus flavus* produces a potent carcinogen called aflatoxin. The accumulation of aflatoxin is influenced by water stress, high temperature, and insect damage. Research also suggests that the type and amount of sugar available in the seed may also influence the amount of aflatoxin accumulated. Few detoxification measures are available once corn is contaminated with aflatoxin. The objective of this research is to 1) identify new sources of low aflatoxin corn, 2) determine the relationship of aflatoxin contamination to other plant traits in corn, and 3) examine the relationship between free radicals in corn, free radical consuming molecules, and aflatoxin contamination in corn.

Aflatoxin levels were measured on 109 corn lines in Missouri, Georgia, and Mississippi. New sources of low aflatoxin corn came from tropical and non-tropical sources. Correlations were conducted between other measurements that were taken on the corn plant and aflatoxin levels. Several traits were negatively correlated with aflatoxin levels such as days to corn ear silking, number of roots growing out at each node, and the width of 10 corn kernels laid together. Genes of interest were identified based on these correlations. DNA sequence of a gene was tested to look for a correlation with a change in aflatoxin levels. An association between *dwarf3* and changes in aflatoxin was identified. *dwarf3* a gene involved in the early portion of the synthesis pathway of the plant hormone gibberellic acid. Gibberellic acid is involved in plant growth processes such as plant height and seed germination.