

THE ROLE OF GENETIC AND PHENOTYPIC DIVERSITY IN MAIZE
AND ITS EFFECTS ON AFLATOXIN ACCUMULATION
BY THE FUNGUS *ASPERGILLUS FLAVUS*

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ABSTRACT

Accumulation of the potent carcinogen, aflatoxin, in maize poses a significant health risk to humans and animals. Most commercially grown maize lines are susceptible to infection by the fungus that synthesizes aflatoxin, and toxin levels can accumulate to dangerously high levels under the influence of a number of environmental and cellular factors. How these factors interact to control aflatoxin levels is poorly understood. The objective of this research was to identify new sources of low aflatoxin maize germplasm and to discover underlying genetic mechanisms leading to low aflatoxin accumulation in maize. Aflatoxin levels were quantified in a large set of diverse maize lines in three locations. Both tropical and temperate sources of low aflatoxin were identified. Correlation of aflatoxin levels with agronomic traits and sequences of genes responsible for some of those traits revealed statistically significant associations with traits related to plant architecture and flowering time, carotenoid content, and haplotypes for genes affecting kernel sugars, plant height and anthocyanin synthesis. Together, the results of these studies identify new sources of low aflatoxin germplasm and suggest avenues for further investigation of factors that regulate aflatoxin accumulation.