

Public Abstract

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Title:GENOTYPIC AND PHENOTYPIC PREDICTORS OF LOW AFLATOXIN ACCUMULATION IN ZEA MAYS

Zea mays L. is one of the world's most important and widely grown crops and is susceptible to a wide range of plant pathogens. One fungal pathogen of particular concern is *Aspergillus flavus* Link, which is capable of producing the secondary metabolite aflatoxin. Aflatoxin poses serious health concerns when consumed by humans and animals and when consumed in large doses can lead to abdominal pain, liver damage, and death. While regulated in the United States, many underdeveloped countries do not have the resources to monitor aflatoxin accumulation in maize and, thus, developing low aflatoxin accumulation commercial maize lines would be of great benefit. The objective of this project was to identify genotypic and phenotypic predictors of low aflatoxin accumulation that could help maize breeders develop a low aflatoxin accumulating line. First, the inheritance pattern of low aflatoxin accumulation was investigated in a series of reciprocal crosses between a high toxin accumulating line and a low toxin accumulating line. The data supported the hypothesis that maternal effects or the interaction between nuclear and maternal genetic components impacts aflatoxin accumulation. Second, the availability of sugars in maize kernels has been shown in laboratory studies to impact aflatoxin production and accumulation in *A. flavus* grown on media. To determine if sugars impact maize grown in the field, aflatoxin accumulation was analyzed in maize starch biosynthesis mutants and four mutants were identified that accumulate significantly high aflatoxin concentrations. These maize mutants have unique phenotypic characteristics such as high sugar concentrations, altered starch ratios and high moisture that could aid *A. flavus* in aflatoxin production. The impact of sugar on aflatoxin accumulation was also evaluated in a diverse set of maize germplasm providing further evidence for the relationship between sugar availability and aflatoxin accumulation. Finally, two QTL chromosome regions were identified in maize cob tissue, a maternally derived tissue. Candidate genes in these regions associated with low aflatoxin accumulation include genes for the transport of sugars and disease resistance. The results of this work reveal the potential impact the maternal parental plant has on low aflatoxin accumulation through the movement of carbohydrates into developing kernels, how maternal tissues (e.g. husks, cob and pericarp) serve as barriers to fungal infection and the location of QTL in the maize genome associated with low aflatoxin accumulation.