# GENOTYPIC AND PHENOTYPIC PREDICTORS OF LOW AFLATOXIN ACCUMULATION IN *ZEA MAYS*

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## ABSTRACT

*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. 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.