

Title Genotypic and phenotypic characterization of response to aflatoxin and secondary traits in maize

Author Melanie Edwards and Javier F Betran

Citation Thesis, Doctor of Philosophy (Plant Breeding). Texas A&M University. 192pages. 2006

Keywords Aflatoxin; Secondary traits; Maize; Heritability

Abstract

One major problem facing maize producers in the southern US is contamination with the mycotoxin aflatoxin, produced by *Aspergillus flavus* (Link: Fr). Aflatoxin is a serious threat to human and animal health, with no resistant commercial hybrid available.

Development of resistance to aflatoxin production has several major limitations. Aflatoxin is highly variable both across and within environments, even under inoculation, requiring several locations and replications for breeding. Additionally, there is no screening method that is reliable, rapid, inexpensive, and allows for high throughput.

Several secondary traits, such as kernel texture, kernel integrity, husk cover, and visible ear rot, have previously shown to be related to aflatoxin accumulation. These traits are easily characterized in the field and are candidates for indirect selection if they are correlated to aflatoxin concentration.

Root lodging, a plant's inability to maintain upright stature is another complex characteristic of root related traits that traditionally is selected for indirectly. It can greatly reduce harvestable yield. It is affected by morphological traits and environmental conditions, but its genetic components are little understood.

This dissertation comprises three studies presented in chapters II, III, and IV. Chapter II involved white and yellow hybrid maize trials as well as quality protein maize trials from several years across Texas environments. Data was analyzed both per and across location to determine repeatability of response to aflatoxin. Additionally, aflatoxin levels were correlated to several secondary characteristics (female flowering, endosperm texture, husk cover, and ear rot ratings) to determine usefulness in indirect selection.

Chapter III was a phenotypic evaluation of a recombinant inbred line (RIL) mapping population, which was derived from divergent parental inbreds Tx811 and CML176. The trials were conducted in two Texas locations, and phenotypic data for aflatoxin concentration, kernel integrity, endosperm texture, female flowering date, and root lodging was collected. Variance components for these traits and genetic and phenotypic correlations were determined.

Chapter IV was a genotypic evaluation of the Tx811/CML176 mapping population using simple sequence repeat markers. Genotypic and phenotypic data were combined to identify quantitative trait loci (QTL) and epistatic interactions for response to aflatoxin and for root lodging.