

AFLATOXIN ACCUMULATION RESISTANCE IN MAIZE

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Introduction

Maize (*Zea mays*) is a staple food of global importance. It can be infected with *Aspergillus flavus*, a fungus that produces the carcinogenic aflatoxin. Host plant resistance is one of the most efficient methods of reducing aflatoxin accumulation in maize. Developing a QTL mapping population helps to identify genes and/or genomic regions responsible for a trait.

Objectives

Identification of novel QTLs from new donor lines contributing to aflatoxin accumulation resistance in maize.

Materials and methods

- An F_{2:3} population was constructed from an initial cross between CML69, an aflatoxin resistant genotype unrelated to all currently known and mapped resistant donor lines, and Va35, a susceptible, southern adapted inbred line.
- 350 SNPs and 60 SSRs were screened on the parents and F₁. 58 SNPs and 14 SSRs polymorphic between the parents were selected and mapped.
- Joinmap, TASSEL and QTL cartographer were used for map creation and data analysis.

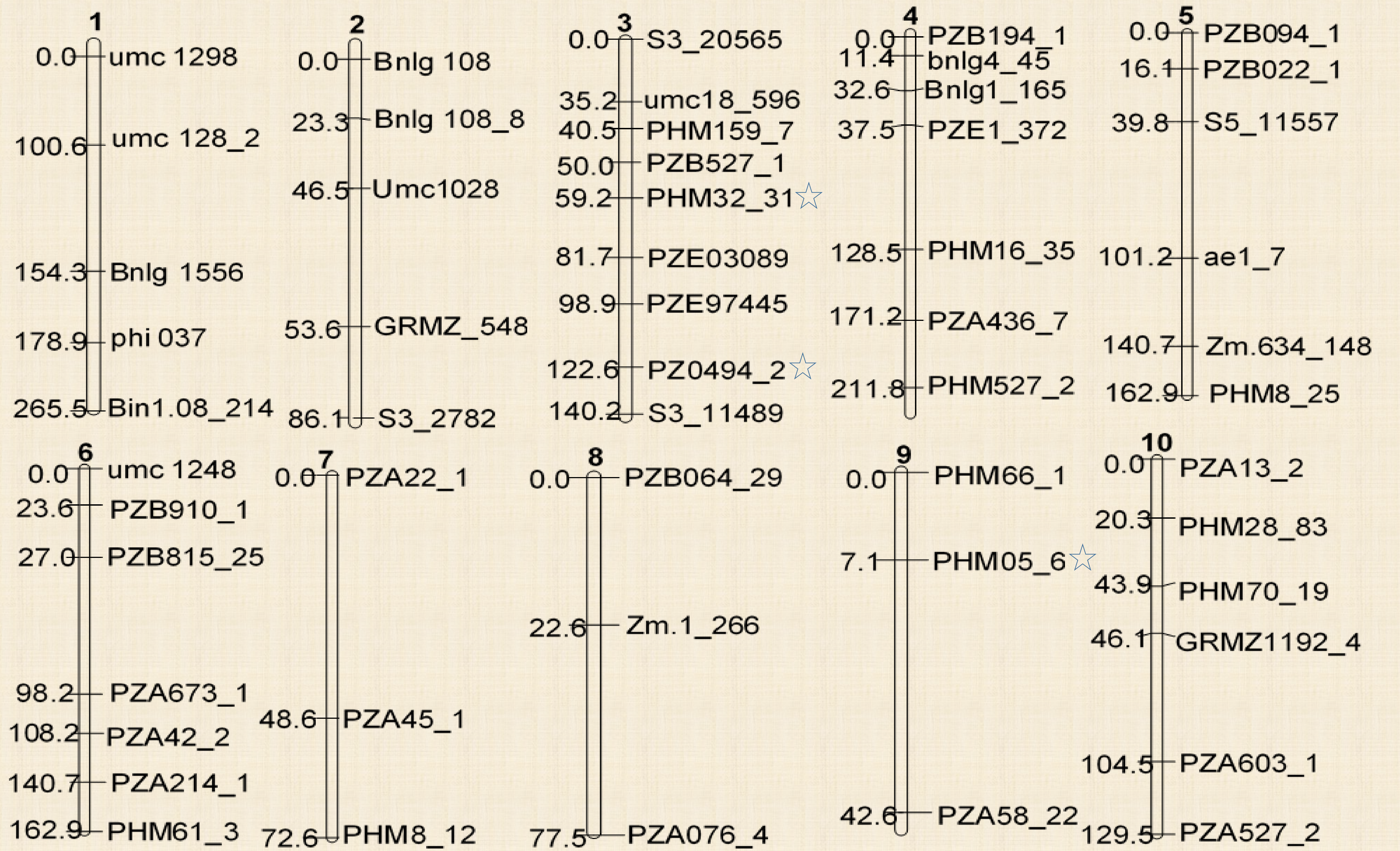


Figure 1: Genetic map showing all 10 chromosomes with the relative distance between the markers.

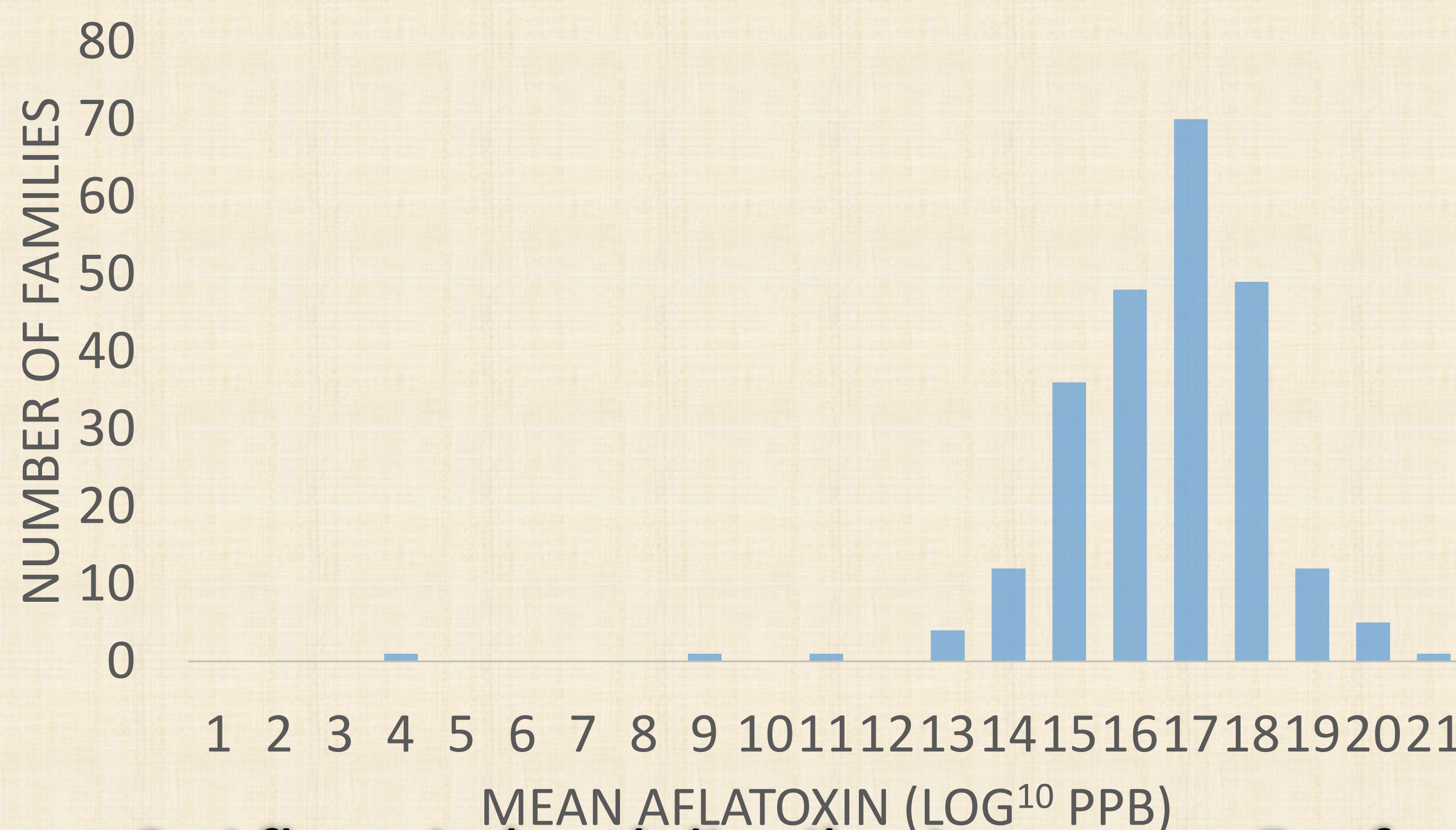


Figure 2: Aflatoxin level distribution across F_{2:3} families

Table 1: Single marker analysis of 3 most significant markers possibly linked to a QTL.

Chr	Marker	pr(F)	R ²
3	1	0.025*	0.0226
3	2	0.012*	0.0274
9	2	0.041*	0.0167

Results and Discussion

Figure 1. Preliminary genetic map showing polymorphic markers and their positions on the chromosome. The map also shows the position of a QTL or gene linked to the trait (☆). Chr. 3 has a marker (PZB0494_2) that falls under a potential QTL as seen by the QTL cartographer output (figure not shown). See Table 1.

Figure 2. Mean distribution curve of aflatoxin levels in the 238 F_{2:3} families in one environment. The uneven distribution is due to the unfavorable environmental conditions for aflatoxin production by *A. flavus*. Both parents also has very low aflatoxin levels due to the same reasons.

Table 1. Single marker analysis suggesting 5 markers linked to QTLs on *Chr* 3 and *Chr* 9. The pr(F) is a measure of the probability that the markers are linked to a QTL with a 95% confidence interval.

Future

- Phenotyping of three more tests (environments) in RCB design for all 238 families in the population is underway.
- More markers are being screened for polymorphisms between the parents and the F₁ of the mapping population to complete the molecular map presented in the study.