

**GENETIC ANALYSIS OF RESISTANCE TO *ASPERGILLUS* EAR ROT AND
AFLATOXIN ACCUMULATION IN MAIZE (*Zea mays* L.) INBRED LINES**

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**A THESIS RESEARCH SUBMITTED IN PARTIAL FULFILMENT OF THE
REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE IN PLANT
BREEDING AND BIOTECHNOLOGY**

**DEPARTMENT OF PLANT SCIENCE AND CROP PROTECTION
FACULTY OF AGRICULTURE
COLLEGE OF AGRICULTURE AND VETERINARY SCIENCES
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2017

DECLARATION

This thesis is my original work and has not been submitted for the award of any degree in any university.

Signed  Date 24/7/2017

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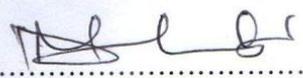
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ABSTRACT

Recurrent aflatoxin contamination in maize has been a major problem in Kenya as it consistently causes loss of produce and lives resulting to massive economic losses. Kenyan maize germplasm are susceptible to aflatoxin accumulation hence there is need to incorporate resistance genes into these germplasm. Therefore, the objective of this study was to improve quality and safety of maize through development of hybrids that are resistant to *Aspergillus flavus* and aflatoxin contamination.

Seventy F₁ hybrids were generated from North Carolina II (NCDII) cross among seventeen inbred lines. The trial was planted in a 5x15 Alpha lattice design in two replicates at KALRO Kiboko and Katumani in 2015. Ears were artificially inoculated with *Aspergillus flavus* spores at mid-silk stage. Data was collected on days to flowering, plant height, ear height, lodging, husk cover, stem borer infestation, ear rots and grain yield. After harvesting, grain was tested for *Aspergillus flavus* infection by plating. Quantification of aflatoxin content in the grains was done by ELISA technique using Accuscan Pro-reader kits.

The level of *Aspergillus flavus* among the hybrids ranged between 100 cfu/g and 2500 cfu/g while that of aflatoxin accumulation was between 2 ng/g and 15000 ng/g. The grain yield ranged from 1.39 t/ha to 5.8 t/ha. Hybrids 18, 31, 37, 56, 59, 60, 58, 65 and 68 were identified as the most resistant with high grain yields. *Aspergillus* ear rot in these hybrids was at 1.9%, while ear damage by stem borer was at 7.2%. The hybrids had an average starch content of 70% and 5% for oil content across the sites. *Aspergillus* ear rot, aflatoxin accumulation and poor husk cover were observed to be directly correlated. However, these traits were indirectly correlated to grain yield. Parents P329, Mp 313E, CKL05003 and Mp719 were identified as the best combiners for resistance with high negative general combining ability (GCA) effects for aflatoxin accumulation and *Aspergillus flavus*. Inbred lines NC298 and (CKL05003/La Posta Seq C7-F180-3-1-1-1-B-B -B)DH152-B-B were the

best combiners for grain yield with the highest positive GCA effects of 0.68 and 0.72 respectively. Parents (CKL05003/La Posta Seq C7-F180-3-1-1-1-B-B -B) DH56-B-B/Mp717, CKL05019/Mp 715 and ([CML444/CML395//DTPWC8F31-1-1-2-2-BB]-4-2-2-1-1-B*4/(9071xBabamgoyo)-3-1-BBB)-B-1-2-3-1-3-B-B/Hi27 had the highest specific combining abilities for resistance to aflatoxin accumulation and parents CKL05003/Hi27, (ZM621A-10-1-1-1-2-B*8/PHG35)-B-16-2-2-B-B/Mp719 and (CKL05003/La Posta Seq C7-F180-3-1-1-1-B-B -B) DH152-B-B/Mp 313E for *Aspergillus flavus* resistance.

This study showed that genetic variations existed among the genotypes hence they were genetically diverse. Husk cover was noted as an important secondary trait in phenotypic selection for resistance to *Aspergillus flavus* and aflatoxin accumulation in maize. Hybrids resistant to *Aspergillus flavus* and aflatoxin accumulation were identified from the study. These germplasm could be incorporated into local breeding programs for improved safe maize productivity. Marker-assisted selection should be considered as an avenue to propel this research further as it is more effective and convenient.

Key words: Maize, Aflatoxin, *Aspergillus flavus*, Hybrid, General combining ability, Specific combining ability.