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Genetic diversity of *Aspergillus flavus* and occurrence of aflatoxin contamination in stored maize across three agro-ecological zones in Kenya

Grace W Gachara¹, Anthony K Nyamache¹, Jagger Harvey², Gbemenou Joselin Benoit Gnonlonfin² and James Wainaina²¹Kenyatta University, Kenya²Biosciences Eastern and Central Africa-International Livestock Research Institute, Kenya

Aflatoxin contamination at post-harvest poses a serious challenge in achieving millennium development goals on food security especially in the developing world. In Kenya, major outbreaks of aflatoxicoses have been attributed to poor post-harvest storage practices. In this study, we conducted a cross-sectional survey within three Agro-ecological zones in Kenya, to determine occurrence and distribution of total aflatoxin in stored maize and the aflatoxigenicity potential of *Aspergillus flavus* in stored maize. The counties selected were; Kitui, Nakuru and Kitale (in Trans-Nzoia County). Sampling sites were selected based on previous aflatoxicoses outbreaks (Kitui) and major maize production areas (Nakuru and Kitale) where little information exists on the occurrence of aflatoxin contamination. A total of one hundred and thirty (130) kernel maize samples were random collected during the period between June and August 2012. Moisture content was determined using the standard oven method and *Aspergillus flavus* was isolated by direct plating technique. Genetic diversity of the isolates was determined by PCR and Single Sequence Repeats (SSR) micro satellites analysis. Positive strains were induced to produce B1 aflatoxins on Yeast Extract Sucrose Agar (YESA) and quantified using competitive ELISA technique. The results indicated mean moisture content of maize ranged between 6% and 34%, although this was found not to be significantly different ($p=0.23>0.05$). However, total aflatoxin contamination of postharvest stored maize samples between sites was significantly different ($p=0.000, <0.05$); with the highest contamination in Kitale at a mean of (9.68 $\mu\text{g/kg}$). *A. flavus* was isolated in 70% (N= 91) of the maize samples collected at postharvest. *A. flavus* isolates with the highest aflatoxigenicity potential were from Nakuru County with mean aflatoxin level at 239.7 $\mu\text{g/kg}$. Genetic distance based on Neighbor Joining (NJ) clustered the *A. flavus* isolates into five main clusters. Principal coordinate Analysis (PCA) analysis showed five distinct clusters with both axes explaining 60.17% of the variance. This study showed widespread distribution of aflatoxin contamination and a highly toxigenic *A. flavus* in stored maize in three major agro ecological zones in Kenya. These results suggest a potential health risk of aflatoxin outbreaks within these areas, thus call for more investigations.

kikogash@gmail.com