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Post Harvest Fungi Diversity and Level of Aflatoxin Contamination in Stored Maize: Cases of Kitui, Nakuru and Trans-Nzoia Counties in Kenya

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Abstract : Aflatoxin contamination of maize in Africa poses a major threat to food security and the health of many African people. In Kenya, aflatoxin contamination of maize is high due to the environmental, agricultural and socio-economic factors. Many studies have been conducted to understand the scope of the problem, especially at pre-harvest level. This research was carried out to gather scientific information on the fungi population, diversity and aflatoxin level during the post-harvest period. The study was conducted in three geographical locations of; Kitui, Kitale and Nakuru. Samples were collected from storage structures of farmers and transported to the Biosciences eastern and central Africa (BecA), International Livestock and Research Institute (ILRI) hub laboratories. Mycoflora was recovered using the direct plating method. A total of five fungal genera (Aspergillus, Penicillium, Fusarium, Rhizopus and Bssyochlamys spp.) were isolated from the stored maize samples. The most common fungal species that were isolated from the three study sites included A. flavus at 82.03% followed by A.niger and F.solani at 49% and 26% respectively. The aflatoxin producing fungi A. flavus was recovered in 82.03% of the samples. Aflatoxin levels were analysed on both the maize samples and in vitro. Most of the A. flavus isolates recorded a high level of aflatoxin when they were analysed for presence of aflatoxin B1 using ELISA. In Kitui, all the samples (100%) had aflatoxin levels above 10ppb with a total aflatoxin mean of 219.2ppb. In Kitale, only 3 samples (n=39) had their aflatoxin levels less than 10ppb while in Nakuru, the total aflatoxin mean level of this region was 239.7ppb. When individual samples were analysed using Vicam fluorometer method, aflatoxin analysis revealed that most of the samples (58.4%) had been contaminated. The means were significantly different ($p=0.00<0.05$) in all the three locations. Genetic relationships of A. flavus isolates were determined using 13 Simple Sequence Repeats (SSRs) markers. The results were used to generate a phylogenetic tree using DARwin5 software program. A total of 5 distinct clusters were revealed among the genotypes. The isolates appeared to cluster separately according to the geographical locations. Principal Coordinates Analysis (PCoA) of the genetic distances among the 91 A. flavus isolates explained over 50.3% of the total variation when two coordinates were used to cluster the isolates. Analysis of Molecular Variance (AMOVA) showed a high variation of 87% within populations and 13% among populations. This research has shown that A. flavus is the main fungal species infecting maize grains in Kenya. The influence of aflatoxins on human populations in Kenya demonstrates a clear need for tools to manage contamination of locally produced maize. Food basket surveys for aflatoxin contamination should be conducted on a regular basis. This would assist in obtaining reliable data on aflatoxin incidence in different food crops. This would go a long way in defining control strategies for this menace.

Keywords : aflatoxin, Aspergillus flavus, genotyping, Kenya
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