

Fingerprinting and Aflatoxin Production of *Aspergillus* Section *Flavi* Associated with Groundnut in Eastern Ethiopia

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Several *Aspergillus* species have the potential to cause aflatoxin contamination, posing a health threat to consumers of susceptible agricultural products such as groundnut, as well as an economic risk through commodity rejection of domestic and international markets. Novel technologies for aflatoxin control target specific DNA sequences of *Aspergillus*; thus, identifying the predominant fungal genotypes that colonize groundnut seed is essential. In this study, 184 *Aspergillus* isolates were obtained from groundnut seeds in eastern Ethiopia. They were analyzed for aflatoxin production by Ultra-Performance Liquid Chromatography, and fingerprinted using 23 Insertion/Deletion markers within the aflatoxin-biosynthesis gene cluster. The species observed included *A. flavus*, *A. tamarii* and *A. parasiticus*. Of the *A. flavus* sampled, L-, S-morphotypes were represented, as well as those deemed sclerotium non-producers (SNP).

All *Aspergillus* isolates tested produced measurable aflatoxins. Analysis of genetic distances by Neighbor Joining, Principal Coordinate Analysis and Structure clustered the isolates into four main groups. **Group I**, the largest, had 88% of the *A. flavus*, including all *A. flavus* L-strains, and *A. tamarii*, and the highest aflatoxin B₁ producer was *A. flavus* (N1436) (77.9 µg/mL). **Group II** contained 52.4% of *A. flavus* S-strains and 47.6% of *A. flavus* (SNP). **Group III** primarily included *A. parasiticus* (87.9%); among which, twenty produced aflatoxins B and G, with up to 50.3 µg/mL of G₁, whilst nine produced only B aflatoxins. **Group IV** was represented by four *A. flavus* S-strains produced aflatoxin B and G types, and two *A. flavus* (SNP). All *Aspergillus* isolates tested produced aflatoxins. This is the first report on aflatoxin contamination and *Aspergillus* genotypes present in groundnut from eastern Ethiopia. Predominant genotypes were identified as candidates for genome sequencing, and to generate a database of Ethiopian *Aspergillus* genomes for the development of effective aflatoxin control strategies in groundnut.