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## Fingerprinting of *Aspergillus* section *Flavi* associated with groundnut (*Arachis hypogaea L*.) and aflatoxin production in Eastern Ethiopia

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A spergillus species cause aflatoxin contamination on seeds, becoming a health threat in agricultural products and leading to commodity rejection by domestic and international markets. Novel technologies for aflatoxin control target specific DNA sequences of *Aspergillus*, thus, identifying the predominant fungal genotypes that colonize groundnut seeds is essential. In this study 184 *Aspergillus* isolates were obtained from groundnut seeds from eastern Ethiopia, were analyzed for aflatoxin production by Ultra-Performance Liquid Chromatography (UPLC) and fingerprinted using 23 insertion/deletions (InDel) within the aflatoxin-biosynthesis gene cluster. Analysis of genetic distances by Neighbor Joining (NJ), Principal Coordinate Analysis (PCoA) and structure clustered the isolates into four main groups. Group-1: 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-2: Contained 21 isolates, 52.4% of *A. flavus* S-strains and 47.6% of *A. flavus*. Group-3: Primarily included A. parasiticus (87.9%); among A. parasiticus isolates, 20 produced aflatoxins B and G, with up to 50.3 µg/mL of G1, whilst nine produced only B aflatoxins. Group-4: Was represented by only six *A. flavus*, four of which were S-strains able to produce the main four aflatoxins. All *Aspergillus* isolates tested produced aflatoxins. This is the first report on aflatoxin production and genotypes of *Aspergillus* present in groundnut in eastern Ethiopia. Predominant genotypes were identified as candidates for DNA sequencing and to generate an exclusive database of Ethiopian *Aspergillus* genomes for the development of effective aflatoxin control strategies in groundnut.

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