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Diversity of *Aspergillus* species associated with groundnut (*Arachis hypogaea* L.) in eastern Ethiopia as revealed by InDels and their potential for aflatoxin production

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Aspergillus species cause aflatoxin contamination, which becomes a health threat in agricultural products and leads to commodity rejection by domestic and international markets. Hence, it is necessary to discriminate diversity and aflatoxin producing species in the eastern Ethiopia. Therefore, the current study was undertaken to elucidate the genetic diversity of *Aspergillus* isolates through InDel (Insertion and Deletions of sequences) markers and evaluate *in vitro* aflatoxin production abilities of the isolates using YES (Yeast Extract Sucrose) medium. A total of 276 isolates were used for genetic diversity fingerprinting of DNA using 23 InDel markers based on aflatoxin biosynthesis gene cluster. Cluster analysis was analyzed by NJ (neighbor joining) and by PCoA (Principal Coordinate Analysis). The *Aspergillus* isolates studied in the current work grouped into three clusters. In addition, 269 isolates were tested for aflatoxin production using UPLC (Ultra Performance Liquid Chromatography). Aflatoxigenic isolates had a maximum of 247 $\mu\text{g mL}^{-1}$ aflatoxin B1 and 139 $\mu\text{g mL}^{-1}$ aflatoxin G₁. This study provides insight into the genetic biodiversity of aflatoxin biosynthesis gene cluster of *Aspergillus* in relation to *in vitro* aflatoxin production of isolates in the country. The prevalence of aflatoxigenic isolates was much higher (93% of the tested isolates) than the non-aflatoxigenic.

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