

ABSTRACT

Aflatoxins (AFs) are poisonous compounds produced by species of fungi belonging to the genus *Aspergillus* mainly *A. flavus* and *A. parasiticus*. However, there are some members of these species that do not produce toxins and have since become of interest for use in Biological Control programs. The species that produce AFs are believed to have clusters of aflatoxin-associated genes that confer aflatoxigenicity. However, recent findings suggest that the presence of aflatoxin genes may not imply aflatoxin production capability. We therefore examined the extent to which the presence or absence of aflatoxin-associated genes (genetic) infers aflatoxigenicity using the Dichlorvos-Ammonia (chemical) method as reference. We report a dissonance between the genetic and chemical methods of ascertaining aflatoxigenicity. Fungi (n = 314) that were morphologically identified as *A. flavus* and *A. parasiticus* were isolated from maize kernels and soil from Eastern Kenya. The fungi were further characterized to confirm their identities using a PCRsequence analysis of the internal transcribed spacer (ITS) region of rDNA which confirmed them to be *Aspergillus* species. We selected and induced 16 isolates in YES media amended with Dichlorvos to produce AFs. Seven of the sixteen isolates were DM-AM positive (aflatoxigenic) but lacked at least one of the key aflatoxin-associated genes. Even more confounding, *A. flavus* isolate (1EM2606) had all aflatoxin-associated genes but was non-aflatoxigenic (DVAM negative) while *A. flavus* (1EM1901) having all genes was aflatoxigenic (DV-AM positive). The genetic abundance of the AF-associated genes among the isolates was as follows: *aflQ* (100%), *aflD* (62.5%) followed by *aflR* (37.5%) and *aflP* (25%). We report that either method alone is limited in ascertaining aflatoxigenicity among *Aspergillus* section *Flavi*. The discordance between presence of aflatoxinassociated genes and aflatoxigenicity may be due to epigenetic factors that affect secondary metabolism, or even other signaling processes that alter toxin production that still remain poorly understood.