

Section: Microbiology, Mycotoxins and Food Safety

Elimination of post-harvest and pre-harvest aflatoxin contamination

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Abstract

Aflatoxins are extremely carcinogenic secondary metabolites produced by *Aspergillus flavus* when this fungus invades crops such as maize, cotton, tree nuts and peanuts prior to harvest, and a host of other commodities after harvest (during storage). Adverse health effects from the ingestion of these toxins have caused regulatory agencies throughout the world to limit the amount of aflatoxins that are permitted in food or feed that is available for sale. This results in undue economic burden on the grower. Strategies to address the food safety and economic issues employ both pre-harvest and post-harvest measures to reduce the risk of aflatoxin contamination in food and feed. Post-harvest measures, such as adequate storage, detection and decontamination or disposal, as well as continuous monitoring of potential contamination during processing and marketing of agricultural commodities, have proved to be crucial and indispensable in ensuring food and feed safety; however, these measures do not address the issue fundamentally. The post-harvest contamination is usually the result of preharvest presence of fungal contamination. Therefore, research focus in the past decades has shifted from post-harvest control to a more preventive approach employing various pre-harvest control measures. Pre-harvest control includes good cultural practices such as insect control, irrigation during drought conditions, planting and harvesting dates. In addition, new biotechnologies such as, 1) the use of non-toxigenic biocompetitive strains of *A. flavus* for biocontrol of aflatoxin contamination, and 2) identification of plant constituents that disrupt aflatoxin biosynthesis or fungal growth and their use in new biochemical marker-based breeding strategies to enhance resistance in crops to aflatoxin, could potentially save the agricultural industry in the U.S. alone hundreds of millions of dollars. Study of the genetics of the aflatoxin biosynthetic pathway for understanding how and why this fungus makes aflatoxins has enabled scientists to examine strategies to interrupt aflatoxin synthesis, thereby preventing aflatoxin contamination of crops. The fungal genome of *A. flavus* has been sequenced to understand the regulation of aflatoxin formation by environmental factors. This information is being used to assist in the development of host-resistance against aflatoxin contamination by studying the effects of various physiological parameters, e.g., drought stress on gene expression in toxigenic fungi.