

## Microbial strategies in controlling aflatoxins

Aflatoxins are a group of structurally related secondary metabolites produced mainly by *Aspergillus flavus* and *Aspergillus parasiticus* (Eaton and Groopman, 1994). They are commonly found in cereals, nuts and animal feeds and create a significant threat to the feed industry and animal production. Several strategies have been developed to avoid or reduce harmful effects of aflatoxins since the 1960's. However, prevention of aflatoxin contamination pre/post harvest or during storage has not been satisfactory and control strategies such as physical removal and chemical inactivation used in feed have their deficiencies, which limit their large scale application. It is expected that progress in the control of aflatoxin contamination will depend on the introduction of technologies for specific, efficient and environmentally sound detoxification. The utilization of biological detoxification agents, such as microorganisms and/or their enzymatic products to detoxify aflatoxins in contaminated feed can be a choice of such technology.

During the past decade, a series of bacteria have been reported to detoxify aflatoxins. Such bacteria include lactic acid bacteria (El-Nezami et al., 2000; Fazeli et al., 2009), *Nocardia corynebacterioides* (Castaneda et al., 2008), *Rhodococcus erythropolis* (Hormisch et al., 2004), *Mycobacterium fluoranthenvorans* (Alberts et al., 2006), *Bacillus licheniformis* (Petchkongkaew et al., 2008), *Stenotrophomonas maltophilia* (Guan et al., 2008), *Myxococcus fulvus* (Guan et al., 2010), et al. Besides, the ability of aflatoxin producing fungi of *Aspergillus* species and other filamentous fungi to biotransform aflatoxins has been reported (Varga et al., 2005; Wu et al., 2009). Additionally, aflatoxin detoxification enzymes such as



laccase, lactoperoxidase, anti-oxidative stress enzymes and some unknown enzymes have been identified from microorganisms (Alberts et al., 2009; Keyhani et al., 2009; Zhao et al., 2010).

Several reports have indicated a consensus that utilization of microorganisms and/or their enzymatic metabolites to detoxify mycotoxins in contaminated feed has advantages, such as mild reaction conditions, target specificity, efficiency and are environmentally friendly (Karlovsky, 1999; Dalié et al., 2010). However, many of the microbial strategies have only showed reduced concentration of aflatoxins and the structure and toxicity of the detoxified products are unclear. More attention should be paid to the detoxification reactions, the structure of biotransformed products and the genes responsible for the detoxification. Further studies could focus on identification of genes responsible for AFB<sub>1</sub> detoxifications.

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