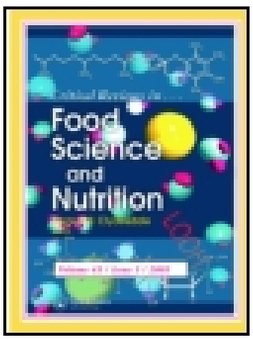

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Review on microbial degradation of aflatoxins

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Abstract

Aflatoxin (AF) contamination presents one of the most insidious challenges to combat, in food safety. Its adulteration of agricultural commodities presents an important safety concern as evident in the incidences of its health implication and economic losses reported widely. Due to the overarching challenges presented by the contamination of aflatoxins (AFs) in foods and feeds, there is an urgent need to evolve cost-effective and competent strategies to combat this menace. In our review, we tried to appraise the cost-effective methods for decontamination of aflatoxins AFs. We identified the missing links in adopting microbial degradation as a palliative to decontamination of aflatoxins AFs and its commercialization in food industries. Cogent areas of further research were also highlighted in the review paper.

Keywords: Aflatoxins, microbial degradation, decontamination, biodegradable products, toxicity

1.0 Introduction

Mycotoxins are secondary fungal metabolites produced by a variety of widespread microscopic toxigenic strains of *Aspergillus*, *Penicillium* and *Fusarium* (Terzi *et al*., 2014). The point of contamination could be due to pre- or post-harvest conditions (Rocha *et al*., 2014). Even though several mycotoxins have been detected in various commodities worldwide (Njobeh *et al*., 2010), the aflatoxins AFs are considered the most important mycotoxins in human foods and animal feeds (Strosnider *et al*., 2006; Yehia, 2014). Aflatoxins attract worldwide attention because of their significant impact on health and trade. In addition, aflatoxins are Of the four major AFs, i.e., aflatoxin B_1 (AFB_1), B_2, G_1 and G_2, the most important in terms of toxicity and occurrence, is AFB_1. In fact, it is one of the most important naturally occurring carcinogen (Makun *et al*., 2012). Aflatoxins generally, are the best known and most intensively researched investigated of all mycotoxins worldwide in the world (Reddy *et al*., 2011; USDA, 2013). Makun *et al*. (2012) reported that aflatoxins AFs are the most trivial mycotoxins in sub-Saharan Africa (SSA) in terms of their occurrence, economic and health effects associated with them.

Due to the impact of mycotoxins on health, it is necessary to mitigate their formation or at best inactivate their presence in food and feed products (Pizzolitto *et al*., 2012). Nevertheless, there are several strategies in preventing, eliminating or inactivating these toxins in foods and feeds have been reported. These strategies include physical approaches such as cooking, roasting, cleaning and milling (Park, 2002; Kabak *et al*., 2006). The chemical approaches include the use of hydrogen peroxide, ozonation and the use of ammonia (Mishra and Das, 2003). These methods can be used singly or complementary to one another (Huwig *et al*., 2001; Wu *et al*., 2009). None of these approaches can however, completely fulfill the desired efficacy, safety and

nutrient retention (Zhao *et al*., 2011). Based on that, the most promising alternative for AF decontamination could be via microbial detoxification (Samuel *et al*., 2013). Microbial detoxification may provide possible removal of these toxic substances in foods or feeds under mild conditions, thus limiting significant losses in the aesthetic quality of food products (Alberts *et al*., 2009; Samuel *et al*., 2014).

Though several reviews have been done on AFs in the literatures as evident in the studies presented by EFSA (2009) and Wu *et al*. (2009), this review presents an update of different studies undertaken on microbial degradation of AF, highlighting the products of AF biodegradation, mechanism of degradation, toxicity of biodegradable products released and experimental approaches adopted.

2.0 Aflatoxins

Aflatoxins were discovered around 1960. This was when 100,000 turkeys died as a result of toxin contamination caused by *Aspergillus flavus* (Quadri *et al.*, 2013). The AFs are predominantly produced by two *Aspergillus* species, i.e *A. parasiticus* and *A. flavus* (Tabata, 2011). Aflatoxins are bis-furan metabolites and 18 different types have been identified (Marin *et al*., 2013). Among the types recognized, are the AFs of public health and agricultural significance. These include aflatoxin B_1[1] (AFB_1), B_2 (AFB_2), G_1 (AFG_1), G_2 (AFG_2), including aflatoxins M_1 (AFM_1) and M_2 (AFM_2), that are hydroxylated metabolites of AFB_1 and AFB_2 respectively (Dors *et al*., 2011). Aflatoxin M_1 and M_2 are bio-transformed in the liver of animals

[1] When AFs are written, the subscripts shows the relative chromatographic mobility (Trucksess and Diaz-Amigo, 2011).

following ingestion of high levels of AFB_1 and AFB_2 (Hell *et al*., 2010). These are subsequently excreted via urine and milk (Trucksess and Diaz-Amigo, 2011).

Major agricultural commodities susceptible to AF contamination include peanuts, maize, cottonseeds, sorghum, cocoa beans, spices, rice, fruits and vegetables (Makun *et al*., 2012). Preliminary detection of AFs is possible since they are innately fluorescent compounds. Under ultraviolet light, the aflatoxin B group emits blue fluorescence, while the G members show green fluorescencing spots. According to Wu and Gulcu (2012), the most potent naturally ocurring liver carcinogen is AFB_1. It has been categorized as a group 1 carcinogen by the International Agency for Research on cancer (IARC) (IARC, 2002). Several studies have reported an order of severity among the chronic and acute toxicities of the various AFs. This order is $AFB_1 > AFG_1 > AFB_2 > AFG_2$, while AFM_1 and AFM_2 are less potent than their precursors. The less potency exhibited by the AFM groups is due to the steric hindrances, chirality and resonance energy of the cyclopentenone ring of the B series, as compared to the six-membered lactone ring of the G series (Haschek and Voss, 2013).

3.0 Degradation of aflatoxins by microorganisms

There is the need to carry out decontamination of AF contaminated agricultural commodities along the food production chain, bearing in mind that carrying out prevention during the production phases can be somewhat challenging, especially on a large scale. The process of decontamination of AFs can be done by physical, chemical and biological methods. Each method could involve the removal of contaminated commodities, inactivation or reduction of the toxin level (Halasz *et al*., 2009). Wang *et al*. (2011) reported that the physical methods are time consuming and may result in the partial removal of the AFs. The use of chemicals significantly

reduces AF concentrations however losses of nutrients, lowering of the aesthetic quality of food or feed and attendant high costs are inevitable (Jard *et al*., 2011).

Based on the disadvantages of the physical and chemical methods, microbial degradation shows promise as a better alternative to AF decontamination. Microbial degradation involves the use of microbial catabolic pathways to detoxify the AFs to less toxic intermediates or end products (Samuel *et al*., 2013). Microbial degradation offers some advantages such as product specificity, mild reactions conditions and feasible processes when applied in food and feed industries (Kolosova and Stroka, 2011).

Two key sites influencing the toxic activities of AFs are the furofuran and lactone rings (Mishra and Das, 2003). Altering their coumarin structure have also been reported to change the mutagenic properties of the AF (Liu *et al*., 1998a). Detoxification of the AF molecule also occurs when there is a cleavage of the difuran ring of the AF molecule (Cao *et al*., 2011). Studies on microbial degradation of AFs are targeted towards these rings. Microbial degradation of AFs has been extensively studied and is now a highly promising area of research. Different AF degrading microorganisms such as bacteria and fungi (including their respective enzymes) have been reported in the literature as elucidated in the subsequent sections of this review.

3.1 Bacterial degradation of aflatoxins

Since over four decades, scientific reports showed that numerous bacteria are capable of degrading aflatoxins (Wu *et al*., 2009). These bacterial species include *Nocardia corynebacteroides, Corynebacterium rubrum and Rhodococcus* spp. (Ciegler *et al*., 1966). Because of short degradation time and non-pigmentation in foods, microbial degradation is preferred in the food and feed industry (Teniola *et al*., 2005).

3.1.1 Lactic acid bacteria

Of all bacteria used to detoxify AFs, lactic acid bacteria (LAB) are the most studied (Oliveira *et al*., 2013). This class of microorganisms has demonstrated a great potential in removing AFs and can be utilized as starter cultures in the fermentation of foods and as additives in food processing (Shetty and Jespersen, 2006). The ability of LABs to detoxify AFs have been attributed to their strong affinity to the toxin (Juodeikiene *et al*., 2012). A number of studies have shown that LAB strains are able to reduce AFs from various matrices, through a binding process (Hathout *et al*., 2011). El-Nezami and co-workers, investigated the ability of two strains of *Lactobacillus rhamnosus* (GG and LC-705) and a *Propionibacterium* spp. to eliminate AFB_1 from intestinal luminal liquid medium of a chicken (El-Nezami *et al*., 2000). According to their report, within one minute, an average of 54% AF degradation was observed. Further investigation on the toxicity and transport of AFB_1 binding by the *Lactobacillus* strain GG using Caco-2 cells, showed that the strain reduced AFB_1 uptake and protected itself against membrane and DNA damage (Gratz *et al*., 2007). The detoxifying prospects of five different LAB cultures investigated for AFB_1 detoxification showed up to 45% reduction in AFB_1 concentration (Oluwafemi *et al*., 2010). Other studies on LAB detoxification of AFs have also been reported (Bovo *et al*., 2014; El-Khoury *et al*., 2011; Topcu *et al*., 2010; Zuo *et al*., 2013) as shown in Table 1. All the above-mentioned LABs were found to be efficient in reducing AF at varying levels.

3.1.2 Miscellaneous bacteria species

About 1000 different microorganisms comprising of algae, bacteria and fungi were studied for their degradation potential by Ciegler *et al*. (1966). Of all the microorganisms studied, only

Nocardia corynebacteroides (formerly known as *Flavobacterium aurantiacum*) recorded up to 70% reduction of AF with no new toxic products formed. The bacteria further irreversibly detoxified AFs in various food samples including milk, corn oil, peanut butter, corn, soybeans and peanuts. *In vivo* assays showed complete detoxification of AF with no new toxic product formed (Ciegler *et al*., 1966). Lillehoj *et al*. (1971) also reported the complete removal of AFM_1 from liquid medium by this bacterium, while Doyle *et al*. (1982) observed that the same bacterium is capable of transforming AFB_1 into aflatoxicol (AFL). *Nocardia corynebacteroides* was also studied by Hao and Brackett (1988) who observed that 23% of AFB_1 was eliminated in non-defatted peanut milk. The degradation mechanism utilized by these bacteria were observed to be an enzymatic pathway dependent process. This occurred through an indefinite binding with the bacterium's genomic DNA (Smiley and Draughon 2000).

Similar studies by Mann and Rehm (1976) reported that the degradation of AFB_1 by *Corynebacterium rubrum* occurred after four days of incubation. A fluorescent compound identified to be aflatoxin R_o (AFR_o) was reported. Total AFB_1 degradation by a *Mycobacterium* strain, isolated from the soil of a coal gas plant after 72 hrs incubation, was also reported by Hormisch *et al*. (2004). Cell-free extracts (CFE) and liquid cultures of *Rhodococcus erythropolis* were also investigated for the degradation of AFB_1 (Teniola *et al*., 2005). Residual AFB_1 (17%) was detected after 48 hrs, with only 3–6% left after 72 hrs. Over 90% degradation of AFB_1 occurred with *N. corynebacterioides* DSM 20151 and loss of mutagenicity was reported of *R.* er*ythropolis* cultures (Alberts *et al*., 2006). (Alberts *et al*., (2006).

Guan *et al*. (2008) reported AFB_1 degradation (83%) by *Stenotrophomonas maltophilia* after 72 hrs of incubation. It was observed that the degradation was primarily enzymatic. The culture

supernatant (CS) of a bacterial strain, *Myxococcus fulvus* ANSM068 after 48 hrs of incubation was reported to reduce AFB_1, AFG_1 and AFM_1 by 72, 68 and 64%, respectively (Zhao *et al*., 2011). Farzaneh *et al*. (2012) likewise reported 95% AFB_1 degradation by a *Bacillus subtilis* strain UTBSP1 isolated from pistachio nuts. A loss in the fluorescence property of the parent AF molecule was observed alongside the degradation process that occurred after the expression of the extracellular enzymes.

Investigations by Samuel *et al*. (2014) showed the ability of *Pseudomonas putida* to degrade AFB_1 to an undetectable level after 24 hrs of incubation. Gas chromatography mass spectrometry (GC-MS) and Fourier transform infra-red spectroscopy (FT-IR) analyses revealed that AFB_1 was degraded and subsequently transformed to AFD_1, AFD_2, and AFD_3 (Figure 1). The percentage reduction in AFB_1 was 100%, while a A change in the lactone and furan ring (presumably, through the reduction of the lactone and the carbonyl moieties y of the furan ring) of the AF molecule was observed. The compounds formed during the process were also reported to be non-toxic (Samuel *et al.*, 2014). while toxicity was reduced. *Cellulosimicrobium funkei* strain was has also been observed to possess a 97% degrading ability and same strain was reported to attenuate the adverse effects of AFB_1 on ducklings (Sun *et al*., 2015).

In a recent study by Eshelli *et al*. (2015), the AFB_1 degradation by a *R. erythropoli*s strain (ATTC 4277) was characterized and elucidated by comprehensive analysis on Liquid Chromatography-Mass Spectrometry (LC-MS) and FT-IR (Figure 2). It was hypothesized that AFB_1 was degraded through a series of reactions to form an aromatic compound (presumably, coumarin structurally-related) with a molecular formula $C_{13}H_{16}O_4$ and a molecular mass of 236.1049.

3.2 Fungi

Although fungal i species produce AFs, certain species and strains have been reported to degrade AFs (Table 1). Wu *et al*. (2009) stated that the fungal i metabolites can lower the pH of a medium and the subsequent acidic condition could reduce AF levels. This class of microorganisms has been identified to possess corresponding genes codings for AF degrading enzymes such as laccases, oxidases and peroxidases (Shcherbakova *et al*., 2015). The degradation of AFB_1, AFB_2, AFG_1 and $AFG_2$the four major AFs by the mycelia um and filtrates of *A. parasiticus* after 24 hrs of incubation, have been reported in several studies (Doyle and Marth, 1978a; 1978b; 1978c; Shih and Marth, 1975). Peroxidase was later confirmed as the enzyme involved in the AF degradation by this fungus (Doyle and Marth, 1979). Hamid and Smith (1987) reported of on AF detoxifying activity by cell free extracts (CFE) and mycelia um of *A. flavus* 102566. Aflatoxin B_1 and G_1 degradation of 23 and 25% were respectively, obtained after 6 days of incubation. Enzymes belonging to the cytochrome P-450 monooxygenase system were suggested to be involved in the degradation process (Hamid and Smith, 1987).

Armillariella tabescens was observed to detoxify AFB_1 spiked media (Liu *et al*., 1998b). The detoxifying ability of this organism was attributed to the enzymes found in the active extract of the mycelium pellets. Alberts *et al*. (2009), reported on the degradation of AFB_1 by culture filtrates of *Pleurotus ostreatus*, *Peniophora* spp., *Bjerkandera adusta*, and *Phanerochaete chrysosporium*. Across the fungal cultures, percentage degradation obtained were 36%, 52%, 28% and 14%, respectively, and this coinciding ed with a loss of fluorescence and mutagenicity. The cultures were also reported to exhibit laccase activity. Wu *et al*. (2009) described fungal strains of *A. niger, A. flavus*, *Eurotium herbariorum* and *Rhizopus* spp. as capable of degrading

AFB_1 by transforming it to AFL. This was attributed to a decrease in the cyclopentenone carbonyl moiety of the AFB_1 molecule. On the other hand, It was also noted that *A. niger* was noted as was being capable of converting AFL to AFB_1 and that the AFB_1 molecule can then be further converted to AFB_{2a}. The entirety contents of AFB_1 and AFL were observed to reduce over time, with a 98.6% degradation and a proposition that both compounds were metabolized to other substances (Figure 3).

3.3 Yeast

Yeast has been known for ages to carry out fermentation in food processing and preservation (Hathout and Ali, 2014). Yeasts have been reported to follow similar mechanism as LAB in binding to AFs as a means of detoxification (Shetty and Jespersen, 2006; Wu *et al*., 2009). In a study by Stanley *et al*. (1993), *Saccharomyces cerevisiae* was used to lessen the toxicity of AF *in vivo*. Results obtained showed that *S. cerevisiae* prevented heart and liver hyperplasia, decreased serum albumin and prevented weight loss in the chicks. Similar reports of yeast binding and subsequent AF detoxification have also been reported by Shetty *et al*. (2007) and Goncalves *et al*. (2015).

3.4 Protozoa

Few studies on the use of protozoa for AF degradation have been reported. Cells of *Tetrahymena pyriformis* decreased AF concentrations by 67% in 48 h, with the formation of a blue fluorescent compound identified as AFR_o (Teunisson and Robertson, 1967). This was later characterized and a molecular weight of 314 kDa recorded (Robertson *et al*., 1970). It was also concluded that *T. pyriformis* reduced the carbonyl moiety in the cyclopentane ring of the AFB_1 molecule to a hydroxyl.

3.5 Enzyme degradation of aflatoxins

Enzymes capable of degrading AFs have also been extracted and purified from different microbial systems. According to Shapira (2004), detoxification using specific enzymes avoids the shortcoming of using applying a whole microorganism, which apart from their degradation activity, may unintentionally impair the organoleptic properties of the product and its safety toxic aspects tendencies. The use of enzymes is far more convenient since they are substrate specific, effective, environmentally friendly and moreover, their application in food and feed industries have been established (Kolosova and Stroka, 2011).

Enzymes responsible for the degradation of AFs degradation have been studied and identified as to include lacasses, peroxidases, oxidases and reductases (Alberts *et al*., 2009; Doyle and Marth, 1979; Taylor *et al*., 2010; Yehia *et al*., 2014; Wu *et al*., 2015). Doyle and Marth (1978d) investigated the effect of lactoperoxidase on AFB_1 and AFG_1. However, low D degradation of AFB_1 (4%) and AFG_1 (5%) were observed after 24 hrs. and P products of degradation obtained were AFB_{2a} and other water soluble compounds. In a separate study by Liu *et al*. (1998b), an enzyme purified from *Armillariella tabescens* (E-20), which was immobilized (Liu *et al*., 1998a) and named aflatoxin-detoxifizyme ADTZ (Liu *et al*., 2001), showed detoxified cation of AFB_1, and consequent completely reducing tion in its toxicity and mutagenicity. In that study, the AF was completely detoxified, and the Infrared (IR) spectra suggested that an enzyme was responsible for opening the difuran ring of AFB_1 that led to its subsequent hydrolysis (Figure 4).

Continuing from of an earlier study by Cao *et al*. (2011), the previously purified ADTZ was characterized and AFB_1 conversion monitored. An Electrospray ionization-tandem mass spectrometry (ESI-MS/MS) analysis and a protein BLAST search inferred that the enzyme is an

AFO, a new oxidase differing from other reported AF-converting enzymes. Similar to earlier observations by Liu *et al*. (1998b), High performance thin layer chromatography (HPTLC) analysis of the AFO also suggested that it hydrolyzed the bisfuran ring system of AFB_1. The AFO was also reported to have acted on versicolorin A, 3,4-dihydro-2H-pyran and furan ring, suggesting that 8,9-unsaturated carbon-carbon bond of AFB_1 is the reactive site for AFO (Wu *et al*., 2015).

Commercial horse radish peroxidase and a partially purified peroxidase were also observed to detoxify up to 60 and 38% AFB_1, respectively (Das and Mishra, 2000), while an purified extracellular enzyme purified from *Pleurotus ostreatus* reportedly showed AF-degradation activity (Motomura *et al*., 2003). The molecular mass of the purified enzyme was estimated to be 90 kDa and observations from fluorescence measurements suggested that the enzymes cleaved the lactone ring of the AF molecule, converting it to AFL.

Taylor *et al*. (2010) identified and characterized $F_{420}H_2$-dependent reductases from *Mycobacteria smegmatis* that catalyzed AF degradation. These enzymes were different from enzymes earlier reported of to degrade ing AF. The $F_{420}H_2$-dependent reductases were reported found to have reduced an α,β-unsaturated ester and subsequently, destabilized the lactone ring (Figure 5). Similar studies on f a purified enzyme from *M. fulvus*, labelled MADE showed that AFM_1 and AFG_1 were degraded to by 97 and 96%, respectively (Zhao *et al*., 2011). The mechanisms of the degradation or end-products were however, not stated.

A manganese peroxidase (MnP) purified from *Phanerochaete sordida* YK-624 showed AFB_1 detoxification of 86% after 48h (Wang *et al*. 2011). Subsequent analysis revealed that AFB_1 was first oxidized to AFB_1-8,9-epoxide by the MnP and then hydrolyzed to AFB_1-8,9-dihydrodiol

(Figure 6). The difuran ring was opened in the subsequent hydrolysis step and a reduction in the mutagenic activity observed detected.

4.0 Conclusion

The severe adverse effects of AF cannot be overemphasized. What is most crucial is to evolve a cost-effective means of detoxifying ication of aflatoxins AFs in foods and feeds before they are consumption and utilized ation of food crops. In addition, since microbial mechanisms offer a better process means of decontamination, efforts should be made to elucidate the processes of degradation using animal models, taking into account that the same microorganism may also be harmful or toxigenic in producing other toxins of health significance. Hence, proper understanding of the harmful effects or toxicity levels of microorganisms used or the products generated thereafter is of paramount importance. Also, toxicological studies in animals are also emphasized. We hope that when all these investigations are painstakingly enunciated, commercialization largescale employment of the efficient and cost-effective methods of for the detoxification of aflatoxins AFs in the food and feed industry ies can be implemented for the overall benefit s of mankind.

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Table 1: Aflatoxin binding or degrading microorganisms, mechanisms and products of degradation

Microorganism	Mechanism of detoxification	Degradation products	Toxicity	References
Bacteria				
Bacillus spp.[a]	Enzymatic	None	ND[b]	Gao *et al*. (2011); Guan *et al*. (2008) & Farzaneh *et al*. (2012)
Bifidobacteria[a]	Binding	None	ND[b]	Peltonen *et al*. (2001)
Brachybacterium spp.[a]	NR[c]	NR[c]	ND[b]	Guan *et al*. (2008)
Brevundimonas spp.[a]	NR[c]	NR[c]	ND[b]	Guan *et al*. (2008)
Cellulosimicrobium spp.[a,d]	Enzymatic	NR[c]	ND[b]	Guan *et al*. (2008); Sun *et al*. (2015)
Corynebacterium rubrum[a]	Enzymatic	AFRo	ND[b]	Mann and Rehm (1976)
Enterobacter spp.[a]	NR[c]	NR[c]	ND[b]	Guan *et al*. (2008)
Flavobacterium aurantiacum[a,d]	Enzymatic	AFL	NT[e]	Doyle *et al*. (1982); Hao and Brackett (1988) & Smiley and Draughon

				(2000)
Klebsiella spp.[a]	NR[c]	NR[c]	ND[b]	Guan *et al*. (2008)
Lactobacillus spp.[a,d]	Binding	NR[c]	NT[e]	El-Khoury *et al*. (2011); El-Nezami *et al*. (2000); Gratz *et al*. (2007); Oluwafemi *et al*. (2010) & Peltonen *et al*. (2001)
Mycobacterium spp.[a]	Enzymatic	NC[f]	ND[b]	Hormisch *et al*. (2004); Teniola *et al*. (2005)
Myxococcus fulvus[a]	Enzymatic	NC[f]	ND[b]	Zhao *et al*. (2011)
Nocardia corynebacteroides[d]	Enzymatic	None	NT[e]	Ceigler *et al*. (1966); Teniola *et al*. (2005) & Tejada-Castaneda *et al*. (2008)
Phoma spp.[a]	Enzymatic	NC[f]	ND[b]	Shantha (1999) & Shcherbakova *et al*. (2015)
Probiotic organisms[d]	Binding	NC[f]	ND[b]	Serrano-Nino *et al*. (2013) & Zuo *et al*. (2013)
Pseudomonas spp.[a]	Enzymatic	AFD_1, AFD_2, AFD_3	LT[g]	Samuel *et al*. (2014) & Sangare *et al*. (2014)

Rhodococcus spp.[a]	Enzymatic	$C_{13}H_{16}O_4$	NT[e]	Alberts *et al*. (2006); Eshelli *et al*. (2015); Guan *et al*. (2008) & Teniola *et al*. (2005)
Stenotrophomonas maltophilia[a]	Enzymatic	NC[f]	ND[b]	Guan *et al*. (2008)
Streptococcus thermophilus[a]	Binding	ND[a]	ND[b]	El-Khoury *et al*. (2011)
Streptomyces spp.[a]	Enzymatic	NC[f]	ND[b]	Eshelli *et al*. (2015)
Fungi				
Absidia repens[a]	Enzymatic	AFRo	ND[b]	Detroy and Hasseltine, (1969)
Alternaria spp.[a]	Inhibition of synthesis	NC[f]	ND[b]	Shantha (1999)
Aspergillus flavus[a]	Enzymatic	AFL, AFL-A, AFL-B & AFB_{2a}	ND[b]	Hamid and Smith (1987) & Wu *et al*. (2009)
Aspergillus niger[a]	Enzymatic	AFL, AFL-A, AFL-B & AFB_{2a}	ND[b]	Ciegler *et al*. (1966); Mann and Rehm (1976) & Wu *et al*. (2009)
Aspergillus parasiticus[a]	Enzymatic	NC[f]	ND[b]	Doyle and Marth (1978a, 1978b, 1978c, 1979); Shih

				and Marth (1975)
Armillariella tabescens[a]	Enzymatic	NC[f]	ND[b]	Liu *et al*. (1998b)
Candida utilis[a]		Benzofuran, tinuvin, dioctyl phthalate	ND[b]	El-Shiekh *et al*. (2007)
Dactylium dendroides[a]	Enzymatic	AFRo	ND[b]	Detroy and Hasseltine (1969)
Mucor spp.[a]	Enzymatic Bioremediation	AFRo, furan-4,5diethyl-2,3-dihydro-2,3-dimethyl, 2-docosane, ketone-2,2 -dimethyl cyclohexyl methyl mannofuranoside	ND[b]	Detroy and Hasseltine (1969); El-Shiekh *et al*. (2007); Mann and Rehm (1976); Shantha (1999)
Paecilomyces lilacimus[a]	Bioremediation	Phenol-bis-(1,1-dimethyl)-4-methyl, methyl dimethoxyphenyl	ND[b]	El-Shiekh *et al*. (2007)

		propanoate, dioctyl phthalate, hexanone		
Penicillium spp.[a]	Enzymatic	Compound similar to AFB_1	ND[b]	Ciegler *et al*. (1966) & El-Shiekh *et al*. (2007)
Peniophora spp.[a]	Enzymatic	None	LT[g]	Alberts *et al*. (2009)
Phanerochaete chrysosporium[a]	Enzymatic	None	LT[g]	Alberts *et al*. (2009)
Phoma spp.[a]	Enzymatic	NC[f]	ND[b]	Shantha (1999) & Shcherbakova *et al*. (2015)
Pleurotus ostreatus[a]	Enzymatic	Other compounds	ND[b]	Alberts *et al*. (2009); Das *et al*. (2014) & Motomura *et al*. (2003)
Rhizopus spp.[a]	Inhibition of synthesis/ degradation	Intermediate compound	LT[g]	Cole and Kirksey (1971); El-Shiekh *et al*. (2007); Kusumaningtyas *et al*. (2006); Wu *et al*. (2009)
Trichoderma spp.[a]	Enzymatic Bioremediation	AFRo, tinuvin, limonene benzofuranone, hexadrotrimethyl	ND[b]	El-Shiekh *et al*. (2007); Mann and Rehm (1976); Shantha (1999)

		benzene, androstanedione		
Protozoa				
Tetrahymena pyriformis[a]	Enzymatic	AFRo	ND[b]	Robertson *et al*. (1970); Teunisson and Robertson (1967)
Yeast				
Saccharomyces cerevisae[a,d]	Binding	NC[f]	ND[b]	El-Shiekh *et al*. (2007); Goncalves *et al*. (2015); Kusumaningtya *et al*. (2006) & Shetty *et al*. (2007)
Enzyme				
AF-detoxifizyme (ADTZ)[a]	Enzymatic	NC[f]	LT[g]	Liu *et al*. (1998a, 1998b, 2001)
AF oxidase (AFO)[a]	Enzymatic			Cao *et al*. (2011) & Wu *et al*. (2015)
Crude enzyme[a]	Enzymatic	NC[f]	ND[b]	Liang *et al*. (2008)
Extracellular enzyme[a]	Enzymatic	AFL	ND[b]	Motomura *et al*. (2003)
Laccase[a]	Enzymatic	NC[f]	LT[g]	Alberts *et al*. (2009)

Lactoperoxidase[a]	Enzymatic	AFB_{2a} and some derivatives	ND[b]	Doyle and Marth (1978d)
Manganese peroxidase[a]	Enzymatic	AFB_1-dihydrodiol	ND[b]	Wang *et al*. (2011) & Yehia *et al*. (2014)
Myxobacteria AF degradation enzyme (MADE)[a]	Enzymatic	NC[f]	ND[b]	Zhao *et al*. (2011)
Peroxidase[a]	Enzymatic	NC[f]	LT[g]	Das and Mishra (2000)
Reductase[a]	Enzymatic	NC[f]	ND[b]	Taylor *et al*. (2010)

Keys*: [a]In vitro; [b]ND – Not Done; [c]NR – Not Reported; [d]In vivo; [e]NT – Not Toxic; [f]NC – Not Characterized; [g]LT – Less Toxic*

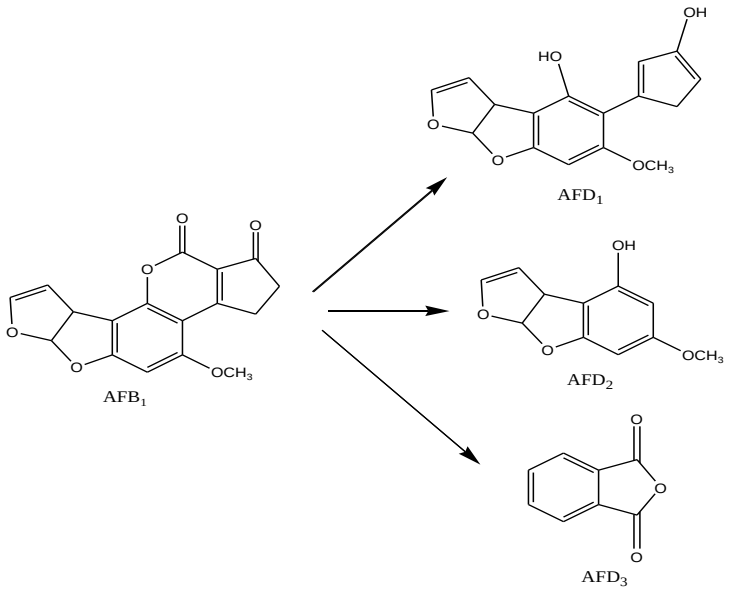

Figure 1: Scheme of AFB_1 degradation by *Pseudomonas putida* (Adapted from Samuel *et al*., 2014)

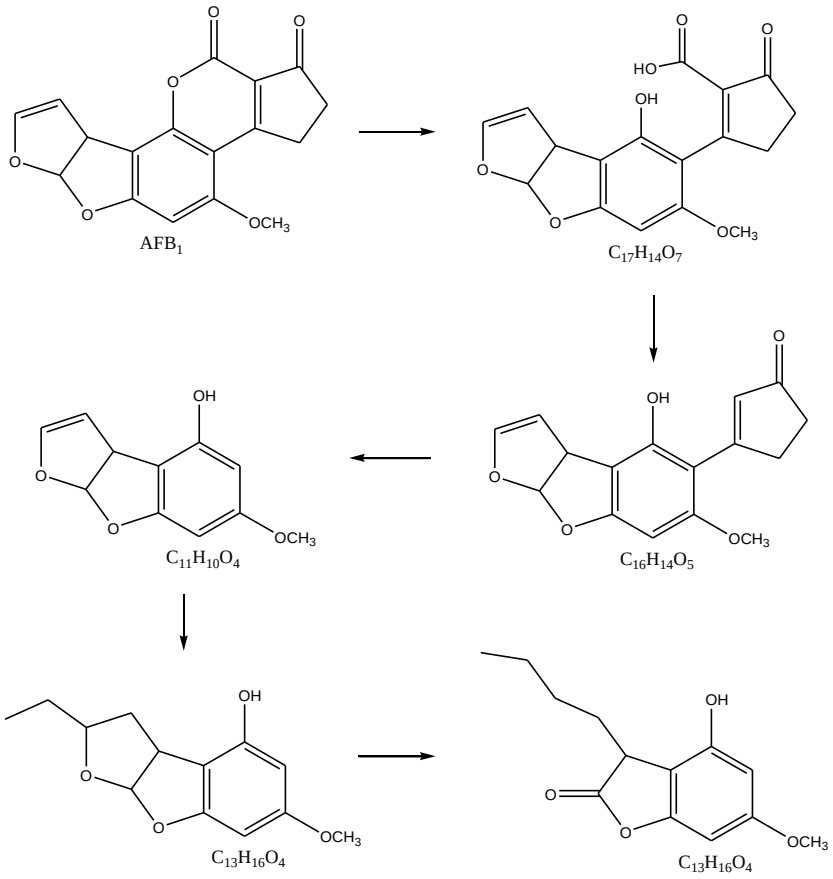

Figure 2: Hypothetical degrading mechanism for AFB_1 by *R. erythropolis* (Adapted from Eshelli *et al.*, 2015)

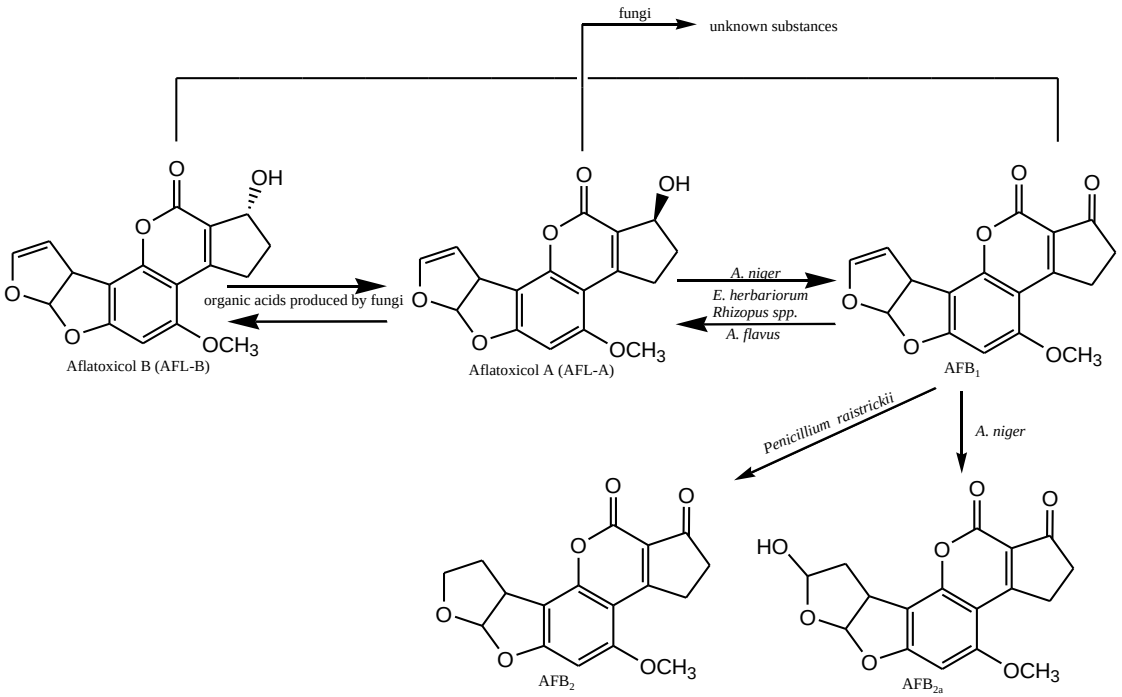

Figure 3: Degradation of AFB_1 by fungi (Adapted from Wu *et al*., 2009)

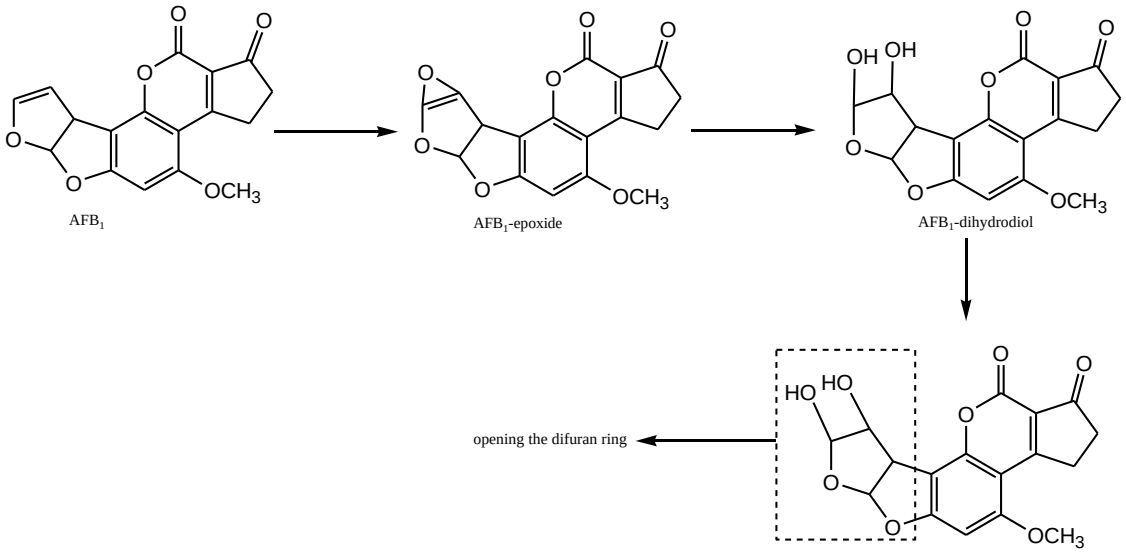

Figure 4: Proposed degradation pathway of AFB_1 by *Armillariella tabescens* (Adapted from Wu *et al.*, 2009)

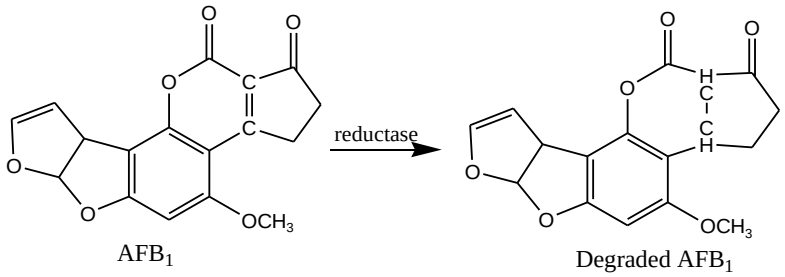

Figure 5: Reduction mechanism of AFB_1 by $F_{420}H_2$-dependent reductases (Adapted from Taylor *et al.*, 2010)

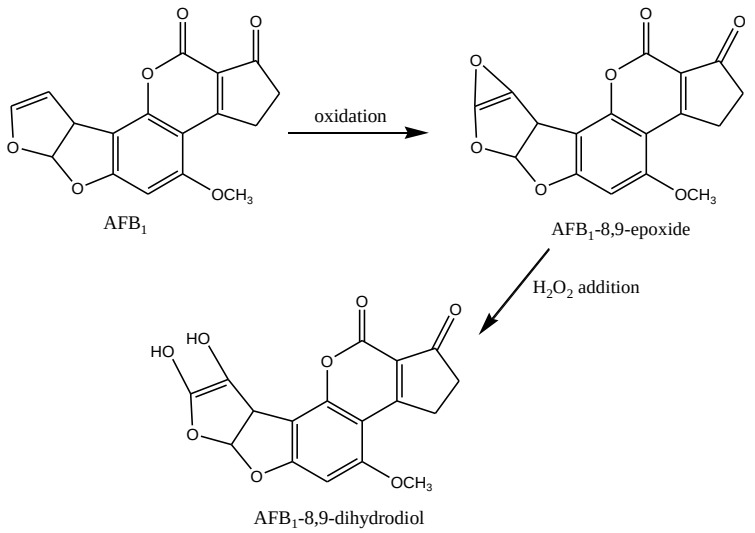

Figure 6: Pathway of degradation of AFB_1 by MnP from *Phanerochaete sordida* YK-624

(Adapted from Wang *et al*., 2011)

