Ind J Clin Biochem (Apr-June 2017) 32(2):124–133
DOI 10.1007/s12291-017-0649-2

REVIEW ARTICLE

Aflatoxins: Implications on Health

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Received: 13 February 2017 / Accepted: 13 March 2017 / Published online: 28 March 2017

Abstract Environmental occurrence of *Aspergillus* and other fungal spores are hazardous to humans and animals. They cause a broad spectrum of clinical complications. Contamination of aflatoxins in agri-food and feed due to *A. flavus* and *A. parasiticus* result in toxicity in humans and animals. Recent advances in aspergillus genomics and aflatoxin management practices are encouraging to tackle the challenges posed by important aspergillus species.

Keywords Aspergilli · Polyketides · Aflatoxins · Toxicity · Genomics

Introduction

Aspergillus species influence human and animal health directly and indirectly with a significant economic impact on the society. *A. flavus* and *A. parasiticus* are the two major species that produce aflatoxins. Several mycotoxins are reported from several other mycotoxigenic fungi of which the aflatoxins are the most toxic and damaging polyketides [1]. Economically important crops such as maize, rice, cottonseed, peanuts, and spices are all susceptible for contamination of aflatoxin. *A. flavus* is the major contributor of aflatoxin in pre and post-harvest agricultural food and feed. It is a major global challenge to manage *Aspergillus* infections in humans and aflatoxin contamination in crops and other food products [2]. Four types of aflatoxins are relevant for humans, animals, agro—food and feeds. These are aflatoxin B_1, B_2, G_1 and G_2.

Approximately 25% of the crops are considered contaminated by mycotoxins of which aflatoxin B_1 is the major toxin (FAO) [3]. Several food materials such as cereals, nuts, milk, spices, vegetables, fruits, oils and meat are prone for aflatoxin contamination. International Agency for Research on Cancer (IARC) conducted evaluation of several chemicals of their carcinogenic potential and classified aflatoxins as most potent natural, known human carcinogens. In view of toxic and carcinogenic effects of aflatoxin contaminated foods, US department of Agriculture (USDA) and Food and Drug Administration (FDA) set the tolerance limit of 20 ppb on foods. EU countries allow much lower ppb concentration of Aflatoxins. Accepted levels for toxins are variable for various foods in different countries.

Aflatoxins are polyketide compounds synthesized by secondary metabolic pathway in *Aspergilli*. As they are carcinogenic, teratogenic and mutagenic in nature, it is a real challenge to prevent and detoxify these compounds. The polyketide biosynthetic machinery imparts the potential to secrete aflatoxins in *Aspergillus flavus* isolates. This pathway also contributes to structural and functional diversity of various other polyketides produced by different *Aspergillus* species. Current review focuses on some important aspects of aflatoxins of *Aspergilli* relevant to human health.

Aflatoxin Producers

Aspergillus species are the main source of aflatoxins in the environment. These species are ubiquitous and universal in

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Fig. 1 Ground nut and maize kernels infested by *Aspergils flavus*

distribution. The high ecological, biological and metabolic diversity of *Aspergillus* species led to exploration of secondary metabolites among these species. The medical 4, agricultural and biotechnological importance of *Aspergillus* species is realized well in the recent past.

Morphological and taxonomical features of *Aspergilli* have some similar and few distinct characters. *A. flavus*, *A. parasiticus* are uniseriate and biseriate, and have mostly dense conidiophores. *A. flavus* and *A.parasiticus* are known to synthesize aflatoxins. Recent researches show that twenty species of *Aspergilli* are capable of producing aflatoxins. Three sections of the genus *Aspergillus*, section *Flavi, Nidulantes* and *Ochraceorosei* are reported to secrete these aflatoxins. These toxins are difuranocoumarin compounds, designated as aflatoxin B_1, B_2, G_1 and G_2 based on their blue or green fluorescence under U.V. light and the relative mobility in thin layer chromatography. Others include P_1, Q_1, B_2A, G_2A which are formed as a result of biotransformation or metabolism of aflatoxins in humans and animals [5]. Aflatoxin M_1 is a hydroxylated form of aflatoxin B_1 formed in animal tissues and fluids as a metabolite of B_1 [6].

The understanding of the secretion of aflatoxin by *A. flavus* came to light during severe outbreak of Turkey X disease in 1961 in U.K. which leads to death of a number of Turkey birds and several other farm animals. At that time aflatoxin is considered as an invisible fluorogenic polyketide compound secreted by *A. flavus*. Subsequently the compounds were designated as "A" for the genus *Aspergillus* and "FLA" for the species *flavus* and toxins as they are toxic. The negative effects of aflatoxin production on crops and human health lead to economic losses.

Aflatoxin Contamination in Food Crops and Feed

Aflatoxin contamination is often observed in several food materials such as cereals, milk, spices, vegetables, fruits, nuts, oils and meat etc. [7, 8]. Cereal grains such as corn, rice, barley, wheat, sorghum, and soybean are also susceptible for *A. flavus* contamination and thereby AFB_1 accumulation. Aflatoxins are produced on cereals both in field (in plants) and storage (in grains). Rice and sorghum, important staple food in various countries are highly susceptible for aflatoxin contamination [9, 10]. Chronic exposure to aflatoxin contaminated food can lead to cancer, nutritional deficiency leading to morbidity and mortality. Hence, the levels of aflatoxins are being monitored strictly in various countries and stipulated guidelines for international trade are also (Fig. 1) formulated. The cut off values for aflatoxin in food are variable in various countries (Table 1).

A high level scientific committee FAO (Food and Agriculture Organization) and WHO (World Health Organisation) on food additives estimated potency values

Table 1 Permissible limits of aflatoxins in different countries

Country	Food items	Limits (μg/kg)
United Kingdom	Nuts, figs, and related products	2–12
United States	Milk, dairy products, Barley, cocoa, coffee, confectionery, corn/maize copra, dairy, dried fruit, feeds, ground nuts/peanuts, infant formula, oats, rice, rye, sorghum, soy, spices, tree nuts, and wheat	0.5–20
European union	Groundnut, peanuts, spices and other food stuff	2–12
Australia	All the food stuff except peanuts	5
	Peanuts and related products	15
India	Nuts, spices, cereals and all other food products	30
China	Rice, sorghum, barley, nuts etc.	5–50
Japan	All the food stuffs	10

for AFB_1 from the epidemiological data. Several reports indicate groundnuts are the main susceptible products for aflatoxin contamination [11]. The US department of Agriculture (USDA) and Food and Drug Administration (FDA) set a tolerance limit of 20 ppb for aflatoxins in view of their toxic effects on foods. However, FDA allows more than 20 ppb in corn and cottonseed meal to be fed for livestock (www.fda.gov/Food/GuidanceRegulation/).

Besides groundnuts, cotton seed and cotton bolls are also susceptible to aflatoxin contamination. Tree nuts such as almonds, walnuts and pistachios also reported to suffer contamination of AFB_1 to a lesser degree. Groundnuts get infected with aflatoxigenic Aspergilli from soil through seed pods. The contamination of toxins can occur in ground nut kernels prior to harvest or during drying and storage also. European union fixed a cut of value of total aflatoxins of 4ug/kg in dried fruits for human use.

Spices

Frequent contamination of Aflatoxin in spices in tropical countries is attributed to atmospheric temperature, humidity and the drying and processing conditions. Several countries reported contamination of aflatoxin in ground red pepper [12–14]. Several other spices such as cumin, black pepper, cardamom, ginger, coriander etc. were also reported to have contamination of *A. flavus* and aflatoxins to a lesser degree compared to cereals [15].

Products

Aflatoxin B_1 when ingested by animals in the contaminated feed is converted into a major metabolite aflatoxin M_1 which is not eliminated or destroyed during pasteurization. Such contamination of aflatoxin M_1 and M_2 are reported from different countries [16, 17].

AFB_1 and AFB_2 will be converted to AFM_1 and AFM_2 in liver and excreted in the milk when the animal ingests aflatoxin in its feed [18]. Hence dairy products are contaminated with AFM_1 and AFM_2. The commission of European communities established a limit for AFM_1 that is 50 μg/kg for milk (www.efsa.europa.eu). Similar regulations are made in developed countries.

The animal food, basically meat and their products are susceptible to aflatoxin contamination as they receive contaminated animal feed [19]. Experimental evidence for aflatoxin metabolites in chicken are well documented [20, 21]. Several animal feed concentrates including cereal grains, soybean products, oil cakes etc. prepared from groundnuts, as base cotton seed, sunflower, palm, copra and fish meal are reported to have contamination of Aflatoxins. Regulation for aflatoxins is being exercised for animal feed in some countries [19]. The total permissible limit for aflatoxins in animal feed range from 0 to 50 ppb with an average of 20 ppb (FAO 2004). However, in developing countries 25–50% show more than 20 ppb of aflatoxins. The range observed is 100–1000 ppb. The permeable limit is 4–20 ppb for feed and food products based on WTO–stipulations.

Aflatoxicosis

Animal Health

The severity of toxicity due to intake of aflatoxin depends on species, age, sex and nutritional status. Major action of toxicity is observed on liver resulting in hepatic damage and observed decreased milk and egg production. Aflatoxicosis in animals depicts symptoms of gastrointestinal dysfunction, reduced reproductivity, reduced feed utilization and efficiency, anaemia and jaundice.

In nursing animals if fed with aflatoxin contaminated feed aflatoxin B_1 will be converted to the metabolite M_1 which will be excreted in milk of dairy cattle. The carcinogenic effect of aflatoxins has been studied and reported in detail. Aflatoxin B_1, M_1, and G_1 are known to cause different types of cancers in different animal species. AFB_1, is the only toxin identified by the International Agency for Research on Cancer (IARC) with sufficient evidence as carcinogen.

Human Health

Several effects of aflatoxin exposure are well studied. Acute aflatoxicosis in humans and animals is reported worldwide. Aflatoxicosis due to chronic exposure at high

and moderate concentrations can lead to acute primary Aflatoxicosis. Symptoms include haemorrhage, acute liver damage, edema, digestion problems and death.

Primary aflatoxicosis results from chronic exposure to Factors Influencing Aflatoxin Production at low to moderate levels. Impaired digestion and slow rate of growth are the main symptoms. Chronic aflatoxicosis includes teratogenic effect associated with congenital malformation. Aflatoxins are also mutagenic and carcinogenic. Mutagenic effect leads to mutation in genetic code, alteration in DNA which lead to chromosomal breaks, rearrangements, loss or gain of chromosome or changes within a gene.

Mechanism of Action of Aflatoxins

Epidemiological data from studies in African countries, particularly in South Africa, South East Asia and India implicate aflatoxins in the hepatobiliary carcinoma, malnutrition, kwashiorkar and marasmus [22–24]. Aflatoxins are clearly associated with aflatoxicosis and other health problems in the humans, livestock and domestic animals. All the types of aflatoxins are lipolytic in nature and are easily absorbed across cell membranes from the site of exposure such as gastrointestinal, respiratory tracts and enter into the blood stream, then spread to various tissues and to the liver. They are metabolized in liver to reactive epoxide intermediate or hydroxylated to less toxic aflatoxin M_1. In humans and susceptible animals, cytochrome P450 microsomal enzyme converts AFB_1 to an epoxide which binds to DNA and albumin in the blood, forms an adduct leading to DNA damage [25]. The epoxide preferentially binds to mitochondrial DNA resulting in hepatocarcinogenesis. The binding of AFB_1 to DNA at guanine site in liver cells affect the genetic code of enzymes which regulate cell growth [26]. This results in formation of tumors. Aflatoxins are known to bind and interfere with enzymes and substrates that are needed in the initiation, transcription and translation processes involved in protein synthesis by forming adducts with DNA, RNA and proteins.

Bioactive Molecules of Aspergillus Species

The versatility of Aspergillus species to produce structurally and biologically complex active molecules is still not well understood.

Aspergillus species particularly *Aspergillus fumigatus*, *Aspergillus flavus* and *Aspergillus parasiticus* secrete a variety of polyketides which include toxins, aflatoxins and virulent factors. The virulence of *Aspergillus* species is multifactorial in nature. Some virulence factors are polyketides and some are multifunctional protein molecules such as ribonucleases. The mechanism of colonization of a niche in the host and immunosuppression, immune invasion in case of human host is not well understood. Similarly, the host-pathogen mechanism in plant system is also not well understood particularly for *A. flavus*. *A. flavus* is metabolically a versatile; saprophyte obtains nutrients for growth and has the ability to secrete hydrolases to degrade complex carbohydrate and protein substrates [27].

Several *A. flavus* isolates are known to produce elastases, which are proteinases in nature, have relevance to human lung infection and invasion [28]. *A. flavus* also secretes polygalactouronases or pectinases that hydrolyze long chain pectins in plant tissues to enter and invade for the nutrients. A specific pectinase was identified to have strong correlation with spread of *A. flavus* isolates between locules of cotton balls (fruits) [29]. Alpha—amylases are another group of enzymes of *A. flavus*, which hydrolyze starch to access endosperm tissue.

Aspergillus flavus secretes extracellular cutinases which are characterized as serine easterases [30]. These enzymes are known to facilitate nutrient capture by the fungus. However, they do not have a dual role in pathogenicity or virulence. The toxins are used by the organisms to withstand competition with other organisms in the environment. It may also have some role in host-pathogen interactions. *Aspergillus fumigatus*, a medically important fungus and known to contaminate mushroom cultures secretes a polyketide pigment known as melanin. *A. fumigatus* produces a protein toxin Asp f1 with multiple functions. It is an important allergen, antigen, has ribonuclease activity and is highly cytotoxic [31, 32]. *A. fumigatus* also produces Asp-hemolysin which induces hemolysis of erythrocytes [33]. Melanin, a complex polyketide pigment of *A. fumigatus*, is considered as a virulent factor known to play an important role in the pathogenesis of Invasive Aspergillosis (IA) in humans.

Other secondary metabolites of *A. fumigatus* include gliotoxin, helvolic acid, fumigacin fumagillin, fumigaclavine A-C, festuclavine, etc. [34]. Gliotoxin is known to be an immunosuppressive compound.

Aspergillus flavus isolates also secrete a diverse group of organic toxic compounds besides multifunctional proteins like allergens, antigens, cytotoxins and most importantly polyketides like aflatoxins. These include oxalic acid, kojic acid, flavacol, aspergillic acid, beta-nitro-propionic acid, endotoxin etc. Some of these compounds exhibit various biological activities which are harmful to the humans and animals. Hence contamination of *A. flavus* and its spores in environment and in the soil affecting various crops through aflatoxins need to be carefully handled by detection, diagnosis and management as they enter the food and feed chain at different stages. Other structurally related compounds to aflatoxin include $AFLGM_1$, parasiticol and aflatoxicol.

Factors Influencing Aflatoxin Production/Conditions for Aflatoxin Production

Flavus has a unique feature of synthesizing a wide variety of structurally and functionally diverse compounds under different conditions of growth. These include culture media, nutrient supply and geographical conditions such as temp., humidity etc. These factors play a role in the synthesis of various polyketides. Few *Aspergillus* species in general produce aflatoxins at an optimum temperature of 25–32 °C, and moisture content a little above 12–16% with a relative humidity of 85%. *A. flavus s*ecretes aflatoxins between 12 and 42 °C and the optimum temp. is considered as 28–30 [35].

Aflatoxins; Genomics

The damaging effect of Aflatoxins on human and animal health, crop productivity and the economic impact on society prompted researchers to look into the biosynthesis of these compounds in *Aspergilli*. Major advancement in *Aspergillus* research is due to the availability of genome sequence information of important *Aspergillus* species. Today it is possible to have better understanding of the biology of important *Aspergilli*.

Aspergillus species have 8 chromosomes and the genome size of some of the important species varies by 30–40 megabases with 50% synteny between them. It harbors 140–500 unique genes. So far only 15,000 ORF are assigned with biological function [36]. Based on bioinformatic approach the transcriptome has been predicted. However, detailed experimental validation is necessary and efforts are on by research groups. Genomic information for most important *Aspergillus* species is now available in publication domain. Several ESTs of *A. fumigatus* (in Indian isolates) are deposited [37, 38].

The whole genome sequence of *Aspergillus flavus* has been updated at several websites and compiled at http://www.aspergillusgenome.org/. Several unique ESTs are generated from the EST bank. It is interesting to note the genome size of *A. flavus* and *A. oryzae* is slightly larger (37 Mb) than other *Aspergilli* (30–34 Mb). *A. flavus* and *A. oryzae* belong to *Aspergillus* section Flavi. Their genomic sequence suggests similarity of the species but they are morphologically distinct. Further, PCR based on ITS regions can identify them from each other. Gene clusters of secondary metabolites in *A. flavus* and *A. oryazae* are similar although species share most of the features, *A oryzae* does not secrete many of the polyketides and toxins produced by *A. flavus.* These two species share most of the genomic content including secondary metabolite gene clusters [39, 40], *A oryzae* does not produce many of the polyketides and toxins of *A. flavus*. In fact, it is highly used in food and fermentation industry. These major differences in these two *Aspergillus* species necessitate characterization and examination of uncharacterized genes involved in secondary metabolite regulation and particularly in the regulation of aflatoxin biosynthesis.

Based on online bioinformatic tools known as SMURF (Secondary Metabolite Unknown Regions Finder) genes associated with enzymes involved in secondary metabolic pathway in *A. flavus* are revealed [41]. These are polyketide synthases, PKS like synthases, nonribosomal peptide synthases, NRPS like synthases, PKS-NRPS enzymes, and phenyl transferases. These enzymes and the other cluster enzymes of Aspergillus species facilitate secretion of certain common classes of compounds such as polyketides, non-ribosomalpeptides, PKS-NRPS hybrids and indole alkaloids [42]. So far only handful of metabolic clusters of *A. flavus* is characterized, although 55gene clusters are predicted [43–46]. Molecular analysis of aflatoxin synthesis and secretion in *A. flavus* and *A. parasiticus* lead to identification of a 75 Kb Gene cluster [47–49]. Two important transcriptional regulators were located on this gene cluster. These are named as *afl R* and *afl S*. The gene cluster along with transcriptional regulator is arranged at the end of chromosome. Further, about 30 co-regulated downstream metabolic genes in the biosynthesis are identified. One of the important compounds in aflatoxin biosynthesis is characterized as sterigmatocystin. It is highly toxic and a carcinogen. This toxin is reported to be synthesized by species of *Nidulantes* and *Versicolor* also.

Most of the gene clusters of Aspergilli are cryptic under a variety of laboratory conditions with the exception to few toxins and a virulent factor [50]. Active research to understand the molecular and biochemical mechanisms for these toxins and virulent factors is in progress. Aflatoxins, ochratoxins and cyclopiazonic acid of Aspergillus species are of agricultural importance A global regulator in Aspergilli is identified and designated as LaeA which is a novel protein in secondary metabolism of *Aspergilli* [51, 52]. Two other proteins *VeA* and *VelB* of Velvet complex, a heterotrimeric nuclear complex (highly conserved in fungi) are hypothesized to activate the secondary metabolite clusters [53–56]. *LaeA* and *VeA,* are shown to regulate aflatoxin and few other toxins [57]. These are also known to play a role in sporulation and secondary metabolism in *A. nidulans* [58]. An important enzyme in polyketide biosynthetic pathway is polyketide synthase (pks). Polyketide synthases of *Aspergilli* are large multifunctional proteins and are of Type I with <1000 amino acids, coded by a single gene in *A. flavus*, other fungi and in bacteria. The pks enzyme of *Aspergillus flavus* and other Aspergillus speices consist of 5–9 domains on a single polypeptide chain and use iterative strategy (repetitive use). The domains are used repeatedly to extend the

polyketide chain to build polyketides such as aflatoxins etc. General architecture of polyketide synthase from different *Aspergillus* species is presented in (Fig. 1).

Aflatoxin gene clusters include *PksA* (size of 6.6 kb) encoding for a polyketide synthase that catalyses the second step in which hexanoyl, tetra hydroxyl anthrone is converted to norsolorinic acid from hexanoate [59–61]. Norsolorinic acid is the first stable compound in the biosynthetic pathway and leads to synthesis of sterigmatocystin and aflatoxins.

The gene cluster is conserved in *A. parasiticus, A. ochraceoroseus, A. nomius, A. pseudotamarii, A.nidulans, A. oryzae* and *A. sojae* etc. [61]. Specificities in the conserved regions in these species may facilitate synthesis of different polyketide toxins. Some do not produce aflatoxins or any other toxin as in the case of *A. oryzae* and *A. sojae*. These two strains are used in the food industry. Several mutations and large deletions are observed in the gene clusters of these two species. Defects in aflatoxin biosynthetic genes and the transcriptional factors are reported in several of these strains. A Zn based transcriptional factor encoded by *aflR* is involved in the expression of the aflatoxin and sterigmatocystin biosynthetic genes. Over expressed and deleted *aflR* demonstrated up regulation of other biosynthetic genes and increased amounts of aflatoxin while deleted *aflR* resulted in absence of these products indicating its important role in the regulation and production of aflatoxins.

In view of variations in the polyketide biochemical pathways among medically and agriculturally important *Aspergillus* species, examination of phylogenetic relationship can lead to assignment of functionality to unexplored polyketide synthases and other enzymes with respect to secondary metabolites [62]. The general molecular architecture of pks enzyme is presented in (Fig. 2).

Molecular Variability in PKS Enzymes, Atoxigenecity and Aflatoxigenecity

It is well known all the isolates of *A. flavus* do not produce aflatoxins. This observation now has been studied with scientific evidence based on the understanding of biochemical pathways for aflatoxin synthesis [63–65]. High degree of molecular diversity of polyketide synthase and the gene cluster enzymes in aflatoxin biosynthetic pathway is being observed in *A. flavus and A. parasiticus* from different geographical regions by various groups [66]. These observations have led to identification of atoxigenicity in *A. flavus* isolates with defective polyketides biosynthetic mechanism [67, 68]. This was exploited for application to cotton field at Arizona for control of aflatoxins by nontoxigenic *A. flavus* isolates [69]. Several reports indicated the usefulness of such isolates [70, 71]. Currently several groups from several countries are working on identification of such strains with defective

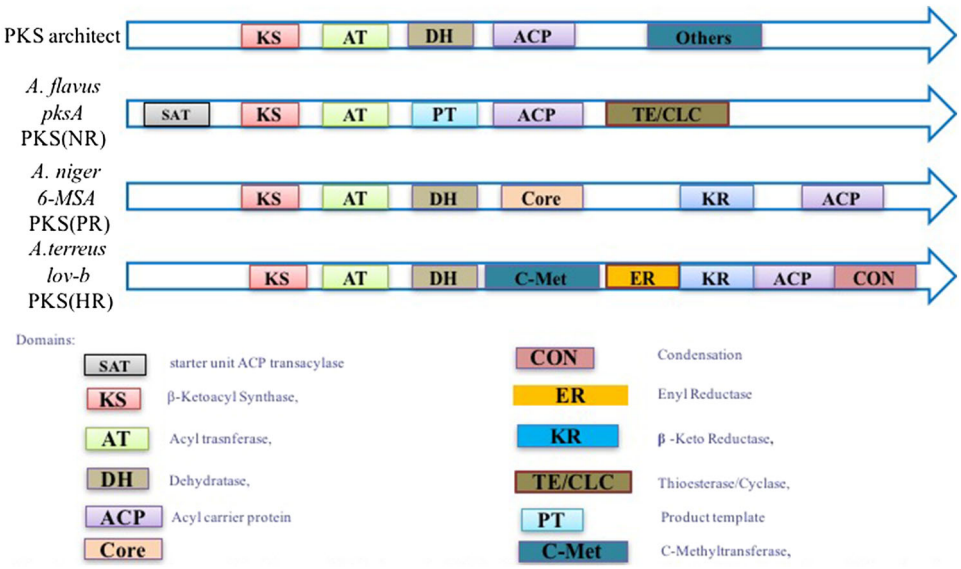

Fig. 2 General architecture of iterative type I PKS. *Aspergillus* PKSs minimally contain ketosynthase (KS), acyl transferase (AT) and acyl carrier protein (ACP) domains. They can be classified into three different groups. I) Non Reduced PKS e.g. pksA from *A. flavus* (*pksL* from *A. parasiticus*) responsible for Aflatoxin synthesis contain SAT, KS, AT, PT, ACP, TE domains. *A. fumigatus* producing 1,3,6,8-tetrahydroxynapthalene (THN) and pksST from *Aspergillus nidulans* contain additional ACP domain. II) Partially reduced PKS e.g. 6-MSA (6-methylsalicylic acid) from *A. niger* secreting antibiotic yanuthone D contains KS, AT, Dh, KR and ACP. III) Highly reducing PKS e.g. *lovB* (lov astatin nanaketide synthease) and *lovF*, are involved in the formation of lovastatin in *A. terreus*. Both PKS gene have KS, AT, DH, CMeT, ER, KR and ACP domains while for *lovB* CON domain is also present

Table 2 Single nucleotide polymorphisms in important genes of *Aspergillus* species

Aspergillus species	SNP/Amino acid substitution reported	Target Protein	Implications
Aspergillus fumigatus	G54, P216, F219, M220, G448	Cyp51A (14α-demethylase)	Pan-azole Resistance
Aspergillus flavus	A/G 591	pksA (Polyketide synthase gene)	Biocontrol VCG isolate
Aspergillus flavus, Aspergillus parasiticus	Multiple	cypX (Aflatoxin Biosynthetic pathway)	Biocontrol VCG isolate
Aspergillus flavus	Multiple	mat1-2 (Matting type locus)	Biocontrol VCG isolate

polyketide biosynthetic pathway for field application and commercialization. Valuable SNPs and deletions in PKs enzyme and the gene cluster enzymes are reported in association with aflatoxin production [68, 72]. However no single identity is associated with atoxigenicity so far. Two specific isolates well characterized for their atoxigenicity are currently reported. They are also available commercially. These include aflaguard and AF36 [73]. K49 and AFCHG2 are also promising isolates [74, 75]. Table 2 projects the molecular variability in PKS enzyme and atoxigenecity of *Aspergillus flavus* isolates along with other known SNP in *Aspergilli*

Toxicity and Potency of Aflatoxin

According to Ames et al. 1990 only dioxins (Td $50 = 6.7 \times 10$ mg/kg/d) significantly exceeds AFB_1(-TD50 $= 9.3 \times 10^{-4}$ mg/kg/d) in its potency. Using TD_{50} parameter aflatoxin B_1 is 1000 times more potent as a carcinogen when compared to benzopyrene [6]. IARC has classified aflatoxins as a group1 carcinogen (IARC 7th annual report on carcinogen 1987) and more than 6000 ng is considered to cause acute toxicity.

Management of Aflatoxin

Economic Impact of Aflatoxins

Economic impact of losses due to aflatoxin contamination in crops and livestock have a direct significance. The cost of regulatory process designed to reduce risk to animal and human health have an economic impact.

Strategies for Removal of Aflatoxins

Removal of aflatoxin was attempted mainly by physical, chemical and biological methods. Decontamination of aflatoxins from animal feed includes use of binders such as Zeolite clays and alluminosilicates. Blending is a method based on mixing contaminated material with uncontaminated ones at a desired ratio based on the level of contamination. Ammoniation is a useful procedure which is successfully operative in many countries. Few chemical agents are effective at laboratory level and need validation for commercialization.

Decontamination of aflatoxins using the microbes such as *Bacillus, Lactobacilli*, and *Pseudomonas* etc. is one of the biological control strategies. *Flavobacterium aurantiacum* B-I84 was reported to remove aflatoxin from liquid media [76]. Simple adsorption method using dead microbes were also used for removal of aflatoxin. Enzymatic methods such as use of chitinase etc. are not economically viable.

Advances in *Aspergillus* research through genomic approaches resulted in better understanding of *A. flavus* molecular diversity in aflatoxin biosynthetic mechanism. Isolates with defective aflatoxin biosynthetic pathway are identified to have a biocontrol potential to eliminate toxigenic *Aspergilli.*

Conclusions

Environmental control of Aspergillus spores and conidia is necessary to avoid complicated allergies and infections due to fungal spores and particularly Aspergillus spores.

Aspergillus flavus and *Aspergillus parasiticus* are the two major species of producers of aflatoxins that contaminate a variety of economically important crops all over the world. Aflatoxins are a major challenge for a quality life. Novel and affordable methods are necessary for detection of agriculturally important *Aspergilli* in crops and agri-feed. A better understanding of host resistance, host pathogen interactions and an insight of the biological mechanisms of these fungi will provide novel methods of control and management of aflatoxins. Further it will also help exploration of new polyketides of human use.

Acknowledgements The authors acknowledge the financial support provided by the Council of Scientific and Industrial Research (CSIR) and the laboratory facilities provided by the Division of Plant Pathology, of Indian Agricultural Research Institute (IARI), New Delhi. Constant support by Dr. Rashmi Agarwal, Head, Division of Plant Pathology, IARI is gratefully acknowledged.

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