

## DECONTAMINATION OF AFLATOXINS WITH A FOCUS ON AFLATOXIN B<sub>1</sub> BY PROBIOTIC BACTERIA AND YEASTS: A REVIEW

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### Review

### ABSTRACT

Food and feed contamination by aflatoxins represents a great challenge for human and animal health. Aflatoxins detoxification using probiotic bacteria and yeasts has been introduced as an inexpensive and promising method. This article is organized with an overview of the potential application of probiotic bacteria and yeasts to eliminate, inactivate or reduce the bioavailability of aflatoxins, especially aflatoxin B<sub>1</sub>, *in vitro* and *in vivo*. Also, a fast glance to beneficial health effects and preservative properties of probiotics followed by the mechanism of binding of aflatoxins by probiotics, influence of different probiotic pretreatments, and the stability of aflatoxin-probiotic complexes are mentioned.



**Keywords:** Detoxification, Probiotic, Adsorption, Aflatoxin, Stability

## INTRODUCTION

Contamination of food and feed by mycotoxins is a severe problem in all countries; hence, decontamination of mycotoxins from food and feed is essential. The food and agriculture organization evaluates that approximately 25% of global food and feed are contaminated with mycotoxins (Zoghi *et al.*, 2017). Mycotoxins are secondary metabolites of mycelia or filamentous fungi associated to the *Penicillium*, *Aspergillus* (A.), and *Fusarium* genera. Production of mycotoxins may happen during the process of production, harvesting, storage or processing, under suitable temperature (between 24 and 37 °C) and humidity (above 13%) conditions (Massoud *et al.*, 2018; Perczak *et al.*, 2018). Several pre- and postharvest methods in order to decrease mycotoxins level in raw materials have been suggested; but, while mycotoxins levels have attained to contamination limited level in a product, it is difficult to eliminate the total toxin amount. Directly or indirectly exposure to mycotoxins may cause teratogenic, mutagenic, estrogenic, haemorrhagic, carcinogenic, immunotoxic, nephrotoxic, hepatotoxic, neurotoxic and immunosuppressive impacts on the health of animals and humans (Haskard *et al.*, 2000; Zoghi *et al.*, 2019).

Aflatoxins are a group of the most repeatedly found mycotoxins in a variety of foods and feeds commodities causing economic losses in industry, veterinary care costs enhancement, and livestock production decline. These toxins are secondary metabolite products of some *Aspergillus* species, especially *A. flavus*, *A. parasiticus* and *A. nomius*. Several factors affect the production of this toxin including water activity, temperature, available nutrients, competitive growth of other microorganisms, and pH-value (Ghofrani Tabari *et al.*, 2018). Various agricultural products may be contaminated by aflatoxins such as cereal grains especially rice, corn, maize, wheat, soya, rye, oats, barley, sorghum, nuts (almonds, peanuts, Pistachio, chestnuts, pumpkin seeds, etc.) and oily seeds such as cottonseed (Fochesato *et al.*, 2018). Aflatoxins can enter the human body directly or indirectly by consuming contaminated products or derived foods, such as dairy products and meats from contaminated livestock, respectively. Exposure to aflatoxins leads to severe effects on human and animal health including chronic intoxications and liver and kidney cancers (Karazhiyan *et al.*, 2016). Once aflatoxins are ingested by animals, they get adsorbed rapidly in the gastro intestinal tract (GIT), because they have low molecular weight, and then appear in blood and milk quickly after 15 minutes and 12 hours of post-feeding, respectively (Martins *et al.*, 2001).

18 types of aflatoxins are identified through toxicological studies, but the major aflatoxins are aflatoxins B<sub>1</sub> (AFB<sub>1</sub>), B<sub>2</sub> (AFB<sub>2</sub>), G<sub>1</sub> (AFG<sub>1</sub>) and G<sub>2</sub> (AFG<sub>2</sub>). These names are related to their fluorescence under UV light (blue (B) or green (G)) and comparative chromatographic migration patterns through thin layer chromatography (TLC) (Lizárraga-Paulín *et al.*, 2011; Rahnama Vosough *et al.*, 2013). *A. flavus* usually produces the B group of aflatoxins, while *A. parasiticus* produces both B and G groups of aflatoxins through several biochemical processes. Among four mentioned aflatoxins, AFB<sub>1</sub> is considered as the most common and dangerous one and exposure to AFB<sub>1</sub> leads to both acute and chronic hepatocellular injury (Jakhar and Sadana, 2004).

Aflatoxin M<sub>1</sub> (AFM<sub>1</sub>) and aflatoxin M<sub>2</sub> (AFM<sub>2</sub>) are metabolic derivatives of AFB<sub>1</sub> and AFB<sub>2</sub>, respectively (Lizárraga-Paulín *et al.*, 2011). When feed containing AFB<sub>1</sub> is ingested by livestock, it can be bio-transformed into AFM<sub>1</sub> (4-hydroxy-AFB<sub>1</sub>) in the liver and excreted in milk, tissues, and urine of animals (Iha *et al.*, 2013; Karazhiyan *et al.*, 2016). AFM<sub>1</sub> is resistant to all stages of dairy processing including pasteurization or sterilization (Prandini *et al.*, 2009; Assaf *et al.*, 2018). Approximately 0.3 to 6.2% of ingested AFB<sub>1</sub> by livestock appears as AFM<sub>1</sub> in milk. Diet type, amount of milk production, breed, health, and rate of digestion can affect the change rate of AFB<sub>1</sub> to AFM<sub>1</sub>. A linear relationship between the AFM<sub>1</sub> concentration in milk and AFB<sub>1</sub> in contaminated feed is reported by Adibpour *et al.* (2016).

The International Agency for Research on Cancer (IARC) categorized AFB<sub>1</sub> and AFM<sub>1</sub> as group 1 that leads to human cancer (IARC, 2016). However AFM<sub>1</sub> is about ten times less toxicogenic, mutagenic and genotoxic than AFB<sub>1</sub>, its carcinogenic effects have been demonstrated in several species (Elsanhoty *et al.*, 2014). AFM<sub>1</sub> is cytotoxic and can also cause DNA damage, gene mutation, chromosomal anomalies and cell transformation in mammalian cells. The Food and Drug Administration (2005) recommended that the maximum acceptable level of AFM<sub>1</sub> in milk is 0.5 µg/kg, and the European Commission (2006) settled this limit to 0.05 µg/kg.

Various strategies have been applied to remove aflatoxins from contaminated food and feed. Elimination of aflatoxins with chemical (addition of chlorinating, oxidizing or hydrolytic agents) and physical (UV light, heat, or ionizing radiation) approaches has some disadvantages, such as possible losses in nutritional value of treated commodities, insufficiency of toxin elimination, and requirement of expensive equipment (Zoghi *et al.*, 2014). In addition, one of the most effective adsorbents for AFB<sub>1</sub> is clay soil-based adsorbent. The layer

structure of this type of adsorbents swells when it is placed in a liquid medium and it can adsorb AFB<sub>1</sub> on its layers and prevent adsorption of AFB<sub>1</sub> by cells in the GIT (Hadiani et al., 2018a). Nevertheless, this group of adsorbents is of low efficiency in adsorbing AFB<sub>1</sub>. Therefore, according to the researches, bioremoval method is an interesting alternative for inexpensive control or reducing of aflatoxins in foodstuffs without losses of nutritional quality or toxic compounds generation. Probiotics are the best candidate for aflatoxins detoxification due to their GRAS (Generally recognized as safe) status.

Recently, several approaches to the removal of aflatoxins using probiotics are demonstrated. This article reviews the potential applications of probiotics in aflatoxin detoxification and the mechanism of aflatoxin binding by probiotics and the aflatoxin-probiotic complex stability are discussed.

## PROBIOTICS AS AFLATOXIN BINDERS

Probiotics are described by FAO (2016) as 'viable microorganisms that, while ingested in sufficient amounts, exert health benefits on the host'. The main benefits for health include: lactose intolerance reduction, gut mucosal immunity support, a possible hypocholesterolemic effect, preventing the diarrheas or respiratory infections, colon cancer or inflammatory bowel disease inhibition, *Helicobacter pylori* or intestinal pathogens prevention, and antimutagenic and anticarcinogenic activities (Sanders et al., 2014; Yu, Chang and Lee, 2015).

Recently, the use of microorganisms, especially probiotics, has been studied for their potential to aflatoxins elimination with an indirect health effect on the host (Bovo et al., 2012). Several probiotic strains have been investigated for their ability to bind aflatoxins (El-Nezami et al., 1998; Bueno et al., 2006; El Khoury et al., 2011; El-Nezami et al., 2002).

*Lactobacillus* (L.) and *Bifidobacterium* (B.) species are the most known commonly probiotic bacteria, as well as the yeast *Saccharomyces* (S.) *cerevisiae* and *Bacillus* species and some strains of *Escherichia* (E.) *coli*. A functional classification of nontoxicogenic, nonpathogenic, and fermentative probiotic bacteria are Lactic acid bacteria (LAB) which are mainly related to the human gastrointestinal tract and widely used in food industry (Zoghi et al., 2017). LAB are Gram-positive, organotrophic, nonsporulating, fermentative rods or cocci, air and acid tolerant, which produce mostly lactic acid as the end-product of carbohydrate fermentation. All of them are anaerobic, but some of them can tolerate low levels of oxygen. *Enterococcus*, *Lactococcus*, *Pediococcus*, *Oenococcus*, *Leuconostoc*, *Streptococcus*, and *Lactobacillus* species are industrially important genera. The genus *Bifidobacteria* is also used as LAB, however they are phylogenetically unrelated and have unique sugar fermentation pathways. LAB are widely used in the world food production, vegetables, meat, and fermented dairy products. LAB play a significant role in improving the flavour, texture, and shelf-life of food products (Perczak et al., 2018).

It is demonstrated that living and dead probiotics are able to decontaminate aflatoxins by attaching the toxin to their cell wall components. This phenomenon can be described as adsorption by components of the cell wall rather than by metabolism or covalent binding (Santos et al., 2006). Capability of nonviable probiotics in aflatoxins decontamination is an important point of view because the viability of probiotics decreases under low pH condition through passing the stomach (Topcu et al., 2010; Hamidi et al., 2013). El-Nezami et al. (1998) reported that five strains of *Lactobacillus* and one *Propionibacterium* were significantly effective in aflatoxin removal from aqueous solution in comparison to *E. coli*. In another study, Peltonen et al. (2001) stated that significant differences in the binding abilities of different amounts of AFB<sub>1</sub> were due to different bacterial cell wall structures.

## Inhibition of aflatoxin biosynthesis by LAB

A few authors also reported the antifungal properties of LAB. The main LAB recognized for this ability belong to *Lactococcus* and *Lactobacillus* (L.) genera. In contrast, it is reported that some LAB strains such as *L. lactis* can motivate aflatoxin accumulation. Coallier-Ascach and Idziak (1985) demonstrated a significant inhibition of aflatoxin accumulation by LAB and reported that this inhibition was not related to a pH decrease or a hydrogen peroxide production but rather to producing a heat stable and low molecular weight metabolite by LAB at the beginning of its growth phase. Gourama and Bullerman (1997) also reported that prevention of aflatoxin synthesis by *Lactobacillus* strain was due to specific bacterial metabolites. Several effective parameters related to antifungal properties of LAB have been investigated including growth medium, temperature, incubation time, pH, and nutritional factors. It was revealed that temperature and period of incubation were significantly affecting the amounts of antifungal metabolite production (Dalié et al., 2010). Gonzalez Pereyra et al. (2018) found that six *Bacillus* sp. strains were capable of decrease aflatoxigenic *A. parasiticus* growth rate significantly and could also decrease AFB<sub>1</sub> concentration.

## FACTORS AFFECTING AFLATOXIN BIOREMOVAL BY PROBIOTICS

Several criteria affect the aflatoxins removal using probiotics such as probiotic strain concentration and specificity, toxin concentration, pH, and incubation time.

## Effect of probiotic strain specificity and concentration

In addition to bacterial strain specificity, the bacterial concentration can also affect the aflatoxin removal. Detoxification of aflatoxins by viable or nonviable probiotic cells is strain dependent (Topcu et al., 2010). In some studies, LAB were considered to be inappropriate binders of AFB<sub>1</sub>. This may be due to the specific LAB strains used in those studies (Shetty and Jespersen, 2006). Similarly, Peltonen et al. (2001) assayed 20 LAB strains and reported that the differences in AFB<sub>1</sub> binding were because of different bacterial strain specificity. So, differences between aflatoxin ability of strains of LAB indicate that binding ability is highly strain dependent. El-Nezami et al. (1998) showed that *L. rhamnosus* strains GG and LC 705 can significantly remove AFB<sub>1</sub> in comparison to other strains of LAB and the removal process was bacterial concentration dependent.

## Toxin concentration effect

Several researchers such as El-Nezami et al. (1998), Elsanhoty et al. (2014) and Peltonen et al. (2001) reported that the amounts of aflatoxin removed by viable and nonviable bacteria depend on initial toxin concentrations. In addition, Pizzolitto et al. (2012) demonstrated that the removal of AFB<sub>1</sub> depended on the LAB strain; because some of LAB strains were more efficient at a low toxin concentration (*L. rhamnosus* at 50 ppb) and other applied LAB were more efficient at high AFB<sub>1</sub> concentration (*L. acidophilus* at 100 ppb and *L. casei* at 500 ppb). According to Shetty et al. (2007) the absolute amount of the AFB<sub>1</sub> removal increased steadily with increasing concentration of AFB<sub>1</sub>; therefore, the initial AFB<sub>1</sub> concentration had a considerable impact on the binding capacity. In contrast, Rahayu et al. (2007) stated that AFB<sub>1</sub> concentration enhancement did not affect the percentage of AFB<sub>1</sub> binding; but, it influenced the binding speed. Also, Lee et al. (2003) reported AFB<sub>1</sub> binding as a linear process and dependent on the toxin concentration at low level of AFB<sub>1</sub>, and a plateau process at higher toxin concentrations.

## Effect of pH-value

Some investigation showed that binding process is not pH dependent exclusively. According to Zinedine et al. (2005) all the assayed *Lactobacillus* spp. removed AFB<sub>1</sub> from 5% to 40% when pH increased from 3 to 5.5. Also, Pranoto et al. (2007) demonstrated that amount of bound AFB<sub>1</sub> by LAB was higher at low pH (< 5) in compare with pH 6 and 7. In another study, Rayes (2013) stated that at pH 8.5 the highest decrease percentage of AFB<sub>1</sub> by a pool of LAB occurred, while at pH 4.5 the lowest removal observed. On the other hand, the highest and lowest AFB<sub>1</sub> removal was at pH 4.5 and 8.5, respectively, when the pool was included a *S. cerevisiae* strain. Hernandez-Mendoza et al. (2009) investigated the binding of *L. reuteri* and *L. casei* with AFB<sub>1</sub> at different pH (6, 7.2, and 8) and incubation time (4 and 12 h). They showed that the highest AFB<sub>1</sub>-binding capacity was at pH 7.2. Furthermore, Topcu et al. (2010) found that the binding of AFB<sub>1</sub> by *Enterococcus faecium* was a pH and incubation time dependent process. In contrast, Bovo et al. (2014) showed no significant differences in the AFB<sub>1</sub> reduction between *L. rhamnosus* strains conditions (spray, in solution or freeze-dried) at pH 3 and 6. So, it can be concluded that the pH dependence of AFB<sub>1</sub> binding vary between bacterial strains. In addition, binding of AFB<sub>1</sub> in a study, was not affected by pH, but binding of AFB<sub>2</sub> considerably influenced by pH. It indicates that different metabolites of the same mycotoxin may show significant differences depend on binding mechanisms.

## Effect of incubation time

Peltonen et al. (2001) stated that the AFB<sub>1</sub> binding by *L. amylovorus* CSCC 5197 was a fast process and increased from 52% (0 h) to 73.2% (72 h). Similarly, Topcu et al. (2010) reported that *Enterococcus faecium* M74 and EF031 strains at 1 h removed almost 65% of the total AFB<sub>1</sub> removed during the whole incubation period (48 h). Bovo et al. (2012) stated that some probiotic strains bound AFM<sub>1</sub> from skimmed milk in 15 min within a range from 13.51 to 37.75%. In another study, it was reported that the percentage of AFB<sub>1</sub> removal was not significantly different between the 0 h and 72 h incubation period (Pizzolitto et al., 2012). In addition, El-Nezami et al. (1998) showed that the AFB<sub>1</sub> removal was fast and no significant different was observed between different incubation times. Motawee and El-Ghany (2011) noted that the percentage of AFM<sub>1</sub> and AFB<sub>1</sub> reduction after 5 h by eight dairy strains of LAB in yoghurt was not considerably less than the whole of storage time. These results suggest that the binding of AFB<sub>1</sub> by probiotics is a rapid process and the removal does not increase with the incubation time, considerably.

## BINDING OF AFLATOXINS BY LAB

Specific strains of LAB are generally the most known probiotics for reducing aflatoxins. It has been reported that different strains of LAB have different effect on AFB<sub>1</sub> removal *in vitro*. This removal is due to binding of bacterial cell wall to the aflatoxin, not bacterial metabolism. It was described that *in vitro* binding of

AFB<sub>1</sub> by LAB is a fast (less than 1 min), strain specific, and reversible process (Bueno et al., 2006; Kankaanpaa et al., 2000).

El Nezami et al. (1998) assayed the capacity of *L. rhamnosus* GG, *L. rhamnosus* LC705, *L. acidophilus*, *L. gasseri*, *L. casei* Shirota, and *Propionibacterium freudenreichii* ssp. *shermanii* JS to bind AFB<sub>1</sub> in a liquid medium and stated that *L. rhamnosus* strains GG and LC705 removed 80% of the toxin. They emphasized that the viability of cells was not a prerequisite for this binding capacity. Then, Haskard et al. (2001) tested 12 viable and non-viable LAB strains and found that *L. rhamnosus* was the best strain to remove AFB<sub>1</sub>. The authors demonstrated that some surface components of the LAB were involved in binding. Also, Peltonen et al. (2001) investigated the binding of AFB<sub>1</sub> by 12 *Lactobacillus*, five *Bifidobacterium* and three *Lactococcus* strains and revealed that two strains of *L. amylovorus* and *L. rhamnosus* removed more than 50% of initial AFB<sub>1</sub> concentration. In addition, Motameny et al. (2012) studied the AFB<sub>1</sub> removal from a gastrointestinal model by *L. rhamnosus*, *L. plantarum*, and *L. acidophilus* and found that all strains were able to AFB<sub>1</sub> detoxification and *L. plantarum* was the most successful (28 %). Elsanhoty et al. (2014) reported that *L. rhamnosus* was the most effective in the binding of AFB<sub>1</sub>, AFB<sub>2</sub>, AFG<sub>1</sub>, and AFG<sub>2</sub> from liquid medium in compared with *L. acidophilus*, *L. sanfranciscensis*, and *B. angulatum* and LAB-aflatoxin complex was stable. On the other hand, Sarimehmetoglu and Küplülü (2004) compared the ability of *Streptococcus thermophilus* ST-36 and *L. delbrueckii* ssp. *bulgaricus* CH-2 to AFM<sub>1</sub> removal from phosphate buffer saline (PBS) and milk. Elgerbi et al. (2006) found that the percentage of AFM<sub>1</sub> binding by *Lactobacillus* spp., *Lactococcus* spp. and *Bifidobacterium* spp. ranged from 4.5-73.1% after 96 hr.

Sezer et al. (2013) reported that *L. plantarum* was more efficient than *L. lactis* in removing AFB<sub>1</sub> from liquid culture (46% and 27%, respectively), but when the two strains were combined, AFB<sub>1</sub> removal reached 81%. Corassin et al. (2013) also revealed that a combination of LAB (*L. rhamnosus*, *L. delbrueckii*, and *B. lactis*) and *S. cerevisiae* could reduce AFM<sub>1</sub> from UHT skim milk, completely. In contrast, El-Khoury et al. (2011) stated that *L. bulgaricus*, *Streptococcus thermophilus* and a mixture of these two bacterium reduced AFM<sub>1</sub> content of milk to 58.5, 37.7 and 46.7%, respectively. It can be concluded that combination of specific probiotic strains may lead to a more aflatoxin removal efficiency than a single one, but may reduce their toxin removal capacity.

Some authors have reported a mathematical model to illustrate the *in vitro* AFB<sub>1</sub> binding to the LAB cell wall. A theoretical model has been suggested by Bueno et al. (2006). This model takes two possible processes into investigation: adsorption (binding) and desorption (release) of AFB<sub>1</sub> to and from the binding site on the LAB surface. This model shows that AFB<sub>1</sub> binds to a number of sites in LAB and allows us to evaluate the number of AFB<sub>1</sub> binding sites and the efficacy of cells to reduce AFB<sub>1</sub> from a liquid medium. So, this model demonstrates that the different abilities of probiotic strains to bind AFB<sub>1</sub> are directly link to the number of binding sites of each probiotic.

## BINDING OF AFLATOXINS BY YEASTS

Data found in the literature indicate that in addition to LAB, other organisms such as *S. cerevisiae* have the potential to bind aflatoxins. Yeast cells can bind to different molecules such as toxins as complexes on their cell wall surfaces (Baptista et al., 2004). Corassin et al. (2013) evaluated the AFM<sub>1</sub> binding ability of *L. rhamnosus*, *L. delbrueckii* ssp. *bulgaricus*, and *B. lactis* in combination with heat-treated *S. cerevisiae*. This mixture could bind with 100% of AFM<sub>1</sub>. In a study, *S. cerevisiae* and *Candida krusei* were tested for AFB<sub>1</sub> binding and they could bind more than 60% (w/w) of the added mycotoxins in PBS. They emphasized the AFB<sub>1</sub> binding was highly strain specific (Shetty and Jespersen, 2006). In another research, when dried yeast and yeast cell wall (include mannan-oligosaccharides) with AFB<sub>1</sub> were added to rat-ration feed, a significant decrease in the toxicity was observed (Baptista et al., 2004).

## MECHANISM OF AFLATOXIN BINDING BY PROBIOTICS

Several researchers studied the mechanism of binding of aflatoxins to probiotics. A review by Shetty and Jespersen (2006) stated that aflatoxin removal by probiotics is due to adhesion to cell wall components, because nonviable and viable probiotics are able to remove aflatoxins *in vitro* with similar efficiency. Possible binding sites include carbohydrates, proteins or a combination of both.

It has been shown that two main components responsible for the binding of AFB<sub>1</sub> by *L. rhamnosus* GG are cell wall polysaccharide and peptidoglycan. In addition, since LAB strain treatment with lipases did not lead to a significant increase in AFB<sub>1</sub> binding, it was supposed that no fatty acids were involved in this adsorption (Lahtinen et al., 2004). Similarly, other authors have suggested that the peptidoglycan of LAB is the most likely site of aflatoxins binding (Haskard et al., 2000; Niderkorn et al., 2009). Yiannikouris et al. (2006) found that a cell wall component of many microorganisms named beta-d-glucans, played a key in the binding of aflatoxins. Recently, it was reported that the binding characteristics of a probiotic strain are possibly depend on the exopolysaccharides produced by the probiotics (Taheur et al., 2017). Also, Haskard et al. (2001) indicated superior involvement of hydrophobic interactions and main role of teichoic acids in aflatoxin binding mechanism.

Similarly, Hernandez-Mendoza et al. (2009) showed that teichoic acids as well as peptidoglycans were important parts of the cell wall which could bind aflatoxin. Another report indicated the main role of teichoic acids in aflatoxin binding by probiotics. Teichoic acids may contribute mainly to hydrophobicity of wall contributed by anionic carbohydrates (Gratz et al., 2004). It can be concluded that binding of probiotics to aflatoxins is a function of fibril network of teichoic acids, peptidoglycans, and polysaccharides. Another mechanistic study conducted by Fochesato et al. (2018), which demonstrated that polysaccharides of *L. rhamnosus* attached aflatoxins. These polysaccharides are in three principal forms: peptidoglycan, cell wall polysaccharide, and teichoic or lipoteichoic acids. The environmental conditions such as pH-value or enzymes would be affecting the three-dimensional structure of the cell wall and the binding sites for aflatoxins. Therefore, it can be concluded that aflatoxin removal is due to the physical binding rather than metabolism, because peptidoglycan is one of the three principal carbohydrate forms of bacterial cell wall.

When acid or heat treatments were used for LAB, it has been demonstrated that LAB ability to remove AFB<sub>1</sub> increased. Also, inserting some basic compounds such as NaOH, Na<sub>2</sub>CO<sub>3</sub>, and isopropanol had negative influence on this binding (El-Nezami et al., 1998). Haskard et al. (2000) investigated the mechanism of binding of *L. rhamnosus* to aflatoxins. They used pronase E and periodate treatments (using periodate causes oxidation of cis OH groups to aldehydes and carbon acid groups) on viable, heat and acid-inactivated probiotic strains and suggested that binding was due to carbohydrate and protein components in cell wall, because a considerable decrease in AFB<sub>1</sub> binding was observed. Heat and acid treatments cause protein denaturation and lead to the exposure of more hydrophobic surfaces. They also reported that AFB<sub>1</sub> binding reduction by urea-treated LAB indicated the key role of hydrophobic interactions in binding. On the other hand, treatments with metal ions such as Na<sup>+</sup> and Ca<sup>2+</sup> showed that electrostatic interactions and hydrogen bonding played only minor role in AFB<sub>1</sub> binding by LAB, because this process was not affected by mono and divalent ions or by changes in pH (2.5–8.5).

## LAB cell wall

Some authors suggested that the significant differences among aflatoxin binding ability of LAB depends on different cell wall structures (El-Nezami et al., 1998; Peltonen et al., 2001; Zinedine et al., 2005; Hernandez-Mendoza et al., 2009; Lahtinen et al., 2004; Pierides et al., 2000). Cell wall structure of LAB is reviewed widely by several researchers (Chapot-Chartier and Kulakauskas, 2014; Elsanhoty et al., 2016; Zoghi et al., 2017; Liu et al., 2018; Zoghi et al., 2019; Nazareth et al., 2020).

Heterogeneous bacteria of LAB, possess a typical gram positive cell wall containing the peptidoglycan matrices, organic acids (teichoic and lipoteichoic acid), proteinaceous surface (S) layer and neutral polysaccharides. These components play various functions including adhesion to macromolecules such as toxins (Perczak et al., 2018). Cell wall polysaccharides are produced by LAB with large variation between different strains (Zoghi et al., 2014). The peptidoglycan consists of polymerized disaccharide N-acetyl-glucosamine-beta (1-4)-N-acetyl muramic acid chains cross-linked by pentapeptide bridges. Disaccharide units of peptidoglycan have three different appendages, including acetyl groups of both N-acetyl-glucosamine and N-acetyl- muramic acid. Some LAB strains such as *Enterococcus faecium*, *Pediococcus pentosaceus*, *L. plantarum*, and *L. casei* have a diverging amino acid sequence of pentapeptide bridge where c-terminal d-alanine is replaced by d-lactate (Grohs et al., 2004).

Teichoic acids are anionic polymers which bind to the peptidoglycan layer via a linkage unit and contribute more than 50% (w/w) of total weight of cell wall. The structure of the linkage unit is glycerol-phospho-N-acetyl mannosaminyl-beta (1-4)- glucosamine. Two types of teichoic acids which are detected from LAB, including poly glycerol phosphate and poly ribitol phosphate teichoic acids. Lipoteichoic acids are structurally similar to teichoic acids but they attach to the plasma membrane instead of peptidoglycan by a glycolipid anchor. The most frequently identified lipoteichoic acid in LAB is the poly glycerol phosphate lipoteichoic acid, which is almost similar to the structure of poly glycerol phosphate teichoic acid (Ambrosini et al., 1996). Some LAB strains such as *Lactobacillus*, *Enterococcus*, *Streptococcus*, *Bifidobacterium* and *Propionibacterium* produce exopolysaccharides containing glucose, rhamnose, galactose, mannose, N-acetylglucosamine, and N-acetylglucosamine (Grohs et al., 2004). Many LAB from the genus *Lactobacillus* are able to produce S-layer proteins. The size of these proteins is 25-50 kDa with calculated pI's ranging from 9.35 to 10.88, and they are highly basic. LAB which cannot produce S-layer proteins have a negative surface charge at neutral pH. Also, it has been reported that the surface charge of S-layer producing *Lactobacillus* are negative. This phenomenon may be due to the involvement of positively charged areas of S-layer proteins in their adhesion to peptidoglycan (Zoghi et al., 2014).

## *S. cerevisiae* cell wall

Except LAB, *S. cerevisiae* is reported to the most used yeast as a probiotic strain in order to aflatoxins removal. *S. cerevisiae* cell wall represents about 30% (w/w) of total weight of the cell and made up of a network of back bone of β-1,3 glucan

with  $\beta$ -1,6 glucan side chains, which is covalently linked to glycosylated mannoproteins. The cell wall mannoprotein includes a very heterogeneous class of glycoproteins. Carbohydrate fraction represents as much as 90% (w/w) of mannoproteins and oligosaccharide of mannan constitutes approximately 50% w/w of the total carbohydrates (Hadiani et al., 2018b). The core contains mannoproteins and branched mannose side chains as well as short and rigid rods like clusters of oligomannosyl chains extend out. Phosphodiester bridges in mannans side chains contribute negative charges on the cell surface. In addition, the cell wall of *S. cerevisiae* is a highly dynamic structure which quickly replies to changes in the environmental stresses (Zoghi et al., 2014). Based on chemical combination and physical nature of cell wall of *S. cerevisiae*, it can be concluded that cell surface presents limitless sites on it in order to physical adsorption of aflatoxins.

According to certain research, it is confirmed that mannan components of the cell wall play a main role in aflatoxin binding by *S. cerevisiae* (Shetty and Jespersen, 2006). The proteins and glucans provide accessible adsorption sites with ability to adsorb aflatoxins through various mechanisms such as hydrogen bonds and ionic or hydrophobic reactions. Heat treatment of *S. cerevisiae* increases permeability of the outer layer of cell wall, due to dissolution of cell-surface mannan and development of adsorption regions (Shetty et al., 2007).

#### EFFECT OF DIFFERENT PROBIOTIC PRETREATMENTS ON AFLATOXIN BINDING

Haskard et al. (2001) revealed that using heat treatment for *L. rhamnosus* GG and LC 705 strains led to significant increase in AFB<sub>1</sub> removal from contaminated defined medium and the stability of LAB-AFB<sub>1</sub> complex. Similarly, Elsanhoty et al. (2014) found that heat treatment of *L. rhamnosus* can significantly enhance its binding to AFM<sub>1</sub> in yoghurt. Reported literature indicates that heat treatment of LAB exhibit higher removal capacity, because of changes on the cell surface (Perczak et al., 2018). Other researchers showed that heat treated yeast reduce aflatoxins more than viable cells. Heating is responsible for protein denaturation or the formation of Maillard reaction products in the cell wall (Shetty et al., 2007; Rahaie et al., 2010).

Several researchers showed that the acid treatment of yeast or LAB caused the highest adsorption of aflatoxin compared with viable and heat-treated probiotic (Haskard et al., 2001; Rahaie et al., 2010; Hegazy et al., 2011). El-Nezami et al. (1998) reported that the binding ability of LAB increased by acid pretreatment. They also stated that acid treatment might break amine linkage in peptides and proteins, producing peptides and amino acids. Moreover, accessible aflatoxin binding sites increase and allow the aflatoxins to bind to the cell wall or its associated components (El-Nezami et al., 2002). According to Haskard et al. (2001) acid treatment may affect cell wall components such as peptidoglycan and polysaccharide by releasing monomers and further fragmentation into aldehydes after the glycosidic linkages break down. The acidic conditions could make AFB<sub>1</sub> to be easily and rapidly bound by constituents of cytoplasmic membrane (Bejaoui et al., 2004). Furthermore, Haskard et al. (2000) noted that hydrophobic interactions were expected in acid-treated LAB; because the protein denaturation may exhibit more hydrophobic binding areas to aflatoxins.

In another study, significant increase in the ability of *L. rhamnosus* GG to bind AFB<sub>1</sub> was observed after treatment with sodium dodecyl sulphate, whereas, treatment with urea showed no effect. One of the probable reasons could be the denaturation of protein by sodium dodecyl sulphate and cell wall isolation consist of peptidoglycan. The exposure of *L. rhamnosus* GG to divalent cations such as Ca<sup>2+</sup> and Mg<sup>2+</sup> or chelators such as EDTA and ethylene glycol tetra-acetic acid, as well as sonication and enzymatic treatments include different specific proteases, did not affect the binding of AFB<sub>1</sub>, may be due to the release of molecules bound to the surface of the bacteria (Lahtinen et al., 2004).

In fact, probiotic pretreatments which lead to protein denaturation, release of some components, and increase of pore size, probably act on the charge distribution change and hydrophobic nature of the bacterial surface and therefore enhance the efficiency of probiotics as adsorbent of aflatoxin (Karazhiyan et al., 2016; Ahlberg et al., 2015).

#### PROBIOTIC-AFLATOXIN COMPLEX STABILITY

Several researchers have reported the partial reversibility of the process of probiotics binding by probiotics (Peltonen et al., 2001; Hernandez-Mendoza et al., 2009); Haskard et al. (2001) studied the stability of 12 LAB-AFB<sub>1</sub> complexes in both viable and nonviable forms (heat and acid treated LAB) after five washing steps with water. They exhibited that up to 71% of the total AFB<sub>1</sub> remained bound and binding of aflatoxins to cell surface is significantly strong. In their investigation, viable cells of *L. rhamnosus* strains LGG and LC105 retained 38 and 50% (w/w) of the bound AFB<sub>1</sub>, respectively. Whereas, non-viable (acid and heat treated) cells retained the highest amount of AFB<sub>1</sub> (66–71% (w/w)). Also, they revealed that autoclaving and sonication treated probiotic bacteria did not release any detectable AFB<sub>1</sub>. The authors concluded that the binding was reversible, but the stability of the complexes depended on strain, treatment and environmental conditions.

Hernandez-Mendoza et al. (2009) reported that about 60–70% of AFB<sub>1</sub> remained bound to the probiotic cells after washing by PBS; so, AFB<sub>1</sub> attached to the bacteria by almost weak and partially reversible bound. Pizzolitto et al. (2012) stated that after five washings with PBS, different LAB cells retained AFB<sub>1</sub> bound close to 50%, and the washing time (1–60 min) did not affect the release percentages. Among a panel of native LAB isolated from Iranian sourdough and dairy products, *L. casei* was reported to have the strongest binding of aflatoxin compared to other *L. plantarum* and *L. fermentum* strains (Fazeli et al., 2009). According to the findings obtained from the washing of AFB<sub>1</sub>-*Enterococcus faecium* complex, the binding of AFB<sub>1</sub> to bacterial cell surface was a reversible process and the stability of the complexes was strain specific (Topcu et al., 2010). Similarly, it was noted that after washing the AFB<sub>1</sub>-*Lactobacillus* complexes, variable amounts of AFB<sub>1</sub> were released back into the solution (Peltonen et al., 2001). Also, the stability of AFB<sub>1</sub>-*Enterococcus faecium* strains (MF4 and GJ40) complexes was found to be high after three washes with PBS (Fernandez Juri et al., 2014). In addition, a stable AFM<sub>1</sub>-LAB (*L. rhamnosus* and *L. plantarum*) complex was showed by Elsanhoty et al. (2014). Moreover, Bevilacqua et al. (2014) described the proportionality of the amount of aflatoxin released into the medium by the number of treatments performed.

According to the above discussion, it is clear that any *in vitro* results must be supported by *in vivo* experiments, because aflatoxins may be released by the continual washing of the bacterial surface in the GIT and negative health implications may be observed. Thus, several studies have attempted to evaluate the stability of the aflatoxin-probiotic complexes in the GIT conditions. It is revealed that defined LAB that show significant adhesion to intestinal cells lose this property when they bind to aflatoxins. Therefore, in the gastrointestinal tract, the bacteria-aflatoxin complex is rapidly excreted (Gratz et al., 2004).

#### IN VIVO STUDIES

Many recent studies revealed that AFB<sub>1</sub> intake can change the morphological and immune function of the intestinal mucosa due to decreasing the percentage of T-cell subsets and the expression level of cytokine mRNA in the small intestine. The mechanism of intestinal tissue poisoning of the host by AFB<sub>1</sub> includes the prevention of oxygen production and inhibition of the free radicals of oxygen (Jiang et al., 2015). Intestinal cells can absorb aflatoxins at high rates (>80%), regardless of the species (Grenier and Applegate, 2013; Wan et al., 2016). Some experimental evidences reported that probiotics could bind aflatoxins within the lumen, so, reducing the negative impacts of aflatoxins and improving gut and liver health (Niderkorn et al., 2009; Gratz et al., 2010).

A few investigations by Slizewska et al. (2010), Hathout et al. (2011), Nikbakht Nasrabadi et al. (2013), and Yadav et al. (2013) indicated the ability of probiotics to decrease genotoxicity impacts and protect animals against oxidative stresses. Hathout et al. (2011) showed that *L. reuteri* and *L. casei* were able to considerably reduce malondialdehyde concentration in the kidney and liver. As aflatoxin toxicity is mainly related to the liver, using probiotics could improve the histological picture and architecture of the liver and serum biochemical parameters.

Besides *in vitro* studies, the AFB<sub>1</sub> binding ability of probiotics was evaluated *ex vivo* in the intestinal lumen of chicken using the chicken duodenum loop technique (El-Nezami et al., 2000). The authors stated that *L. rhamnosus* GG, *L. rhamnosus* LC705, and *Propionibacterium freudenreichii* removed 54, 44, and 36% of the AFB<sub>1</sub>, respectively from the soluble fraction of the luminal fluid within 1 min. It can be concluded from these findings that AFB<sub>1</sub> binding by LAB appears in physiological conditions in animals, which may represents a way to reduce AFB<sub>1</sub> bioavailability in the organism. El Nezami et al. (2006) continued their research in Egypt and investigated the effect of a combination of *L. rhamnosus* LC705 and *Propionibacterium freudenreichii* on AFB<sub>1</sub> levels in human feces samples from 20 healthy volunteers. The mentioned probiotic strains were administered two times per day (at a dosage of 2.5×10<sup>10</sup> CFU/day) for five weeks by volunteers and the control group received a placebo. The marker for biologically effective dose of AFB<sub>1</sub> was the adduct AFB<sub>1</sub>-N7-guanine. High level of this adduct in the urinary excretion is associated to a high risk of liver cancer (Vinderola and Riteni, 2015). The fecal samples were positive for AFB<sub>1</sub> with a range from 1.8 to 6 µg AFB<sub>1</sub>/kg feces for 11 volunteers. A significant reduction in urinary excretion of AFB<sub>1</sub>-N7-guanine and fecal aflatoxin levels was observed for volunteers after receiving the probiotic mixture compared to volunteers receiving a placebo.

Kankaanpaa et al. (2000) showed that aflatoxin binding by *L. rhamnosus* LGG and LC105 considerably reduced adhesion properties of the probiotic strains and facilitates excretion of immobilized AFB<sub>1</sub>. Similarly, Gratz et al. (2004) reported that pre-exposure of *L. rhamnosus* GG to AFB<sub>1</sub> decreases its binding with intestinal mucus and leads to faster removal. Also, it was shown that addition of *S. cerevisiae* to the animal diet reduced aflatoxin toxicities; thus, possible stability of the yeast-aflatoxin complex was indicated through the GIT (Shetty and Jespersen, 2006; Armando et al., 2012). Similar results reported by Gratz et al. (2006) who found that *L. rhamnosus* GG was able to modulate AFB<sub>1</sub> uptake in rats, increased fecal AFB<sub>1</sub> excretion in rats and reduced liver injury. As demonstrated, *L. casei* Shirota can decrease AFB<sub>1</sub> absorption in the GIT even after a long period of toxin exposure (Hernandez-Mendoza et al., 2010).

**Nikbakht Nasrabadi et al. (2013)** also found that *L. casei* Shirota could reduce the blood serum level of AFB<sub>1</sub> in rats and improved the adverse effect of AFB<sub>1</sub> on rats' body weight and plasma biochemical parameters. This result is consistent with **Hernandez-Mendoza et al. (2009)** who stated that *L. reuteri* was able to bind to AFB<sub>1</sub> in all intestinal sections under normal conditions of the GIT. On the other hand, another study revealed that the probiotic mixture could only retard the AFB<sub>1</sub> absorption in duodenal loops and considerably decrease the AFB<sub>1</sub> adsorption in the intestinal mucus (**Gratz et al., 2005**).

**Fochesato et al. (2018)** reported that dynamics of AFB<sub>1</sub> adsorption and desorption by *L. rhamnosus* RC007 were strongly affected by the salivary environment. The knowledge of the adsorption dynamics of AFB<sub>1</sub> with a probiotic strain will allow predicting its behavior at each stage of the GIT.

## CONCLUSION

Aflatoxins frequently contaminate the food and feed at various levels. So, for the food industry, it has always been an uphill task to control the aflatoxins level in the products. It is suggested that probiotic strains with high aflatoxin binding abilities can be used in food industries as additives in small quantities without compromising the characteristics of the final product and thus can avoid accumulation of this toxic compound and decrease its toxic effects. Many studies have demonstrated varying efficiency of some selected probiotics in removing aflatoxins. Tables 1 and 2 demonstrate several kinds of probiotics applied for decontamination of food and feed from AFB<sub>1</sub> and AFM<sub>1</sub>, respectively.

**Table 1** Several kinds of probiotics applied for decontamination of aflatoxin B<sub>1</sub>

Probiotic species	Strain	Medium kind	Probiotic concentration (CFU/mL)	Probiotic Condition	Initial AFB <sub>1</sub> Concentration	AFB <sub>1</sub> removal %	Explanation	Reference
<i>Flavobacterium aurantiacum</i>	NRRL B-184	aqueous solution		Viable Heat-treated Proteinase-treated DNase-treated	2 ppm	74.5 55 34.5 80.5	At 30 °C for 24 h	Smiley & Draughon, 2000
<i>L. acidophilus</i> <i>L. casei Shirota</i> <i>L. gasseri</i> <i>L. rhamnosus</i> <i>L. rhamnosus</i>	ATCC 4356 YIT 9018 ATCC 33323 GG LC-705	Liquid media		Viable Heat-treated	5,10,50 mg/mL	55-67 33-58 48-68 75-82 75-82	0-72 h incubation period at 37 °C. Toxin concentration and temperature dependent process	El-Nezami et al., 1998
<i>S. cerevisiae</i>		aqueous solution	2×10 <sup>8</sup>	Viable Acid-treated Cell wall	2 ppm	44.45 73.35 73.03		Ghofrani Tabari et al., 2018
<i>L. rhamnosus</i>	GG	aqueous solution	1×10 <sup>9</sup>	Viable Acid-treated Cell wall	2 ppm	46.46 75.52 75.28		Ghofrani Tabari et al., 2018
<i>Enterococcus faecium</i>	EF031 M74	aqueous solution	1×10 <sup>10</sup>	Viable non-viable	5 mg/L	23.4 - 37.5 19.3- 30.5	48 h incubation period pH 7	Topcu et al., 2010
<i>Enterococcus faecium</i>	GJ40	aqueous solution	1×10 <sup>8</sup>	Viable heat-killed cells	50 ppb 100 ppb	24-27 17-24	48 h incubation period pH 7	Fernandez Juri et al., 2014
<i>Enterococcus faecium</i>	MF4	aqueous solution	1×10 <sup>8</sup>	Viable heat-killed cells	50 ppb 100 ppb	36-42 27-32	48 h incubation period pH 7	Fernandez Juri et al., 2014
<i>Lactobacillus</i> sp.	G7 PDS3	aqueous solution	1×10 <sup>10</sup>	Viable nonviable	5 mg/L	69.11 73.75	48 h incubation period	Damayanti et al., 2017
<i>L. rhamnosus</i>	RC007	Simulated GIT	1×10 <sup>8</sup>	viable	93.89 ng/g	82.39	Under GIT conditions	Fochesato et al., 2018
<i>L. rhamnosus</i>	GG	cottonseed	1×10 <sup>9</sup>	Viable heat killed acid killed	5 µg/L 10 µg/L 20 µg/L	44-49	slow process 24 h incubation period	Rahnama Vosough et al., 2013
<i>Lactococcus lactis</i> <i>Sterptococcus thermophilus</i>		phosphate buffer solution	10 <sup>7</sup> – 10 <sup>8</sup>	Dead cells (by boiling)	2 µg/L	86.1 100	Strong stability of complex	Shahin, 2007
<i>Lactococcus lactis</i> <i>Sterptococcus thermophilus</i>		phosphate buffer solution	10 <sup>7</sup> – 10 <sup>8</sup>	viable	2 µg/L	54.35 81	Strong stability	Shahin, 2007
<i>L. kefir</i>	KFLM3	milk	8.4 × 10 <sup>7</sup>	viable	1 µg/mL	80-100		Taheur et al., 2017
<i>L. acidophilus</i>	E-94507 CSCC 5361	aqueous solution	1×10 <sup>10</sup>	viable	2 mg/mL	18.2 20.7 57.8	24 h incubation period at 37 °C.	Peltonen et al., 2001
<i>L. amylovorus</i>	CSCC 5197 CSCC 5160	aqueous solution	1×10 <sup>10</sup>	viable	2 mg/mL	59.7	24 h incubation period at 37 °C.	Peltonen et al., 2001
<i>L. delbrueckii</i> <i>subsp. bulgaricus</i> <i>L. helveticus</i> <i>L. fermentum</i> <i>L. johnsonii</i> <i>L. plantarum</i> <i>B. Lactis</i> <i>B. Longum</i>	CSCC 5142 E-79098 CSCC 5094 CSCC 5304 CSCC 1941	aqueous solution	1×10 <sup>10</sup>	viable	2 mg/mL	17.3 34.2 22.6 30.1 28.4 48.7 37.5 45.7	24 h incubation period at 37 °C. Reversible binding	Peltonen et al., 2001

<i>B. animalis</i>								
<i>L. acidophilus</i>	24	liquid medium	$1 \times 10^7$	viable	1.5; 3.75; 7.5; 15	15-24	Pizzolitto et al., 2012	
<i>S. cerevisiae</i>	CECT 1891		$8 \times 10^9$		$\mu\text{g/mL}$			
<i>L. paracasei</i>	LOCK0920	Fecal water		hydrogen peroxide-treated		22	Slizewska et al., 2010	
<i>L. brevis</i>	LOCK0944							
<i>L. plantarum</i>	LOCK0945							
<i>S. cerevisiae</i>	LOCK0140							
<i>L. brevis</i>		Maize grain		Heat-treated viable	80 ng/g	33-75 33	72 h incubation period	Oluwafemi & Da-Silva, 2009
<i>L. delbrueckii</i> <i>subsp. bulgaricus</i>		Maize grain		Viable Heat killed	80 ng/g	50 56	72 h incubation period	Oluwafemi & Da-Silva, 2009
<i>L. plantarum</i>		Maize grain		Viable Heat killed		75 95	48 h incubation period	Oluwafemi et al., 2010
<i>L. casei</i>	Shirota	aqueous solution	$2-3 \times 10^9$	viable	4.6 $\mu\text{g/mL}$	15-68	4 & 12 h incubation period	Hernandez-Mendoza et al., 2009
<i>L. casei</i>	Defensis					35-60		
<i>B. bifidum</i>						35-60		
<i>S. cerevisiae</i>		Corn for mice feed		viable		72	6 weeks incubation period	Motameny et al., 2012
<i>S. cerevisiae</i>	A 18 26.1.11	Indigenous fermented foods	$1 \times 10^9$	Viable, heat and acid treated cells	1 to 20 $\mu\text{g/mL}$	53 48	20 to 37 °C	Shetty et al., 2007
<i>L. rhamnosus</i>	GG	Aqueous solution		viable		61	Time-dependent process	Gratz et al., 2007
<i>L. plantarum</i>	PTCC 1058			viable		45 100	1 h incubation period 90 h incubation period	Khanafari et al., 2007
<i>L. johnsonii</i>						38.8		
<i>L. paracasei</i>				viable		30	24 h incubation period	Peltonen et al., 2000
<i>L. salivarius</i>	LM2-118					17		
<i>B. lactis</i>	Bb-12					18		
<i>L. casei</i>		Aqueous solution	$10^6-10^9$	viable	30 $\mu\text{g/mL}$	79.7	0-80 h incubation period pH=3-9	Hussien, 2008
<i>B. bifidum</i>						90		
<i>L. acidophilus</i>						84.3		
<i>L. rhamnosus</i>	GG	Aqueous solution		Treatment with: Sodium dodecyl sulphate Urea CaCl <sub>2</sub> MgCl <sub>2</sub> EDTA EGTA		89 78 49 54 49 50		Lahtinen et al., 2004
<i>B. breve</i> <i>Propionibacterium freudenreichii</i>	Bbi99/E8 shermanii JS	aqueous solution	$10^7-10^8$	viable	2 g/L	21.4 12.5	1 h incubation period at 37 °C	Halttunen et al., 2008
<i>L. plantarum</i>	BS22	GIT of broiler chickens	$1.0 \times 10^8$	viable	50 $\mu\text{g/kg}$	50	28 days incubation period	Zeng et al., 2018
<i>L. brevis</i>	Lb1	Liquid media		viable	10 $\mu\text{g/mL}$	4.46	48 h incubation period at 30 °C pH=6.5	Zinedine et al., 2005
<i>L. casei</i>	Lc12					22.28		
<i>L. lactis</i>	Lb5					16.81		
<i>L. lactis</i>	Lb8					20.26		
<i>L. plantarum</i>	Lb7					2.14		
<i>L. plantarum</i>	Lb9					5.21		
<i>L. rhamnosus</i>	Lb44					25.27		
<i>L. rhamnosus</i>	Lb21					23.01		
<i>L. rhamnosus</i>	Lb31					31.12		
<i>L. rhamnosus</i>	Lb103					30.77		

<i>L. rhamnosus</i>	Lb50					44.89		
<i>Leuconostoc mesenteroides</i>	Ln13					2.15		
<i>Pediococcus acidilactici</i>	P5					1.80		
<i>L. rhamnosus</i>	GG	aqueous solution	$1 \times 10^{10}$	Viable	5 µg/mL	66	Treatment with Pronase E	Haskard et al., 2000
				Heat-treated		72		
				Acid-treated		85		
<i>L. rhamnosus</i>	GG	aqueous solution	$1 \times 10^{10}$	Viable	5 µg/mL	76	Treatment with Lipase	Haskard et al., 2000
				Heat-treated		74		
				Acid-treated		89		
<i>L. rhamnosus</i>	GG	Phosphate buffer	$1 \times 10^{10}$	Viable	5 µg/mL	86		Haskard et al., 2000
				Heat-treated		85		
				Acid-treated		91		
<i>L. rhamnosus</i>	GG	aqueous solution	$1 \times 10^{10}$	Viable	5 µg/mL	60	Treatment with Periodate	Haskard et al., 2000
				Heat-treated		49		
				Acid-treated		36		
<i>L. rhamnosus</i>	GG	aqueous solution	$1 \times 10^{10}$	Viable	5 µg/mL	83	Treatment with Iodate	Haskard et al., 2000
				Heat-treated		84		
				Acid-treated		80		
<i>L. rhamnosus</i>	GG	aqueous solution	$1 \times 10^{10}$	Viable	5 µg/mL	64	Treatment with Urea (8 M)	Haskard et al., 2000
				Heat-treated		60		
				Acid-treated		50		
<i>L. rhamnosus</i>	GG	water	$1 \times 10^{10}$	Viable	5 µg/mL	76		Haskard et al., 2000
				Heat-treated		83		
				Acid-treated		84		

**Legend:** L. is abbreviation of *Lactobacillus*; S. is abbreviation of *Saccharomyces*; B. is abbreviation of *Bifidobacterium*

**Table 2** Several kinds of probiotics applied for detoxification of aflatoxin M<sub>1</sub>

probiotic	Strain	Medium kind	Probiotic concentration (CFU/mL)	Probiotic Condition	Initial AFM <sub>1</sub> Concentration	AFM <sub>1</sub> removal %	Explanation	References
<i>L. acidophilus</i>	LA-5	yoghurt	1×10 <sup>8</sup>	viable	0.1, 0.5, 0.75 µg/L	90	in the presence and absence of yoghurt starter	Adibpour et al., 2016
<i>L. rhamnosus</i>	GG	liquid media	5×10 <sup>8</sup> - 10 <sup>10</sup>	Viable and heat treated	50, 100 µg/L	63	18 h incubation period at 37 °C Partial reversible	Assaf et al., 2018
<i>S. cerevisiae</i>		yoghurt	2.1×10 <sup>9</sup>	viable, acid-, heat- and ultrasound-treated	100, 500 and 750 pg/mL	74.2- 76.4	different storage times (1, 7, 14 and 21 days)	Karazhiyan et al., 2016
<i>L. plantarum</i>	MON03	liquid medium	1×10 <sup>9</sup>	viable	100 mg/kg	93	24 h incubation period	Ben Salah-Abbe's et al., 2015
<i>L. bulgaricus</i> <i>Streptococcus thermophilus</i>		yogurt	1×10 <sup>6</sup>	viable	50 µg/L	58.5 37.7	14 h incubation period at 37 °C	El Khoury et al., 2011
<i>L. acidophilus</i>	LA1	milk		Viable Heat killed		18.3 25.5		Pierides et al., 2000
<i>L. delbrueckii subsp. Bulgaricus</i> <i>Streptococcus thermophilus</i>	ST-36	Milk PBS Milk PBS				27.6 18.7 39.16 29.42	4 h incubation period at 37 °C pH dependent	Sarimehmetoglu & Küplülü, 2004
<i>L. gasseri</i>		milk		Viable Heat killed		30.8 61.5		Pierides et al., 2000
<i>L. rhamnosus</i> <i>L. lactis</i> <i>L. lactis</i>	LC705 cremoris ARH74			Heat killed Viable Heat killed		50 40.4 38.9		
<i>L. acidophilus</i> <i>L. reuteri</i> <i>L. rhamnosus</i> <i>L. johnsonii</i> <i>B. bifidum</i>	NRRL B-4495 NRRL B-14171 NRRL	milk		viable	10 ng/mL	22.72 26.5 24.54 32.2 45.17	37 °C	Serrano-Niño et al., 2013

**Legend:** L. is abbreviation of *Lactobacillus*; S. is abbreviation of *Saccharomyces*; B. is abbreviation of *Bifidobacterium*.

Aflatoxin removal mainly relies on aflatoxin binding to probiotic cell walls rather than bacterial metabolism. This removal was described as a reversible phenomenon, probiotic strain- and dose-dependent, and did not affect the viability of probiotics. Binding is related to some protein and carbohydrate components in the cell wall of probiotics. The stability and strength of binding of probiotics to aflatoxins is also a key consideration for evaluation of probiotic strains ability to decline aflatoxins. The binding stability depends on the environmental conditions (such as pH), probiotic strain, amino acid composition of peptidoglycan structure, formation medium conditions and the treatment used to investigate stability. According to previous studies, aflatoxin binding could be permanent if the probiotic strains are dead, whereas the living probiotics may release some of the aflatoxin content with time. As reported, treated probiotic cells with physical and chemical treatments (high temperature, adding metal ions or acids, alkaline and enzymatic treatments) seems to increase their aflatoxin binding efficiency due to the impact of hydrophobic and electrostatic interactions. This is quite related to the probiotic cell wall components, mainly peptidoglycans and exopolysaccharides. Even though probiotic effect can be varied between species and strains of probiotics, the most efficient probiotic strains could be applied as biological detoxifying agents in various kinds of food and livestock feed frequently contaminated by aflatoxins in order to increase food safety.

As reported by several researches, under appropriate *in vitro* conditions, *L. rhamnosus* and *L. bulgaricus* have high potential for removal of AFB<sub>1</sub> and AFM<sub>1</sub>, respectively. *In vivo* studies are all in agreement that aflatoxin binding by probiotics is in fact better at lower pH, therefore, the probiotics have the ability to bind with aflatoxins in the small intestine and subsequently preventing toxicity of aflatoxin. Despite the promising research findings, future studies should also focus on the potential release of aflatoxins (from probiotics) after ingestion and the dose of toxicity of the bound aflatoxin compared to its unbound form.

Until now, all the studies have been conducted bench scale and there are not any applicable industrial reports for probiotics application in detoxification of aflatoxins from foods. So, further research on the pilot and industrial scale of such process is required. Also, future study on screening of new probiotic strains, combination of different probiotic strains, improvement of culture conditions, genetic engineering, and modeling of bioprocess would be required in this field of research.

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