REVIEW

Bio-detoxification of mycotoxin-contaminated feedstuffs: Using lactic acid bacteria and yeast

Alaleh Zoghi[1], **Svetoslav Dimitrov Todorov**[2], **Kianoush Khosravi-Darani**[1*]
[1] Department of Food Technology Research, National Nutrition and Food Technology Research Institute, Faculty of Nutrition Sciences and Food Technology, Shahid Beheshti University of Medical Sciences, Tehran 19395-4741, Iran
[2] ProBacLab, Department of Advanced Convergence, Handong Global University, Pohang, Gyeongbuk 791-708, Republic of Korea

Abstract: Mycotoxins contaminations in feedstuffs are one of the principal concerns worldwide nowadays, related to the fact that they may evoke health problems in animals and consequently in humans. Biodetoxification of mycotoxins by application of beneficial microorganisms (lactic acid bacteria or yeasts) is one of the well-known, relatively low-cost, easy, efficient, safe, and green approaches for the reduction of mycotoxins presence in feeds. The use of beneficial microorganisms as feed additives to remove mycotoxins is widely practiced in the industrial production of animal feed. In this overview, we aim to summarize the great potential of beneficial microorganisms as bio-detoxificant, including a summary of various reported detoxification activities of lactic acid bacteria or yeasts against mycotoxins with relevance for feedstuff. The principal focus is the detoxification of mycotoxins in livestock, poultry, and aquatic feed using beneficial microorganisms. The mechanisms of the detoxification process and effective factors in this process are also covered. This review article could be useful for biotechnologists, investigators, and animal feed manufacturers who have challenges regarding the existence of mycotoxins in feed, and help them to find the best method for feed bio-decontamination.

Keywords: Bioremediation, probiotic, decontamination, degradation, binding, mycotoxins

Abbreviations: LAB: lactic acid bacteria; S-layer: surface layer; EPS: exopolysaccharide; GIT: gastrointestinal tract; *L.*: *Lactobacillus*; *S.*: *Saccharomyces*; *E.*: *Enterococcus*; *B.*: *Bifidobacterium*; *Lc.*: *Lactococcus*; ZEA: Zearalenone; AFB_1: Aflatoxin B_1; T-2 toxin: Trichothecene-2 toxin; DON: Deoxynivalenol; OTA: Ochratoxin A; FB_1 and FB_2: Fumonisin B_1 and B_2

Correspondence to: Kianoush Khosravi-Darani. Research Department of Food Technology, National Nutrition and food Technology Research Institute, Faculty of Food and Nutrition Sciences, Shahid Beheshti University of Medical Sciences, P.O. Box: 19395-4741, Tehran, Iran; E-mail: k.khosravi@sbmu.ac.ir

Received: April 28, 2024; **Accepted:** August 25, 2024; **Published Online:** September 2, 2024
Citation: Zoghi, A., Todorov, S.D., Khosravi-Darani, K., 2024. Bio-detoxification of mycotoxin-contaminated feedstuffs: Using lactic acid bacteria and yeast. *Applied Environmental Biotechnology*, 9(1): 62-75. http://doi.org/10.26789/AEB.2024.01.007

1 Introduction

The contamination of animal feed commodities with different mycotoxins has always been considered as a worldwide problem but has become in strong focus in recent years related to increasing evidence of the relevance of the intoxication not only for the animals but also for possible transmission via the food chain to humans (Liu et al., 2022). In general, mycotoxins are metabolites produced by several fungal species, known as toxins with strong effects on humans and other animals, and are considered as a concern by the health authorities associated with their strong toxicity, mutagenic and carcinogenic properties, in addition to other adverse effects (Zoghi et al., 2014).

The concentrations of mycotoxins in primary feed materials, such as corn, grass, or clover normally need to be present below suggested by controlling authorities, while they will be processed into feed products, since these metabolites generally are not affected by exposure to high and low temperatures processing, and not subject to natural degradation, even after a long storage period (Kosicki et al., 2016). According to a global survey reported by Gruber-Dorninger et al. (2019), practically 90% of produced feed commodities and especially primary feed materials produced worldwide were detected to be contaminated with at least one type of mycotoxin, evidence of the contaminations with mycotoxin-producing molds at some stage of production or storage. Moreover, contaminations with multiple mycotoxins were found in 64% of these samples. It is evident, that some environmental conditions during storage time may stimulate growth and toxin production by fungi, including the temperature of 25-30°C and moisture of grains (16-30%, w/w), as well as humidity of gas phase (80-100%, v/v). Taking into consideration that usually, the content of mycotoxins may not decrease during the preparation of feed, transforming the problem even more relevant (Kosicki et al., 2016; 2019).

Different methods have been suggested and applied for the removal of mycotoxin, such as physical methods (washing, heat treatment, irradiation, and using adsorbents, such as activated carbon and clay) (Vila-Donat et al., 2018) and chem-

icals (ammonia and ozone) (Conte et al., 2020). However, all of these procedures have their own proper limitations, such as leaving chemical residues and reducing the nutritional quality and organoleptic properties of feed. Biodetoxification has been introduced as a highly specific, effective, and successful approach, which is also considered as safe for humans and other animals, and environmentally friendly; been considered as part of the "green technologies" (Śliżewska et al., 2016; Zhu et al., 2017). Some special microbial species with the potential for biodetoxification needed to as well safe for application in feed products, to belong to GRAS species, with no undesirable side effects should be considered, as part of the concept "Safety is Priority" (Tan et al., 2014).

Among all applicable microorganisms, LAB and other microorganisms with probiotic properties are preferred for this purpose besides other beneficial aspects for animal health and productivity due to stimulating the immune system and modulating gut microbiota (Wang et al., 2019; Nasrollahzadeh et al., 2022). Most of the LAB are considered as nonpathogenic and nontoxigenic and several of them were characterized as probiotics. Moreover, the mentioned microorganisms can be involved in the production of hydrolytic enzymes for decomposing different carbohydrates (specially saccharose and maltose) and can be involved in increasing the activity of the specific enzymatic systems (Śliżewska and Piotrowska, 2014). The most applicable genera of probiotic yeasts with biodetoxification properties were *S. cerevisiae* and *S. boulardii*, while effective LAB genera belong to *Lactobacillus* (re-classified in different Genera since April 2020 (Zheng et al., 2020)), *Bifidobacterium*, *Streptococcus*, *Lactococcus*, *Bacillus*, and *Enterococcus* (Perczak et al., 2018). Biodetoxification of feed products by different microorganisms with probiotic properties was reported for some mycotoxins, including OTA, AFB_1, ZEA, FB_1, FB_2, and DON (Deepthi et al., 2016; Moretti et al., 2018; 2019; 2020; Ragoubi et al., 2021). In general, the aim of this review is to present the role of LAB and yeast as beneficial organisms involved in the reduction and/or inactivation of mycotoxins in feedstuff.

2 Mycotoxins in Feedstuff

The most prevalent mycotoxins found in feed were reported to be AFs, OTA, trichothecenes including DON and T-2 toxin, as well as ZEA and fumonisins (Liew and Mohd-Redzwan, 2018; Ben Hassouna et al., 2022). A schematic representation of the presence of mycotoxins in feedstuff is demonstrated in Figure 1. In the European Union surveys, the most frequently reported mycotoxins in feed were AFB_1 ($> 98\%$), DON ($\sim 90\%$), and ZEA (70%) (Streit et al., 2012). AFs have a wide range of biological effects on different animals and clearly lead to serious intoxications. The guidance value for the presence of AFs in feedstuff (at 12% moisture) is 0.005-0.05 mg/kg (Chlebicz and Śliżewska, 2020; Abraham et al., 2022). Moreover, was reported that AFs have half-maximal lethal dose values varying from about 0.3 mg/kg of BW in rabbits to around 18 mg/kg of BW reported in rats (FDA, 2016).

The toxic doses and defenselessness of AFs depend on the dose and duration of exposure, species, gender, physiological conditions, nutritional status, and age. Levels of AFs have been recorded in domestic (including cattle, buffaloes, camels, horses, sheep, goats, dogs, and pigs) and wild animals (deer and Rhesus monkeys) (Iqbal et al., 2019) and various toxic effects of AFs in animals have been reported (Olinda et al., 2016).

The molds can grow in soil, cross-contaminate different food and feed commodities, and reach humans and other animals. Animals fed with contaminated feed can cumulate the AFs and pass the mycotoxin via eggs, milk products, and meat to humans (Fratamico et al., 2008). AFs can be particularly toxic for children and shown to be related to stunted growth, delayed physical and intellectual development, and

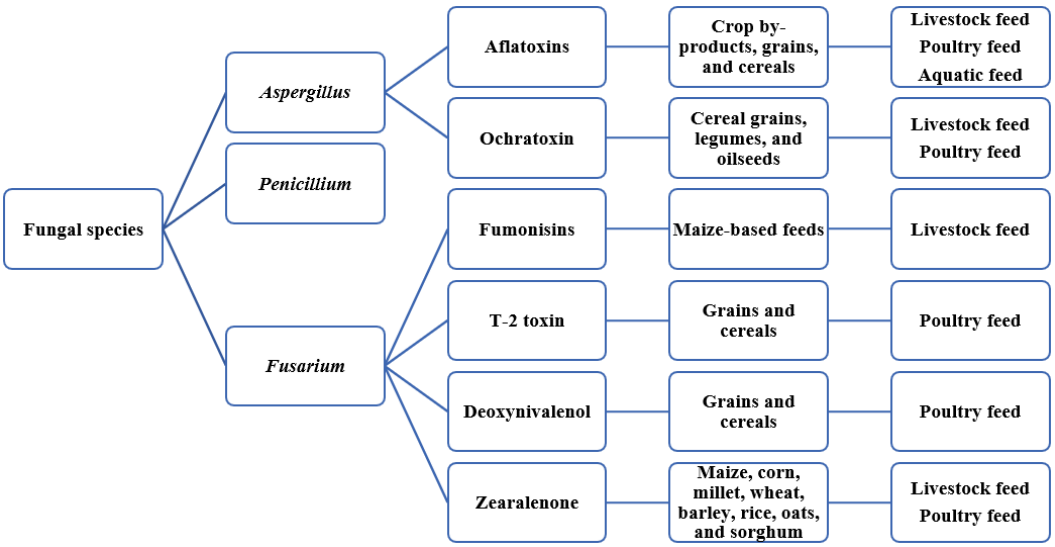

Figure 1. Schematic representation of the presence of mycotoxins in feedstuff.

damage to the liver, including to be associated with liver cancer (Abbas, 2005). Adults normally have a better tolerance to exposure to AFs; however, even thus, their health status can be compromised. In general, all animal species can be considered susceptible to the effect of AFs (Hudler, 1998).

OTA is predominantly found in cereal grains, legumes, and oilseeds as well as in the tissue and organs of animals, most probably cumulated after a feed with mycotoxin-contaminated sources. Several toxicological effects of OTA were also described (Śliżewska and Piotrowska, 2014). The guidance value in feedstuff (with 12% moisture) for OTA is 0.05-0.25 mg/kg (Chlebicz and Śliżewska, 2020). The toxin was recorded posteriorly in the histological material of tissues and organs of different animals, and even in human blood and breast milk (Clark and Snedeker, 2006). Was shown that OTA can be associated with carcinogenic, neurotoxicity, immunosuppression, immunotoxicity, and nephropathies health consequences not only for humans but for different domestic and wild animals (O'Brien and Dietrich, 2005).

ZEA production occurs in geographical regions with humid and warm climates in the preharvest stage in comparison to the storage period. It can disrupt the estrous cycles in animals (Kowalska et al., 2016). Swine is the most vulnerable animal to ZEA even at 1 ppm contamination of diet (Chaytor et al., 2011). The guidance value of ZEA in feed (12% w/w moisture) is 0.1-3 mg/kg (Chlebicz and Śliżewska, 2020). ZEA has been detected at 120 μg/L (49% from 1,820 samples in China), 104 μg/L (45% from 5,402 samples in Australia), and 87 μg/L (40% from 1,402 samples in Japan) (Rodrigues and Naehrer, 2012). ZEA is a mycotoxin, that interacts with receptors associated with estrogen and causes infertility, including abortion, especially in swine farming (Ropejko and Twarużek, 2021). Moreover, the toxic mode of action of ZEA is associated with a combination with deoxynivalenol in soiled samples, and often its toxicity is increased when combined with other toxins (Peillod et al., 2021). One of the major problems is that ZEA, as well some several other mycotoxins, is resistant to the effect of high-temperature treatments (Massoud and Zoghi, 2022; Prossnitz and Barton, 2014).

Among 4 types of Trichothecenes (Haque et al., 2020), DON is the major toxin synthesized by *Fusarium* commonly detected in grains and cereals. Several toxic effects are reported due to acute exposure to high doses of DON. Pigs are the most sensitive animals to exposure through their cereal-rich diet (Pinton and Oswald, 2014). T-2 is the most acutely toxic type among the 4 categories of trichothecenes in animals, anyway, vulnerability depends on animal species, especially in dairy cows (Haque et al., 2020). The guidance values in feedstuff (12% moisture) for T-2/HT-2 and DON are 0.25-2.0 and 0.9-12.0 mg/kg, respectively (Chlebicz and Śliżewska, 2020).

Fusarium verticillioides and *Fusarium proliferatum* can synthesize fumonisins by growth on maize-based feeds. The toxicity of fumonisins to animals is due to the collapse of sphingolipid metabolism (Haque et al., 2020), as well as hepatotoxic, nephrotoxic, and immunosuppressing effects, especially in poultry and rats (Deepthi et al., 2016). Several toxicologic effects are reported resulting from the contamination of fumonisins in horses and pigs (Ashiq, 2014). The guidance value in feedstuff (12% moisture) for FB_1 and FB_2 is 5.0-60 mg/kg (Chlebicz and Śliżewska, 2020).

3 Factors Influencing the Detoxification Ability of LAB and Yeast

Mycotoxin removal by LAB and other microorganisms depends on different variables, including pH, incubation temperature and time, specificity of bacterial strain, inoculum, and initial mycotoxin concentration (Zoghi et al., 2021b). Chlebicz and Slizewska (2020) reported the biodetoxification ability of strains belonging to *L. brevis*, *L. casei*, *L. paracasei*, *L. plantarum*, *L. reuteri*, *L. rhamnosus*, and *S. cerevisiae* to FB_1 and FB_2. The range of bio removal efficiency varied from 62 to 77% and 67 to 74% for bacterial and yeast strains. After 24 h of incubation, the content of DON removal reached 19-39% when *Lactobacillus* sp. strains and 22-43% when *S. cerevisiae* was applied, respectively. The concentration of T-2 toxin, AFB_1, and ZEA was also reduced by 61%, 60%, and 57% by different *Lactobacillus* spp., correspondingly, and 69%, 65%, and 52% by *S. cerevisiae*, correspondingly. However, *L. rhamnosus* was the most effective LAB for the bio-removal of ZEA, DON, AFB_1, and fumonisins (Chlebicz and Śliżewska, 2020). Therefore, it is clear that the detoxification capacity of LAB was revealed to be strictly strain-specific.

Muaz et al. (2021) suggested and confirmed that detoxification needs to be regarded as a fast process and attachments between cells and mycotoxins normally occur in a few minutes. A similar was reported by Zhao et al. (2016), who reported that fumonisins can attach to lactobacilli quickly and normally occur in the 1 h of interactions between mycotoxin and bacterial cells. Moreover, Pizzolitto et al. (2012) pointed out that the process can be almost immediate, and binding even after 1 minute of interaction between bacterial cells and mycotoxins can be fact. Usually, it is shown that the mycotoxins adsorption process by LAB and yeast is quick and begins immediately after their direct contact (Zoghi et al., 2017).

It was suggested that pH can be considered as one of the important influencing factors in mycotoxin removal by LAB and yeast. Hsu et al. (2018) evaluated the role of *Bacillus licheniformis* in the removal of ZEA and pointed out that pH increases from 2.5- 6.0, enhancing the bio-removal of the mycotoxin. Moreover, Guo et al. (2018) showed that pH increasing from 3.0 to 5.0 can influence the increase in adsorption of OTA, ZEA, and AFB_1 in the presence of kefir-isolated bacteria consortium by 94%, 100%, and 82%,

respectively. On the opposite, Tiziri et al. (2023) stated that the removal ability of viable LAB cells increased with a decrease in pH from 6 to 5. Furthermore, Bovo et al. (2014) reported no significant difference in AFB_1 reduction efficacy when a strain of *L. rhamnosus* was applied to two different pH values (3.0 and 6.0). In another study, the highest and lowest AFB_1 elimination by LAB was detected at pH 8.0 and 4.4, respectively (Rayes, 2013). In the different experimental study was claimed that mycotoxins reduction by some specific probiotics can be pH-dependent and more efficient removal processes were recorded at pH values near neutral (Elsanhoty et al., 2016). These different reports could be due to the difference between strains, detoxification conditions, and mycotoxin type.

The LAB role in the detoxification processes is clearly related to the concentration of the mycotoxin (Zoghi et al., 2017), most probably depending on the ability of the microbial cells to adsorb or metabolize mycotoxin can play a limiting factor in the efficacy of the processes. Armando et al. (2013) reported increasing binding ability of *S. cerevisiae* RC016 from 27%, 43%, 68%, and 79.6% followed by increasing mycotoxin of FB_1 concentration at 1, 5, 20, and 50 μg/ml, respectively.

3.1 Effect of LAB pretreatment on detoxification

Was suggested that pretreating LABs can influence the mycotoxin detoxification process (Zoghi et al., 2021a). As part of the applied approach, denaturation of proteins can occur and result in the alteration in charge distribution, specific changes in the hydrophobic surface re-arrangement in bacterial surface, and therefore as well influence and improve the mycotoxins adsorption (Zoghi et al., 2021b). The structure of the cell wall in *Bacillus* and *Lactobacillus* includes teichoic acids, and peptidoglycans, with the inclusion of specific polysaccharides and proteins. The specific structure and thickness of the cell wall can be reduced and as a consequence, their pore size may enhance when cells are exposed to acid and/or heat treatments. Moreover, some of the amide bindings in the structure of the peptidoglycans can be broken as a consequence of the effect of the acid. Even, some of the glycosidic links in polysaccharides can be affected by Maillard reactions (among peptides and polysaccharides as a consequence of the heat treatments). Also, proteins can be simply denatured by acid and/or heat treatments (Tinyiro et al., 2011).

The adsorption abilities of the LABs may change by pretreatment with heat due to possible changes in the peptidoglycan structure, including an increase of the porosity and break of existing glycosidic links between polysaccharides (Lee et al., 2017). It has already shown that the high-temperature pretreatment may involve the development of binding sites via specific hydrophobic bindings with mycotoxins (Teodorowicz et al., 2017).

The adsorption abilities of the LABs are also influenced by changes in the pH and acid treatments, associated with an increase in porosity, which may influence the thickness of the cell wall peptidoglycan, and break the amide bonds in the peptidoglycans (Lee et al., 2017). The acid pretreatment of bacteria can have an effect on the decrease of the cell wall specific thickness and enhances the size as the monomers, released from proteins and amide and glycosidic linkages in peptides and polysaccharides break (Zou et al., 2012). However, acid pretreatment of *Bacillus* leads to a significant decrease in ZEA absorption in comparison to untreated cells, implying that low pH sites are most probably unfavorable for the microbial degradation and adsorption of ZEA by that specific *Bacillus* strain (Wang et al., 2017).

LABs and some other probiotics by applying alkaline pretreatments are able to reduce and even eliminate the coating compounds present on the bacterial surface and in this way involved in the change of the availability of the binding sites. As a consequence, the acidic groups most probably will be neutralized and this will affect the whole cell's, surface electronegativity (Wang et al., 2015). The ability of the bacterial cells to increase their binding capacity after the cell wall's degradation was shown to be associated with the improvement of viability of the peptidoglycans amount (Zoghi et al., 2021a).

4 Detoxification of Mycotoxins in Feed by LAB and Yeast

Table 1 shows some LAB and yeast species recently used for mycotoxins detoxification from feedstuffs (2012 onwards).

4.1 Livestock feed

Sources of contamination of livestock with mycotoxin are normally cereals, oilseeds, leguminous seeds, as well as industrial and crop by-products (Coppock et al., 2018). A strain of *E. faecium*, recovered from the feces of healthy dogs has been shown to reduce the levels of AFB_1 in feed. These strains were suggested to be applied as promising pet feed additives for aflatoxin detoxification (Fernandez Juri et al., 2014). For strain of *S. cerevisiae* CECT 1891 was also shown to have the ability to adsorb aflatoxin into its cell wall components. Moreover, that particular strain of *S. cerevisiae* was shown as well to be resistant to salivary and gastrointestinal environmental conditions, making him a good probiotic candidate (Pizzolitto et al., 2012). These benefits may increase the possibility of its use as a feed additive for livestock with mycotoxin-reducing properties. Watanakij et al. (2020) reported on the use of extracellular fraction obtained from *Bacillus subtilis* BCC42005 as a soaking agent for maize with the aim of reduction of aflatoxins and the results showed a reduction of AFB_1 after 120 min contact time. Therefore, specific strains of LAB and yeast, as feed additives, are ef-

Table 1. Several LABs and yeasts applied for feed detoxification (recent 11 years)

Species	Mycotoxin	Feed	Microorganism concentration (CFU/ml)	Initial toxin concentration	Toxin removal	Experimental condition	Mechanism of detoxification	References
Berevibacillus laterosporus	AFB_1	Quails feed	1.5×10^{10}	5 µg/ml	57.30%	37 °C for 4 h	Adsorption	Bagherzadeh Kasmani et al., 2012
L. gallinarum PL 149	AFB_1	Poultry feed	108	100 ng/ml	65%	37°C for 2 h	Adsorption	Azeem et al., 2019
Bacillus Megaterium, Bacillus amyloliquefaciens, Bacillus subtilis	AFB_1	Poultry feed	109	750 µg/L	47%	37 °C	Biotransformation into less toxic products	Galarza-Seeber et al., 2015
L. plantarum CIDCA 83114	AFB_1	Poultry feed	$1–2\times10^{8}$	500 µg/L	90%	freeze-dried bacteria-zeolite mixture	Adsorption into the bacterial cell wall	Moretti et al., 2018
L. acidophilus ATCC 20552, *B. angulatum* DSMZ 20098	AFB_1	Water	109		8.9 - 21.6%	22 or 37°C for 5 min to 24 h	Detailed data unavailable	Elsanhoty et al., 2016
S. cerevisiae	AFB_1	Corn for mice feed				6 weeks incubation period	Detailed data unavailable	Motameny et al., 2012
Bacillus velezensis DY3108	AFB_1	Maize grain	108	500 µg/L	91.50%	80 °C for 24 h	Biotransformation into less toxic products	Shu et al., 2018
Bacillus shackletonii L7	AFB_1	Liquid feed		100 µg/L	92.10%	37 °C for 72 h	Biotransformation into less toxic products	Xu et al., 2017
Bacillus subtilis, Bacillus licheniformis, Bacillus pumilus	AFB_1, OTA	Shrimp feed	5×10^{10}	1.000 ng/ml	> 50%	pH 2, 6	Adsorption into the bacterial cell wall	Calvet et al., 2020
L. plantarum R1096	AFB_1 OTA	Wheat	1010	40 ng/mL	76% 70%	25 °C for 24 h pH 6	Binding to the bacterial cell wall	Tiziri et al., 2023
L. plantarum 1QB147 *L. plantarum* 3QB361	AFB_1 ZEA	Potassium phosphate buffer	109	1.0 mg/ml 2.0 µg/ml	78% 82%	37 °C for 20 min	Adsorption into the bacterial cell wall	Møller et al., 2021
L. rhamnosus CECT 278 T	OTA	MRS broth	108	0.6 µg/ml	97%	37 °C for 24 h	Enzymatic degradation	Luz et al., 2018
Bacillus subtilis	ZEA	Maize	10^5 to 10^6	5 mg/kg	56%	37°C for 24 h	Degradation	Chen et al., 2019
Bacillus subtilis ANSB01G	ZEA	Complete pig feed	500 ng/ml	5 µg/ml	83.00%	37 °C for 48 h in the dark	Degradation	Lei et al., 2014
Bacillus amyloliquefaciens LN	ZEA	Corn meal medium	1010	5 µg/ml	92%	37°C for 24 h	Adsorption into the bacterial cell wall	Lee et al., 2017
Bacillus licheniformis CK1	ZEA	Corn meal medium	108	5 µg/ml	73.00%	37°C, pH 7.0	Adsorption into the bacterial cell wall	Hsu et al., 2018
L. paracasei, Lc. lactis, S. cerevisiae	ZEA	Aqueous solution	18×10^{8}	2 µg/ml	55.30% 47.40% 57.00%	37 °C for 24 h	Adsorption and degradation	Rogowska et al., 2019
L. acidophilus CIP 76.13T, *L. delbrueckii* subsp. *Bulgaricus* CIP 101027T	ZEA DON	Liquid feed	10^5 to 10^6		23% 30%	37°C for 48 h	Degradation	Ragoubi et al., 2021
L. paracasei LHZ-1	DON	Liquid culture		50 µg/mL	40.70%		Adsorption into the bacterial cell wall	Zhai et al., 2019
Bacillus subtilis ASAG 216	DON	Luria–Bertani medium	109	100 µg/mL	81.10%	37°C for 48 h	Detailed data unavailable	Jia et al., 2021
S. cerevisiae ŁOCK 0119	DON FB_1, FB_2 AFB_1 ZEA T-2 toxin	PBS solution	108	100µg/mL	22–43% 67–74% 65% 52% 69%	37 or 30 °C for 24 h	Adsorption into the bacterial cell wall	Chlebicz and Śliżewska, 2020
L. plantarum MYS6	FB_1	Maize-based feeds	106	10 µg/mL	61.70%	37°C for 2 and 4 h.; pH 7.4	Adsorption into the bacterial cell wall	Deepthi et al., 2016
Bacterial consortium SAAS79	FB_1	Cereal-based feeds	108	10 µg/mL	>90%	28-35 °C for 24 h.; pH 5-7	Enzymatic transformation into low-toxicity metabolites	Zhao et al., 2019
L. plantarum FS2, *L. delbrueckii* subsp. *delbrueckii* CIP 57.8T *Pediococcus pentosaceus* D39	FB_1 FB_2	Maize based Fermented cereals	1013	125 µg/ml	80%	37°C for 24 h	Adsorption	Dawlal et al., 2019
Lentilactobacillus buchneri, L. gasseri	AFs	rye silage	1.25×10^{11} CFU/g	13.49 µg/kg	16.75%	30 °C for 24 h	Adsorption into the bacterial cell wall	Juráček et al., 2022
L. plantarum CECT 749 CFS	AFB_1 FB_1	Corn kernels and corn ears	107		73.7 to 99.7%	37 °C for 72 h	Adsorption into the bacterial cell wall	Nazareth et al., 2020
L. buchneri, L. lactis, L. plantarum, L. lactis	ZEA	Corn silage	250,000 CFU/g		40–60%	25°C for 30 days	Adsorption	Gallo et al., 2022

Abbreviations: *Lactobacillus: L.*; *Saccharomyces: S.*; *Bifidobacterium: B.*; *Lactococcus: Lc.*; Zearalenone: ZEA; Aflatoxin B_1: AFB_1; Trichothecene-2 toxin: T-2 toxin; Deoxynivalenol: DON; Ochratoxin A: OTA; Fumonisin B_1 and B_2: FB_1 and FB_2.

fective in the adsorption of AFB_1 from feedstuff and the efficiency could depend on the different strains.

Bacillus subtilis ANSB01G, a strain isolated from the intestinal chyme of the broiler, was shown to be involved in the reduction of ZEA (Lei et al., 2014). Moreover, Ju et al. (2019) also reported on the elimination of ZEA by two strains (*Bacillus subtilis* and *Bacillus natto*) after 48 h with efficacity of 100% and 88% respectively; As well, these two previously mentioned strains presented good ZEA degradation ability in corn flour and soy flour. During the microbial degradation of ZEA, both estrogenic compounds, such as α-zearalenone and β-zearalenone, and non-estrogenic compounds, such as 1-(3,5-dihydroxy-phenyl)-10'-hydroxy-1'E-undecene-6'-one, can be produced that are less toxic than ZEA. *Bacillus licheniformis* CK1 was able to degrade ZEA into non-estrogenic or less estrogenic compounds in animal feed and even reduce the adverse effects of ZEA in the gilts (Fu et al., 2016). Also, *Bacillus* velezensis A2 can also degrade ZEA (7.45 μg/ml) in a Luria-Bertani medium after 3 days. It could be applicable as a feed additive to decontaminate the feed (Wang et al., 2018a). *Bacillus cereus* BC7 recovered from moldy contaminated animal feeds has been also reported for 100% and 89.31% bio-removal of experimentally contaminated with 10 mg/L ZEA Luria-Bertani medium or laboratory prepared simulated gastric fluid, respectively. *Bacillus cereus* BC7 was shown to significantly protect the experimental mice against the toxic effects of ZEA (Wang et al., 2018b). Plant-derived AFB_1 BCC 47723 isolated from Thai fermented vegetable products reduced ZEA from feedstuff by the efficiency of 0.5-23% (Adunphatcharaphon et al., 2021). Niderkorn et al. (2008) showed the possibility of binding of ZEA to *Streptococcus thermophilus* in animal feed. They showed a 91% efficiency of binding at the beginning which was then reduced to 67% after 18 h.

Interaction, including the ability of *L. pentosus* X8 and AFB_1 B7 to bind with fumonisins (FB_1 and FB_2), has also been reported from the maize-based feed. Bio-removal depends clearly on some environmental conditions, including pH, as well as incubation temperature and time. Both viable and dead bacteria cells were able to bind (Zhao et al., 2016). In addition, beneficial properties for 3 strains of *Propionibacterium* have been reported for bio-removal of FB_1 and FB_2 in experimental conditions in MRS broth (pH 4.0) (Niderkorn et al., 2006). The reported results pointed out that the mentioned bacterial species were more effective for the bio-removal of FB_2 in comparison to FB_1. Also, Niderkorn et al. (2006) demonstrated that LAB, for comparison with propionibacteria were unable to trap FB_1 and FB_2 in neutral pH.

The high efficiency of using coculture of LAB strains with *S. cerevisiae* for degradation of OTA has been also reported. Around 31.9 to 47.7% reduction in OTA content was observed after incubation at 30°C or 37°C for 24 h. Moreover, OTA was also reduced in the soiled feed down to 2 mg/kg, *in vivo* condition by a combination of LAB and Saccharomyces species (Markowiak et al., 2019). In another study, seven inactivated LAB strains (including AFB_1 1QB147, *Levilactobacillus* spp. 1QB459, 3QB398, and *L. plantarum* 3QB361) were able to endorse a reduction of 78% of AFB_1, 90% of OTA, and 82% of ZEA, which are abundant in cereal-based feed. It is relevant to underline, that this specific reduction is not only strain-specific but as well can be varied depending on the environmental pH (Møller et al., 2021).

4.2 Poultry feed

Aflatoxicosis is one of the principles responsible for toxins with strong negative effects and associated causing economic problems in the poultry industry (Iqbal et al., 2019). Ducks followed by turkeys, quails, broilers, and layers are the most vulnerable birds affected by the AFs (Sana et al., 2019). Was suggested and shown efficacity of *Bacillus subtilis* ANSB060, strain isolates from the fish gut that can inhibit the growth of *Aspergillus flavus*, moreover, be associated with degradation of AFs to less toxic compounds, and the same time can be resistant to adverse conditions such as simulated gastric and intestinal environments. Even more, its detoxification effect was confirmed by *in vivo* experiments and showed that in a chicken broiler fed with peanuts naturally contaminated with AFs; laying hens exposed to certain levels of AFs strengthened the case for its utility as a feed additive (Ma et al., 2012). In a different study, the positive effects of *S. cerevisiae* were linked to several health-beneficial aspects against AFB_1 in poultry feeds (Zoghi et al., 2014). Śliżewska and Smulikowska (2011) reported the impact of fermentation of feeds with probiotic bacteria and yeast strains and positive consequences on the reduction of the content of AFB_1. The same authors reported a 55% decrease in AFB_1 content (with an initial concentration of 1 mg/kg) after only 6 h fermentation with *L. paracasei* LOCK 0920, *L. brevis* LOCK 0944, AFB_1 LOCK 0945, as well as *S. cerevisiae* LOCK 0140, in a broiler feed. However, the bio-removal efficiency of AFB_1 was 39% with an initial presence of 5 mg/kg, placing on the dose-dependent outcome of the efficacity of probiotic cultures in bio-degradation of AFs (Śliżewska and Smulikowska, 2011). Tiziri et al. (2023) determined the detoxification properties of viable and heat-inactivated cells of eleven LAB strains, isolated from Algerian fermented foods, toward AFB_1 and OTA in wheat. They claimed that both viable and nonviable cells of all LAB strains were able to remove AFB_1 and OTA, with efficiency varying between the strains and higher for AFB_1 with nonviable cells.

Śliżewska and Piotrowska (2014) reported detoxification of OTA from chicken feed by *L. brevis* LOCK 0944, *L. paracasei* LOCK 0920, and AFB_1 LOCK 0945 together with *S. cerevisiae* LOCK 0140. The results showed a 73% reduction in the presence of OTA (with initial levels of 1 mg/kg), after 6-hour fermentation. However, as well as in the case of AFs previously reported by the same researchers (Śliżewska and

Smulikowska, 2011), at higher content OTA (5 mg/kg), removal efficiency dropped to 55%. Abrunhosa et al. (2014) proposed the application of *Pediococcus parvulus* for the reduction of OTA in a liquid system and reported a 90% reduction of OTA in the first 20 h of the fermentation processes. Moreover, the authors pointed out the link between applied incubation temperature and the importance of the inoculum size: different strains of *Lactobacillus* spp. showed the ability for 50% bio-detoxification of OTA even after 30 min incubation at pH 6.2 (Piotrowska, 2020). Kapetanakou et al. (2012) investigated OTA bio-detoxification by strains belonging to *L. sakei*, *L. casei*, and *Streptococcus salivarius* with the best efficacity for bio-removal (20%) recorded at pH 5.0.

Xu et al. (2016) reported on 95.7% and 62.1% decrease in ZEA content with initial content of 3 and 1 ppm, respectively, in wheat by *Bacillus amyloliquefaciens* ZDS-1. A strain of *S. cerevisiae*, isolated from grapes, was shown to be involved in degrading of ZEA rather than simply absorbing it. In the mentioned study, the authors applied nutrient yeast dextrose broth as model culture media for culture and after 2 days showed that ZEA was degraded completely into α-zearalenone and β-zearalenone by applied yeast strain (Zhang et al., 2016).

Zou et al.(2012) evaluated the ability for bio-detoxification properties for strains of AFB_1, *L. lactis*, *L. casei*, and *L. brevis* of DON in a fermentation process after 3 days. However, after 2 days, bio-removal efficiency reached the maximum while no change was observed until the 3^{rd} day. Evaluated strains of AFB_1 showed the best activity for DON bio-detoxification. *L. paracasei* evaluated strains were effective on DON in detoxification processes (Zhai et al., 2019). The binding ability for evaluated *L. rhamnosus* and *Propionibacterium freudenreichii* strains has been reported for their efficacity related to DON, HT-2, and T-2 toxins (El-Nezami et al., 2002).

4.3 Fish and aquatic feed

LAB was shown to play an essential role in aquacultures with proven effects on enhancing growth, disease resistance, and feed efficiency. Fish aquacultures contribute to providing high-quality proteins for humans and other animals and also play important financial contributions to the communities' growth (Jamal et al., 2019). Certain aquaculture species like catfish, Indian common carp, tilapia, trout, sturgeon, and shrimps are prone to aflatoxicosis (Iqbal et al., 2019). The LAB can be added directly to the water or as feed additives. Their ability for absorbing or degrading mycotoxins is reported (Wang et al., 2017).

Elsanhoty et al. (2016) reported a higher binding ability for *L. rhamnosus* to AFB_1 in a liquid medium and compared these properties to L. sanfranciscensis, *L. acidophilus*, and *B. angulatum*. They also showed the stability of the complex of LAB to AF. Halttunen et al. (2007) assessed the exclusion of AFB_1 from aqueous solution by *L. rhamnosus* LC705, *L. rhamnosus* GG, *B. breve* Bbi99/E8, and *Propionibacterium freudenreichii* subsp. *shermanii* JS. The most efficient removal of AFB_1 was observed with *B. brevis* Bbi by 21.4%. Topcu et al. (2010) investigated the detoxification of AFB_1 from water by *E. faecium* M74. This probiotic strain removed 19.3 to 30.5% of AFB_1 throughout a 48-h incubation period. The results also showed high stability of the AFB_1 complexes with the applied bacterial strains. It is important to underline that both, live and dead cells could decrease toxin content at almost the same rate. In another study, AFB_1 and *Lc. lactis* strains were able to decrease the content of AFB_1 in model solutions by 46% and 27%, respectively. Synergistic effect of coculture by AFB_1 and *Lc. lactis* experimental strains in bio-detoxification processes (81%) were approved in comparison to applying a single strain (Sezer et al., 2013).

In general, it can be concluded that choosing the appropriate LAB or yeast with potential probiotic properties, aimed for each mycotoxin removal in livestock, poultry, fish and aquatic feed is important, though the detoxification process is highly strain-specific. On the other hand, using LAB or yeast with probiotic properties could be more useful, because of their several health benefits besides their ability to mycotoxin removal; So, they can be used as feed additives without worrying about the side effects of utilizing these microorganisms for animals. In addition, applying optimal experimental conditions plays a major role in the decontamination process.

5 Mechanisms of Detoxification

As previously reported (Sadiq et al., 2019), the mechanism of mycotoxin bio-detoxification is associated with biodegradation and/or adsorption into the cell walls with non-covalent bonds (in most cases Van der Waals forces) and results in the reduction of mycotoxins bioavailability in the gastrointestinal tract or other systems (Guan et al., 2021). It is observed that physiologically active and/or dead bacterial or yeast cells are able to interfere and attach the mycotoxins and, in this way, eliminate their values. These processes were mostly confirmed based on evidence for cell wall adsorption, and lees the formation of covalent bonds (Hamidi et al., 2013). Mycotoxin degradation involves the microorganisms producing certain metabolites including some acids, specific phenolic compounds, different bioactive peptides, and fatty acids which result in to change in mycotoxin structure and toxicity (Theumer et al., 2018; Muhialdin et al., 2020). Proteolytic enzymes have the main role in the degradation of mycotoxins and change their structure (Guan et al., 2021) (See Figure 2). The main enzymes produced by LAB/yeast involved in mycotoxin degradation in feedstuff are demonstrated in Table 2.

LABs are able to establish specific non-covalent bonds between mycotoxins and bacterial cell surfaces (Ansari and Rezaei, 2022). The bacterial S-layers possess different linking sites responsible for the attachment to the mycotoxins by non-covalent links (Zoghi et al., 2018). LABs are also able to

Table 2. Produced enzymes by lactic acid bacteria and yeast involved in mycotoxin degradation in feedstuff

Enzyme	LAB/yeast	Mycotoxin	Mechanism of degradation	References
Laccase	*Bacillus licheniformis* ANSB821	AFB_1	Through free radical generation	Guo et al., 2020
Lactonase	*Bacillus subtilis* RC1B, *Bacillus cereus* RC1C, *Bacillus mojavensis* RC3B	AFB_1	Hydrolysis of the AFB_1 lactone ring	González Pereyra et al., 2019
Unknown	*Bacillus* sp.	ZEA	Phosphorylation	Zhu et al., 2021
Lactonohydrolase	*L. reuteri*	ZEA	Hydrolysis of the ZEA lactone ring	Liu et al., 2019
Carboxy-peptidase	*S. cerevisiae*	OTA	Hydrolysis of the amide bond	Abrunhosa et al., 2010
Unknown	*Bacillus* sp. LS100	DON	Reductive de-epoxidation	Islam et al., 2012
3-O-acetyltransferases	*S. cerevisiae* RW2802	DON	Acetylation of DON	Khatibi et al., 2011
Unknown	*Eubacterium* BBSH 797	T-2 toxin	Reductive de-epoxidation	Fuchs et al., 2002

Abbreviations: *Lactobacillus: L.*; *Saccharomyces: S.*; Zearalenone: ZEA; Aflatoxin B_1: AFB_1; Trichothecene-2 toxin: T-2 toxin; Deoxynivalenol: DON; Ochratoxin A: OTA.

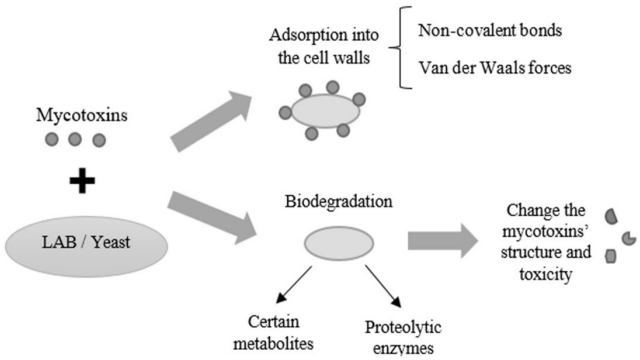

Figure 2. Schematic representation of the mechanism of mycotoxin bio-detoxification by lactic acid bacteria (LAB) and yeast.

synthesize specific EPS from basic carbohydrates, an important player in the detoxification progressions of mycotoxins (Oleksy-Sobczak et al., 2020). It was also observed that the primary role in binding processes is the cell wall peptidoglycan and polysaccharides part of the bacterial membrane, presenting a key role in the formation of complexes and further detoxification processes (Liu et al., 2020). Peptidoglycans, part of the bacterial walls, and especially disaccharides are directly involved in interactions between mycotoxins and some pentapeptide bridges. The acetyl groups of the N-acetyl-muramic and N-acetyl-glucosamine as well can alter and the C6 in muramic acid can be replaced by teichoic acid (Zoghi et al., 2014). Teichoic acid is an anionic structure, representing almost half of the cell wall's weight. However, needs to be mentioned, that lipoteichoic and teichoic acids are highly similar in their structures (Khosravi Darani et al., 2020). Moreover, was also reported on the specificity in the variety of interaction and binding abilities for different mycotoxins to bacterial and yeast cells is clearly associated with having specific variations in the cell wall structures (Zoghi et al., 2014; Khosravi Darani et al., 2020; Zoghi et al., 2021a). The specificity of the cell wall thickness and uniqueness of the diameter relation represents a relation between potential mycotoxin reduction and the present cell wall area. After exposing the cell walls to the low pH and heat treatments, it was observed that the cell wall thickness was connected to removal ability in a positive way (Wang et al., 2019).

It was suggested that ZEA elimination by bacterial or yeast cells occur normally through the following specific stages: absorption stage - normally this is a rapid and highly efficient strain-specific process and is followed by the second stage - in most cases a slower process and related to ZEA diffusion into microbial cells (Król et al., 2018). As well, previously assessed that the ZEA elimination processes by *Bacillus* spp. were not a simple adsorption process. The capacity of ZEA exclusion by adsorption by *Bacillus* strains was less significant compared to the metabolization occurring by specific secretase (Xu et al., 2016). ZEA removal by the strain of AFB_1 was suggested and associated with the changes in protein organizations of AFB_1 cell wall after treatment by SDS and when ZEA reduction was highly affected. Therefore, the bio-removal based on the hydrophobicity interactions was pointed as the principal mechanism in ZEA decrease performed by AFB_1 (Adunphatcharaphon et al., 2021). The adsorption mechanism of *Bacillus* spp. was the same that has been reported for *Lactobacillus* spp. and other Gram-positive bacteria, due to the similarity in the cell walls. ZEA is generally adsorbed by the cell surface based on hydrophobic interactions and the specific carbohydrates from the *Lactobacillus* spp. cell walls (Tinyiro et al., 2011). Furthermore, several *Bacillus* strains have been found capable of degrading ZEA to ZEA-14-phosphate (Zhu et al., 2021).

Chen et al. (2019), suggested that the osteolytic activity of LAB can play a significant role in the ZEA degradation and reported on the decreased concentration of DON and converted to 3-keto-DON or 3-epi-DON, a less toxic derivative, in PBS as an effect of interaction with LAB and suggested that observed results are a consequence of the activity of some unidentified extracellular enzymes. Also,

de-epoxidation of the C12,13 epoxide ring of trichothecenes (T-2 toxin and DON) by unknown enzymes from *Bacillus* sp. has been reported. The reduced toxicity of de-epoxy derivatives of T-2 toxin and DON was stated (Abraham et al., 2022).

Fumonisin was shown to have a propensity to attach to the peptidoglycan in LAB cell walls. It was shown that tricarboxylic acid in the LAB can play a key role in this attachment process, therefore reported that hydrolyzed fumonisin can have a less binding affinity (Zoghi et al., 2014). Zhao et al. (2016) as well confirmed that peptidoglycans were principal biding molecules for mycotoxins attachments and that teichoic acid was less involved in the bindings processes. Martinez Tuppia et al. (2017) described that the bio-removal of FB_1 was primarily associated with specific biodegradation processes and physical adsorption. However, mycotoxin removal cannot be postulated which was based on the same processes for all strains of *Lactobacillus* spp. in the study.

Vosough et al. (2014) showed that the AFB_1-binding ability of viable (43%), heat-killed (49%), and acid-killed *L. rhamnosus* GG (50%) was not different. These results indicate that AFB_1 was not removed based on the metabolic processes, but because it becomes physically bound to molecular components of the probiotic, most probably part of the cell walls. The main mechanism was the binding of LAB to AFB_1, pointing out that the AF reduction is generally through the physical binding and the involvement of the peptidoglycans in the carbohydrate forms in the bacteria cell wall (Khosravi Darani et al., 2020). On the other hand, it has been demonstrated that laccases and other enzymes that depolymerize polyaromatic lignin can oxidize AFs. These enzymes usually need extra co-substrates or mediators, which may restrict their usefulness for removing AFs from the feed (Abraham et al., 2022). Recently, it was discovered that AFB_1 can be converted into the 3-hydroxy epimers, AFQ_1, and epi-AFQ_1, without the use of redox mediators by the bacterial laccase CotA from *Bacillus licheniformis* ANSB821 (Guo et al., 2020). The two epimers have no harmful effects on people. It was determined that AFQ_1 was 18 times less hazardous than AFB_1.

A study by Ragoubi et al. (2020) showed a higher reduction in OTA content in thermally inactivated probiotics which shows the binding mechanism of biodetoxification. Heat-treated cells showed a higher OTA adsorption in PBS in comparison to intact cells which shows heat-induced loss of active site of absorption in the cell wall. Also, the amide bond of OTA can be hydrolyzed by carboxypeptidase, which can be produced by *S. cerevisiae*, to form non-toxic phenylalanine and ochratoxin α (Abraham et al., 2022).

6 Mycotoxin-(LAB/yeast) Complex Stability *In vitro*

LAB and yeast application for the mycotoxins reduction and removal from feedstuffs relates to as well their complex stability in the GIT. Depending on the specificity of the probiotics, some can permanently colonize the GIT, however, others can be rather characterized as transit microbiota. Several LAB and yeast, evaluated as potential or effective probiotics, have the ability to adhere to the cells of the GIT with a high degree of strain-specific properties. In case of the elimination of mycotoxins, adherence to the epithelial cells will be considered as a significant health hazard, since this will be keeping the mycotoxins in the host. However, most probiotics can be characterized by a significant reduction of their adherence ability to the epithelial cells of the GIT after binding to mycotoxins. Thus, the formed complex between the probiotic and mycotoxin is normally rapidly passed via the GIT and excreted (Zoghi et al., 2021a; Zoghi et al., 2021b). Moreover, it is important that these formed bonds would not dissociate in the GIT. The stability of the builder complex between the probiotics and mycotoxins is associated with several environmental parameters (Hsu et al., 2018).

Some reports proposed that the mycotoxins' attachment to the cell wall of LAB and yeasts occurred via binding and releasing. According to a recent study, the stability of the complex of toxin-*Saccharomyces* is higher which indicates forming a specific complementary structure between mannose on the yeast membrane and mycotoxins (Guan et al., 2021). Zhao et al. (2015) observed that ZEA removal by AFB_1 strain can be a fact, but the process of interaction between the toxin and the bacterial cell was partially reversible. Petruzzi et al. (2016) indicated 25% stability of the complex of *S. cerevisiae* to mycotoxin in simulated digestive conditions for 6 h. Pizzolitto et al. (2012) showed a 49% release of LAB-AF bound after 5-step items of washing with PBS, and even an increase in washing duration from 1 to 60 min, however, does not improve the effect on percentage release. Moreover, was shown that the binding in the complex of *E. faecium*- AFB_1 was a reversible process as well. The conclusion was that the stability of the cells/mycotoxin complexes depends primarily on the applied bacteria strains, a strain-specific phenomenon (Topcu et al., 2010). Bevilacqua et al. (2014) showed that the binding of AF -yeast was not enough stable, and toxin was released from the complex, too. The stability of *Enterococcus*-AFB_1 was enough high even after 3 times of washing with PBS (Fernandez Juri et al., 2014). It is important to mention, that all mentioned *in vitro* experiments are positive indications for the beneficial role of LAB and yeasts in the bio-removal of mycotoxins, however, all of them must be cleared *in vivo* models as mycotoxins may be released from the formed complexes with LAB and yeast surface after washing and enter to animal body and potential negative health consequences may occur.

7 Conclusions

Different mycotoxins are produced by the fungal species and can be present in feedstuffs which can have serious health consequences for animals and humans. The most common mycotoxins existing in animal feed are AFB_1, DON, and ZEA. Feed detoxification by specific beneficial microorganisms is a green technology to reduce and control several health risks. Several LABs and yeast strains are proven for their role in the reduction and removal of mycotoxins from feeds. As summarized, Table 1 shows some of the recent research (2012 onwards) contributions, in which LABs and yeasts have been used for detoxification in feedstuffs. Mycotoxins' binding to the yeast/LAB's cell wall structure and mycotoxins' degradation are the key mechanisms by which they are detoxified. According to previous studies, *Lactobacillus* strains, especially AFB_1 and *L. paracasei*, are the most effective LAB for adsorbing AFB_1 and DON in feedstuff, respectively. Also, *Bacillus* sp., particularly *Bacillus subtilis*, has been found to be more effective in degrading AFB_1, DON, and ZEA into less toxic compounds. It could be due to these LAB characteristics for providing binding with mycotoxins or producing efficient enzymes for mycotoxin degradation.

The merits of LABs and yeasts for detoxification include the fact that they can be directly applicable in feedstuffs, have a simple bioactivity property, are economical, and are able to perform their detoxification properties quickly. The detoxification ability is clearly strain-specific (it means that different LAB or yeast strains might able to remove a particular mycotoxin or not) and can vary in different incubation times, specific temperature and pH, adequate inoculum size, and be able to reduce and eliminate mycotoxin concentration. The most efficient LAB and yeast strains should be applied for bio-decontamination mycotoxins and to enhance feed safety. Therefore, before using them as mycotoxin detoxification agents in feed, a variety of criteria including the feed's own characteristics, the potential mycotoxins and their fungal producers, as well as LAB/yeast strains, should be taken into account. However, even if clearly shown that LAB and yeast strains can be positively involved in the detoxication of mycotoxin processes, more assessments *in vitro* and *in vivo* are needed to describe the biochemical basis of the detoxification mechanisms and also to optimize the effective conditions and increase removal yield. A deeper comprehension of the biochemical processes involved in LAB/yeast detoxification will shed light on the creation of possible mycotoxin-detoxifying bioactive substances. In fact, applications of LAB and yeasts in the effective removal of mycotoxins can be regarded as a perspective research field with importance for animal and human health.

Even though there are several research projects regarding probiotics application in feedstuffs, more data on the practical implementation and benefits in the feed industry is still needed. Additionally, determining probiotic behavior and benefits in various *in vivo* processes associated with safe feedstuff production is needed. Several models *in vitro* and their results should be protected by *in vivo* tests to validate the effects of the LAB or yeast on mycotoxins availability and toxicity. Moreover, different further studies in model conditions, including the digestive system will contribute to clarifying the obtained results in the *in vitro* experiments. In this review article, the biodetoxification of normal adult and healthy animal feed has been investigated. Therefore, more complementary studies in this field are needed for biodecontamination of special animal feed, such as young or sick animals, for which the maximum doses of mycotoxin are different.

Author Contributions

Zoghi - Conceptualization, Investigation, Writing original draft, Review & editing. Todorov and Khosravi-Darani - Conceptualization, Investigation, Review & editing.

Acknowledgments

The authors have no further acknowledgments to declare. The manuscript was prepared solely by the authors, whose contributions are declared herein.

Conflict of Interest

No conflict of interest was reported by all authors.

References

Abbas, H.K., 2005. Aflatoxin and Food Safety. CRC Press. ISBN: 978-0-8247-2303-3.

Abraham, N., Chan, E.T.S., Zhou, T., Seah, S.Y.K., 2022. Microbial detoxification of mycotoxins in food. Frontiers in Microbiology, 13: 957148. https://doi.org/10.3389/fmicb.2022.957148

Abrunhosa, L., Inês, A., Rodrigues, A.I., Guimarães, A., Pereira, V.L., Parpot, P., Venâncio, A., 2014. Biodegradation of ochratoxin A by Pediococcus parvulus isolated from Douro wines. International Journal of Food Microbiology, 188: 45-52. https://doi.org/10.1016/j.ijfoodmicro.2014.07.019

Abrunhosa, L., Paterson, R.R.M. and Venâncio, A., 2010. Biodegradation of ochratoxin A for food and feed decontamination. Toxins, 2: 1078-1099. https://doi.org/10.3390/toxins2051078

Adunphatcharaphon, S., Petchkongkaew, A. and Visessanguan, W., 2021. *in vitro* mechanism assessment of zearalenone removal by plant-derived *Lactobacillus* plantarum BCC 47723. Toxins, 13: 286. https://doi.org/10.3390/toxins13040286

Ansari, F. and Rezaei, K., 2022. Biological detoxification of mycotoxins by binding them with certain microorganisms: A review. Microbiology, Metabolites and Biotechnology, 5(1): 56-69.

Armando, M., Galvagno, M., Dogi, C., Cerrutti, P., Dalcero, A., Cavaglieri, L., 2013. Statistical optimization of culture conditions for biomass production of probiotic gut-borne Saccharomyces cerevisiae strain able to reduce fumonisin B1. Journal of Applied Microbiology, 114: 1338-1346. https://doi.org/10.1111/jam.12144

Ashiq, S., 2014. Natural occurrence of mycotoxins in food and feed: Pakistan perspective. Comprehensive Reviews in Food Science and Food Safety, 14(2): 159-175. https://doi.org/10.1111/1541-4337.12122

Azeem, N., Nawaz, M., Anjum, A.A., Saeed, S., Sana, S., Mustafa, A., Yousuf, M.R., 2019. Activity and anti-aflatoxigenic effect of indigenously characterized probiotic lactobacilli against Aspergillus flavus—A common poultry feed contaminant. Animals, 9: 166-175. https://doi.org/10.3390/ani9040166

Bagherzadeh Kasmani, F., Karimi Torshizi, M.A., Allameh, A., Shariatmadari, F., 2012. A novel aflatoxin-binding *Bacillus* probiotic: Performance, serum biochemistry, and immunological parameters in Japanese quail. Poultry Science, 91: 1846-1853. http://dx.doi.org/10.3382/ps.2011-01830

Ben Hassouna, K., Ben Salah-Abbès, J., Chaieb, K., Abbès, S., 2022. Mycotoxins occurrence in milk and cereals in North African countries - a review. Critical Reviews in Toxicology, 52(8): 619-635. https://doi.org/10.1080/10408444.2022.2157703

Bevilacqua, A., Petruzzi, L., Corbo, M.R., Baiano, A., Garofalo, C., Sinigaglia, M., 2014. Ochratoxin A released back into the medium by Saccharomyces cerevisiae as a function of the strain, washing medium and fermentative conditions. Journal of Science of Food and Agriculture, 94: 3291-3295. http://dx.doi.org/10.1002/jsfa.6683

Bovo, F., Franco, L.T., Rosim, R., Favaro, E., Trindade, C.S., Fernandes De Oliveira, C.A., 2014. The ability of *Lactobacillus* rhamnosus in solution, spray-dried or lyophilized to bind aflatoxin B1. Journal of Food Research, 3: 35-41. https://doi.org/10.5539/jfr.v3n2p35

Calvet, R.M., Nóbrega, M.M.G.P., Costa, A.P.R., Pereyra, C.M., Monte, A.M., Muratori, M.C.S., 2020. *in vitro* anti-mycotoxin activity of probiotic (*Bacillus* spp) and microalgae (Chaetoceros gracilis) for aflatoxin B1 and ochratoxin A used to feed Litopenaeus vannamei. Research, Society and Development, 9(11): e5499119998. https://doi.org/10.33448/rsd-v9i11.9998

Chaytor, A.C., Hansen, J.A., van Heugten, E., See, M.T., Kim, S.W., 2011. Occurrence and decontamination of mycotoxins in swine feed. Asian-Australasian Journal of Animal Sciences, 24: 723-738. https://doi.org/10.5713/ajas.2011.10358

Chen, S.W., Wang, H.T., Shih, W.Y., Ciou, Y.A., Chang, Y.Y., Ananda, L., Wang, S.Y., Hsu, J.T., 2019. Application of zearalenone (ZEN)-detoxifying *Bacillus* in animal feed decontamination through fermentation. Toxins, 11: 330-341. https://doi.org/10.3390/toxins11060330

Chlebicz, A. and Śliżewska, K., 2020. *in vitro* detoxification of Aflatoxin B1, deoxynivalenol, fumonisins, T-2 toxin and zearalenone by probiotic bacteria from genus *Lactobacillus* and Saccharomyces cerevisiae yeast. Probiotics and Antimicrobial Proteins, 12: 289-301. https://doi.org/10.1007/s12602-018-9512-x

Clark, H.A. and Snedeker, S.M., 2006. Ochratoxin A: its cancer risk and potential for exposure. Journal of Toxicology and Environmental Health Part B: Critical Reviews, 9(3): 265-296. https://doi.org/10.1080/15287390500195570

Conte, G., Fontanelli, M., Galli, F., Cotrozzi, L., Pagni, L., Pellegrini, E., 2020. Mycotoxins in feed and food and the role of ozone in their detoxification and degradation: an update. Toxins, 12: 486. https://doi.org/10.3390/toxins12080486

Coppock, R.W., Christian, R.G. and Jacobsen, B.J., 2018. Aflatoxins in veterinary toxicology basic and clinical principles. In: Gupta RC, editor. Academic Press, Cambridge, United States, p. 983-994.

Dawlal, P., Brabet, C., Thantsha, M.S., Buys, E.M., 2019. Visualisation and quantification of fumonisins bound by lactic acid bacteria isolates from traditional African maize-based fermented cereals, ogi and mahewu. Food Additives and Contaminants Part A, 36(2): 296-307. https://doi.org/10.1080/19440049.2018.1562234

Deepthi, B.V., Poornachandra Rao, K., Chennapa, G., Naik, M.K., Chandrashekara, K.T., Sreenivasa, M.Y., 2016. Antifungal attributes of *Lactobacillus* plantarum MYS6 against fumonisin producing *Fusarium proliferatum* associated with poultry feeds. PLoS One, 11(6): e0155122. https://doi.org/10.1371/journal.pone.0155122

El-Nezami, H.S., Chrevatidis, A., Auriola, S., Salminen, S., Mykkanen, H., 2002. Removal of common *Fusarium* toxins *in vitro* by strains of *Lactobacillus* and *Propionibacterium*. Food Additives and Contaminants, 19: 680-686.

Elsanhoty, R.M., Al-Turki, I.A. and Ramadan, M.F., 2016. Application of lactic acid bacteria in removing heavy metals and aflatoxin B1 from contaminated water. Water Science Technology, 74(3): 625-638. https://doi.org/10.2166/wst.2016.255

Fernandez Juri, M.G., Dalcero, A.M. and Magnoli, C.E., 2014. *in vitro* aflatoxin B1 binding capacity by two *Enterococcus* faecium strains isolated from healthy dog faeces. Journal of Applied Microbiology, 118: 574-582. http://dx.doi.org/10.1111/jam.12726

Food and Drug Administration (FDA), 2016. Bad Bug Book: Foodborne pathogenic microorganisms and natural toxins. 2nd ed. Accessed Nov. 1. http://www.fda.gov/downloads/Food/FoodborneIllnessContaminants/UCM297627.pdf.

Fratamico, P.M., Bhunia, A.K. and Smith, J.L., 2008. Foodborne Pathogens: Microbiology and Molecular Biology. Norofolk, UK: Horizon Scientific Press. ISBN 978-1-898486-52-7.

Fu, G., Ma, J., Wang, L., Yang, X., Liu, J.R., Zhao, X., 2016. Effect of degradation of zearalenone-contaminated feed by *Bacillus licheniformis* CK1 on postweaning female piglets. Toxins, 8: 300. https://doi.org/10.3390/toxins8100300

Fuchs, E., Binder, E.M., Heidler, D., Krska, R., 2002. Structural characterization of metabolites after the microbial degradation of type a trichothecenes by the bacterial strain BBSH 797. Food Additives and Contaminants, 19: 379-386.

Galarza-Seeber, R., Latorre, J.D., Hernandez-Velasco, X., Wolfenden, A.D., Bielke, L.R., Menconi, A., Hargis, B.M., Tellez, G., 2015. Isolation, screening and identification of *Bacillus* spp. as direct-fed microbial candidates for aflatoxin B 1 biodegradation. Asian Pacific Journal of Tropical Biomedicine, 5(9): 702-706. https://doi.org/10.1016/j.apjtb.2015.07.014

Gallo, A., Fancello, F., Ghilardelli, F., Zara, S., Spanghero, M., 2022. Effects of several commercial or pure lactic acid bacteria inoculants on fermentation and mycotoxin levels in high-moisture corn silage. Animal Feed Science and Technology, 286: 115256. https://doi.org/10.1016/j.anifeedsci.2022.115256

González Pereyra, M.L., Martínez, M.P. and Cavaglieri, L.R., 2019. Presence of aiiA homologue genes encoding for N-acyl homoserine lactone-degrading enzyme in aflatoxin B 1-decontaminating *Bacillus* strains with potential use as feed additives. Food and Chemical Toxicology, 124: 316-323. https://doi.org/10.1016/j.fct.2018.12.016

Gruber-Dorninger, C., Jenkins, T. and Schatzmayr, G., 2019. Global mycotoxin occurrence in feed: A ten-year survey. Toxins, 11: 375. https://doi.org/10.3390/toxins11070375

Guan, Y., Chen, J., Nepovimova, E., Long, M., Wu, W., Kuca, K., 2021. Aflatoxin detoxification using microorganisms and enzymes. Toxins, 13: 46-63. https://doi.org/10.3390/toxins13010046

Guo, C., Guo, M., Zhang, S., Qin, D., Yang, Y., Li, M., 2018. Assessment of patulin adsorption efficacy from aqueous solution by water-insoluble corn flour. Journal of Food Safety, 38(1): e12397. https://doi.org/10.1111/jfs.12397

Guo, Y., Qin, X., Tang, Y., Ma, Q., Zhang, J., Zhao, L., 2020. CotA laccase, a novel aflatoxin oxidase from *Bacillus licheniformis*, transforms aflatoxin B1 to aflatoxin Q1 and epi-aflatoxin Q1. Food Chemistry, 325: 126877. https://doi.org/10.1016/j.foodchem.2020.126877

Halttunen, T., Collado, M.C., El-Nezami, H., Meriluoto, J., Salminen, S., 2007. Combining strains of lactic acid bacteria may reduce their toxin and heavy metal removal efficiency from aqueous. Letters in Applied Microbiology, 46(2): 160-165. https://doi.org/10.1111/j.1472-765X.2007.02276.x

Hamidi, A., Mirnejad, R., Yahaghi, E., Behnod, V., Mirhosseini, A., Amani, S., 2013. The aflatoxin B1 isolating potential of two lactic acid bacteria. Asian Pacific Journal of Tropical Biomedicine, 3: 732-736. http://dx.doi.org/10.1016/S2221-1691(13)60147-1

Haque, M.A., Wang, Y., Shen, Z., Li, X., Saleemi, M.K., He, C., 2020. Mycotoxin contamination and control strategy in human, domestic animal and poultry: A review. Microbial Pathogenesis, 142: 104095. https://doi.org/10.1016/j.micpath.2020.104095

Hsu, T.C., Yi, P.J., Lee, T.Y., Liu, J.R., 2018. Probiotic characteristics and zearalenone-removal ability of a *Bacillus licheniformis* strain. PLoS One, 13(4): e0194866. https://doi.org/10.1371/journal.pone.0194866

Hudler, G.W., 1998. Magical Mushrooms, Mischievous Molds: The Remarkable Story of the Fungus Kingdom and Its Impact on Human Affairs. Princeton University Press. ISBN 978-0-691-07016-2.

Iqbal, M., Abbas, M., Adil, M., Nazir, A., Ahmad, I., 2019. Aflatoxins biosynthesis, toxicity and intervention strategies: A review. Chemistry International, 5(3): 168-191. https://doi.org/10.5281/zenodo.1570747

Islam, R., Zhou, T., Young, J.C., Goodwin, P.H., Pauls, K.P., 2012. Aerobic and anaerobic de-epoxydation of mycotoxin deoxynivalenol by bacteria originating from agricultural soil. World Journal of Microbiology and Biotechnology, 28: 7-13. https://doi.org/10.1007/s11274-011-0785-4

Jamal, M.T., Abdulrahman, I.A., Al Harbi, M., Chithambaran, S., 2019. Probiotics as alternative control measures in shrimp aquaculture: A review. Journal of Applied Biology and Biotechnology, 7(03): 69-77. https://doi.org/10.7324/JABB.2019.70313

Jia, R., Cao, L.R., Liu, W.B., Shen, Z.Y., 2021. Detoxification of deoxynivalenol by *Bacillus subtilis* ASAG 216 and characterization the degradation process. European Food Research and Technology, 247: 67-76. https://doi.org/10.1007/s00217-020-03607-8

Ju, J., Tinyiro, S.E., Yao, W., Yu, H., Guo, Y., Qian, H., Xie, Y.F., 2019. The ability of *Bacillus subtilis* and *Bacillus natto* to degrade zearalenone and its application in food. Journal of Food Processing and Preservation, 43(10): e14122. https://doi.org/10.1111/jfpp.14122

Juráček, M., Felšöciová, S., Bíro, D., Šimko, M., Gálik, B., Rolinec, M., Hanušovský, O., Bujko, J., Kalúzová, M., Kačániová, M., 2022. The effect of lactic acid bacteria addition on microbiota and occurrence of mycotoxins in rye silages. Journal of Central European Agriculture, 23(2): 342-350. https://doi.org/10.5513/JCEA01/23.2.3540

Kapetanakou, A.E., Kollias, J.N., Drosinos, E.H., Skandamis, P.N., 2012. Inhibition of A. Carbonarius growth and reduction of ochratoxin A by bacteria and yeast composites of technological importance in culture media and beverages. International Journal of Food Microbiology, 152: 91-99. https://doi.org/10.1016/j.ijfoodmicro.2011.09.010

Khatibi, P.A., Newmister, S.A., Rayment, I., McCormick, S.P., Alexander, N.J., Schmale, D.G., 2011. Bioprospecting for trichothecene 3-o-acetyltransferases in the fungal genus *Fusarium* yields functional enzymes with different abilities to modify the mycotoxin deoxynivalenol. Applied and Environmental Microbiology, 77: 1162-1170. https://doi.org/10.1128/AEM.01738-10

Khosravi Darani, K., Zoghi, A., Jazayeri, S., Cruz, A.G., 2020. Decontamination of Aflatoxins with a focus on Aflatoxin B1 by probiotic bacteria and yeasts: a review. Journal of Microbiology Biotechnology and Food Science, 10: 424-435. https://doi.org/10.15414/jmbfs.2020.10.3.424-435

Kosicki, R., Blajet-Kosicka, A., Grajewski, J., Twaruzek, M., 2016. Multi-annual mycotoxin survey in feed materials and feeding stuffs. Animal Feed Science and Technology, 215: 165-180. https://doi.org/10.1016/j.anifeedsci.2016.03.012

Kowalska, K., Habrowska-Górczy´nska, D.E. and Piastowska-Ciesielska, A.W., 2016. Zearalenone as an endocrine disruptor in humans. Environmental Toxicology and Pharmacology, 48: 141-149. https://doi.org/10.1016/j.etap.2016.10.015

Król, A., Pomastowski, P., Rafińska, K., Railean-Plugaru, V., Walczak, J., Buszewski, B., 2018. Microbiology neutralization of zearalenone using *Lactococcus* lactis and *Bifidobacterium* sp. Analytical and Bioanalytical Chemistry, 410: 943-952. https://doi.org/10.1007/s00216-017-0555-8

Lee, A., Cheng, K.C. and Liu, J.R., 2017. Isolation and characterization of a *Bacillus* amyloliquefaciens strain with zearalenone removal ability and its probiotic potential. PLoS ONE, 12(8): e0182220. https://doi.org/10.1371/journal.pone.0182220

Lei, Y.P., Zhao, L.H., Ma, Q.G., Zhang, J.Y., Zhou, T., Gao, C.Q., Ji, C., 2014. Degradation of zearalenone in swine feed and feed ingredients by *Bacillus subtilis* ANSB01. World Mycotoxin Journal, 7(2): 143-151. https://doi.org/10.3920/wmj2013.1623

Liew, W.P.P. and Mohd-Redzwan, S., 2018. Mycotoxin: its impact on gut health and microbiota. Frontiers in Cellular and Infection Microbiology, 8: 60. https://doi.org/10.3389/fcimb.2018.00060

Liu, F., Malaphan, W., Xing, F., Yu, B., 2019. Biodetoxification of fungal mycotoxins zearalenone by engineered probiotic bacterium *Lactobacillus* reuteri with surface-displayed lactonohydrolase. Applied Microbiology and Biotechnology, 103: 8813-8824. https://doi.org/10.1007/s00253-019-10153-1

Liu, A., Zheng, Y., Liu, L., Chen, S., He, L., Ao, X., Yang, Y., Liu, S., 2020. Decontamination of aflatoxins by lactic acid bacteria. Current Microbiology, 77: 3821-3830. https://doi.org/10.1007/s00284-020-02220-y

Liu, M., Zhao, L., Gong, G., Zhang, L., Shi, L., Dai, J., Han, Y., Wu, Y., Khalil, M.M., Sun, L., 2022. Invited review: Remediation strategies for mycotoxin control in feed. Journal of Animal Science and Biotechnology, 13(1): 19. https://doi.org/10.1186/s40104-021-00661-4

Luz, C., Ferrer, J., Mañes, J., Meca, G., 2018. Toxicity reduction of ochratoxin A by lactic acid bacteria. Food and Chemical Toxicology, 112: 60-66. https://doi.org/10.1016/j.fct.2017.12.030

Ma, Q.G., Gao, X., Zhou, T., Zhao, L.H., Fan, Y., Li, X.Y., Lei, Y.P., Ji, C., Zhang, J.Y., 2012. Protective effect of *Bacillus subtilis* ANSB060 on egg quality, biochemical and histopathological changes in layers exposed to aflatoxin B1. Poultry Science, 91: 2852-2857. https://doi.org/10.3382/ps.2012-02474

Markowiak, P., Śliżewska, K., Nowak, A., Chlebicz, A., Zybikowski, A., Pawowski, K., Szeleszczuk, P., 2019. Probiotic microorganisms detoxify ochratoxin A in both a chicken liver cell line and chickens. Journal of Science of Food and Agriculture, 99: 4309-4318. https://doi.org/10.1002/jsfa.9664

Martinez Tuppia, C., Atanasova-Penichon, V., Chéreau, S., Ferrer, N., Marchegay, G., Savoie, J., Richard-Forget, F., 2017. Yeast and bacteria from ensiled high moisture maize grains as potential mitigation agents of fumonisin B1. Journal of Science of Food and Agriculture, 97: 2443-2452. https://doi.org/10.1002/jsfa.8058

Massoud, R. and Zoghi, A., 2022. Potential probiotic strains with heavy metals and mycotoxins bioremoval capacity for application in foodstuffs. Journal of Applied Microbiology, 133(3): 1288-1307. https://doi.org/10.1111/jam.15685

Møller, A., Freire, L., Rosim, R.E., Margalho, L.P., Balthazar, C.F., Franco, L.T., Sant'Ana, A.S., Corassin, C.H., Rattray, F.P., Oliveira, C.A.F., 2021. Effect of lactic acid bacteria strains on the growth and aflatoxin production potential of Aspergillus parasiticus, and their ability to bind aflatoxin B1, ochratoxin A, and zearalenone *in vitro*. Frontiers in Microbiology, 12: 655386. https://doi.org/10.3389/fmicb.2021.655386

Moretti, A.F., Gamba, R.R., Puppo, J., Malo, N., Gómez-Zavaglia, A., Peláez, A.L., Golowczyc, M.A., 2018. Incorporation of *Lactobacillus* plantarum and zeolites in poultry feed can reduce aflatoxin B1 levels. Journal of Science of Food and Agriculture, 55: 431-436. https://doi.org/10.1007/s13197-017-2923-y

Motameny, R., Sadeghi, A.A., Dehghan-Banadaky, M., Chamani, M., Abolhassani, M., 2012. Effect of some acid treated bacteria on reduction of impure aflatoxin B1 in ruminant gastrointestinal model. Journal of American Science, 7: 213-217.

Muaz, K., Riaz, M., Oliveira, C.A.F., Akhtar, S., Ali, S.W., Nadeem, H., Park, S., Balasubramanian, B., 2021. Aflatoxin M1 in milk and dairy products: global occurrence and potential decontamination strategies. Toxin Reviews, 1-18. https://doi.org/10.1080/15569543.2021.1873387

Muhialdin, B.J., Saari, N., Meor Hussin, A.S., 2020. Review on the biological detoxification of mycotoxins using lactic acid bacteria to enhance the sustainability of foods supply. Molecules, 25(11): 2655-2667. https://doi.org/10.3390/molecules25112655

Nasrollahzadeh, A., Mokhtari, S., Khomeiri, M., Saris, P., 2022. Mycotoxin detoxification of food by lactic acid bacteria. International Journal of Food Contaminants, 9. https://doi.org/10.1186/s40550-021-00087-w

Nazareth, T.D.M., Luz, C., Torrijos, R., Quiles, J.M., Luciano, F.B., Mañes, J., Meca, G., 2020. Potential application of lactic acid bacteria to reduce aflatoxin B1 and fumonisin B1 occurrence on corn kernels and corn ears. Toxins, 12: 21. https:// doi.org/10.3390/toxins12010021

Niderkorn, V., Boudra, H. and Morgavi, D.P., 2006. Binding of *Fusarium* mycotoxins by fermentative bacteria *in vitro*. Appl. Environ. Microbiol. 101, 849-856.

Niderkorn, V., Boudra, H., Morgavi, D.P., 2008. Stability of the bacteriabound zearalenone complex in ruminal fluid and in simulated gastrointestinal environment *in vitro*. World Mycotoxin Journal, 1: 463-467. https://doi.org/10.3920/WMJ2007.1010

O'Brien, E. and Dietrich, D.R., 2005. Ochratoxin A: the continuing enigma. Critical Reviews in Toxicology, 35(1): 33-60. https://doi.org/10.1080/10408440590905948

Oleksy-Sobczak, M., Klewicka, E., Piekarska-Radzik, L., 2020. Exopolysaccharides production by *Lactobacillus* rhamnosus strains - optimization of synthesis and extraction conditions. LWT-Food Science and Technology, 122: 109055. https://doi.org/10.1016/j.lwt.2020.109055

Olinda, R.G., Lima, J.M., de Lucena, R.B., do Vale, A.M., Batista, J.S., de Barros, C.S.L., Riet-Correa, F., Dantas, A.F.M., 2016. Acute aflatoxicosis in swines in Northeastern Brazil. Acta Science Veterenian, 44: 124-129.

Peillod, C., Laborde, M., Travel, A., Mika, A., Bailly, J.D., Cleva, D., 2021. Toxic effects of fumonisins, deoxynivalenol and zearalenone alone and in combination in ducks fed the maximum eutolerated level. Toxins, 13(2): 152. https://doi.org/10.3390/toxins13020152

Perczak, A., Goliński, P., Bryla, M., Wacękiewicz, A., 2018. The efficiency of lactic acid bacteria against pathogenic fungi and mycotoxins. Archives of Industrial Hygiene and Toxicology, 69: 32-45. https://doi.org/10.2478/aiht-2018-69-3051

Petruzzi, L., Corbo, M.R., Sinigaglia, M., Bevilacqua, A., 2016. Ochratoxin a removal by yeasts after exposure to simulated human gastrointestinal conditions. Journal of Food Science, 81: 2756-2760. https://doi.org/10.1111/1750-3841.13518

Pinton, P. and Oswald, I.P., 2014. Effect of deoxynivalenol and other Type B trichothecenes on the intestine: a review. Toxins, 6: 1615-1643. https://doi.org/10.3390/toxins6051615

Piotrowska, M., 2014. The adsorption of ochratoxin A by *Lactobacillus* species. Toxins, 6: 2826-2839. https://doi.org/10.3390/toxins6092826.

Pizzolitto, R.P., Salvano, M.A. and Dalcero, A.M., 2012. Analysis of fumonisin B1 removal by microorganisms in co-occurrence with aflatoxin B1 and the nature of the binding process. International Journal of Food Microbiology, 156: 214-221. https://doi.org/10.1016/j.ijfoodmicro.2012.03.024

Prossnitz, E.R. and Barton, M., 2014. Estrogen biology: new insights into GPER function and clinical opportunities. Molecular and Cellular Endocrinology, 389(1-2): 71-83. https://doi.org/10.1016/j.mce.2014.02.002

Ragoubi, C., Quintieri, L., Greco, D., Mehrez, A., Maatouk, I., D'Ascanio, V., Landoulsi, A., Avantaggiato, G., 2020. Mycotoxin removal ability of *Lactobacillus* acidophilus cip 76.13 and *L. brevis* cip 102806t isolated from humans. Journal of Clinical Gastroenterology, 54: S29.

Ragoubi, C., Quintieri, L., Greco, D., Mehrez, A., Maatouk, I., D'Ascanio, V., Landoulsi, A., Avantaggiato, G., 2021. Mycotoxin removal by *Lactobacillus* spp. and their application in animal liquid feed. Toxins, 13: 185-200. https://doi.org/10.3390/toxins13030185

Rayes, A.A.H., 2013. Removal of aflatoxin B1 from experimentally contaminated whole milk using a pool of probiotic strains of lactic acid bacteria and baker's yeast Saccharomyces cerevisiae. New York Science Journal, 6: 84-90.

Rodrigues, I. and Naehrer, K., 2012. A three-year survey on the worldwide occurrence of mycotoxins in feedstuffs and feed. Toxins, 4: 663-675. https://doi.org/10.3390/toxins4090663

Rogowska, A., Pomastowski, P., Walczak, J., Railean-Plugaru, V., Rudnicka, J., Buszewski, B., 2019. Investigation of zearalenone adsorption and biotransformation by microorganisms cultured under cellular stress conditions. Toxins, 11: 463. https://doi.org/10.3390/toxins11080463

Ropejko, K. and Twarużek, M., 2021. Zearalenone and its metabolites-General overview, occurrence, and toxicity. Toxins, 13(1): 35. https://doi.org/10.3390/toxins13010035

Sadiq, F.A., Yan, B., Tian, F., Zhao, J., Zhang, H., Chen, W., 2019. Lactic acid bacteria as antifungal and anti-mycotoxigenic agents: A comprehensive review. Comprehensive Reviews in Food Science and Food Safety, 18: 1403-1436. https://doi.org/10.1111/1541-4337.12481

Sana, S., Anjum, A.A., Yaqub, T., Nasir, M., Ali, M.A., Abbas, M., 2019. Molecular approaches for characterization of aflatoxin producing Aspergillus flavus isolates from poultry feed. Pakistan Veterinarian Journal, 39: 169-174. https://doi.org/10.29261/pakvetj/2019.031

Sezer, Ç., Güven, A., Oral, N.B., Vatansever, L., 2013. Detoxification of aflatoxin B1 by bacteriocins and bacteriocinogenic lactic acid bacteria. Turkish Journal of Veterinary and Animal Sciences, 37: 594-601. https://doi.org/10.3906/vet-1301-31

Shu, X., Wang, Y.T., Zhou, Q., Li, M.H., Hu, H., Ma, Y.H., 2018. Biological degradation of aflatoxin B1 by cell-free extracts of *Bacillus velezensis* DY3108 with broad PH stability and excellent thermostability. Toxins, 10(8): 330. https://doi.org/10.3390/toxins10080330

Śliżewska, K., Nowak, A. and Smulikowska, S., 2016. Probiotic preparation reduces faecal water genotoxicity and cytotoxicity in chickens fed ochratoxin A contaminated feed (*in vivo* study). Acta Biochimica Polonica, 63(2): 281-286. https://doi.org/10.18388/abp.2015_1094

Śliżewska, K. and Piotrowska, M., 2014. Reduction of ochratoxin A in chicken feed using probiotic. Annals of Agricultural and Environmental Medicine, 21(4): 676-680. https://doi.org/10.5604/12321966.1129913

Śliżewska, K. and Smulikowska, S., 2011. Detoxification of afiatoxin B1 and change in microflora pattern by probiotic *in vitro* fermentation of broiler feed. Journal of Animal Feed Science, 20: 300-309. https://doi.org/10.22358/jafs/66187/2011

Streit, E., Schatzmayr, G., Tassis, P., Tzika, E., Marin, D., Taranu, I., Tabacu, C., Nicolau, A., Aprodu, I., Puel, O., Oswald, I.P., 2012. Current situation of mycotoxin contamination and co-occurrence in animal feed-focus on Europe. Toxins, 4(10): 788-809. https://doi.org/10.3390/toxins4100788

Tan, H., Hu, Y., He, J., Wu, L., Liao, F., Luo, B., He, Y., Zuo, Z., Ren, Z., Zhong, Z., 2014. Zearalenone degradation by two Pseudomonas strains from soil. Mycotoxin Research, 30: 191-196. https://doi.org/10.1007/s12550-014-0199-x

Teodorowicz, M., Van Neerven, J. and Savelkoul, H., 2017. Food processing: the influence of the maillard reaction on immunogenicity and allergenicity of food proteins. Nutrition, 9: 835. https://doi.org/10.3390/nu9080835

Theumer, M.G., Henneb, Y., Khoury, L., Snini, S.P., Tadrist, S., Canlet, C., Audebert, M., 2018. Genotoxicity of aflatoxins and their precursors in human cells. Toxicology Letters, 287: 100-107. https://doi.org/10.1016/j.toxlet.2018.02.007

Tinyiro, S.E., Wokadala, C., Xu, D., Yao, W., 2011. Adsorption and degradation of zearalenone by *Bacillus* strains. Folia Microbiologica, 56: 321-327. https://doi.org/10.1007/s12223-011-0047-8

Tiziri, B., Durand, N., Bendali, F., Piro-Metayer, I., Zinedine, A., Salah-Abbès, J., Abbes, S., Montet, D., Riba, A., Brabet, C., 2023. *in vitro* detoxification of aflatoxin B1 and ochratoxin A by lactic acid bacteria isolated from Algerian fermented foods. Biological Control, 179: 105181.
https://doi.org/10.1016/j.biocontrol.2023.105181

Topcu, A., Bulat, T., Wishah, R., Boyac, I.H., 2010. Detoxification of aflatoxin B1 and patulin by *Enterococcus* faecium strains. International Journal of Food Microbiology, 139(3): 202-205.
https://doi.org/10.1016/j.ijfoodmicro.2010.03.006

Vila-Donat, P., Marín, S., Sanchis, V., Ramos, A.J., 2018. A review of the mycotoxin adsorbing agents, with an emphasis on their multi-binding capacity, for animal feed decontamination. Food and Chemical Toxicology, 114: 246-259.
https://doi.org/10.1016/j.fct.2018.02.044

Vosough, P.R., Sani, A.M., Mehraban, M., Karazhyan, R., 2014. *in vitro* effect of *Lactobacillus* rhamnosus GG on reduction of aflatoxin B1. Nutrition and Food Science, 44: 32-40.
https://doi.org/10.1108/NFS-11-2012-0122

Wang, G., Yu, M., Dong, F., Shi, J., Xu, J., 2017. Esterase activity inspired selection and characterization of zearalenone degrading bacteria *Bacillus* pumilus ES-21. Food Control, 77: 57-64.
https://doi.org/10.1016/j.foodcont.2017.01.021

Wang, L., Yue, T., Yuan, Y., Wang, Z., Ye, M., Cai, R., 2015. A new insight into the adsorption mechanism of patulin by the heat-inactive lactic acid bacteria cells. Food Control, 50: 104-110.
https://doi.org/10.1016/j.foodcont.2014.08.041

Wang, N., Li, P., Wang, M., Chen, S., Huang, S., Long, M., Yang, S., He, J., 2018b. The protective role of *Bacillus velezensis* A2 on the biochemical and hepatic toxicity of zearalenone in mice. Toxins, 10: 449.
https://doi.org/10.3390/toxins10110449

Wang, N., Wu, W., Pan, J., Long, M., 2019. Detoxification strategies for zearalenone using microorganisms: a review. Microorganisms, 7: 208-222.
https://doi.org/10.3390/microorganisms7070208

Wang, W., Sun, J., Liu, C., Xue, Z., 2016. Application of immunostimulants in aquacultur: current knowledge and future perspectives. Aquaculture Research, 1-23.
https://doi.org/10.1111/are.13161

Wang, Y., Zhang, J., Wang, Y., Wang, K., Wei, H., Shen, L., 2018a. Isolation and characterization of the *Bacillus cereus* BC7 strain, which is capable of zearalenone removal and intestinal flora modulation in mice. Toxicon, 155: 9-20.
https://doi.org/10.1016/j.toxicon.2018.09.005

Watanakij, N., Visessanguan, W. and Petchkongkaew, A., 2020. Aflatoxin B1-degrading activity from *Bacillus subtilis* BCC 42005 isolated from fermented cereal products. Food Additives and Contaminants Part A: Chemistry, Analysis, Control, Exposure and Risk Assessment, 37: 1579-1589.
https://doi.org/10.1080/19440049.2020.1778182

Xu, J., Wang, H., Zhu, Z., Ji, F., Yin, X., Hong, Q., Shi, J., 2016. Isolation and characterization of *Bacillus* amyloliquefaciens ZDS-1: exploring the degradation of zearalenone by *Bacillus* spp. Food Control, 68: 244-250.
https://doi.org/10.1016/j.foodcont.2016.03.030

Xu, L., Ahmed, M.F., Sangare, L., Zhao, Y.J., Selvaraj, J.N., Xing, F.G., 2017. Novel aflatoxin-degrading enzyme from *Bacillus* shackletonii L7. Toxins, 9(1): 36.
https://doi.org/10.3390/toxins9010036

Zhai, Y., Hu, S., Zhong, L., Lu, Z., Bie, X., Zhao, H., Zhang, C., Lu, F., 2019. Characterization of deoxynivalenol detoxification by *Lactobacillus* paracasei LHZ-1 isolated from Yogurt. Journal of Food Protection, 82: 1292-1299.
https://doi.org/10.4315/0362-028X.JFP-18-581

Zhang, H., Dong, M., Yang, Q., Apaliya, M.T., Li, J., Zhang, X., 2016. Biodegradation of zearalenone by Saccharomyces cerevisiae: possible involvement of ZEN responsive proteins of the yeast. Journal of Proteome research, 143: 416-423.
https://doi.org/10.1016/j.jprot.2016.04.017

Zhao, H., Wang, X., Zhang, J., Zhang, J., Zhang, B., 2016. The mechanism of *Lactobacillus* strains for their ability to remove fumonisins B1 and B2. Food and Chemical Toxicology, 97: 40-46.
https://doi.org/10.1016/j.fct.2016.08.028

Zhao, L., Jin, H., Lan, J., Zhang, R., Ren, H., Zhang, H., Yu, G., 2015. Detoxification of zearalenone by three strains of *Lactobacillus* plantarum from fermented food *in vitro*. Food Control, 54: 158-164.
https://doi.org/10.1016/j.foodcont.2015.02.003

Zhao, Z., Zhang, Y., Gong, A., Liu, N., Chen, S., Zhao, X., Li, X., Chen, L., Zhou, C., Wang, J., 2019. Biodegradation of mycotoxin fumonisin B1 by a novel bacterial consortium SAAS79. Applied Microbiology and Biotechnology, 103(17): 7129-7140.
https://doi.org/10.1007/s00253-019-09979-6

Zheng, J., Wittouck, S., Salvetti, E., Franz, C.M.A.P., Harris, H.M.B., Mattarelli, P., O'Toole, P.W., Pot, B., Vandamme, P., Walter, J., Watanabe, K., Wuyts, S., Felis, G.E., Gänzle, M.G., Lebeer, S., 2020. A taxonomic note on the genus *Lactobacillus*: Description of 23 novel genera, emended description of the genus *Lactobacillus* Beijerinck 1901, and union of Lactobacillaceae and Leuconostocaceae. International Journal of Systematic and Evolutionary Microbiology, 70(4): 2782-2858.
https://doi.org/10.1099/ijsem.0.004107

Zhu, Y., Hassan, Y.I., Lepp, D., Shao, S., Zhou, T., 2017. Strategies and methodologies for developing microbial detoxification systems to mitigate mycotoxins. Toxins, 9(4): 130.
https://doi.org/10.3390/toxins9040130

Zhu, Y., Drouin, P., Lepp, D., Li, X.Z., Zhu, H., Castex, M., 2021. A novel microbial zearalenone transformation through phosphorylation. Toxins, 13: 294.
https://doi.org/10.3390/toxins13050294

Zoghi, A., Khosravi-Darani, K. and Hekmatdoost, A., 2021a. Effects of pretreatments on patulin removal from apple juices using lactobacilli: binding stability in simulated gastrointestinal condition and modeling. Probiotics and Antimicrobial Proteins, 13: 135-145.
https://doi.org/10.1007/s12602-020-09666-3

Zoghi, A., Khosravi-Darani, K. and Sohrabvandi, S., 2014. Surface binding of toxins and heavy metals by probiotics. Mini-Reviews in Medicinal Chemistry, 14: 84-98.

Zoghi, A., Khosravi-Darani, K., Sohrabvandi, S., Attar, H., Alavi, S.A., 2017. Effect of probiotics on patulin removal from synbiotic apple juice. Journal of Science of Food and Agriculture, 97: 2601-2609.
https://doi.org/10.1002/jsfa.8082

Zoghi, A., Khosravi-Darni, K. and Sohrabvandi, S., 2018. Patulin removal from synbiotic apple juice using *Lactobacillus* plantarum ATCC 8014. Journal of Applied Microbiology, 126: 1149-1160.
https://doi.org/10.1111/jam.14172

Zoghi, A., Massoud, R., Todorov, S.D., Chikindas, M.L., Popov, I., Smith, S., Khosravi-Darani, K., 2021b. Role of the lactobacilli in food biodecontamination: Friends with benefits. Enzyme and Microbial Technology, 150: 109861.
https://doi.org/10.1016/j.enzmictec.2021.109861

Zou, Z.Y., He, Z.F., Li, H.J., Han, P.F., Meng, X., Zhang, Y., Zhou, F., Ouyang, K.P., Chen, X.Y., Tang, J., 2012. *in vitro* removal of deoxynivalenol and T-2 toxin by lactic acid bacteria. Food Science and Biotechnology, 21: 1677-1683.
https://doi.org/10.1007/s10068-012-0223-x