



**PROCEEDINGS OF ABSTRACTS
VIII. INTERNATIONAL
AGRICULTURAL, BIOLOGICAL,
LIFE SCIENCE CONFERENCE
AGBIOL 2026**

06-09 SEPTEMBER 2026

ISTANBUL, TÜRKİYE



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**Organized by
Trakya University
İstanbul Beykent University
International Researchers Association**

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WELCOME NOTES

You are welcome to our VIII. AGBIOL Conference that is organized by Trakya University, Beykent University and International Researchers Association. The aim of our conference is to present scientific subjects of a broad interest to the scientific community, by providing an opportunity to present their work as oral or poster presentations that can be of great value for global science arena. Our goal was to bring three communities, namely science, research and private investment together in a friendly environment of Edirne, Turkey in order to share their interests and ideas and to get benefit from the interaction with each other.

In September 2018, we organized the first AGBIOL Conference with more than 700 scientists and researchers from all over the world with over 800 scientific papers. Due to COVID-19 situation, II. AGBIOL 2020 has organized fully on-line event which was one of the biggest online conferences in recent years in the world with 499 papers and 1133 authors with 333 oral and 166 e-poster presentations from 55 countries. Due to COVID-19 situation, AGBIOL 2021 was organized online again. AGBIOL 2022 conference was organized with a worldwide participation from 44 countries over 522 papers contributed by over 1300 authors. AGBIOL 2023 was organized with a record and worldwide participation from 33 countries 833 papers contributed by over 2000 authors with 522 oral and 311 poster presentations. AGBIOL 2024 consisted of 835 papers contributed by about 2000 authors with worldwide record participation again from 55 countries with 522 oral and 311 poster presentations. AGBIOL 2025 was organized with a worldwide record participation from 60 countries 988 papers contributed over 2300 authors with 400 oral and 588 poster presentations.

The AGBIOL 2026 is normal participation as well as with online participation in Beykent University in Istanbul, Turkey on 06-09 September, 2026. The program included oral talks by invited prominent scientists and oral and e poster presentations by participants in selected topics from the submitted abstracts focusing on Agriculture, Biology and Life Sciences topics.

There is a worldwide record participation again in AGBIOL 2026 from 61 countries 1057 papers contributed over 2500 authors then 800 of them were accepted and then the conference was organized with 390 oral and 410 poster presentations.

With care for our nature and environment, we aim the green congress, meaning that as little as possible papers will be used. Abstract book is published in electronic book and is distributed to the participants by e mail for online participants. All the e-posters are prepared in electronic form and then submit to via the conference e mail and exhibited in electronical poster boards as well as in online e poster hall in our web page during the conference.

The participants with paid conference fee accessed all the normal and virtual presentation talks in each session, as well as to visit the virtual poster hall via preliminary provided. The abstracts were published in the Conference Abstract and Proceedings Book. Participants might send us their full papers, which based on their preferences are published either in our Conference Abstract and Proceedings Book or in selected International Indexed Scientific Journals.

Conference Topics:

Agriculture, Forestry, Life Sciences, Agricultural Engineering, Aquaculture and Biosystems, Animal Science, Biomedical science, Biochemistry and Molecular Biology, Biology, Bioengineering, Biomaterials, Biomechanics, Biophysics, Bioscience, Biotechnology, Botany, Chemistry, Chemical Engineering, Earth Sciences, Environmental Science, Food Science, Genetics and Human Genetics, Medical Science, Machinery, Pharmaceutical Sciences, Physics, Soil Science.

We would like to thank all of you for joining this conference and we would like to give also special thanks to TUBITAK and collaborators for giving us a big support to organize this event.

Prof Dr Yalcin KAYA

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FOODBORNE MYCOTOXINS AND THE HUMAN MICROBIOME: A HACCP-BASED RISK ASSESSMENT APPROACH

Natalija Atanasova-Pancevska^{1*}, Aleksandra Markovska², Daniela Todevska³

¹Ss. Cyril and Methodius University in Skopje, Faculty of Natural Sciences and Mathematics – Skopje, Institute of Biology, Department of Microbiology and Microbial Biotechnology, Skopje, North Macedonia

*corresponding author: natalijaap@gmail.com, natalija@pmf.ukim.mk

² Quality Consulting, North Macedonia

³ Faculty of Agriculture, Goce Delcev University, Stip, North Macedonia

ABSTRACT

Mycotoxins, toxic secondary metabolites produced by fungi such as *Aspergillus*, *Fusarium*, and *Penicillium*, represent one of the most significant chemical hazards in food systems. They contaminate cereals, nuts, fruits, and processed products, posing risks not only through acute toxicity but also via chronic exposure that can disrupt the human gut microbiome. The microbiome, a complex ecosystem of bacteria, fungi, and archaea, plays a central role in digestion, immune regulation, and metabolic homeostasis. Evidence suggests that mycotoxins such as aflatoxins, ochratoxin A, fumonisins, and deoxynivalenol can alter microbial diversity, reduce beneficial taxa, and promote dysbiosis, thereby increasing susceptibility to gastrointestinal disorders, metabolic dysfunction, and immune imbalance.

This review synthesizes current knowledge on the ecological interactions between foodborne mycotoxins and the human microbiome, emphasizing the need for integrated risk assessment. The Hazard Analysis and Critical Control Points (HACCP) framework provides a systematic approach to identifying and controlling hazards at critical points in food production and processing. Applying HACCP principles to mycotoxin contamination involves monitoring agricultural practices, storage conditions, and processing steps where fungal growth and toxin production are most likely.

By incorporating microbiome-focused biomarkers, such as microbial diversity indices, short-chain fatty acid levels, NF-κB activation, and metabolomic signatures, into HACCP risk assessment, food safety management can evolve beyond traditional toxicological thresholds to include microbial resilience and host health outcomes. Case studies highlight how HACCP interventions, including improved grain storage, rapid detection methods, and biocontrol strategies, reduce mycotoxin exposure. Ultimately, aligning HACCP with microbiome research offers a proactive strategy to mitigate the long-term health consequences of mycotoxin contamination. This interdisciplinary approach underscores the importance of integrating food safety, microbiology, and public health perspectives to safeguard consumer wellbeing and ensure sustainable food systems.

Keywords: Foodborne mycotoxins, Human gut microbiome, Microbiome dysbiosis, HACCP framework, Critical control points, Risk assessment, Food safety management

INTRODUCTION

Mycotoxins are toxic secondary metabolites produced by fungi such as *Aspergillus*, *Fusarium*, and *Penicillium*. They contaminate staple foods including cereals, nuts, coffee, dried fruits, and spices, and represent one of the most significant chemical hazards in food safety (Khan, 2024). Chronic exposure to mycotoxins has long been associated with hepatotoxicity, nephrotoxicity, immunosuppression, and carcinogenesis (Mafe & Büsselberg, 2026). More recently, attention has shifted to their impact on the human gut microbiome, a complex ecosystem essential for digestion, immune regulation, and metabolic homeostasis.

Evidence indicates that mycotoxins disrupt microbial diversity, reduce beneficial taxa, and promote dysbiosis. For example, deoxynivalenol (DON) impairs short-chain fatty acid production and increases intestinal inflammation (Mafe & Büsselberg, 2026), while aflatoxin B₁ alters microbial composition and epithelial barrier integrity (Khan, 2024). These bidirectional interactions are critical: gut microbes can metabolize and detoxify certain mycotoxins, but they can also bioactivate others, amplifying toxicity (Mafe & Büsselberg, 2026).

The Hazard Analysis and Critical Control Points (HACCP) framework provides a systematic approach to identifying and controlling hazards at critical points in food production. Applying HACCP principles to mycotoxin contamination involves monitoring agricultural practices, storage conditions, and processing steps where fungal growth and toxin production are most likely (Khan, 2024). Integrating microbiome endpoints into HACCP risk assessment could enhance food safety management by considering not only toxicological thresholds but also microbial resilience and host health outcomes.

TYPES OF FOODBORNE MYCOTOXINS

Aflatoxins

Produced mainly by *Aspergillus flavus* and *A. parasiticus*, aflatoxins are potent hepatotoxins and carcinogens. Aflatoxin B₁ is the most toxic, linked to liver cancer and immune suppression (Mafe & Büsselberg, 2024). Studies show that aflatoxins disrupt gut microbial balance, reducing beneficial *Lactobacillus* and *Bifidobacterium* populations, while increasing opportunistic pathogens (Mafe & Büsselberg, 2026).

Ochratoxin A (OTA)

Generated by *Aspergillus* and *Penicillium* species, OTA contaminates cereals, coffee, and dried fruits. It is nephrotoxic and immunotoxic, and recent findings suggest it alters gut microbial composition, impairing epithelial barrier function and promoting dysbiosis (Khan, 2024). OTA exposure has been linked to reduced microbial diversity and increased inflammatory signaling pathways such as NF- κ B (Mafe & Büsselberg, 2026).

Fumonisin

Produced by *Fusarium verticillioides*, fumonisins contaminate maize and maize-based products. Fumonisin B₁ interferes with sphingolipid metabolism and has been associated with esophageal cancer (Mafe & Büsselberg, 2024). In the gut, fumonisins disrupt microbial

communities and impair short-chain fatty acid production, contributing to intestinal inflammation (Mafe & Büsselberg, 2026).

Deoxynivalenol (DON)

Also known as vomitoxin, DON is produced by *Fusarium graminearum* and contaminates wheat, barley, and maize. DON induces gastrointestinal distress and immune dysregulation. It reduces microbial richness, impairs SCFA production, and increases pro-inflammatory cytokines, thereby exacerbating dysbiosis (Khan, 2024; Mafe & Büsselberg, 2026).

Zearalenone (ZEN)

Produced by *Fusarium* species, ZEN is an estrogenic mycotoxin found in maize and wheat. It disrupts hormonal balance and reproductive health. In the gut, ZEN alters microbial composition and may promote the growth of taxa capable of metabolizing estrogen-like compounds, further complicating host–microbe interactions (Mafe & Büsselberg, 2026).

MICROBIOME IMPACTS OF FOODBORNE MYCOTOXINS

The gut microbiome refers to the diverse community of microorganisms living in the digestive tract, primarily in the intestines. These microorganisms play essential roles in digestion, nutrient absorption, and the synthesis of certain vitamins and hormones. The balance and composition of the gut microbiome can significantly impact overall health, including metabolic function, mental health, and immune response.

Each individual has a unique gut microbiome influenced by various factors, including genetics, diet, lifestyle, and environmental exposures. Maintaining a balanced and diverse gut microbiome is crucial for supporting various bodily functions and promoting overall well-being.

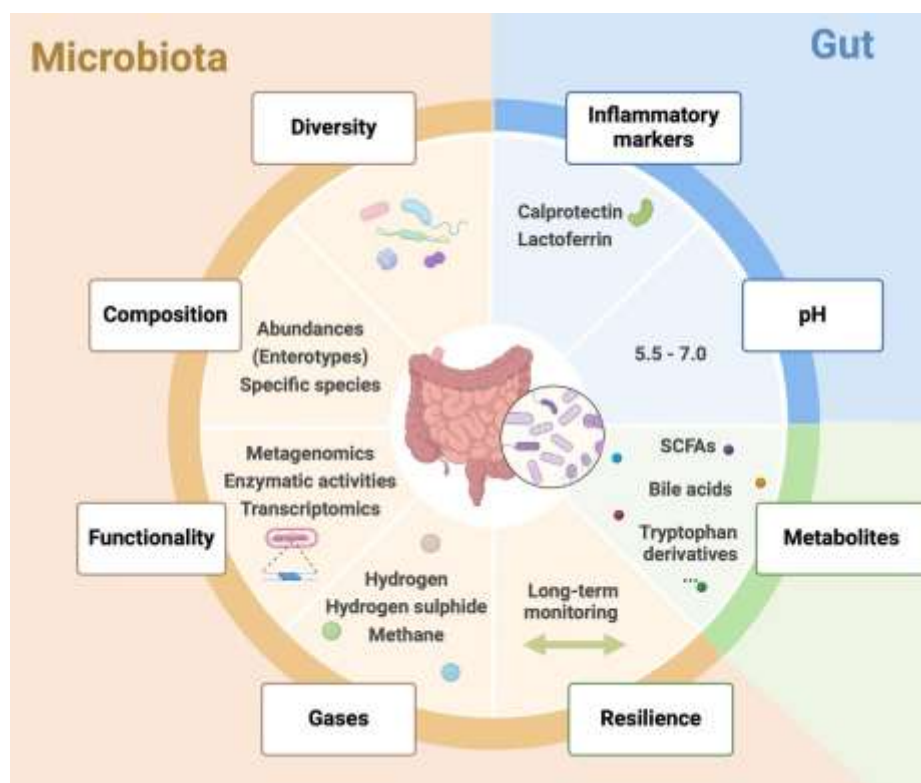


Figure 1. Potential markers of a healthy gut microbiota. A healthy gut microbiota is characterised by a diverse and balanced community of microorganisms that perform vital functions for the host. Several key markers have been proposed to assess these, including microbial diversity, composition (abundances, enterotypes, specific species), functionality (metagenomics, enzymatic activities, transcriptomics) and resilience (through long-term monitoring). Production of important metabolites like SCFAs, bile acids and tryptophan derivatives, as well as gases (hydrogen, hydrogen sulfide, methane), are potential indicators.

Additionally, gut health indicators such as pH levels and the presence of inflammation markers (like calprotectin, lactoferrin) can be used for assessing overall gut health. SCFAs, short-chain fatty acids (from Van Hul et al., 2024).

Exposure to foodborne mycotoxins can disrupt this balance, leading to microbiome dysbiosis and downstream health consequences.

Alterations in Microbial Diversity

Aflatoxins, particularly aflatoxin B₁, reduce beneficial taxa such as *Lactobacillus* and *Bifidobacterium* while promoting opportunistic pathogens (Chalaśkiewicz et al., 2025). This imbalance increases intestinal permeability and weakens epithelial barrier integrity (Mafe & Büsselberg, 2026).

Metabolic Effects

Deoxynivalenol (DON) is one of the most studied mycotoxins. It reduces the production of short-chain fatty acids (SCFAs), which are crucial for gut health and immune modulation. DON exposure also elevates pro-inflammatory cytokines, contributing to chronic intestinal inflammation (Li et al., 2019). Fumonisin, especially fumonisin B₁, disrupt sphingolipid metabolism and alter microbial composition, reducing *Clostridiaceae* and *Campylobacteraceae*

while increasing *Ruminococcaceae* and *Faecalibacterium* (Yunus Zeebone et al., 2023; Zhang et al., 2021).

Immune Dysregulation

Ochratoxin A (OTA) is nephrotoxic and immunosuppressive, but also directly affects the microbiome. OTA activates NF- κ B signaling, leading to chronic inflammation and reduced microbial diversity (Więckowska et al., 2025; Izco et al., 2021). Dysbiosis caused by OTA increases susceptibility to infections and metabolic disorders.

Bidirectional Interactions

The relationship between mycotoxins and the microbiome is bidirectional. Gut microbes can metabolize and detoxify certain mycotoxins, but they may also bioactivate others, amplifying toxicity (Mafe & Büsselberg, 2026). This dual role highlights the need for integrated risk assessment approaches that consider microbial resilience alongside toxicological thresholds.

HACCP CONTROL POINTS FOR MYCOTOXIN MANAGEMENT

The Hazard Analysis and Critical Control Points (HACCP) framework provides a systematic approach to identifying, evaluating, and controlling hazards in food production. When applied to mycotoxins, HACCP emphasizes prevention at critical stages rather than relying solely on end-product testing. Integrating microbiome considerations into HACCP adds a novel dimension, ensuring that food safety strategies also protect gut microbial health.

1. Primary Production (Agriculture)

Critical Control Point (CCP): Crop cultivation and harvesting

Mycotoxins such as aflatoxins and fumonisins originate in the field, particularly under warm and humid conditions (Khan, 2024).

Preventive measures: crop rotation, resistant varieties, biocontrol agents (e.g., *Aspergillus flavus* biocompetitive strains).

Microbiome relevance: reducing contamination at source minimizes downstream exposure that disrupts gut microbial diversity.

2. Post-Harvest Handling and Storage

Critical Control Point (CCP): Grain drying and storage

Improper drying and high moisture favor fungal growth and OTA production (Izco et al., 2021).

Preventive measures: rapid drying to <13% moisture, controlled humidity, aeration systems.

Microbiome relevance: OTA exposure is linked to NF- κ B activation and dysbiosis (Więckowska et al., 2025).

3. Processing and Manufacturing

Critical Control Point (CCP): Milling, sorting, and detoxification steps

DON and ZEN often persist through processing; sorting and cleaning reduce contamination (Li et al., 2019).

Emerging technologies: enzymatic detoxification, microbial biotransformation.

Microbiome relevance: microbial detoxification strategies may preserve gut microbial resilience.

4. Distribution and Retail

Critical Control Point (CCP): Packaging and transport

Contamination can occur during storage and distribution if conditions favor fungal growth.

Preventive measures: HACCP monitoring of supply chains, traceability systems.

Microbiome relevance: minimizing chronic low-dose exposure reduces risk of long-term dysbiosis.

5. Consumption and Public Health Monitoring

Critical Control Point (CCP): Consumer awareness and biomarker surveillance

Incorporating microbiome-sensitive biomarkers into HACCP risk assessment could provide early warning of subclinical effects (Mafe & Büsselberg, 2026).

Public health programs should integrate dietary monitoring with microbiome analysis to assess cumulative impacts.

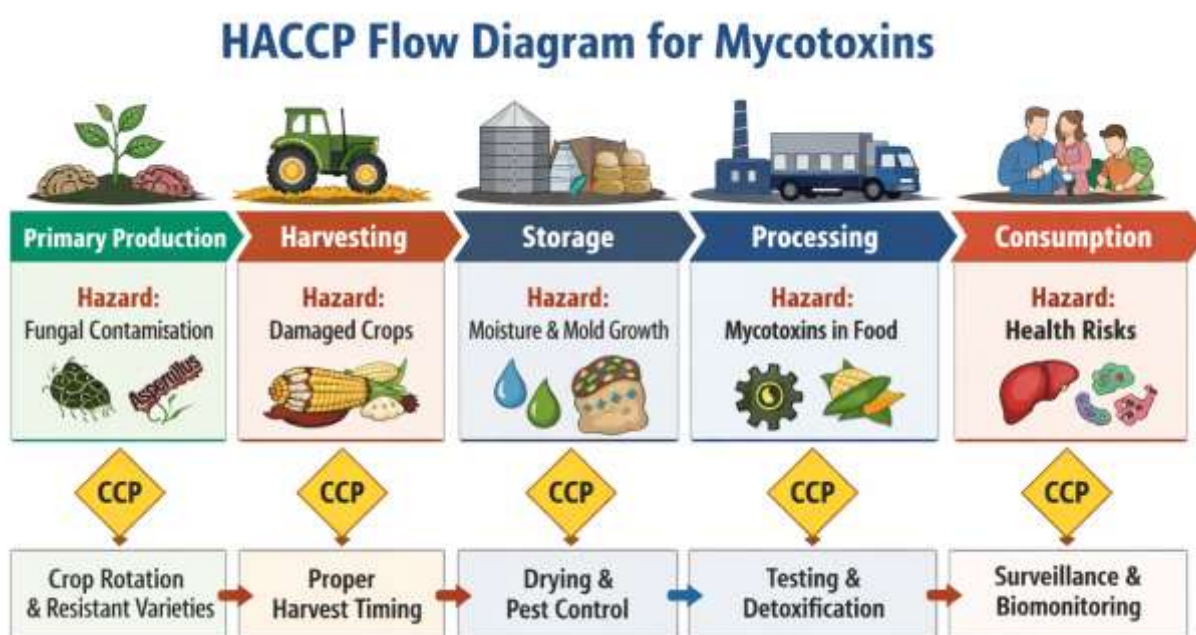


Figure 2. HACCP flow diagram for mycotoxin control in food systems

MICROBIOME BIOMARKERS IN FOOD SAFETY

In recent years, food safety science has begun to recognize that the human gut microbiome is not only a passive target of dietary contaminants but also an active participant in shaping health outcomes. This realization has led to the proposal of microbiome biomarkers as complementary tools within HACCP-based risk assessment frameworks. Unlike traditional monitoring, which focuses on detecting chemical residues such as aflatoxins or fumonisins in food products, microbiome biomarkers provide a biological readout of how these toxins affect host physiology even at low, chronic exposure levels.

One of the most widely studied indicators is microbial diversity. Healthy gut ecosystems are characterized by high richness and evenness, measured through indices such as Shannon and Simpson. Exposure to aflatoxin B₁ has been shown to reduce microbial diversity, weakening the resilience of the gut ecosystem and increasing susceptibility to opportunistic pathogens (Chalaśkiewicz et al., 2025). This decline in diversity can therefore serve as an early warning biomarker of toxin-induced dysbiosis.

Another critical set of biomarkers involves short-chain fatty acids (SCFAs), including acetate, propionate, and butyrate. These metabolites are produced by gut microbes during fiber fermentation and play essential roles in maintaining intestinal barrier integrity and modulating immune responses. Studies demonstrate that deoxynivalenol (DON) and fumonisins significantly reduce SCFA production, leading to impaired gut function and chronic inflammation (Li et al., 2019; Yunus Zeebone et al., 2023). Monitoring SCFA levels in fecal or blood samples thus provides a functional biomarker of microbiome health under toxin stress.

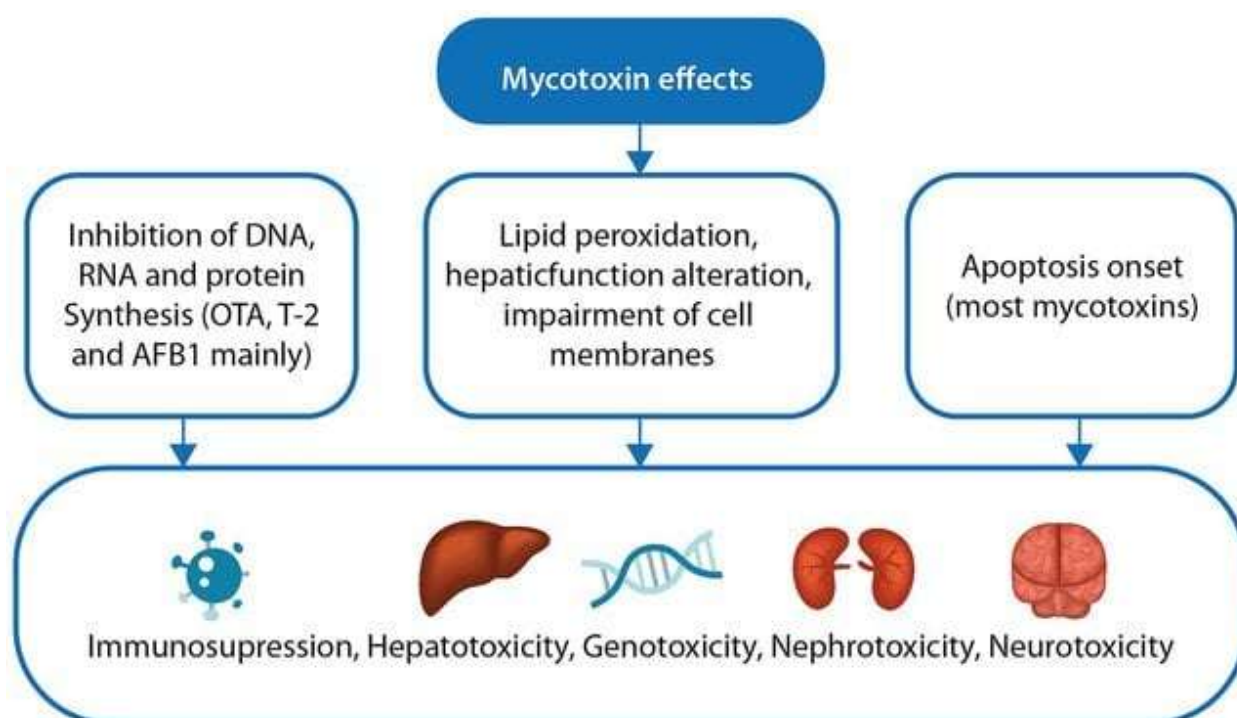


Figure 3. Major mechanisms of mycotoxin toxicity and their effects. Different mechanisms of mycotoxins can affect different organs and tissues in birds such as inhibition of protein synthesis, lipid peroxidation, hepatic function impairment, apoptosis modulation, among others. DNA, deoxyribonucleic acid; RNA, ribonucleic acid; OTA, ochratoxin; AFB1, aflatoxin B1 (from Gómez-Osorio et al., 2024).

The immune system offers another layer of biomarker evidence. Mycotoxins such as ochratoxin A (OTA) activate NF- κ B signaling, resulting in elevated levels of pro-inflammatory cytokines like IL-6 and TNF- α . These cytokines are measurable in serum and reflect immune dysregulation linked to microbiome imbalance (Więckowska et al., 2025; Izco et al., 2021). Their inclusion in HACCP monitoring would allow food safety systems to capture not only chemical hazards but also their biological consequences.

Beyond immune markers, metabolomic signatures provide a systems-level perspective. Alterations in bile acids, sphingolipids, and estrogen-like metabolites have been associated with fumonisin and zearalenone exposure (Zhang et al., 2021). These shifts reveal how toxins disrupt host-microbe metabolic interactions, offering highly specific biomarkers for risk assessment.

Finally, probiotic resilience markers highlight the protective role of beneficial microbes. The survival and activity of taxa such as *Lactobacillus* and *Bifidobacterium* under toxin stress can serve as indicators of microbiome robustness. Probiotic supplementation has been shown to mitigate DON and OTA effects, suggesting that resilience markers could guide preventive interventions within HACCP frameworks (Mafe & Büsselberg, 2026).

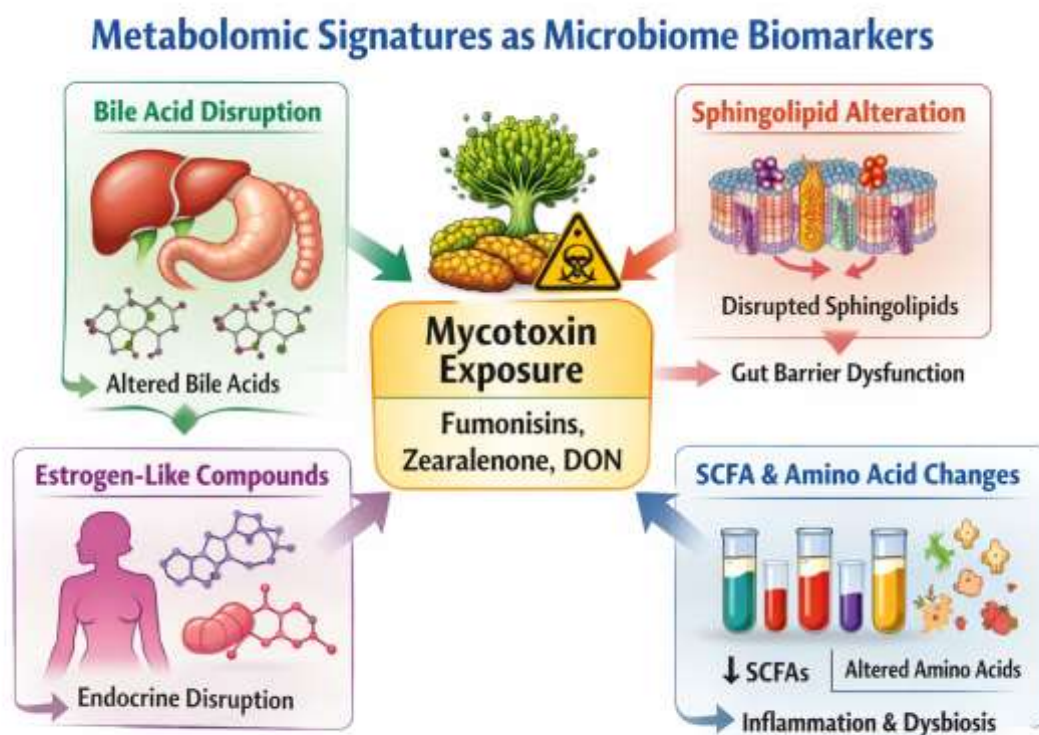


Figure 4. Metabolomic signatures as microbiome biomarkers in food safety. Mycotoxin exposure alters bile acid metabolism, sphingolipid integrity, estrogen-like compounds, and SCFA/amino acid profiles, providing measurable indicators of toxin impact on gut health.

CONCLUSION

The interplay between foodborne mycotoxins and the gut microbiome represents a critical frontier in modern food safety research. Mycotoxins such as aflatoxins, ochratoxin A, deoxynivalenol, fumonisins, and zearalenone exert not only direct toxicological effects but also profound influences on microbial composition, metabolism, and immune regulation. These interactions reshape the intestinal ecosystem, leading to dysbiosis, inflammation, and metabolic imbalance.

Integrating microbiome-based indicators into the HACCP framework transforms food safety from a purely chemical surveillance system into a biological risk-assessment model. By monitoring microbial diversity, SCFA production, cytokine activation, and metabolomic signatures, HACCP can detect early biological responses to contamination long before clinical symptoms appear. This approach aligns with the principles of preventive toxicology and precision nutrition, emphasizing resilience and health maintenance rather than reactive control.

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