Editorial

**Guarding our food: keeping it safe in a changing world through multidisciplinary approaches**

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As a society increasingly reliant on a complex global food system, ensuring food safety has become paramount (Fung et al., 2018; Nayak and Waterson, 2019). Here in the Asiatic region, with its diverse ecosystems and unique culinary traditions, safeguarding our food supply presents a multifaceted challenge (Downs et al., 2020). Here, I tried to explain why it’s important to use different scientific fields together to tackle food safety and security.

The Asian region faces a unique set of food safety challenges. The emergence of infectious diseases, coupled with the rise of antibiotic-resistant pathogens due to their increased use in intensive agriculture, poses a significant threat (Kim and Ahn, 2022; Okaiyeto et al., 2024). Additionally, the region’s diverse climates create ideal conditions for the proliferation of mycotoxin-producing fungi, contaminating staple crops like rice and wheat (Medina et al., 2017; Perrone et al., 2020). These factors necessitate a paradigm shift towards a holistic approach to ensure food safety.

Agricultural microbiology offers a powerful tool for safeguarding food at its source (Anand et al., 2022). By studying the microbial communities associated with regional crops and livestock, researchers can identify beneficial microbes that act as biocontrol agents (Suman et al., 2022; Masenya et al., 2024). These microbes suppress the growth of harmful pathogens in the field, reducing the risk of contamination before harvest (Wang et al., 2022). Understanding the intricate relationship between plants and their associated microbial communities in the rhizosphere can further inform strategies for promoting healthy soil ecosystems, ultimately fostering plant resilience against pathogens (Chauhan et al., 2023; Thepbandit and Athinuwat, 2024).

Bioinformatics empowers scientists to unlock the vast potential of high-throughput sequencing technologies. This allows for the rapid and accurate identification of microorganisms present in food samples (Gupta and Verma, 2019; Satam et al., 2023). By comparing these sequences to comprehensive databases of known pathogens and beneficial microbes, bioinformatics provides crucial insights into potential food safety risks (Alkema et al., 2016; Jagadeesan et al., 2019). Additionally, bioinformatics facilitates the development of novel detection methods with improved sensitivity and specificity for identifying specific pathogens relevant to the region (Behl et al., 2021; Vashisht et al., 2023).

Molecular pathology offers a deeper understanding of how foodborne pathogens cause disease at the molecular level. By examining the interaction of these pathogens with host cells, researchers can identify key virulence factors specific to pathogens prevalent in the Asian region (Rafiq et al., 2022; Juszczuk-Kubiak, 2024). This knowledge paves the way for the development of targeted therapies and preventative measures. Additionally,
molecular pathology can be used for outbreak investigations, enabling swift interventions to prevent further illness (Foxman, 2012; Bumunang et al., 2023).

The Asiatic region boasts a rich diversity of plants with unique medicinal properties. Phytochemistry explores the vast array of natural compounds produced by these plants, many of which possess antimicrobial properties (Oppedisano et al., 2023). By isolating and characterizing these bioactive molecules, scientists can develop plant-derived antimicrobials specifically suited to combatting regional foodborne threats. This approach offers a sustainable and potentially safer alternative to traditional chemical preservatives (Alzandi et al., 2021; Farid et al., 2023; Pinto et al., 2023). Additionally, understanding the natural defense mechanisms employed by regional plants against microbial colonization can inspire the development of novel strategies for enhancing food crop resistance to pathogens (Srikamwang et al., 2023).

These disciplines are not isolated entities; their synergy unlocks a new level of understanding towards food safety. Agricultural microbiologists can leverage bioinformatics to analyze the complex microbial communities in agricultural environments specific to the region (Gangola et al., 2023; Masenya et al., 2024). Molecular pathologists can utilize bioinformatics tools to identify novel virulence factors in newly emerged pathogens prevalent in the region. Phytochemists can collaborate with agricultural microbiologists to explore the potential of plant-derived antimicrobials against specific foodborne pathogens relevant to the region (Doxey et al., 2019; Venbrux et al., 2023).

To ensure a safe and sustainable food supply for future generations, continued investment in collaborative research across the Asian region is paramount. By establishing interdisciplinary research centers that bring together scientists from diverse fields, we can foster cross-pollination of ideas and accelerate the development of innovative solutions tailored to the region’s specific food safety challenges (Lin, 2017). Additionally, advancements in high-throughput sequencing, metagenomics, and artificial intelligence will further empower researchers to rapidly identify and characterize foodborne threats specific to the region (Oon et al., 2023; Vashisht et al., 2023).

The responsibility for food safety extends beyond the realm of scientific research. It encompasses the entire food production chain, from farmers and food processors to regulatory bodies and consumers (Hamilton et al., 2023). Open communication and collaboration between these stakeholders are crucial for implementing effective food safety measures at all stages (Baba and Esfandiari, 2023). This collaborative effort, coupled with the integration of the aforementioned scientific disciplines, holds immense promise for safeguarding our food supply and ensuring the well-being of future generations in the Asian region. By harnessing the power of science, technology, and regional collaboration, we can cultivate a safer and healthier food system for all.

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**Data availability**
Not applicable.

**Conflict of interest**
None to declare.

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**References**


