Food and Agriculture Organization of the United Nations

World Health Organization

Joint FAO/WHO expert meeting on microbiological risk assessment on the use of omics-based technologies in microbiological risk assessment

FAO HQ, Rome, Italy, 2-6 March 2026

SUMMARY AND CONCLUSIONS

Issued in March 2026

A Joint FAO/WHO Expert Meeting on Microbiological Risk Assessment (JEMRA) on the use of omics-based technologies in microbiological risk assessment (MRA) was convened in Rome, Italy, from 2–6 March 2026. The meeting brought together international experts to review recent scientific developments, available information and practical experience related to the application of omics-based technologies in microbiological food safety and MRA. The Expert Committee examined the current and potential use of genomics, transcriptomics, proteomics, metabolomics, and related approaches in supporting hazard identification, hazard characterization, exposure assessment, and risk characterization. The Expert Committee reviewed two Codex Alimentarius documents about MRA and management and provided suggestions on areas where advances in omics-based technologies could be incorporated to update them.

This document summarizes the conclusions of the meeting. A full report will be published by FAO and WHO.

The meeting participants are listed in Annex 1 of this summary report. Maarten Nauta served as Chairperson and Bing Wang as Rapporteur.

More information on this work is available at:

http://www.fao.org/food-safety/en/

and

https://www.who.int/foodsafety/en/

Background

In response to a request from the Codex Alimentarius Committee on Food Hygiene (CCFH) for scientific advice, FAO and WHO convened a Joint FAO/WHO Expert Meeting on Microbiological Risk Assessment (JEMRA) to evaluate the role of omics-based technologies in microbiological risk assessment (MRA). Since the publication of the Microbiological Risk Assessment – Guidance for Food (FAO/WHO, 2021)[1], rapid advancements in analytical methods that generate extensive molecular data have transformed food microbiology, surveillance and outbreak investigation. These developments have generated new types of data with potential relevance for hazard identification, hazard characterization, exposure assessment, and risk characterization.

The objective of this meeting was to assess whether, and to what extent, current MRA guidance could be updated to incorporate the application of omics-based technologies and omics-derived data. Specifically, the Expert Committee was tasked with: (i) compiling an overview of omics-based technologies currently available and applicable to microbiological food safety; (ii) for those currently applied in MRA, reviewing their benefits, limitations, and practical challenges; (iii) evaluating how omics-derived data can inform different steps of the MRA process as defined by Codex Alimentarius and (iv) identifying considerations for practical implementation.

Omics-based technologies, including genomics, transcriptomics, proteomics, metabolomics and related approaches, enable detailed characterization of microbial identity, relatedness, genetic determinants, functional potential and expressed traits. The meeting focused on how omics-derived data can be integrated into MRA in a fit-for-purpose manner, while maintaining transparency, scientific rigor, and consistency with risk analysis principles.

This Executive Summary reflects the key findings and conclusions of the meeting and serves as the basis for a more detailed technical report.

Overview of omics-based technologies and their application in microbiological food safety

- For the specific purpose of conducting MRA, “omics-based technologies” refer to methods that generate extensive molecular data to characterize microbial identity, relatedness, functional potential and/or activity at the system level, whether applied to individual isolates or complex communities.
- Omics-based technologies have more discriminatory power than previously used classifications (e.g., species, serotype, phage type, etc.).
- Genomics is being used for detection, surveillance, outbreak investigation, source attribution, and characterization of foodborne hazards.
- Proteomics, transcriptomics, metabolomics, and related methods are supporting the characterization of the behaviour of microorganisms.
- Several methodological challenges remain in the interpretation and application of omics-derived data in microbiological food safety. These include issues such as low prevalence of pathogens in food, the need for cultivation in some applications, as well as the difficulty in

[1] FAO and WHO. 2021. *Microbiological risk assessment - Guidance for food*. Microbiological Risk Assessment Series No. 36. Rome. https://doi.org/10.4060/cb5006en

distinguishing between viable and non-viable microorganisms when interpreting molecular signals.

Application of omics-based technologies in MRA

General considerations on the application of omics-derived data in MRA

- Genomics-derived data enhance foodborne disease surveillance, epidemiological investigations and source attribution, strengthening the evidence linking specific strains or subtypes to adverse health effects, and thereby improving the data used in MRA.
- In current applications of MRA, whole genome sequence analyses are primarily used to inform subgrouping of microorganisms based on phenotypic traits relevant to risk, such as virulence, antimicrobial resistance (AMR), or environmental fitness.
- The relevance of incorporating omics-based subgrouping into an MRA may be evaluated during the design phase of the assessment, for example through sensitivity analyses or in relation to the risk management questions outlined in the risk profile.
- A range of analytical approaches, including genome-wide association studies and machine learning, may support the identification of genomic markers associated with phenotypes relevant to MRA.
- Associations between omics-based markers and phenotypes should be interpreted with caution, as high predictive accuracy does not necessarily imply biological causality and risk-relevant phenotypes may be influenced by multiple genetic and environmental factors.
- The level of evidence supporting omics-based markers may vary, ranging from dataset-specific statistical associations to experimentally validated markers. The level of evidence should be considered in relation to the intended use within MRA.
- In practice, the application of omics-based markers in MRA may involve three general stages: (i) definition and characterization of the risk-relevant phenotype; (ii) identification and validation of omics-derived markers associated with the phenotype; and (iii) implementation of validated markers in surveillance, monitoring and specific phenotypic characterizations to inform risk assessment activities.

Hazard identification

- In current MRA practice, the application of omics-based technologies at the hazard identification stage remains generally limited to genomics. Combined with associated metadata and resulting data analyses, genomics can enhance hazard identification by providing high-resolution characterization of microorganisms.
- Genomics enhances traditional data inputs (e.g., epidemiological surveillance, outbreak investigations, food monitoring data, source attribution) for hazard identification by adding high-resolution characterization of genotypes associated with illness, enabling comparability and standardized documentation. Still, genomics-derived data must be interpreted alongside epidemiological and traceback evidence and metadata.

Hazard characterization

- Examples from published studies illustrate how omics-based approaches can reveal differences in virulence and disease severity between pathogen subgroups and their associations with host groups. These insights support a shift from species-level assumptions of equal virulence toward subgroup- and potentially host-specific hazard characterization models, which may reduce uncertainty in dose–response relationships.

- Effective integration of omics-derived data into hazard characterization requires combined interpretation of genomic, phenotypic, and epidemiological evidence.

Exposure assessment

- Genomic surveillance can determine whether certain subgroups are over- or under-represented in specific food commodities.
- Genomics-derived data may allow for the refinement of prevalence estimates of subgroups in food commodities rather than a prevalence estimate of a single population at species level.
- Omics-based markers can be associated with phenotypes relevant to exposure assessment (e.g., growth ability, environmental fitness, heat resistance), enabling subgroup-specific modelling of microbial behaviour.
- Integration of omics-derived data into exposure assessment requires validated genotype–phenotype associations, as currently many omics-based markers lack established biologically meaningful relationships with microbial behaviour.

Risk characterization

- Examples from published studies demonstrate that omics-derived data can be used to define pathogen subgroups based on virulence potential or ecological fitness, which can then be incorporated into hazard characterization and exposure assessment to estimate subgroup-specific risks. Although only a limited number of studies have used genomic information for every step, these examples illustrate that subgroup-specific risk estimation is feasible.
- Combining subgroup prevalence, environmental fitness traits and virulence parameters allows estimation of the relative contribution of different pathogen subgroups to the risk of the pathogen under consideration.

How omics-based technologies can change microbiological risk management

- For risk management, omics-derived data may impact the risk profile and the formulation of the statement of purpose, as the hazard can be more specifically defined based on enhanced inputs from source attribution, outbreak investigations, and surveillance.
- Informed by MRA, the omics-based classification decreases uncertainty in the risk estimate received by the risk managers.
- When omics-based classification shows differences in prevalence and microbial behaviour across food commodities, the resulting variation in risk between food commodities can inform the design of targeted intervention strategies.
- Risk management strategies can address specific omics-based classification(s), allowing enhanced efficiency by directing efforts towards the most relevant risks and enabling the refinement or prioritization of intervention measures.

Practical considerations

- Omics-derived data used in MRA should rely on standardized and well-documented laboratory methods including sampling, bioinformatic pipelines, metadata quality, and analytical approaches.
- Omics-derived data should be interpreted alongside phenotypic, experimental, and epidemiological evidence to reduce uncertainty in MRA.
- Challenges in using omics-based technologies include the lack of access to appropriate laboratory and computational infrastructure and financial resources, as well as the lack of trained personnel in data generation, analysis, and interpretation.
- Provision of capacity building may improve the adoption of omics-based technologies in MRA, especially in low- and middle-income countries.
- In some cases, omics-based subgroups can be categorized by specific markers that can then be detected by non-omics methods, meaning that applying MRA informed by omics does not necessarily require routine use of omics-based technologies.
- Omics-derived data used in MRA should adhere to FAIR (Findable, Accessible, Interoperable, Reusable) principles and be accompanied by robust, standardized metadata. Data sharing and governance frameworks should support access to omics-derived data.
- Risk communication involving omics-based classifications may require conveying more detailed information about a hazard beyond the species level. This may increase complexity in communication among risk assessors, risk managers, and other stakeholders.

Outlook

- Further technological advancements are foreseen that will impact the potential of using omics-based technologies in MRA. These include but are not limited to culture-independent methods, artificial intelligence-driven analyses and tools for data integration and analytics.
- In microbiology, there is an expected emergence of new variants or strains, which may lead to the emergence of new hazards and may require continuous updates of omics-based classifications.
- The global spread of AMR across human, animal and environmental reservoirs highlights the need to better understand the role of food systems in AMR transmission, where omics-based approaches may support improved characterization and tracking of resistance determinants.
- Future MRA will benefit from using omics-based technologies in a one-health approach.

Conclusions

Recent advances in omics-based technologies provide new opportunities to enhance MRA by enabling high-resolution characterization of microorganisms, their functional traits and ecological behaviour in agrifood systems. When combined with phenotypic characterization, omics-derived information can improve hazard identification, refine hazard characterization and support more targeted exposure assessment, ultimately reducing uncertainty in risk estimates.

The Expert Committee emphasized that omics-derived data complement rather than replace established MRA methods. The interpretation of omics-based markers requires careful consideration of genotype–phenotype relationships, levels of supporting evidence, and associated uncertainties. Integration of omics-derived data into MRA, therefore, requires transparent documentation of analytical methods, bioinformatic pipelines, metadata and assumptions, as well as continued reliance on phenotypic, epidemiological and experimental evidence.

Application of omics-based technologies requires a suitable laboratory, computational infrastructure, and trained personnel. However, even if this infrastructure does not allow routinely performing omics-based technologies, results on classification based on omics-derived data obtained by others can be applied using more conventional molecular techniques, such as PCR.

The Expert Committee reviewed Codex Alimentarius guidelines (Codex Principles and guidelines for the conduct of microbiological risk assessment, CXG 30-1999[2] and Codex Principles and guidelines for the conduct of microbiological risk management (MRM), CXG 63-2007[3]). While the current Codex Alimentarius guidelines on the conduct of MRA and management provide a robust framework, the meeting noted that certain elements may benefit from clarification or refinement to reflect the emerging role of omics-derived data. The Expert Committee provided specific comments on areas where advances in the application of omics-technologies in microbiological risk analysis could be incorporated to update these documents. For specific recommended modifications, please refer to Annex 2.

[2] https://www.fao.org/fao-who-codexalimentarius/sh-proxy/it/?lnk=1&url=https%253A%252F%252Fworkspace.fao.org%252Fsites%252Fcodex%252FStandards%252FCXG%2B30-1999%252FCXG_030e_2014.pdf

[3] https://www.fao.org/fao-who-codexalimentarius/sh-proxy/it/?lnk=1&url=https%253A%252F%252Fworkspace.fao.org%252Fsites%252Fcodex%252FStandards%252FCXG%2B63-2007%252FCXG_063e.pdf

Annex 1: List of participants

EXPERTS

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TECHNICAL RESOURCE PERSONS

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SECRETARIAT

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Annex 2: Recommendations on the modification of Codex Alimentarius documents about microbiological risk assessment and management

Please refer to the full report for rationales for the recommended modifications.

- *Codex Principles and guidelines for the conduct of microbiological risk assessment, (CXG 30-1999)*

5.3 Hazard identification

Recommend adding: **Hazard identification may be refined when omics-based classification reveals associations between genomic sequences and phenotypic traits linked to increased virulence, environmental fitness, or transmission potential, when relevant to risk.**

5.6 Risk Characterization

Recommend adding: **When omics-based approaches enable classification of hazards into biologically meaningful subgroups, this classification should be applied consistently across all relevant components of the risk assessment, including exposure assessment and hazard characterization. However, omics-based classification information may not always be available for each component. In such cases, risk assessors may need to rely on knowledge of the hazard in its broader, non-classified form, while explicitly acknowledging and characterizing the resulting uncertainty.**

- *Codex Principles and guidelines for the conduct of microbiological risk management (MRM), (CXG 63-2007)*

8.1, Under "*When establishing or re-designing monitoring systems in countries, the following aspects should be considered*", in the second bullet, add 'bioinformaticians' as shown below:

> *Interdisciplinary teams of epidemiologists,* ***bioinformaticians*** *and food safety experts should be formed to investigate foodborne illness to identify the food vehicles and the series of events that lead to illnesses.*

Annex 1, in "*1. Hazard-food commodity combination(s) of concern*", add the bolded text to the first bullet as shown below

> *Hazard(s) of concern;* ***the hazard may be specified based on omics-based classification***

Annex 1, in "*2. Description of public health problem*", add the bolded text as a new black bullet above "*Characteristics of disease*"

- ***Variation between subgroups of the hazard, for example based on omics-based classification***

Annex 1, in "*2. Description of public health problem*", under the black bullet "*Epidemiology of foodborne diseases*", add the bolded text as a new white bullet at the end as shown below:

- ***Source attribution data (e.g., based on omics)***