Archives of Microbiology (2026) 208:109
https://doi.org/10.1007/s00203-025-04675-8

REVIEW

Food-borne bacterial pathogens: emerging approaches in detection and prevention

Zaryab Shafi[1] · Mohammad Shahid[2] · Rahul Singh[3]

Received: 6 November 2025 / Revised: 12 December 2025 / Accepted: 17 December 2025 / Published online: 12 January 2026

Abstract

Food-borne bacterial pathogens remain a major public health concern, causing extensive illness and economic losses worldwide. Conventional detection methods are often slow and insufficient for identifying viable but non-culturable pathogens. Recent microbiological, biotechnological and bioinformatic advances have markedly improved food safety monitoring. Rapid molecular assays (PCR, qPCR, microarrays), next-generation sequencing, metagenomics, and emerging CRISPR-based diagnostics enable faster and more accurate pathogen detection and outbreak tracing. Bioinformatic tools—including genomic databases, phylogenetics, and machine-learning models—support predictive risk assessment and real-time surveillance. Preventive innovations such as bacteriophages, probiotics, antimicrobial peptides, nanotechnology-based interventions, and engineered microbes provide sustainable alternatives to chemical preservatives. Key challenges include variability across food matrices, biosafety considerations, and limited integration of multi-omics approaches into routine workflows. Overall, these emerging strategies offer improved precision and responsiveness for detecting and preventing food-borne bacterial pathogens.

Communicated by Yusuf Akhter

✉ Zaryab Shafi
shaikhzaryabshafi@gmail.com

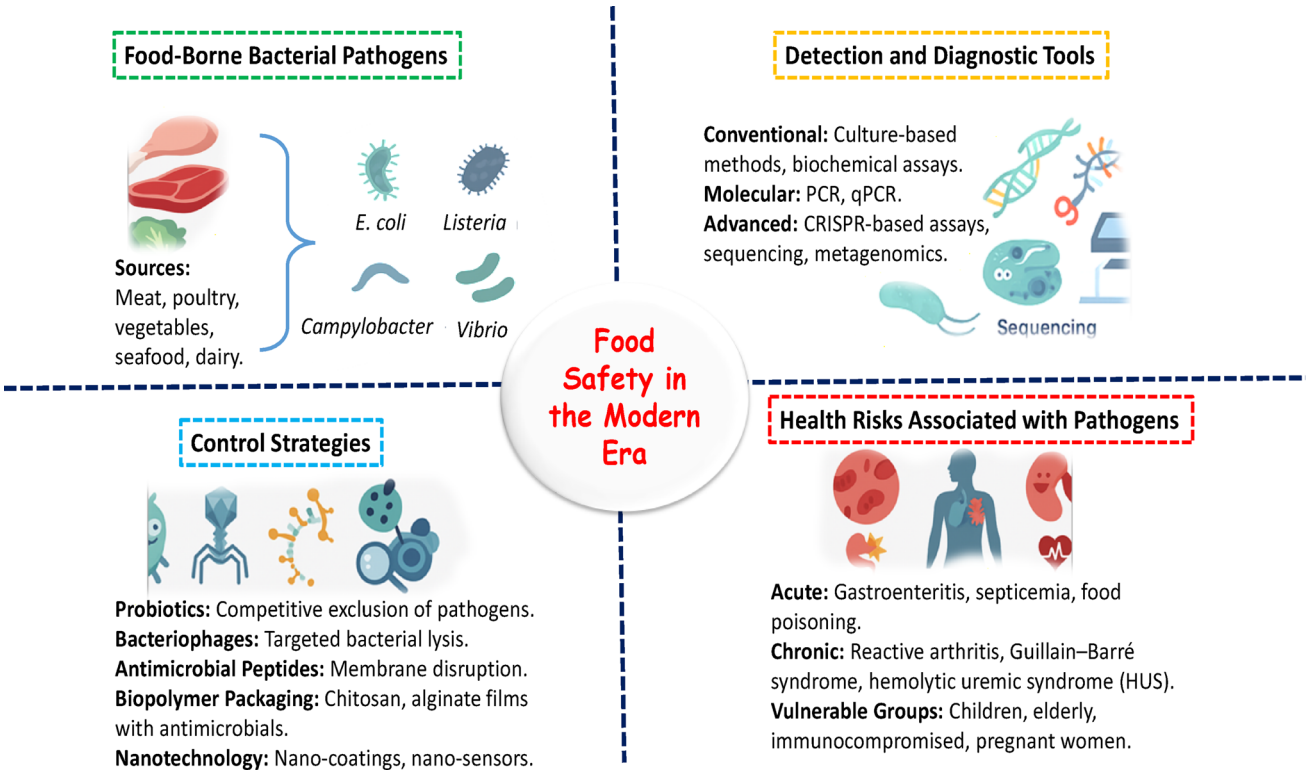
✉ Rahul Singh
Rahulsingh.jnu@gmail.com

[1] Department of Biosciences, Integral University, Lucknow, Uttar Pradesh 226026, India

[2] Marwadi University Research Center, Department of Agriculture, Faculty of Science, Marwadi University, Rajkot, Gujarat 360003, India

[3] Department of Bioengineering, Integral University, Lucknow, Uttar Pradesh 226026, India

Graphical abstract



Keywords Bacterial pathogens · CRISPR-based detection · Emerging approaches · Food safety · Metagenomics · Molecular diagnostics

Introduction

Food safety has become a critical global health concern due to the increasing complexity of food production, processing, and distribution systems (Garcia et al. 2020). The modern food supply chain spans continents, linking producers, processors, retailers, and consumers. While globalization enhances food accessibility, it also amplifies the risk of contamination and facilitates rapid international spread of food-borne pathogens (Newell et al. 2010). The World Health Organization (WHO) estimates that 600 million individuals suffer from food-borne illnesses annually, resulting in 420,000 deaths, with children under five accounting for nearly 30% of these fatalities (Almaary 2023; Bryce et al. 2005). Economic impacts are similarly substantial, including treatment costs, productivity losses, trade disruptions, and erosion of consumer trust.

Food-borne disease burden is unevenly distributed, with low- and middle-income countries disproportionately affected due to limited infrastructure, insufficient sanitation, and weak surveillance systems (Grace 2023). However, industrialized nations experience large-scale outbreaks linked to centralized production and global trade. Climate change and antimicrobial resistance further complicate risk dynamics by altering pathogen ecology and facilitating emergence of hard-to-control strains (Lio et al. 2023). Extreme weather events increase contamination risks in food and livestock systems, while antibiotic-resistant food-borne bacteria present growing management challenges (Duchenne et al. 2021).

Bacterial pathogens remain the leading cause of food-borne diseases due to their high prevalence and capacity for severe illness (Elbehiry et al. 2023). Salmonella spp. continues to be a major etiological agent of salmonellosis, often associated with poultry, eggs, and dairy products (Galán-Relaño et al. 2023). Enterohemorrhagic *Escherichia coli*, particularly O157:H7, causes bloody diarrhea and hemolytic uremic syndrome (HUS), frequently linked to undercooked beef, contaminated produce, and unsafe water sources (Werner et al. 2024). *Listeria monocytogenes*, notable for thriving under refrigeration, poses severe risks to pregnant women, neonates, and immunocompromised individuals (Luesth 2021; Murtaza et al. 2025). *Campylobacter* spp., commonly associated with undercooked poultry, is a major cause of gastroenteritis and has been linked to

Guillain–Barré syndrome (Myintzaw et al. 2023). Toxigenic *Clostridium perfringens* and *C. botulinum* also contribute significantly to food poisoning and botulism, respectively (Finnie and Uzal 2022).

Foundational control measures remain essential. Good Agricultural Practices (GAPs), Good Manufacturing Practices (GMPs), and Hazard Analysis and Critical Control Points (HACCP) form the backbone of preventive food safety by promoting hygiene, sanitation, environmental monitoring, and identification of critical risk points across the food chain. Traditional interventions such as heating, refrigeration, and proper storage are effective but increasingly challenged by antimicrobial resistance, consumer preference for minimally processed foods, and climate-driven fluctuations in pathogen survival. These constraints underscore the need for modern technologies that complement conventional practices and provide rapid, eco-friendly solutions.

Classical detection methods—including culture-based, biochemical, and immunological assays—are reliable but slow, labour-intensive, and limited in detecting viable but non-culturable (VBNC) pathogens (Kabiraz et al. 2023; Wideman et al. 2021). Molecular approaches such as PCR and ELISA improve sensitivity and specificity but remain constrained by cost, equipment requirements, and limited antigenic scope (Ashraf et al. 2025). Concurrently, antibiotic overuse in agriculture accelerates antimicrobial resistance development (Farrukh et al. 2025), and excessive reliance on chemical preservatives raises concerns regarding long-term health and environmental safety (Rathee et al. 2023). These limitations highlight the urgency for innovative diagnostic and preventive platforms.

Recent evidence (2021–2024) demonstrates that pathogens like *Salmonella*, *Listeria*, and Shiga toxin–producing *E. coli* are rapidly adapting to environmental stressors encountered during processing and storage, enhancing persistence in previously inhospitable conditions. Surveillance reports document a rise in multidrug-resistant strains associated with outbreaks, emphasizing the need for more sophisticated monitoring and integrated diagnostic frameworks (Grace 2023). Incorporating these findings situates the present review within current scientific discourse and underscores the need for predictive, technology-driven food safety systems.

Biotechnology and bioinformatics now offer transformative capabilities for pathogen detection, characterization, and control. Advances in genomics, proteomics, and metabolomics allow high-resolution analysis of virulence factors, resistance determinants, and adaptive strategies (Pérez-Llarena and Bou 2016). Whole-genome sequencing (WGS) has become a cornerstone of outbreak tracing, enabling precise identification of contamination sources. CRISPR-based diagnostics and biosensors support near real-time detection in complex food matrices. Bioinformatic pipelines facilitate interpretation of large genomic datasets, enabling temporal and spatial surveillance of pathogen evolution (Siddiqui 2024). Machine learning and artificial intelligence tools increasingly model contamination risks, simulate pathogen behavior under variable conditions, and inform targeted interventions (Towfek and Elkanzi 2024).

Unlike earlier reviews that address microbiology, biotechnology, and bioinformatics separately, this article integrates these domains within a unified systems-based framework. By linking pathogen ecology, molecular diagnostics, biocontrol strategies, and computational modeling, the review emphasizes how modern tools collectively support anticipatory rather than reactive food safety. Integrating multi-omics datasets with machine-learning models and quantitative microbial risk assessment (QMRA) enables proactive detection, early warning systems, and improved decision-making. The goal of this review is to assess how these innovations spanning WGS, metagenomics, CRISPR diagnostics, biosensors, and AI-driven surveillance can be leveraged to build scalable, cost-effective, and globally accessible food safety solutions. This synthesis aims to guide researchers, policymakers, and industry stakeholders toward more resilient, data-driven food protection systems in an increasingly interconnected world.

Microbiological insights into food-borne bacterial pathogens

Food-borne bacterial pathogens represent a diverse group of microorganisms with unique microbiological traits that allow them to persist in food chains, interact with host systems, and cause illness. Understanding their taxonomy, physiology, virulence factors, and survival mechanisms is essential for designing effective detection and control strategies.

Taxonomy, physiology, and virulence factors

The taxonomy of food-borne pathogens has been refined significantly through advances in molecular microbiology and genome sequencing. *Salmonella* spp., for example, belong to the family Enterobacteriaceae and are classified into more than 2,600 serovars based on antigenic differences. Among them, *S. enterica* serovar *Typhimurium* and *S. enterica* serovar *Enteritidis* are most frequently implicated in human infections (Mkangara 2023). Similarly, *Escherichia coli* encompasses both commensal strains and pathogenic lineages, such as enterohemorrhagic (EHEC), enterotoxigenic (ETEC), and enteropathogenic (EPEC)

types, each defined by distinct virulence factors (Naidoo and Zishiri 2025). *Listeria monocytogenes*, classified within the genus *Listeria*, is notable for its ability to thrive at refrigeration temperatures and in high-salt environments, making it a persistent threat in ready-to-eat foods (Manyi-Loh and Lues 2025). Its virulence is largely attributed to the expression of listeriolysin O (LLO), a pore-forming toxin that facilitates escape from phagosomes (Banerji et al. 2021). *Campylobacter* spp., especially *C. jejuni* and *C. coli*, are microaerophilic organisms requiring reduced oxygen conditions, and their pathogenicity involves adhesins, cyto-lethal distending toxin (CDT), and flagella-driven motility (Sadek et al. 2023). Spore-forming species such as *Clostridium perfringens* and *C. botulinum* produce potent enterotoxins and neurotoxins, respectively, which are key virulence factors linked to food poisoning and botulism (Rawson et al. 2023). These examples show that virulence factors are not uniform but pathogen-specific, often shaped by environmental pressures and genetic plasticity. Earlier studies have revealed how horizontal gene transfer contributes to the acquisition of toxin genes and antibiotic resistance, thereby enhancing pathogenic potential (Liu et al. 2022).

Pathogen–host interactions and infection mechanisms

Food-borne bacterial pathogens employ sophisticated strategies to invade host tissues, evade immune defenses, and establish infection. For instance, Salmonella uses type III secretion systems (T3SS) encoded in pathogenicity islands (SPI-1 and SPI-2) to inject effector proteins into host cells, leading to cytoskeletal rearrangements and intracellular survival (Worley 2025). Early studies demonstrated that these effector proteins facilitate bacterial uptake by non-phagocytic cells, ensuring successful colonization of the intestinal epithelium (Sansonetti 2001). *E. coli* O157:H7 adheres tightly to enterocytes using intimin, a surface protein encoded by the eae gene, forming characteristic attaching and effacing lesions (Stevens and Frankel 2015).

Shiga toxins further contribute to systemic complications such as haemolytic uremic syndrome (HUS) (Exeni et al. 2018). *L. monocytogenes* is a classic example of intracellular pathogens, relying on internalins (InlA and InlB) for cell entry, followed by actin-based motility that allows spread from cell to cell without extracellular exposure (Pizarro-Cerda and Cossart 2018). In the case of *Campylobacter*, host colonization involves flagella-mediated motility, chemotaxis, and toxin-mediated disruption of host cell signaling pathways (da Silva Bras 1998). *Clostridium botulinum*, on the other hand, exerts its pathogenicity through the release of botulinum neurotoxin, which blocks acetylcholine release at neuromuscular junctions, leading to paralysis (Rawson et al. 2023).

Survival strategies in food and environment

Food-borne bacteria exhibit remarkable adaptability, enabling them to persist in food processing environments, resist stresses, and survive under hostile conditions (Alvarez-Ordonez et al. 2015). One of the most well-studied strategies is biofilm formation, where pathogens such as *Salmonella*, *Listeria*, and *E. coli* produce extracellular polymeric substances (EPS) that develop protective niches on food surfaces and industrial equipment (Bai et al. 2021). Initial biofilm research indicated that not only does it improve survival, but also makes these communities more resistant to disinfectants and antibiotics, which makes it difficult to eradicate (Sharma et al. 2019). The other important mechanism is stress adaptation. An example is L. monocytogenes using stress response regulators such as sigmaB to endure acid, osmotic and oxidative stresses in the food environments (Wiktorczyk-Kapischke et al. 2021). Acid tolerance responses (ATR) are triggered by E. coli and Salmonella and the survivors can cross the gastric barrier (Foster 2001). On the same note, *Campylobacter* is aerotolerant even though it is microaerophilic, which allows it to persist in food handling and storage (Pokhrel et al. 2022). Spores, especially *Clostridium* spp., enhance heat, desiccation and chemical resistance. Food processing activities like cooking and canning spores can survive and be able to germinate under favourable conditions resulting into outbreaks. The research on the biology of the spores previously showed the significance of the dipicolinic acid and small acid-soluble proteins (SASPs) in the maintenance of long-term stability (Setlow et al. 2006).

Emerging and re-emerging pathogens

Although classical pathogens still occupy a central role in the agenda, there is an ever-growing number of bacteria that pose threats, as the environment, globalization, and microbial evolution drive the evolution of novel threats. *Cronobacter sakazakii* is a formerly thought-to-be-rare opportunistic pathogen that has come into the limelight because of its role in powdered infant formula contamination, as well as leading to meningitis and sepsis in infants (Chauhan et al. 2023). Likewise, *Arcobacter* spp. which are closely related to *Campylobacter* are also becoming more and more widely identified in poultry and dairy products and are implicated in gastrointestinal illness in humans. The re-emergence of pathogens is also critical, and it is commonly supported by antimicrobial resistance (AMR) (Chibwe et al. 2025). The cases of multidrug-resistant strains of *Salmonella*, *E. coli*,

and *Listeria* have been documented at a global level this fact complicates treatment and raises the severity of outbreaks (Bisola Bello et al. 2024).

Although individual pathogens differ in virulence factors, reservoirs, and transmission routes, their behavior in food environments reveals several shared patterns. Many species demonstrate the ability to persist under stress, form biofilms, and adapt to temperature fluctuations, contributing to their survival across diverse food matrices. Comparative evidence shows that pathogens such as Listeria monocytogenes and Salmonella enterica exhibit stronger resilience under cold and osmotic stress, whereas Campylobacter remains more sensitive yet highly infectious. These similarities and differences highlight the need for detection systems that account for both pathogen-specific traits and broader ecological strategies that enable persistence in modern food systems.

Recent mechanistic studies reveal that *Salmonella enterica serovar Typhimurium* adapts to antimicrobial stress through modulation of efflux pump systems such as AcrAB-TolC, enhancing survival under sublethal exposure. Likewise, *Listeria monocytogenes* demonstrates cold-shock resilience through activation of the prfA regulon, which coordinates virulence gene expression and supports persistence in refrigerated foods. These mechanistic insights illustrate the adaptive strategies that complicate detection and control effort.

Additionally, climate change is altering pathogen ecology, expanding the geographical distribution of food-borne bacteria and creating conditions for novel reservoirs and transmission routes. Earlier studies emphasized how molecular typing and whole-genome sequencing (WGS) have been crucial in identifying and tracking emerging pathogens, offering insights into their evolution and spread (Vashisht et al. 2023). Table 1 highlights not only the clinical relevance of these pathogens but also their ability to adapt through mechanisms such as biofilm formation, spore production, and stress tolerance, which complicates detection and control strategies. The infection pathways, virulence mechanisms, and associated health impacts of major food-borne bacterial pathogens are summarized schematically in Fig. 1.

Detection techniques and diagnostic tools

Conventional microbiological methods

Traditional culture-dependent assays remain foundational in food microbiology because they allow recovery of viable isolates for downstream characterization, including serotyping, antimicrobial susceptibility profiling, and whole-genome sequencing (Ahmad et al. 2024). Standard workflows typically involve selective enrichment, isolation, and phenotypic confirmation (Taskila et al. 2012). *Salmonella spp.*, for example, are enriched in Rappaport–Vassiliadis or selenite broth before plating on XLD or Hektoen agar (Neyaz et al. 2024), whereas Listeria monocytogenes is isolated using Oxford or PALCAM agar (Jamali et al. 2013). Biochemical confirmations (TSI, urease, citrate, indole tests) remain routine (Rhoden 1980), and automation systems such as API and VITEK improve standardization (Gupta and Agarwal 2024). Immunoassays—including ELISA and latex agglutination—enable rapid antigen or toxin detection, widely applied for C. botulinum neurotoxin and E. coli O157:H7 (Gurtler and Pavia 2020; Xu et al. 2019).

Despite their reliability, culture-based approaches typically require 2–7 days, lack sensitivity for low-abundance or VBNC organisms (Jackson et al. 2009), and are prone to false negatives due to competitive microflora or inhibitory matrices (Ferone et al. 2020). These limitations drive adoption of molecular and biotechnological tools while retaining culture methods as confirmatory standards (McVey et al. 2021; Rajapaksha et al. 2019).

Molecular approaches

PCR and qPCR

PCR enables detection of pathogen-specific loci within hours. Widely used markers include invA for Salmonella (Haffar and Gilbride 2010) and hlyA for *L. monocytogenes* (Liu et al. 2012). qPCR provides quantitative detection with high analytical sensitivity—detecting as few as 10–100 CFU/g E. coli O157:H7 after enrichment (Wang et al. 2007a, b)—and is now common in regulatory testing (Kralik and Ricchi 2017; Mangal et al. 2016).

RT-PCR

RT-PCR targets mRNA, offering discrimination of viable, metabolically active cells where DNA-based assays may overestimate contamination (Bustin 2022). Applications include detection of viable *L. monocytogenes* in ready-to-eat foods (Amagliani et al. 2021) and monitoring stress-induced gene expression in *Salmonella* and *E. coli* (Han et al. 2018).

Multiplex PCR

Multiplex assays reduce time and cost by simultaneously amplifying multiple targets. Assays combining invA, uidA, and hlyA enable simultaneous screening for *Salmonella*, *E. coli*, and *Listeria* in raw foods (Kim et al. 2007). Recent

Table 1 Major Food-Borne bacterial pathogens: Taxonomy, Diseases, virulence Factors, and survival strategies

Pathogen	Taxonomy (Genus, Family)	Common food sources	Major diseases (Acute/chronic)	Virulence factors	Survival strategies (Biofilm, spore, stress adaptation)	Vulnerable populations	References
Salmonella enterica	Enterobacteriaceae	Poultry, eggs, produce	Salmonellosis (gastroenteritis),	T3SS, endotoxin, adhesion proteins	Acid tolerance, biofilm on surfaces	Children, elderly	Bhunia (2018)
Escherichia coli O157:H7	Enterobacteriaceae	Beef, vegetables, milk	Hemorrhagic colitis, HUS	Shiga toxins, intimin, adhesins	Acid resistance, VBNC state	Children	Mirza (2015)
Listeria monocytogenes	Listeriaceae	Dairy, ready-to-eat meats	Listeriosis (meningitis)	LLO, internalins	Cold tolerance, biofilm	Pregnant women, neonates	Wang et al. (2021)
Campylobacter jejuni	Campylobacteraceae	Poultry, milk	Campylobacteriosis, Guillain–Barre syndrome	CDT, adhesins, motility	Aerotolerance, VBNC	General, immunocompromised	Pokhrel (2024)
Clostridium botulinum	Clostridiaceae	Canned foods, fish	Botulism	Neurotoxins (BoNTs)	Spore formation	All, especially elderly	Jarosz et al. (2022)
Cronobacter sakazakii	Enterobacteriaceae	Powdered infant formula	Neonatal meningitis, sepsis	Capsule, siderophores	Desiccation resistance, biofilm	Neonates, infants	Saad (2018)
Arcobacter butzleri	Campylobacteraceae	Poultry, dairy products	Enteritis, diarrhea	Adhesins, toxins, motility	Biofilm formation, aerotolerance	General population	Milesi (2011)
Shigella dysenteriae	Enterobacteriaceae	Contaminated water, vegetables	Dysentery, HUS	Shiga toxin, invasion plasmid antigens	Stress adaptation, VBNC	Malnourished children,	Mirza (2015)
Vibrio cholerae	Vibrionaceae	Contaminated water, seafood	Cholera (acute watery diarrhea)	Cholera toxin, TCP pili	VBNC, biofilm	Children, poor sanitation	Bhuniya (2018)
Vibrio parahaemolyticus	Vibrionaceae	Raw seafood, shellfish	Acute gastroenteritis	TDH, TRH toxins, hemolysins	Salt tolerance, VBNC	Seafood consumers	Letchumanan (2019)
Aeromonas hydrophila	Aeromonadaceae	Seafood, vegetables	Gastroenteritis, wound infections	Hemolysins, enterotoxins	Biofilm formation, stress adaptation	Immunocompromised individuals	Lee (2023)
Yersinia enterocolitica	Enterobacteriaceae	Pork, milk, untreated water	Yersiniosis (mesenteric lymphadenitis)	Invasin, YadA adhesin	Cold tolerance, biofilm	Children, elderly	Wang (2016)
Bacillus cereus	Bacillaceae	Rice, pasta, dairy	Food poisoning (emetic, diarrheal)	Enterotoxins, cereulide toxin	Spore formation, stress adaptation	All age groups	Haque et al. (2021)
Staphylococcus aureus	Staphylococcaceae	Dairy, meats, salads	Staphylococcal food poisoning	Enterotoxins, superantigens	Biofilm, toxin stability	All age groups	Ibrahim (2020a, b)
Clostridium perfringens	Clostridiaceae	Cooked meat, stews	Food poisoning (diarrheal)	Enterotoxins (CPE)	Spore formation	All age groups	Shrestha et al. (2018)
Enterococcus faecalis	Enterococcaceae	Cheese, fermented foods	Opportunistic infections, bacteremia	Aggregation substance, cytolysin	Biofilm, antibiotic resistance	Immunocompromised	Krawczyk et al. (2021)

Table 1 (continued)

Pathogen	Taxonomy (Genus, Family)	Common food sources	Major diseases (Acute/chronic)	Virulence factors	Survival strategies (Biofilm, spore, stress adaptation)	Vulnerable populations	References
Helicobacter pylori	Helicobacteraceae	Milk, contaminated water	Gastritis, gastric cancer	CagA, VacA toxins	Acid adaptation, biofilm	Adults, high-risk populations	Delgado Carreño et al. (2018)
Pseudomonas aeruginosa	Pseudomonadaceae	Meat, dairy, hospital foods	Opportunistic infections, septicemia	Elastase, exotoxin A	Biofilm, antibiotic resistance	Hospitalized patients	Urgancı et al. (2022)
Edwardsiella tarda	Enterobacteriaceae	Fish, aquatic foods	Gastroenteritis, septicemia	Hemolysins, siderophores	Biofilm, VBNC	General population	Michael and Abbott (1993)
Brucella spp.	Brucellaceae	Unpasteurized dairy, meat	Brucellosis (systemic infection)	Lipopolysaccharides, urease	Intracellular survival	Rural and farming populations	Hasan et al. (2021)

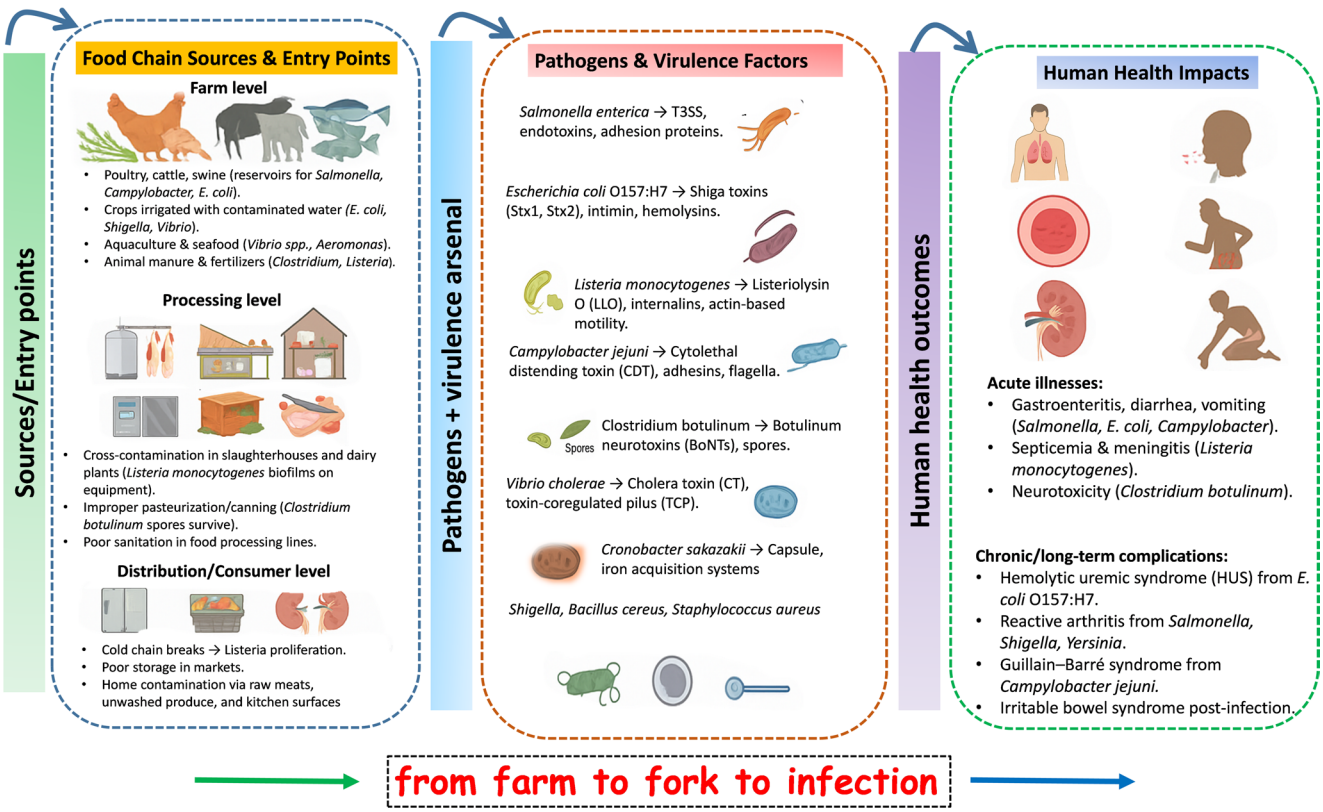


Fig. 1 Infection pathways of food-borne bacterial pathogens, highlighting sources, virulence factors, and associated health impacts from acute gastroenteritis to chronic complications, with global drivers such as antimicrobial resistance and climate change

panels also detect AMR genes, improving surveillance of multidrug-resistant strains (Dung et al. 2024).

DNA microarrays

Microarrays allow high-throughput hybridization-based detection of pathogens, virulence factors, and resistance genes (Lopez-Campos et al. 2012). Early platforms simultaneously identified *Salmonella*, *Listeria*, and *E. coli* O157:H7 (Call 2005). Although cost and technical complexity remain barriers, integration with bioinformatics and NGS has expanded their utility (Wolff et al. 2021; Mishra et al. 2024). Molecular tools considerably shorten diagnostic timelines and enhance accuracy but are increasingly

complemented—and in some cases replaced—by next-generation genomic approaches.

Approaches for differentiating viable and dead cells in modern detection systems

A major limitation of contemporary molecular and sequencing-based detection platforms is their inability to reliably distinguish viable bacteria from dead or inactivated cells, which can result in overestimation of contamination levels. Several emerging strategies aim to overcome this challenge. Viability PCR (vPCR) incorporates DNA-intercalating dyes such as propidium monoazide (PMA) or ethidium monoazide (EMA), which selectively inhibit amplification of DNA from membrane-compromised cells, thereby enriching signals derived from viable organisms (Li et al. 2017). RNA-based assays—including RT-PCR and RT-qPCR—target short-lived mRNA transcripts that reflect active metabolism, providing improved specificity for detecting living cells (Bustin 2022). Flow cytometry coupled with fluorescent viability stains allows rapid, single-cell discrimination and has been widely applied to assess viable but non-culturable (VBNC) states in foodborne pathogens (Oliver 2010). Additional complementary tools such as metabolomic fingerprinting and ATP bioluminescence offer real-time insights into microbial physiological activity, supporting more accurate viability assessments in complex food matrices (Venkateswaran et al. 2023). Continued refinement and integration of these approaches into molecular workflows are essential for improving accuracy in pathogen surveillance, particularly where VBNC cells pose a significant risk.

Advanced biotechnological systems

CRISPR-based diagnostics

CRISPR–Cas platforms such as SHERLOCK and DETECTR leverage sequence-specific cleavage to produce rapid, ultra-sensitive detection signals (Ganger et al. 2017; Singh et al. 2022). SHERLOCK has detected *E. coli* O157:H7 at femtomolar levels (Gootenberg et al. 2017), while DETECTR has been applied to *L. monocytogenes* (De et al. 2023). Coupling with isothermal amplification (RPA, LAMP) enables field-deployable formats that identify *Salmonella* in milk within an hour (Yin et al. 2023; Patel et al. 2024).

Next-generation sequencing

NGS and whole-genome sequencing (WGS) provide comprehensive resolution of pathogen genomes, supporting source attribution, virulence profiling, and AMR surveillance. WGS has guided outbreak investigations, such as tracing *L. monocytogenes* contamination in frozen vegetables (Madad et al. 2023) and differentiating Salmonella strains in poultry outbreaks (Kipper et al. 2021). Platforms including Illumina, Ion Torrent, and Oxford Nanopore broaden analytical capabilities for plasmids and mobile elements (Hu et al. 2021; Yaqub et al. 2024). Global networks such as GenomeTrakr and PulseNet facilitate international surveillance (WHO 2023).

Metagenomics

Shotgun metagenomics enables culture-independent detection of entire microbial communities, revealing pathogens present at low levels or in VBNC states (Ramamurthy et al. 2014). Applications include identifying *Campylobacter* in poultry-processing environments (Soro et al. 2020) and uncovering hidden diversity in dairy products. Challenges include high sequencing costs and difficulty distinguishing live from dead cells, though advances in computational pipelines are improving feasibility (Chen et al. 2021; Singh and Gouda 2024).

Bioinformatic and biomathematical applications

Genomic databases

Extensive genomic repositories—GenBank, ENA, DDBJ—enable rapid identification and comparative analyses of food-borne pathogens (Okido et al. 2022). Specialized systems like GenomeTrakr and PulseNet integrate genomic and epidemiological data, supporting outbreak tracing for *Salmonella*, *L. monocytogenes*, and *E. coli* (Brown et al. 2017; Gensheimer et al. 2025; Ottesen et al. 2020).

Phylogenetic analysis and outbreak tracing

High-resolution approaches such as SNP analysis and wgMLST reconstruct transmission pathways with precision surpassing PFGE (Blanc et al. 2020). WGS-based phylogeny has linked poultry-derived Salmonella isolates to patient cases (Allard et al. 2012) and identified persistent L. monocytogenes strains in food-processing facilities (van de Merwe et al. 2024).

Machine learning and predictive surveillance

Machine learning models analyze genomic, environmental, and production data to forecast contamination risks (Soroushianfar et al. 2025). Examples include predicting AMR in Salmonella and E. coli using genomic inputs (Nguyen et al. 2019) and estimating Listeria persistence

in processing plants using facility-level metadata (Gupta and Adhikari 2022). ML-based predictive microbiology improves simulation of pathogen responses to fluctuating temperature, pH, and storage conditions (Fernandez et al. 2011; Khoiri and Moussango 2024; Kusuma et al. 2024)

Integrating predictive microbiology and bioinformatics

Predictive microbiology models describe microbial growth and survival under varying environmental conditions (Baranyi and Roberts 1994). Databases such as ComBase and PMP support quantitative microbial risk assessment (QMRA), enabling scenario analysis for processing and storage variables (Ross et al. 2009). Coupling these models with genomic and metagenomic data—via platforms like Galaxy, MEGA, and MiGA—strengthens understanding of pathogen adaptation mechanisms. Machine learning enhances these frameworks by capturing nonlinear interactions in complex food matrices (Xiao et al. 2025). When integrated with genomic surveillance systems (GenomeTrakr, PulseNet), predictive tools enable near–real-time forecasting of outbreak clusters and contamination hotspots. Machine-learning models such as Random Forest and XGBoost are increasingly applied to microbial risk prediction, with XGBoost often outperforming traditional tree-based ensembles on large, multidimensional genomic datasets (Chen and Guestrin 2016; Liang et al. 2021). Typical WGS-to-prediction pipelines integrate sequence quality filtering, genome assembly, annotation, and extraction of virulence or antimicrobial resistance (AMR) determinants, which are then used as input features for ML classification or regression models (Zhou et al. 2020; Green et al. 2022). These structured workflows enhance the precision, interpretability, and predictive capacity of modern pathogen surveillance systems by linking genomic signatures with contamination risk or outbreak likelihood.

Each detection strategy contributes uniquely to modern food safety surveillance. Culture-based methods remain essential for viability confirmation, PCR-based assays provide rapid targeted detection, and advanced platforms such as CRISPR, NGS, and metagenomics offer deep genomic insight. Bioinformatics and predictive analytics unify these approaches, enabling proactive, data-driven food safety management. Table 2; Fig. 2 summarize the comparative characteristics and chronological evolution of these methods.

Biotechnological and engineering approaches for control

In recent decades, biotechnology and engineering have offered novel solutions that move beyond chemical preservatives and antibiotics, aligning with consumer demand for natural, sustainable, and safe interventions. Prominent approaches include the use of probiotics and bacteriophages, antimicrobial peptides, nanotechnology-based interventions, genetic engineering of beneficial microbes, and biopolymer-based food packaging.

Probiotics and bacteriophages in food safety

Probiotics are beneficial microorganisms, primarily lactic acid bacteria (LAB), that can inhibit pathogenic bacteria through competitive exclusion, production of antimicrobial metabolites, and modulation of gut microbiota (Anjana and Tiwari 2022). Early studies demonstrated that *Lactobacillus rhamnosus* reduced adhesion of *E. coli* O157:H7 to intestinal cells, highlighting its protective role (Li et al. 2020). Similarly, *L. plantarum* and *Lactobacillus casei* have been shown to inhibit *Listeria monocytogenes* growth in dairy products by producing organic acids and bacteriocins (Pisano et al. 2022). Bacteriophages (viruses that specifically infect bacteria) represent another promising tool. They offer high specificity against pathogens without disturbing beneficial microflora (Lopetuso et al. 2019). Phage-based products, such as ListShield™ and EcoShield™, have been approved for use in controlling *Listeria monocytogenes* and *E. coli* O157:H7 in ready-to-eat foods (Vikram et al. 2020). An early application by Higgins et al. (2005) showed that phage treatment reduced *Salmonella* colonization in poultry by several log units. Phage cocktails are particularly valuable in addressing the emergence of phage-resistant bacterial mutants, a limitation of single-phage therapy (Pal et al. 2024). Together, probiotics and bacteriophages provide eco-friendly alternatives to antibiotics, with potential applications both in food preservation and in enhancing host resistance to food-borne infections. Recent mechanistic studies demonstrate that phage–biofilm co-evolution significantly influences control efficacy, as bacteriophages adapt to penetrate extracellular polymeric structures while biofilms simultaneously acquire resistance traits such as receptor masking (Chan et al. 2016; Abedon 2017). Probiotic strains also exhibit targeted antagonism through the production of bacteriocins, including nisin and pediocin, which disrupt pathogen cell membranes and inhibit quorum-sensing pathways (Cotter et al. 2013; Chikindas et al. 2018). Comparative antimicrobial assessments show that phage application can reduce Salmonella and Listeria counts by approximately 2–4 log CFU under controlled conditions

Table 2 Conventional, molecular, and advanced detection methods for food-borne pathogens

Detection Method	Principle/Target	Pathogens Detected	Sensitivity/LOD	Time to Result	Advantages	Limitations	References
Culture-based	Growth on selective/differential media	*Salmonella*, *Listeria*, *E. coli*	Moderate	2–7 days	Gold standard, isolates obtained	Slow, misses VBNC	Malabadi et al. (2024)
Biochemical assays (API, VITEK)	Enzyme activity, sugar fermentation	Enterobacteriaceae	Moderate	1–2 days	Simple, standardized	False positives/negatives	Abbas and Radhi (2016)
PCR/qPCR	DNA amplification of virulence genes	*Salmonella*, *Listeria*, *E. coli* O157:H7	High (10–100 CFU)	Few hours	High sensitivity & specificity	Susceptible to matrix inhibitors	Garrido-Maestu et al. (2015)
RT-PCR	RNA transcripts detection	*Viable Salmonella*, *Listeria*	Very high	Few hours	Detects live pathogens	Expensive, complex	Ye et al. (2012)
Multiplex PCR	Multiple primers for multi-target amplification	*Salmonella*, *E. coli*, *Listeria*	High	Hours	Multi-pathogen detection	Cross-reactivity issues	Xu et al. (2016)
DNA Microarrays	Hybridization with probes	Multiple bacterial species	High	1–2 days	Large-scale profiling	Costly, requires prior sequence knowledge	Wang et al. (2007a, b)
NGS (WGS)	Whole-genome sequencing	All food-borne pathogens	Very high	1–2 days	Strain-level resolution, outbreak tracing	High cost, bioinformatics needed	Oniciuc et al. (2018)
Metagenomics	Shotgun sequencing of all DNA	Mixed microbial communities	High	1–3 days	Detects unculturable pathogens	Expensive, complex analysis	Kergourlay et al. (2015)
CRISPR-based assays	Cas12/13 collateral cleavage	*Salmonella*, *E. coli*, *Listeria*	Extremely high	< 1 h	Portable, real-time	Still emerging technology	Sahel et al. (2024)
Loop-mediated Isothermal Amplification (LAMP)	DNA amplification at constant temperature	*Salmonella*, *Listeria*, *Campylobacter*	High (10 CFU)	30–60 min	Rapid, does not require thermal cycler	Primer design critical, non-specific amplification	Kreitlow et al. (2021)
Immunoassays (ELISA, lateral flow)	Antibody-antigen binding	*E. coli*, *Salmonella*, *Listeria*	Moderate to high	1–4 h	Inexpensive, widely used	May need enrichment, cross-reactivity	Fogaça et al. (2021)
Biosensors (electrochemical, optical)	Signal changes upon pathogen binding	*Salmonella*, *Listeria*, *E. coli*, *Vibrio*	High (single-cell level possible)	Minutes to 2 h	Portable, sensitive	Expensive, device calibration required	Vizzini et al. (2019)
MALDI-TOF Mass Spectrometry	Protein/peptide mass fingerprinting	*Listeria*, *Salmonella*, *E. coli*	High	Minutes to hours	Rapid, accurate identification	Database-dependent, requires isolates	Calo-Mata et al. (2016)
Isothermal RPA	DNA amplification at low temperatures	*E. coli*, *Salmonella*	High	20–40 min	Works at low constant temperatures	Sensitive to contamination	Li et al. (2019)
Fluorescence in situ Hybridization	Fluorescent probes hybridizing to rRNA	*Listeria*, *Salmonella*	Moderate	Few hours	Visual confirmation of cells	Time-consuming sample prep	Almeida et al. (2010)
Microfluidics-based detection	Miniaturized channels for pathogen analysis	Multiple bacterial pathogens	High	1–3 h	Miniaturized, high throughput	Expensive, requires microfabrication	Hussain et al. (2024)
Lab-on-a-chip systems	Integrated chip combining multiple assays	Multiple pathogens simultaneously	High	1–2 h	Combines detection steps	Costly, needs skilled operators	Yoon and Kim (2012)
Nanopore seq.	Single molecule sequencing	food-borne pathogens	Very high	Hours	Long reads, no amp.	Error-prone, costsly	Zhou et al. (2022)
SPR sensors	Resonance signal shifts due to binding	*Listeria*, *Salmonella*, *Vibrio*	High	Minutes	Real-time monitoring	Requires advanced equipment	Raghu and Kumar (2020)

Table 2 (continued)

Detection Method	Principle/Target	Pathogens Detected	Sensitivity/LOD	Time to Result	Advantages	Limitations	References
Digital PCR	Partitioned DNA amplification for precise quantification	*Salmonella*, *E. coli*	Extremely high	Hours	Precise quantification of low-abundance targets	Expensive, requires special devices	Kong et al. (2022)

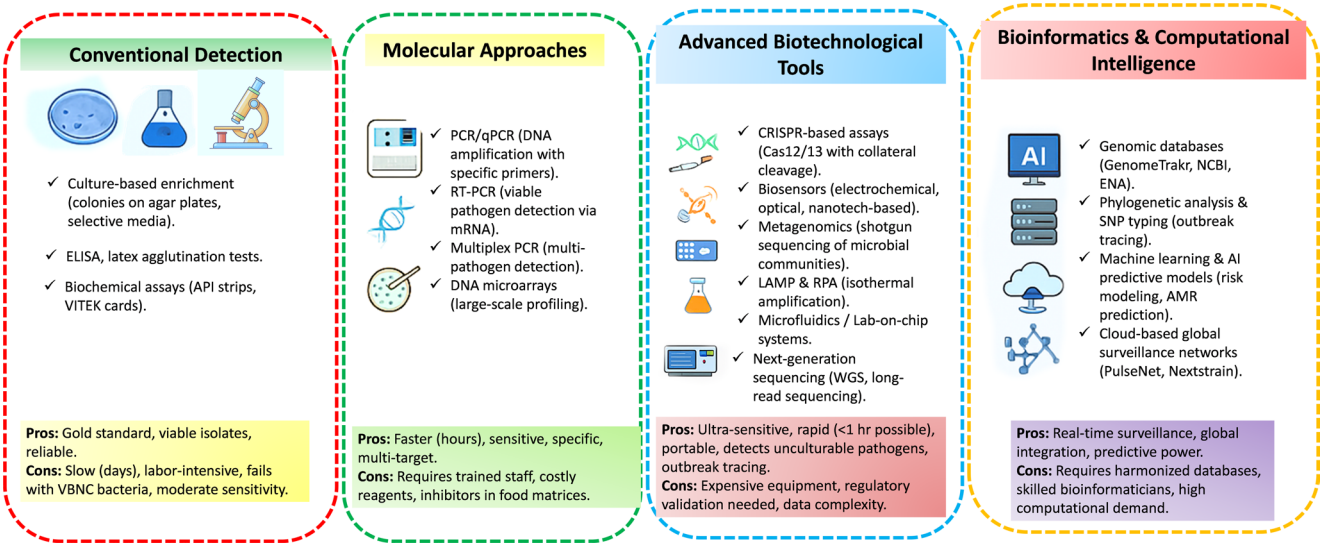


Fig. 2 Evolution of pathogen detection from conventional and molecular methods to advanced biotechnological and bioinformatic tools, enabling rapid, high-resolution surveillance

(Viazis et al. 2011; Sillankorva et al. 2012), while bacteriocin-rich probiotic formulations and antimicrobial peptides often achieve MIC values in the low µg/mL range against major food-borne pathogens (Galvez et al. 2007; Yang et al. 2014). These mechanistic insights highlight how biological interactions shape the effectiveness of emerging control strategies.

Antimicrobial peptides and engineered bacteriocins

Antimicrobial peptides (AMPs) are small, naturally occurring molecules produced by bacteria, fungi, and plants that disrupt microbial cell membranes or interfere with essential cellular processes. Nisin, produced by *Lactococcus lactis*, is one of the best-studied bacteriocins and has been used commercially as a food preservative since the 1960s (Ghosh et al. 2021). Earlier research showed that nisin effectively inhibits *Clostridium botulinum* spores in canned foods (Mazzotta et al. 1997). Modern biotechnology has expanded the scope of AMPs through engineering of bacteriocins for enhanced activity, stability, and spectrum. For example, engineered derivatives of nisin have shown stronger inhibitory effects against multidrug-resistant *Staphylococcus aureus* (Zhao and Kuipers 2021). Similarly, pediocin produced by *Pediococcus acidilactici* has been applied in meat preservation, inhibiting *Listeria monocytogenes* (Nieto-Lozano et al. 2006). The combination of AMPs with other hurdles, such as mild heat or high-pressure processing, further enhances their effectiveness. This synergistic approach has been demonstrated in dairy, meat, and vegetable systems. Engineered bacteriocins are now being explored as precision antimicrobials that can selectively target pathogens while preserving beneficial microbiota.

Nanotechnology-based interventions

Nanotechnology offers innovative solutions in food safety through nano-sensors, nano-coatings, and nano-carriers. Nano-sensors provide rapid, sensitive detection of pathogens and toxins in food systems (Mahajan et al. 2025). For example, gold nanoparticle-based biosensors have been used to detect *Salmonella* spp. in chicken meat within minutes (Ghazy et al. 2024). Similarly, carbon nanotube-based sensors have shown high sensitivity in detecting *Listeria* contamination. Antimicrobial surfaces can be formed by nanoparticles that are included in packaging materials. Polymer films have also been incorporated with silver nanoparticles (AgNPs), which have an excellent antibacterial effect

against bacteria on fresh produce and meat (Kraśniewska et al. 2020). Titanium dioxide and zinc oxide nanoparticles are also antimicrobial agents based on the reactive oxygen species (ROS) formation (Venkatasubbu et al. 2016). Nanotechnology provides the opportunity to release essential oils and bacteriocins in a controlled way. Research revealed that oregano oil encapsulated in chitosan nanoparticles enhanced its effect as an antimicrobial agent in minced beef contaminated with *E. coli* O157:H7 (Hadian et al. 2017).

Genetic engineering of beneficial microbes for pathogen inhibition

Genetic engineering has provided avenue to expand the antimicrobial potential of useful microbes used in food systems. Engineered microbes can also increase the levels of antimicrobials or new compounds by introducing new metabolic pathways or improving on existing ones (Lee et al. 2009). An example is to modify recombinant *Lactococcus lactis* strains that have enhanced the production of nisin, which is better at inhibiting Listeria monocytogenes (Ni et al. 2017). Alternatives involve the expression of non-host heterologous bacteriocins or enzymes to destroy the cell walls of pathogens through engineering of LAB. Cotter et al. (2005) found in a study that genetically modified *Lactobacillus* strains had a higher production of enhanced bacteriocin with prolonged action against gram-negative pathogens. In addition, engineered probiotics are able to provide protective molecules directly into the gastrointestinal tract. In particular, *E. coli* Nissle 1917 has been engineered to produce antimicrobial peptide onto enteric pathogens (Geldart et al. 2018). These strategies enhance not only food preservation, but also decrease the colonization risk in consumers. Recent advances in engineered probiotics have also strengthened biological strategies for controlling foodborne pathogens. Prof. Matthew Chang and his team at NUS, Singapore, have developed programmable *E. coli* Nissle strains capable of sensing pathogen signals and producing targeted antimicrobial responses (Ng et al. 2013). Their work includes engineered probiotics that release bacteriocins or neutralizing molecules only upon pathogen detection, minimizing disruption to native gut microbiota (Hwang et al. 2017). More recent efforts demonstrate living therapeutics that degrade virulence factors and modulate host–pathogen interactions, offering promising preventive tools against gastrointestinal infections (Ho et al. 2021).

Biopolymer-based food packaging for pathogen control

Biopolymer-based packaging materials provide eco-friendly alternatives to synthetic plastics while offering active antimicrobial functionality. Polysaccharides (chitosan, alginate), proteins (gelatin, whey protein), and lipids are commonly used as biopolymeric matrices (George and Abraham 2006). Chitosan, derived from chitin, has inherent antimicrobial properties against bacteria and fungi. Studies have shown that chitosan films incorporated with essential oils inhibit *Salmonella* and *E. coli* O157:H7 on fresh vegetables (El-Zehery et al. 2022). Similarly, alginate-based coatings enriched with plant extracts have been used to extend the shelf life of fruits while suppressing bacterial growth (Ghosh et al. 2024). Silver nanoparticle-incorporated starch films reduced *Listeria* counts on cheese during storage (Paidari et al. 2024).

Across biotechnological interventions, a clear pattern emerges: successful control strategies often pair targeted biological mechanisms with broader ecological considerations. Probiotics and bacteriophages offer precision suppression of pathogens, yet their performance varies with food matrix composition. Antimicrobial peptides and nanomaterials provide versatile applications but require careful assessment of safety and stability. Biopolymer packaging supports sustained pathogen inhibition while also enhancing shelf life. Comparing these tools reveals that no single approach is universally effective; instead, layered interventions that combine microbial, chemical, and material-based solutions provide the most robust and adaptable control framework.

Biotechnological and engineering approaches are redefining pathogen control strategies in food systems. Probiotics and bacteriophages offer natural biological control, while antimicrobial peptides and engineered bacteriocins provide precision-targeted interventions. A consolidated view of biotechnological and engineering strategies for pathogen control, including probiotics, bacteriophages, antimicrobial peptides, nanotechnology, engineered microbes, and biopolymer-based packaging, is provided in Table 3. The mechanistic basis of probiotics, phages, antimicrobial peptides, nanotechnology, engineered microbes, and biopolymer packaging in food-borne pathogen control is depicted in Fig. 3.

Health risks and preventive strategies for food-borne bacterial pathogens

Food-borne bacterial pathogens continue to pose serious public health challenges worldwide, contributing to illnesses that range from mild gastroenteritis to life-threatening systemic infections. Their impact extends beyond acute disease, disproportionately affecting vulnerable populations and generating substantial economic burdens.

Table 3 Biotechnological and engineering approaches for pathogen control in food systems

Approach	Mechanism of action	Target pathogens	Applications in food	Advantages	Limitations/ challenges
Probiotics	Competitive exclusion, acid/bacteriocin	*Salmonella*, *E. coli*, *Listeria*	Dairy, fermented foods, poultry	Natural, safe, gut microbiota modulation	Variable efficacy, strain-specific
Bacteriophages	Lytic infection of bacteria	*Salmonella*, *E. coli* O157:H7, *Listeria*	Ready-to-eat foods, poultry	Highly specific, natural	Resistance may develop
Antimicrobial peptides (Nisin, Pediocin)	Pore formation, cell wall disruption	*Listeria*, *Clostridium*	Dairy, meats, canned foods	Safe, GRAS status	Narrow spectrum, cost
Engineered bacteriocins	Modified AMPs with enhanced activity	*MDR pathogens*	Meat, dairy, bio-preservatives	High potency, specificity	Regulatory approval needed
Nanotechnology (nano-coatings, sensors)	Antimicrobial activity (ROS, ion release), rapid detection	*Salmonella*, *Listeria*, *E. coli*	Packaging, surface coatings, biosensors	Multi-functional, real-time detection	Safety & toxicity concerns
Genetic engineering of beneficial microbes	Enhanced bacteriocin/ enzyme production	*Pathogens* in dairy/ meats	Fermented foods, probiotics	Targeted control	Ethical/regulatory issues
Biopolymer(Chitosan, Alginate)	Antimicrobial coatings, controlled release	*Salmonella*, *E. coli*, *Listeria*	Fruits, vegetables, dairy, meats	Biodegradable, eco-friendly	Shelf-life limitations
Essential oil-loaded nanoparticles	Slow release of antimicrobial essential oils	*E. coli*, *Salmonella*, *Listeria*	Meat, dairy, fresh produce	Improved stability and delivery of essential oils	Cost of nanoparticle formulation
Cold plasma treatment	Microbial inactivation via reactive species	*Salmonella*, *Listeria*, *E. coli*, *Campylobacter*	Surface decontamination of produce, meats	Non-thermal, chemical-free	Limited penetration, expensive
High-pressure processing (HPP)	Cell membrane disruption under high pressure	*Listeria*, *E. coli*, *Salmonella*	Packaged meats, juices, dairy	Maintains food quality, non-thermal	Cost, equipment intensive
Ozone-based decontamination	Oxidative stress-induced microbial inactivation	*Salmonella*, *E. coli*, *Listeria*	Fresh produce, grains, meat	Effective broad-spectrum method	Equipment costs, safety concerns
Edible coatings with plant extracts	Barrier function + release of bioactive compounds	*Salmonella*, *Listeria*, *fungi*	Fruits, vegetables, meat products	Edible, consumer-friendly	Limited scalability, variable efficacy
Synbiotics (probiotic + prebiotic)	Gut microbiota modulation and pathogen inhibition	*E. coli*, *Salmonella*, *Clostridium*	Dairy, infant formulas	Synergistic effect of probiotics and prebiotics	Cost, formulation challenges
RNA interference (RNAi) technology	Silencing pathogen virulence genes	*Listeria*, *Salmonella*	Genetically engineered crops and food systems	Targets virulence without killing beneficial microbes	Regulatory hurdles, delivery challenges
Photodynamic inactivation (PDI)	Photosensitizers + light generating ROS	*Listeria*, *E. coli*, *Salmonella*	Fresh produce, juices, dairy	Eco-friendly, non-thermal	Requires light source, penetration limits
Magnetic NP-based pathogen removal	Magnetic separation of pathogens	*E. coli*, *Salmonella*	Beverages, dairy, meats	Rapid removal of pathogens	Cost, recovery efficiency

Understanding these risks, alongside effective mitigation strategies, is essential for strengthening global food safety frameworks.

Acute and chronic health effects

A wide range of pathogens cause acute gastrointestinal symptoms such as diarrhoea, fever, abdominal cramps, and nausea. *Salmonella enterica* remains one of the most common causes of food-borne gastroenteritis (Pal et al. 2015), while *Campylobacter jejuni* is a leading contributor to enteric infections in both developed and developing regions (Kaakoush et al. 2015). Some pathogens cause more severe complications: Shiga toxin–producing E. coli O157:H7 may lead to hemorrhagic colitis and haemolytic uremic syndrome (HUS), particularly in children (Bruyand et al. 2018); *Listeria monocytogenes* can progress to septicaemia or meningitis, especially in neonates and immunocompromised individuals (Velanti et al. 2021); and *Clostridium botulinum* produces neurotoxins that can result in fatal botulism (Rao 2021). Long-term sequelae such as reactive arthritis following *Salmonella*, *Shigella*, or *Yersinia* infection, and post-infectious irritable bowel syndrome, have also been documented (Connor 2016).

Vulnerable populations and disproportionate risks

Certain demographic groups experience heightened susceptibility due to physiological or immunological factors. Children are particularly vulnerable because of immature immune defenses (Casanova 2015). Severe outbreaks of *Cronobacter sakazakii* linked to powdered infant formula

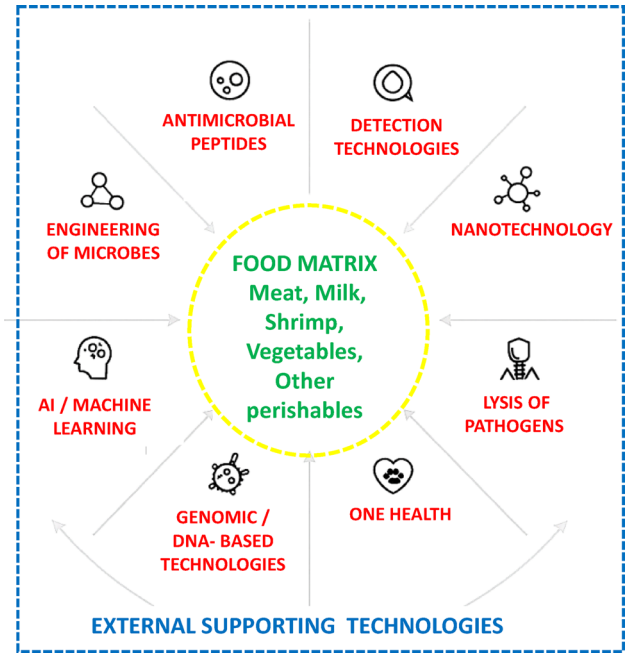


Fig. 3 Concentric schematic illustrating core microbial inhibition processes within food matrices and the external supporting technologies that enhance detection, control, and overall food safety

have resulted in neonatal meningitis and high mortality rates (Henry and Fouladkhah 2019). Older adults also face elevated risks due to weakened immunity and comorbidities, with *Listeria monocytogenes* frequently associated with hospitalization in this group (Schuchat and Broome 2005). Immunocompromised individuals—including patients undergoing chemotherapy or receiving immunosuppressive treatment—are prone to opportunistic infections such as those caused by Aeromonas spp. (Janda and Abbott 1999). Pregnant women represent another vulnerable category, as *Listeria monocytogenes* can cross the placental barrier and cause miscarriage or neonatal infection (Vázquez-Boland et al. 2017). These patterns underscore the importance of targeted guidelines for high-risk foods such as unpasteurized dairy, raw sprouts, and ready-to-eat meat products.

Economic and societal burdens

Food-borne illnesses impose substantial global economic losses due to healthcare costs, productivity reductions, legal liabilities, and disruptions in food trade. In the United States alone, the annual cost of food-borne diseases exceeds $15 billion (Hoffmann et al. 2015). Low- and middle-income countries experience productivity losses totaling approximately $95 billion per year as a result of unsafe food (Grace 2015). Large-scale recalls triggered by bacterial contamination further contribute to financial losses and erode public confidence in food systems. Broader societal consequences include food insecurity and reduced market stability, particularly in regions where safe alternatives are limited (Unnevehr 2022). Cost–benefit analyses consistently show that preventive strategies such as HACCP yield greater economic advantages compared to post-outbreak interventions (Makwavarara 2018). Decade-wise epidemiological patterns further illustrate the persistent burden of major food-borne pathogens. Global surveillance data show that Salmonella infections have remained among the highest contributors to food-borne illness over the past 20 years, with only marginal decline despite improved monitoring (Havelaar et al. 2015; Kirk et al. 2015). Campylobacter prevalence continues to rise in many regions, now surpassing *Salmonella* in several high-income countries according to long-term EFSA and CDC trend reports (EFSA & ECDC 2023; CDC 2022). Reports of *Listeria monocytogenes* have remained relatively stable but show increased severity in elderly and immunocompromised groups (Swaminathan and Gerner-Smidt 2007; Silk et al. 2013). *Shiga t*oxin–producing *E. coli* infections demonstrate periodic spikes linked to large outbreaks rather than gradual reduction, as reflected in WHO and CDC outbreak analyses (WHO 2018; Heiman et al. 2015). These decade-level trends reinforce that the global burden remains substantial and underscore the need for enhanced surveillance and proactive detection systems.

Core preventive and precautionary strategies

Preventing food-borne bacterial diseases requires coordinated farm-to-fork approaches that integrate agricultural, industrial, consumer-level, and regulatory measures.

Good agricultural and manufacturing practices (GAPs and GMPs)

GAPs minimize contamination at the production level through clean irrigation water, manure management, and hygiene practices—approaches strengthened following *E. coli* O157:H7 outbreaks linked to leafy greens (Viazis et al. 2025). GMPs extend these principles to processing environments, where hygienic design, sanitation routines, and personnel training significantly reduce contamination risks, including *Listeria monocytogenes* in ready-to-eat foods (Luber et al. 2011). Together, these practices form the foundation of modern food safety systems (Iranloye and Okonkwo 2023).

Hazard analysis and critical control points (HACCP)

HACCP provides a structured system for identifying and controlling potential hazards in food production (Ibrahim 2020a, b). As a globally recognized standard (Radu et al. 2023), HACCP has reduced contamination incidents in the

seafood and dairy industries, particularly those involving *Vibrio*, *Salmonella*, and *Listeria* (Tzouros and Arvanitoyannis 2000; Chon et al. 2021).

Cold chain integrity and storage practices

Maintaining appropriate temperatures inhibits bacterial growth. Pathogens like *Salmonella*, *E. coli*, and *Campylobacter* proliferate rapidly under ambient conditions (Solow et al. 2003), while breaches in cold chain systems correlate strongly with outbreaks (Pedro et al. 2023). Pathogens such as Listeria monocytogenes can grow even at refrigeration temperatures, emphasizing the need for rigorous monitoring (Leong et al. 2016).

Consumer-level hygiene and food handling

Cross-contamination, improper thawing, and inadequate cooking remain major contributors to household-level food-borne illness. Public health campaigns focused on the principles of "clean, separate, cook, and chill" have effectively reduced outbreak incidence (Nossier 2013). Proper cooking (e.g., > 74 °C for poultry) and good hand hygiene can reduce up to 40% of food-borne cases (Gautam 2015).

Regulatory frameworks and policy measures

Regulatory bodies—including FDA, EFSA, and FSSAI—set microbiological standards, enforce HACCP, and regulate antimicrobial use in agriculture (Jha and Singh 2025). For example, the EU ban on antibiotic growth promoters in 2006 helped decrease resistant *Enterococcus* and *Salmonella* strains (EMA 2017). Codex Alimentarius standards support international harmonization (Lee et al. 2021). National systems for recalls, surveillance, and risk communication further strengthen food safety, alongside investments in infrastructure and workforce training (Pinstrup-Andersen and Watson 2011).

Integrated perspective

A comprehensive, multi-layered strategy—spanning GAPs, GMPs, HACCP, cold chain management, consumer hygiene, and regulatory actions—forms a robust defense against food-borne pathogens. When applied consistently across the entire food system, these measures significantly reduce contamination risks and lower the global burden of food-borne illness.

Challenges and limitations

Despite significant advancements in biotechnological and bioinformatic tools for food safety, several challenges continue to limit their widespread application. These limitations can be broadly categorized as follows:

Variability in food matrices and detection inconsistencies

The heterogeneous nature of food matrices remains a major obstacle to accurate pathogen detection. Physical, chemical, and microbial complexity—ranging from high-fat dairy products to leafy vegetables—can contribute to inconsistent results (Bergwerff and Debast 2021). Matrix inhibitors may interfere with PCR amplification, while enrichment steps may fail to recover pathogens that are present in low numbers or in a viable but non-culturable (VBNC) state (Wilson 2003). These challenges can lead to false negatives, delaying outbreak response.

Diagnostic ambiguities and risk of false results

False positives and false negatives pose significant concerns in both molecular and biosensor-based detection platforms (Ho et al. 2012). Cross-reactivity among closely related species, contamination during sample preparation, and the inability to detect sub-lethally injured bacteria may compromise diagnostic accuracy. Such ambiguities may result in either undetected risks or unnecessary product recalls, both of which have serious health and economic consequences.

Biosafety, ethical considerations, and ecological risks

Innovative control methods such as bacteriophage therapy and genetically engineered microbes show strong potential but raise biosafety and ecological concerns. Issues related to horizontal gene transfer, unintended environmental persistence, and long-term safety remain under investigation (Colavecchio and Goodridge 2018). Similarly, the use of nanomaterials in packaging has sparked debate regarding potential toxicity and environmental accumulation, highlighting the need for rigorous risk assessment prior to commercial adoption (Lacourt et al. 2024).

Scalability and feasibility in low-resource settings

Advanced technologies such as next-generation sequencing, metagenomics, and CRISPR-based diagnostics require substantial financial investment, robust infrastructure, and skilled personnel. In many low- and middle-income

regions—where the burden of food-borne illness is highest—such resources are limited, creating a gap between technological innovation and practical application (Grace 2023). Developing cost-effective, portable, and user-friendly diagnostic tools is essential to bridge this gap.

Integration challenges for multi-omics and bioinformatics

Although genomics, proteomics, and metabolomics generate rich datasets for understanding pathogen dynamics, the integration of these tools into routine surveillance remains limited. Challenges include data standardization, interoperability of databases, and the need for advanced analysis pipelines (Vashisht et al. 2023). Limited global harmonization among surveillance systems further restricts effective cross-border outbreak tracing.

Need for infrastructure, regulation, and cross-sector coordination

The full potential of modern biotechnological and bioinformatic platforms can only be realized with strong regulatory frameworks, trained personnel, and sustained investment in data and laboratory infrastructure. Multisector collaboration between academia, industry, and regulatory agencies is essential to resolve these limitations and support the transition of advanced technologies into practical, scalable food safety solutions (Griffiths et al. 2017).

Future perspectives

Future directions in food-borne pathogen detection and control are moving toward rapid, data-driven, and highly integrated systems powered by advances in biotechnology and computational intelligence. Portable diagnostics, CRISPR-based assays, next-generation sequencing, and biosensors will continue to shorten detection times, while multi-omics platforms will enable real-time pathogen profiling. Artificial intelligence is expected to play a central role by supporting early outbreak prediction, automated decision-making, and continuous surveillance through integration with genomic pipelines, IoT-based monitoring, and smart processing environments. Emerging AI tools—including digital twins, risk-forecasting models, and anomaly-detection algorithms—will strengthen proactive control by identifying contamination hotspots and anticipating antimicrobial resistance trends. On the intervention side, precision tools such as engineered phages, antimicrobial peptides, and smart packaging will offer targeted and sustainable control options. Together, these innovations signal a shift from reactive responses to predictive, automated, and resilient food safety systems, underscoring the need for interoperable AI frameworks, bias-free algorithms, and secure data infrastructures to enable global adoption.

Conclusion

Food-borne bacterial pathogens continue to challenge global food safety because of their adaptability, ecological persistence, and increasing antimicrobial resistance. This review highlights how advances in microbiology, biotechnology, and bioinformatics—including CRISPR-based assays, next-generation sequencing, metagenomics, and machine-learning tools—are transforming pathogen detection, control, and risk assessment. Integrating multi-omics data with computational modeling supports a shift toward anticipatory food safety systems capable of preventing outbreaks rather than reacting to them, especially when aligned with One Health principles. Moving forward, the impact of these innovations will depend on their translation into affordable, scalable, and field-ready solutions. Strengthening data-sharing networks, improving interoperability of analytical platforms, and expanding AI-driven surveillance will be essential for global adoption. To support this transition, researchers should prioritize low-cost diagnostics and robust predictive tools, policymakers must enhance surveillance and digital infrastructure, and industry should integrate rapid detection and smart monitoring technologies. Together, these efforts will advance more resilient, prevention-focused, and sustainable food safety systems.

Acknowledgements The authors express deep gratitude to Integral University, Lucknow-226026, India, for their generous support of this work. We are also thankful for the support received from the Department of Science and Technology–Funds for Improvement of Science and Technology Infrastructure (DST-FIST), with grant acknowledgment and sanction number (SR/FST/LS-1/2017/13(C)). Additionally, we extend our appreciation to Integral University for providing the manuscript communication number (IU/R&D/2025-MCN0004162).

Author contributions **Zaryab Shafi: ** Conceptualization; Software; Writing-original draft; Writing-review & editing. **Mohammad Shahid: ** Data curation; Writing - original draft. Data curation; Formal analysis; Writing-review & editing. **Rahul Singh: ** Conceptualization; Supervision; Project administration; Writing-review & editing.

Funding Not applicable.

Data availability No datasets were generated or analysed during the current study.

Declarations

Conflict of interest The authors declare no competing interests.

References

Abbas YA, Radhi GF (2016) Rapid identification of Enterobacter Spp. Islated from hospitals in Basrah Province by automated system (Vitek® 2 Compact). Int J Micro Biology Genet Monocular Biology Res 2(2):9–20

Abedon ST (2017) Phage therapy of biofilms: Exploiting biofilm vulnerabilities. Bacteriophage, 7(1):e1252884

Ahmad S, Lohiya S, Taksande A, Meshram RJ, Varma A, Vagha K, Ahmad S Jr, Sr VA (2024) A comprehensive review of innovative paradigms in microbial detection and antimicrobial resistance: beyond traditional cultural methods. Cureus 16(6):1-8

Allard MW, Luo Y, Strain E, Li C, Keys CE, Son I, Stones R, Musser SM, Brown EW (2012) High resolution clustering of Salmonella enterica serovar Montevideo strains using a next-generation sequencing approach. BMC Genomics 13(1):32

Almaary KS (2023) Food-borne diseases and their impact on health. Biosci Biotechnol Res Asia 20(3):745–755

Almeida C, Azevedo NF, Fernandes RM, Keevil CW, Vieira MJ (2010) Fluorescence In situ hybridization method using a peptide nucleic acid probe for identification of Salmonella spp. In a broad spectrum of samples. Appl Environ Microbiol 76(13):4476–4485

Alvarez-Ordonez A, Broussolle V, Colin P, Nguyen-The C, Prieto M (2015) The adaptive response of bacterial food-borne pathogens in the environment, host and food: implications for food safety. Int J Food Microbiol 213:99–109

Amagliani G, Blasi G, Scuota S, Duranti A, Fisichella S, Gattuso A, Gianfranceschi MV, Schiavano GF, Brandi G, Pomilio F, Gabucci C (2021) Detection and virulence characterization of Listeria monocytogenes strains in ready-to-eat products. Foodborne Pathog Dis 18(9):675–682

Anjana A, Tiwari SK (2022) Bacteriocin-producing probiotic lactic acid bacteria in controlling dysbiosis of the gut microbiota. Front Cell Infect Microbiol 12:851140

Ashraf Z, Naseer MU, Shah SH, Shah S, Khan MA, Zulfiqar I (2025) COMPARATIVE EFFECTIVENESS OF ELISA, PCR, AND NGS FOR EMERGING INFECTIOUS DISEASES. Insights-Journal Health Rehabilitation 3(2 Health Rehab):700–706

Ashrafudoulla M, Ulrich MS, Toushik SH, Nahar S, Roy PK, Mizan FR, Park SH, Ha SD (2023) Challenges and opportunities of non-conventional technologies concerning food safety. World's Poult Sci J 79(1):3–26

Bai X, Nakatsu CH, Bhunia AK (2021) Bacterial biofilms and their implications in pathogenesis and food safety. Foods 10(9):2117

Banerji R, Karkee A, Kanojiya P, Saroj SD (2021) Pore-forming toxins of foodborne pathogens. Compr Rev Food Sci Food Saf 20(3):2265–2285

Baranyi J, Roberts TA 1994 A dynamic approach to predicting bacterial growth in food. Int J Food Microbiol 23(3-4):277-294

Bergwerff AA, Debast SB (2021) Modernization of control of pathogenic micro-organisms in the food-chain requires a durable role for immunoaffinity-based detection methodology—a review. Foods 10(4):832

Bhadra L, Dhiman P, Srivastava A, Patel A, Ratrey P, Kumar A, Datta B (2024) Processed food microbiology and safety: Risks, trends and future perspectives. Industrial microbiology and biotechnology: an insight into current trends. Springer Nature Singapore, Singapore, pp 175–227

Bhunia AK (2018) Salmonella enterica. Foodborne microbial pathogens: mechanisms and pathogenesis. Springer New York, New York, NY, pp 271–287

Bisola Bello A, Olamilekan Adesola R, Idris I, Yawson Scott G, Alfa S, Akinfemi Ajibade F (2024) Combatting extensively drug-resistant salmonella: a global perspective on outbreaks, impacts, and control strategies. Pathogens Global Health 118(7–8):559–573

Blanc DS, Magalhães B, Koenig I, Senn L, Grandbastien B (2020) Comparison of whole genome (wg-) and core genome (cg-) MLST (BioNumericsTM) versus SNP variant calling for epidemiological investigation of Pseudomonas aeruginosa. Front Microbiol 11:1729

Brown EW, Gonzalez-Escalona N, Stones R, Timme R, Allard MW (2017) The rise of genomics and the promise of whole genome sequencing for Understanding microbial foodborne pathogens. Foodborne pathogens: virulence factors and host susceptibility. Springer International Publishing, Cham, pp 333–351

Bruyand M, Mariani-Kurkdjian P, Gouali M, De Valk H, King LA, Le Hello S, Bonacorsi S, Loirat C (2018) Hemolytic uremic syndrome due to Shiga toxin-producing Escherichia coli infection. Med Et Maladies Infectieuses 48(3):167–174

Bryce J, Boschi-Pinto C, Shibuya K, Black RE (2005) WHO estimates of the causes of death in children. Lancet 365(9465):1147–1152

Bustin SA (2002) INVITED REVIEW quantification of mRNA using real-time reverse transcription PCR (RT-PCR): trends and problems. J Mol Endocrinol 29:23–39

Bustin SA (2022) Molecular quantification of mRNA: Approaches, challenges, and applications in viability assessment. J Mol Diagn 24(3):245–258. https://doi.org/10.1016/j.jmoldx.2021.11.005

Call DR (2005) Challenges and opportunities for pathogen detection using DNA microarrays. Crit Rev Microbiol 31(2):91–99

Calo-Mata P, Carrera M, Böhme K, Caamaño-Antelo S, Gallardo JM, Barros-Velázquez J, Cañas B (2016) Novel peptide biomarker discovery for detection and identification of bacterial pathogens by LC-ESI-MS/MS

Casanova JL (2015) Severe infectious diseases of childhood as Monogenic inborn errors of immunity. Proc Natl Acad Sci 112(51):E7128–E7137

CDC (2022) Foodborne Diseases Active Surveillance Network (FoodNet): Annual report. Centers for Disease Control and Prevention

Chan BK, Turner PE, Kim S, Mojibian HR, Elefteriades J, Narayan D (2016) Phage treatment of an aortic graft infected with *Pseudomonas aeruginosa*. Cell Host Microbe 20(5):671–676 (Contains mechanistic discussion on phage adaptation relevant to biofilms.)

Chauhan R, Tall BD, Gopinath G, Azmi W, Goel G (2023) Environmental risk factors associated with the survival, persistence, and thermal tolerance of cronobacter Sakazakii during the manufacture of powdered infant formula. Crit Rev Food Sci Nutr 63(33):12224–12239

Chen T, Guestrin C (2016) XGBoost: A scalable tree boosting system. Proceedings of the 22nd ACM SIGKDD international conference on knowledge discovery and data mining, 785–794

Chen H, Li J, Yan S, Sun H, Tan C, Liu M, Liu K, Zhang H, Zou M, Xiao X (2021) Identification of pathogen (s) in infectious diseases using shotgun metagenomic sequencing and conventional culture: a comparative study. PeerJ 9:e11699

Chibwe M, Odume ON, Nnadozie CF (2025) Campylobacter—an emerging pollutant of aquatic environments. Emerging Pollut: Protect Water Quality Health People Environ 35–65

Chikindas ML, Weeks R, Drider D, Chistyakov VA, Dicks LMT (2018) Functions and emerging applications of bacteriocins. Curr Opin Biotechnol 49:23–28

Chon JW, Koo R, Song KY, Kang IB, Kim DH, Bae D, Kim H, Kim SH, Seo KH (2021) Strategies for expanding HACCP certification rate using an awareness survey of dairy farmers. Int J Dairy Technol 74(3):453–461

Colavecchio A, Goodridge LD (2018) Phage therapy approaches to reducing pathogen persistence and transmission in animal production environments: opportunities and challenges. Preharvest Food Safety 289–308

Connor BA (2016) Post-Infectious sequelae of travelers' diarrhea: reactive Arthritis, Guillain-Barré syndrome, and irritable bowel syndrome. Curr Trop Med Rep 3(3):102–107

Cotter PD, Ross RP, Hill C (2013) Bacteriocins: A viable alternative to antibiotics? Nat Rev Microbiol 11(2):95–105

Cotter PD, Hill C, Ross RP 2005 Bacteriocins: developing innate immunity for food. Nat Rev Microbiol 3(10):777-788

da Silva Bras AML (1998) Campylobacter jejuni virulence mechanisms: characterisation and regulation. University of Leicester (United Kingdom)

De Puig Guixe H, Najjar D, Wiederoder MS, Reilly D, McGraw-Manza SK, Collins JJ (2023) CRISPR/Cas cell-free sensors for rapid detection of pathogenic *Escherichia coli*, *Salmonella enterica*, and *Listeria monocytogenes* in complex food and environmental samples

Delgado Carreño CV, Rojas B (2018) Helicobacter pylori in water sources and food products: a constant public health problem

Duchenne R, Ranghoo-Sanmukhiya VM, Neetoo H (2021) Impact of climate change and climate variability on food safety and occurrence of foodborne diseases. Food Secur Safety: Afr Perspect, 451–474

Dung TTN, Phat VV, Vinh C, Lan NPH, Phuong NLN, Ngan LTQ, Thwaites G, Thwaites L, Rabaa M, Nguyen AT, Duy PT (2024) Development and validation of multiplex real-time PCR for simultaneous detection of six bacterial pathogens causing lower respiratory tract infections and antimicrobial resistance genes. BMC Infect Dis 24(1):164

EFSA & ECDC (2023) The European Union One Health 2023 zoonoses report

El-Zehery HR, Zaghloul RA, Abdel-Rahman HM, Salem AA, El-Dougdoug KA (2022) Novel strategies of essential oils, chitosan, and nano-chitosan for Inhibition of multi-drug resistant: E. coli O157: H7 and Listeria monocytogenes. Saudi J Biol Sci 29(4):2582–2590

Elbehiry A, Abalkhail A, Marzouk E, Elmanssury AE, Almuzaini AM, Alfheeaid H, Alshahrani MT, Huraysh N, Ibrahem M, Alzaben F, Alanazi F (2023) An overview of the public health challenges in diagnosing and controlling human foodborne pathogens. Vaccines, 11(4):725

EMA Committee for Medicinal Products for Veterinary Use (CVMP) and EFSA Panel on Biological Hazards (BIOHAZ), Murphy D, Ricci A, Auce Z, Beechinor JG, Bergendahl H, Breathnach R, Bureš J, Da Silva D, Hederová JP, J. and, Hekman P (2017) EMA and EFSA joint scientific opinion on measures to reduce the need to use antimicrobial agents in animal husbandry in the European Union, and the resulting impacts on food safety (RONAFA). EFSA J 15(1):e04666

European Food Safety Authority and European Centre for Disease Prevention and Control

Exeni RA, Fernandez-Brando RJ, Santiago AP, Fiorentino GA, Exeni AM, Ramos MV, Palermo MS (2018) Pathogenic role of inflammatory response during Shiga toxin-associated hemolytic uremic syndrome (HUS). Pediatr Nephrol 33(11):2057–2071

Farrukh M, Munawar A, Nawaz Z, Hussain N, Hafeez AB, Szweda P (2025) Antibiotic resistance and preventive strategies in foodborne pathogenic bacteria: A comprehensive review. Food Sci Biotechnol 34(10):2101–2129

Fernández JC, Hervás C, Martínez-Estudillo FJ, Gutiérrez PA (2011) Memetic Pareto evolutionary artificial neural networks to determine growth/no-growth in predictive microbiology. Appl Soft Comput 11(1):534–550

Ferone M, Gowen A, Fanning S, Scannell AG (2020) Microbial detection and identification methods: bench top assays to omics approaches. Compr Rev Food Sci Food Saf 19(6):3106–3129

Finnie JW, Uzal FA (2022) Pathology and pathogenesis of brain lesions produced by clostridium perfringens type D epsilon toxin. Int J Mol Sci 23(16):9050

Flörl L, Meyer A, Bokulich NA (2025) Exploring sub-species variation in food microbiomes: a roadmap to reveal hidden diversity and functional potential. Appl Environ Microbiol 91(5):e00524–e00525

Fogaça MBT, Bhunia AK, Lopes-Luz L, de Almeida EPRP, Vieira JDG, Bührer-Sékula S (2021) Antibody-and nucleic acid–based lateral flow immunoassay for Listeria monocytogenes detection. Anal Bioanal Chem 413(16):4161–4180

Foster JW (2001) Acid stress responses of Salmonella and E. coli: survival mechanisms, regulation, and implications for pathogenesis. J MICROBIOLOGY-SEOUL- 39(2):89–94

Galán-Relaño Á, Díaz V, Huerta Lorenzo A, Gómez-Gascón B, Rodríguez LM, Carrasco MªÁ, Jiménez E, Pérez Rodríguez F, Márquez A (2023) R.J., Salmonella and salmonellosis: An update on public health implications and control strategies. *Animals*, *13*(23), p.3666

Galvez A, Abriouel H, Lopez RL, Ben Omar N (2007) Bacteriocin-based strategies for food biopreservation. Int J Food Microbiol 120(1–2):51–70

Ganger S, Harale G, Majumdar P (2023) Clustered regularly interspaced short palindromic repeats/CRISPR-associated (CRISPR/Cas) systems: Discovery, structure, classification, and general mechanism. CRISPR/Cas-Mediated genome editing in plants. Apple Academic, pp 65–97

Garcia SN, Osburn BI, Jay-Russell MT (2020) One health for food safety, food security, and sustainable food production. Front Sustainable Food Syst 4:1

Garrido-Maestu A, Chapela MJ, Peñaranda E, Cabado AG (2015) Re-evaluation of enhanced qPCR prevalidated method for next-day detection of Salmonella spp., Shigella spp., Escherichia coli O157 and Listeria monocytogenes. Food Biotechnol 29(4):317–335

Gautam O (2015) *Food hygiene intervention to improve food hygiene behaviours, and reduce food contamination in Nepal: an exploratory trial* (Doctoral dissertation, London School of Hygiene & Tropical Medicine)

Geldart KG, Kommineni S, Forbes M, Hayward M, Dunny GM, Salzman NH, Kaznessis YN (2018) Engineered E. coli Nissle 1917 for the reduction of vancomycin-resistant Enterococcus in the intestinal tract. Bioeng Translational Med 3(3):197–208

Gensheimer K, Allard MW, Timme RE, Brown E, Hintz L, Pettengill J, Strain E, Tallent SM, Vélez LF, King E, Shea SL (2025) Genomic surveillance of foodborne pathogens: advances and Obstacles. J Public Health Manage Pract 31(3):351–359

George M, Abraham TE (2006) Polyionic hydrocolloids for the intestinal delivery of protein drugs: alginate and chitosan—a review. J Controlled Release 114(1):1–14

Ghazy A, Nyarku R, Faraj R, Bentum K, Woube Y, Williams M, Alocilja E, Abebe W (2024) Gold nanoparticle-based plasmonic detection of Escherichia coli, Salmonella enterica, Campylobacter jejuni, and Listeria monocytogenes from bovine fecal samples. Microorganisms 12(6):1069

Ghosh T, Purkait A, Garai B, Banerjee A (2021) Microbial production of bacteriocins and its applications in food preservation: a review. J Food Process Preserv 5:1–2

Ghosh M, Hemanth P, Rahman M, Kardile NB, Gaikwad ST, Kumar S (2024) Advancement and effectiveness of Aloe Vera (Aloe Barbadense miller) and sodium alginate based natural coatings for extending the shelf life of fruits and vegetables. Eur J Nutr Food Saf 16(11):109–129

Gootenberg JS, Abudayyeh OO, Lee JW, Essletzbichler P, Dy AJ, Joung J, Verdine V, Donghia N, Daringer NM, Freije CA, Myhrvold C 2017 Nucleic acid detection with CRISPR-Cas13a/C2c2. Sci 356(6336):438-442

Grace D (2023) Burden of foodborne disease in low-income and middle-income countries and opportunities for scaling food safety interventions. Food Secur 15(6):1475–1488

Grace D 2015 Food safety in low and middle income countries. Int J Environ Res Pub Health 12(9):10490-10507

Green MR, Zaman MH, Warnow T (2022) Machine learning-based prediction of antimicrobial resistance using whole-genome sequencing data. Nat Commun 13(1):1–11

Griffiths E, Dooley D, Graham M, Van Domselaar G, Brinkman FS, Hsiao WW (2017) Context is everything: harmonization of critical food microbiology descriptors and metadata for improved food safety and surveillance. Front Microbiol 8:1068

Gupta P, Adhikari A (2022) Novel approaches to environmental monitoring and control of Listeria monocytogenes in food production facilities. Foods 11(12):1760

Gupta A, Agarwal J (2024) Automation techniques in aerobic bacteriology. Automated diagnostic techniques in medical microbiology. Springer Nature Singapore, Singapore, pp 39–66

Gurtler V, Pavia CS (2020) Immunological methods in microbiology, vol 47. Academic

Hadian M, Rajaei A, Mohsenifar A, Tabatabaei M (2017) Encapsulation of Rosmarinus officinalis essential oils in chitosan-benzoic acid nanogel with enhanced antibacterial activity in beef cutlet against Salmonella typhimurium during refrigerated storage. Lwt 84:394–401

Haffar M, Gilbride KA (2010) The utility and application of real-time PCR and FISH in the detection of single-copy gene targets in Escherichia coli O157: H7 and Salmonella typhimurium. Can J Microbiol 56(3):254–262

Han D, Hung YC, Bratcher CL, Monu EA, Wang Y, Wang L (2018) Formation of sublethally injured Yersinia enterocolitica, Escherichia coli O157: H7, and Salmonella enterica serovar enteritidis cells after neutral electrolyzed oxidizing water treatments. Appl Environ Microbiol 84(17):e01066–e01018

Haque MA, Khan A, He C (2021) Feed-borne Bacillus cereus: an emerging threat to food chain related hazard, safety and pathogenic potentiality. Veterinary Pathobiology Public Health 1:251–269

Hasan TH, Kadhum HA, Alasedi KK (2021) Brucella spp. Virulence factors. Int J Pharm Res 13(1):09752366

Havelaar AH, Kirk MD, Torgerson PR, Gibb HJ, Hald T, Lake RJ, Praet N, Bellinger DC, de Silva NR, Gargouri N, Speybroeck N, Cawthorne A (2015) & World Health Organization Foodborne Disease Burden Epidemiology Reference Group

Heiman KE, Mody RK, Johnson SD, Griffin PM, Gould LH (2015) Escherichia coli O157 outbreaks in the united States, 2003–2012. Clin Infect Dis 61(6):1043–1051

Henry M, Fouladkhah A (2019) Outbreak history, biofilm formation, and preventive measures for control of cronobacter Sakazakii in infant formula and infant care settings. Microorganisms 7(3):77

Higgins JP, Higgins SE, Guenther KL, Huff W, Donoghue AM, Donoghue DJ, Hargis BM 2005 Use of a specific bacteriophage treatment to reduce Salmonella in poultry products. Poult Sci 84(7):1141-1145

Ho CY, Lai YC, Chen IW, Wang FY, Tai WH (2012) Statistical analysis of false positives and false negatives from real traffic with intrusion detection/prevention systems. IEEE Commun Mag 50(3):146–154

Ho CL, Tan HQ, Kyriakopoulos S, Chang MW (2021) Engineered microbial therapeutics for targeted modulation of host–pathogen interactions. Nat Commun 12:1–12

Hoffmann SA, Maculloch B, Batz M (2015) Economic burden of major foodborne illnesses acquired in the United States

Hu T, Chitnis N, Monos D, Dinh A (2021) Next-generation sequencing technologies: an overview. Hum Immunol 82(11):801–811

Hussain M, He X, Wang C, Wang Y, Wang J, Chen M, Kang H, Yang N, Ni X, Li J, Zhou X (2024) Recent advances in microfluidic-based spectroscopic approaches for pathogen detection. Biomicrofluidics 18(3):031505

Hwang IY, Tan MH, Koh E, Chang MW (2017) Reprogramming probiotics to target pathogens using synthetic genetic circuits. ACS Synth Biol 6:421–430

Ibrahim OO (2020a) Introduction to hazard analysis and critical control points (HACCP). EC Microbiol 16(3):1–7

Ibrahim OO (2020b) Staphylococcus aureus a gram-positive coccid bacterium causing microbial infections, and toxins symptoms including food poisoning. EC Microbiol 16:61–76

Iranloye YM, Okonkwo CE (2023) The role of good agricultural practices (GAPs) and good manufacturing practices (GMPs). Food Safety and Toxicol: Present Future Perspect 417

Jackson DN, Davis B, Tirado SM, Duggal M, Van Frankenhuyzen JK, Deaville D, Wijesinghe MAK, Tessaro M, Trevors JT (2009) Survival mechanisms and culturability of Campylobacter jejuni under stress conditions. Antonie Van Leeuwenhoek 96(4):377–394

Jamali H, Chai LC, Thong KL (2013) Detection And isolation of Listeria spp. And Listeria monocytogenes in ready-to-eat foods with various selective culture media. Food Control 32(1):19–24

Janda JM, Abbott SL (1999) Unusual food-borne pathogens: Listeria monocytogenes, Aeromonas, Plesiomonas, and Edwardsiella species. Clin Lab Med 19(3):553–582

Jarosz A, Grenda T, Goldsztejn M, Kozak B, Kwiatek K (2022) Potential risk of botulinum neurotoxin-producing clostridia occurrence in canned fish. J Veterinary Res 66(4):605

Jha P, Singh AK (2025) Regulatory compliance and food safety standards. Engineering solutions for sustainable food and dairy production: innovations and techniques in food processing and dairy engineering. Springer Nature Switzerland, Cham, pp 463–487

Kaakoush NO, Castaño-Rodríguez N, Mitchell HM, Man SM (2015) Global epidemiology of Campylobacter infection. Clin Microbiol Rev 28(3):687–720

Kabiraz MP, Majumdar PR, Mahmud MC, Bhowmik S, Ali A (2023) Conventional and advanced detection techniques of foodborne pathogens: A comprehensive review. Heliyon 9(4):1-24

Kergourlay G, Taminiau B, Daube G, Vergès MCC (2015) Metagenomic insights into the dynamics of microbial communities in food. Int J Food Microbiol 213:31–39

Khoiri S, Moussango VD (2024) A short review on Harnessing bioinformatics for food safety: computational approaches to detecting foodborne pathogens. J Adv Health Inf Res 2(3):109–114

Kim JS, Lee GG, Park JS, Jung YH, Kwak HS, Kim SB, Nam YS, Kwon ST (2007) A novel multiplex PCR assay for rapid and simultaneous detection of five pathogenic bacteria: Escherichia coli O157: H7, Salmonella, Staphylococcus aureus, Listeria monocytogenes, and vibrio parahaemolyticus. J Food Prot 70(7):1656–1662

Kipper D, Orsi RH, Carroll LM, Mascitti AK, Streck AF, Fonseca AS, Ikuta N, Tondo EC, Wiedmann M, Lunge VR (2021) Recent evolution and genomic profile of Salmonella enterica serovar Heidelberg isolates from poultry flocks in Brazil. Appl Environ Microbiol 87(21):e01036–e01021

Kirk MD, Pires SM, Black RE, Caipo M, Crump JA, Devleesschauwer B, Dopfer D, Fazil A, Fischer-Walker CL, Hald T, Hall AJ, Keddy KH, Lake RJ, Lanata CF, Torgerson PR, Havelaar AH, Angulo FJ (2015) World health organization estimates of the global and regional disease burden of 22 foodborne bacterial, protozoal, and viral diseases, 2010: A data synthesis. PLoS Med 12(12):e1001921

Kong J, Fan C, Liao X, Chen A, Yang S, Zhao L, Li H (2022) Accurate detection of Escherichia coli O157: H7 and Salmonella enterica serovar typhimurium based on the combination of next-generation sequencing and droplet digital PCR. LWT 168:113913

Kralik P, Ricchi M (2017) A basic guide to real time PCR in microbial diagnostics: definitions, parameters, and everything. Front Microbiol 8:108

Kraśniewska K, Galus S, Gniewosz M (2020) Biopolymers-based materials containing silver nanoparticles as active packaging for food applications–a review. Int J Mol Sci 21(3):698

Krawczyk B, Wityk P, Gałęcka M, Michalik M (2021) The many faces of Enterococcus spp.—commensal, probiotic and opportunistic pathogen. Microorganisms 9(9):1900

Kreitlow A, Becker A, Ahmed MF, Kittler S, Schotte U, Plötz M, Abdulmawjood A (2021) Combined loop-mediated isothermal amplification assays for rapid detection and one-step differentiation of Campylobacter jejuni and Campylobacter coli in meat products. Front Microbiol 12:668824

Kusuma I, Rahmadhia SN, Ma'arif A (2024) Exploring the role of biotechnology and biodiversity in achieving sustainable and nutritional food systems

Lacourt C, Mukherjee K, Garthoff J, O'Sullivan A, Meunier L, Fattori V (2024) Recent and emerging food packaging alternatives: chemical safety risks, current regulations, and analytical challenges. Compr Rev Food Sci Food Saf 23(6):e70059

Lee H (2023) Mesophilic Aeromonas spp. Isolated from ready-to-eat seafood: insight into antimicrobial resistance, virulence factors, and growth kinetics in food

Lee SY, Kim HU, Park JH, Park JM, Kim TY (2009) Metabolic engineering of microorganisms: general strategies and drug production. Drug Discovery Today 14(1–2):78–88

Lee JG, Lee Y, Kim CS, Han SB (2021) Codex alimentarius commission on ensuring food safety and promoting fair trade: harmonization of standards between Korea and Codex. Food Sci Biotechnol 30(9):1151–1170

Leong D, Alvarez-OrdÃ³Ã±ez A, Jooste P, Jordan K (2016) Listeria monocytogenes in food: Control by monitoring the food processing environment. Afr J Microbiol Res 10(1):1–14

Letchumanan V (2019) Prevalence and characterisation of antibiotic resistance of vibrio parahaemolyticus from seafood in Selangor, Malaysia (Doctoral dissertation, University of Malaya (Malaysia))

Li B, Chen JQ, Wang X (2017) Viability PCR for distinguishing live and dead bacteria: PMA and EMA applications in food microbiology. Food Microbiol 62:1–13. https://doi.org/10.1016/j.fm.2016.09.012

Li J, Ma B, Fang J, Zhi A, Chen E, Xu Y, Yu X, Sun C, Zhang M (2019) Recombinase polymerase amplification (RPA) combined with lateral flow immunoassay for rapid detection of Salmonella in food. Foods 9(1):27

Li N, Pang B, Li J, Liu G, Xu X, Shao D, Jiang C, Yang B, Shi J (2020) Mechanisms for Lactobacillus rhamnosus treatment of intestinal infection by drug-resistant Escherichia coli. Food Funct 11(5):4428–4445

Liang Q, Bible PW, Liu Y, Zou B, Wei L, Xu J (2021) Deep and ensemble learning approaches for antimicrobial resistance prediction: comparative evaluation and model interpretation. Brief Bioinform 22(6):bbab296

Lio MS, Favara R, Maugeri G, Barchitta A, M. and, Agodi A (2023) How antimicrobial resistance is linked to climate change: an overview of two intertwined global challenges. Int J Environ Res Public Health 20(3):1681

Liu P, Mizue H, Fujihara K, Kobayashi H, Kamikado H, Tanaka T, Honjoh KI, Miyamoto T (2012) A new rapid real-time PCR method for detection of Listeria monocytogenes targeting the HlyA gene. Food Sci Technol Res 18(1):47–57

Liu G, Thomsen LE, Olsen JE (2022) Antimicrobial-induced horizontal transfer of antimicrobial resistance genes in bacteria: a mini-review. J Antimicrob Chemother 77(3):556–567

Lopetuso LR, Giorgio ME, Saviano A, Scaldaferri F, Gasbarrini A, Cammarota G (2019) Bacteriocins and bacteriophages: therapeutic weapons for gastrointestinal diseases? Int J Mol Sci 20(1):183

López-Campos G, Martínez-Suárez JV, Aguado-Urda M, López-Alonso V (2012) Microarray detection and characterization of bacterial foodborne pathogens. Springer Sci & Bus Media.

Luber P, Crerar S, Dufour C, Farber J, Datta A, Todd EC (2011) Controlling Listeria monocytogenes in ready-to-eat foods: working towards global scientific consensus and harmonization–recommendations for improved prevention and control. Food Control 22(9):1535-1549.

Lüth S (2021) Molecular surveillance of Listeria monocytogenes in Germany to control transmission along food supply chains and to prevent human listeriosis cases (Doctoral dissertation)

Madad A, Marshall KE, Blessington T, Hardy C, Salter M, Basler C, Conrad A, Stroika S, Luo Y, Dwarka A, Gerhardt T (2023) Investigation of a multistate outbreak of Listeria monocytogenes infections linked to frozen vegetables produced at individually quick-frozen vegetable manufacturing facilities. J Food Prot 86(8):100117

Mahajan P, Sethi A, Singla M, Bhardwaj DK, Kaur B (2025) Nanotechnology in food: advances in Processing, Packaging, Safety, and emerging challenges. J Food Chem Nanotechnol 11(2):83–96

Makwavarara T (2018) Use of a modified hazard analysis and critical control points (HACCP) approach for the evaluation of bovine brucellosis control programmes. University of Pretoria (South Africa)

Malabadi RB, Sadiya MR, Kolkar KP, Chalannavar RK (2024) Pathogenic Escherichia coli (E. coli) food borne outbreak: detection methods and controlling measures. Magna Scientia Adv Res Reviews 10(01):052–085

Mangal M, Bansal S, Sharma SK, Gupta RK (2016) Molecular detection of foodborne pathogens: A rapid and accurate answer to food safety. Crit Rev Food Sci Nutr 56(9):1568–1584

Manyi-Loh CE, Lues R (2025) Listeria monocytogenes and Listeriosis: The Global Enigma. Foods 14(7):1266

Mazzotta AS, Crandall AD, Montville TJ (1997) Nisin resistance in clostridium botulinum spores and vegetative cells. Appl Environ Microbiol 63(7):2654–2659

McVey C, Elliott CT, Cannavan A, Kelly SD, Petchkongkaew A, Haughey SA (2021) Portable spectroscopy for high throughput food authenticity screening: advancements in technology and integration into digital traceability systems. Trends Food Sci Technol 118:777–790

Michael J, Abbott SL (1993) Infections associated with the genus edwardsiella: the role of Edwardsiella Tarda in human disease. Clin Infect Dis 17(4):742–748

Milesi S (2011) Emerging pathogen Arcobacter spp. in food of animal origin

Mirza N (2015) Immune response to Shiga toxin producing *Escherichia coli*: Detection of antibodies against outer membrane proteins of the bacteria in healthy population of Bangladesh (Doctoral dissertation, Brac University)

Mishra A, Roy S, Shaikh NI, Malave P, Mishra A, Alam MA, Ghorpade Y, Hasan MR, Nizam A (2024) Recent advances in multiplex aptasensor detection techniques for food-borne pathogens: a comprehensive review of novel approaches. Biosens Bioelectron X 16:100417

Mkangara M (2023) Prevention and control of human Salmonella enterica infections: an implication in food safety. Int J Food Sci 2023(1):8899596

Murtaza B, Ling-ling G, Wang L, Li X, Ali A, Saleemi MK, Xu Y (2025) Mycotoxin detection in corn and distillers dried grains for food security. Renew Sustain Energy Rev 210:115194

Myintzaw P, Jaiswal AK, Jaiswal S (2023) A review on campylobacteriosis associated with poultry meat consumption. Food Reviews Int 39(4):2107–2121

Naidoo N, Zishiri OT, Presence (2025) Pathogenicity, antibiotic resistance, and virulence factors of *Escherichia coli*: a review. Bacteria 4(1):16

Newell DG, Koopmans M, Verhoef L, Duizer E, Aidara-Kane A, Sprong H, Opsteegh M, Langelaar M, Threfall J, Scheutz F, van der Giessen J (2010) Food-borne diseases—the challenges of 20 years ago still persist while new ones continue to emerge. Int J Food Microbiol 139:S3–S15

Neyaz LA, Alghamdi HS, Alghashmari RM, Alswat SS, Almaghrabi RO, Bazaid FS, Albarakaty FM, Elbanna K, Abulreesh HH (2024) A comprehensive review on the current status of culture media for routine standardized isolation of Salmonella and Shigella spp. from contaminated food. J Umm Al-Qura Univ Appl Sci pp.1–14

Ng WL, Hwang IY, Chang MW (2013) Engineered probiotics for detection and control of pathogenic bacteria using quorum-sensing mechanisms. Biotechnol J 8:1130–1141

Nguyen M, Long SW, McDermott PF, Olsen RJ, Olson R, Stevens RL, Tyson GH, Zhao S, Davis JJ (2019) Using machine learning to predict antimicrobial mics and associated genomic features for nontyphoidal Salmonella. J Clin Microbiol 57(2):10–1128

Ni ZJ, Zhang XY, Liu F, Wang M, Hao RH, Ling PX, Zhu XQ (2017) Effect of co-overexpression of Nisin key genes on Nisin production improvement in Lactococcus lactis LS01. Probiotics Antimicrob Proteins 9(2):204–212

Nieto-Lozano JC, Reguera-Useros JI, Pelaez-Martinez MDC, de la Torre AH (2006) Effect of a bacteriocin produced by pediococcus acidilactici against Listeria monocytogenes and clostridium perfringens on Spanish Raw meat. Meat Sci 72(1):57–61

Nossier E (2013) The risk level associated with food acquisition and management practices of low income individuals. Rutgers The State University of New Jersey, School of Graduate Studies

Okido T, Kodama Y, Mashima J, Kosuge T, Fujisawa T, Ogasawara O (2022) DNA data bank of Japan (DDBJ) update report 2021. Nucleic Acids Res 50(D1):D102–D105

Oliver JD (2010) Recent findings on the viable but nonculturable state in pathogenic bacteria. FEMS Microbiol Rev 34(4):415–425. https://doi.org/10.1111/j.1574-6976.2009.00200.x

Oniciuc EA, Likotrafiti E, Alvarez-Molina A, Prieto M, Santos JA, Alvarez-Ordóñez A (2018) The present and future of whole genome sequencing (WGS) and whole metagenome sequencing (WMS) for surveillance of antimicrobial resistant microorganisms and antimicrobial resistance genes across the food chain. Genes 9(5):268

Ottesen A, Ramachandran P, Chen Y, Brown E, Reed E, Strain E (2020) Quasimetagenomic source tracking of Listeria monocytogenes from naturally contaminated ice cream. BMC Infect Dis 20(1):83

Paidari S, Esmaeili Y, Ibrahim SA, Vahedi S, Al-Hilifi SA, Zamindar N (2024) Application of nanoparticles to enhance the microbial quality and shelf life of food products. Microbial biotechnology in the food industry: Advances, challenges, and potential solutions. Springer International Publishing, Cham, pp 75–102

Pal M, Merera O, Abera F, Rahman MT, Hazarika RA (2015) Salmonellosis: A major foodborne disease of global significance. Beverage Food World 42(12):21–24

Pal N, Sharma P, Kumawat M, Singh S, Verma V, Tiwari RR, Sarma DK, Nagpal R, Kumar M (2024) Phage therapy: an alternative treatment modality for MDR bacterial infections. Infect Dis 56(10):785–817

Patel A, Wolfram A, Desin TS (2024) Advancements in Detection Methods for Salmonella in Food: A Comprehensive Review. Pathogens 13(12):1075

Pedro AL, Rodolfo RV, Arturo MHP, Nazmín TGD, Antonio SJL (2023) Cold chain relevance in the food safety of perishable products. Foods Raw Mater 11(1):116–128

Pérez-Llarena FJ, Bou G (2016) Proteomics as a tool for studying bacterial virulence and antimicrobial resistance. Front Microbiol 7:410

Pinstrup-Andersen P, Watson II DD (2011) Food policy for developing countries: the role of government in global, national, and local food systems. Cornell University Press

Pisano MB, Fadda ME, Viale S, Deplano M, Mereu F, Blažić M, Cosentino S (2022) Inhibitory effect of Lactiplantibacillus plantarum and Lactococcus lactis autochtonous strains against Listeria monocytogenes in a laboratory cheese model. *Foods*, *11*(5), p.715

Pizarro-Cerda J, Cossart P (2018) Listeria monocytogenes: cell biology of invasion and intracellular growth. Microbiol Spectr 6(6):10–1128

Pokhrel D (2024) Campylobacter jejuni survival under environmental stressors. Mississippi State University

Pokhrel D, Thames HT, Zhang L, Dinh TT, Schilling W, White SB, Ramachandran R, Sukumaran T (2022) A., Roles of aerotolerance, biofilm formation, and viable but non-culturable state in the survival of *Campylobacter jejuni* in poultry processing environments. Microorganisms 10(11):2165

Radu E, Dima A, Dobrota EM, Badea AM, Madsen DØ, Dobrin C, Stanciu S (2023) Global trends and research hotspots on HACCP and modern quality management systems in the food industry. Heliyon *9*(7):1-24

Raghu HV, Kumar N (2020) Rapid detection of Listeria monocytogenes in milk by surface plasmon resonance using wheat germ agglutinin. Food Anal Methods 13(4):982–991

Rajapaksha P, Elbourne A, Gangadoo S, Brown R, Cozzolino D, Chapman J (2019) A review of methods for the detection of pathogenic microorganisms. Analyst 144(2):396–411

Ramamurthy T, Ghosh A, Pazhani GP, Shinoda S (2014) Current perspectives on viable but non-culturable (VBNC) pathogenic bacteria. Front Public Health 2:103

Rao AK (2021) Clinical guidelines for diagnosis and treatment of botulism, 2021. MMWR Recommendations Rep, 70

Rathee P, Sehrawat R, Rathee P, Khatkar A, Akkol EK, Khatkar S, Redhu N, Türkcanoğlu G, Sobarzo-Sánchez E (2023) Polyphenols: natural preservatives with promising applications in food, cosmetics and pharma industries; problems and toxicity associated with synthetic preservatives; impact of misleading advertisements; recent trends in preservation and legislation. Materials 16(13):4793

Rawson AM, Dempster AW, Humphreys CM, Minton NP (2023) Pathogenicity and virulence of Clostridium botulinum. Virulence 14(1):2205251

Rhoden DL (1980) Isolation and identification of Enterobacteriaceae in the clinical bacteriology laboratory. US Department of Health and Human Services, Public Health Service, Center for Disease Control, Bureau of Laboratories, Bacteriology Division, Clinical Bacteriology Branch

Ross T, Rasmussen S, Fazil A, Paoli G, Sumner J 2009 Quantitative risk assessment of Listeria monocytogenes in ready-to-eat meats in Australia. Int J Food Microbiol 131(2-3):128-137

Saad MTA (2018) Aetiology of potentially pathogenic bacteria from neonatal feeding tubes. Nottingham Trent University (United Kingdom)

Sadek SA, Shaapan RM, Barakat AM (2023) Campylobacteriosis in poultry: a review. J World's Poult Res 13(2):168–179

Sahel DK, Giriprasad G, Jatyan R, Guha S, Korde A, Mittal A, Bhand S, Chitkara D (2024) Next-generation CRISPR/Cas-based ultrasensitive diagnostic tools: current progress and prospects. RSC Adv 14(44):32411–32435

Sansonetti P (2001) December. Phagocytosis of bacterial pathogens: implications in the host response. Semin Immunol 13:381–390 6

Schuchat A, Broome CV (2005) Infections Caused by Listeria monocytogenes. HARRISONS PRINCIPLES Intern Med 16(1):837

Setlow B, Atluri S, Kitchel R, Koziol-Dube K, Setlow P (2006) Role of dipicolinic acid in resistance and stability of spores of Bacillus subtilis with or without DNA-protective α/β-type small acid-soluble proteins. J Bacteriol 188(11):3740–3747

Sharma D, Misba L, Khan AU (2019) Antibiotics versus biofilm: an emerging battleground in microbial communities. Antimicrob Resist Infect Control 8(1):76

Shrestha A, Uzal FA, McClane BA (2018) Enterotoxic clostridia: clostridium perfringens enteric diseases. Microbiol Spectr 6(5):10–1128

Siddiqui MF (2024) The role of bioinformatics in molecular biology: tools and techniques for data analysis. Multidisciplinary J Biochem 1(2):64–73

Silk BJ, Date KA, Jackson KA, Pouillot R, Holt KG, Graves LM, Hurd S, Austin JL, Mahon BE (2013) Trends in listeriosis in the united States, 2001–2011. Foodborne Pathog Dis 10(7):543–549

Sillankorva S, Oliveira R, Azeredo J (2012) Bacteriophages and their role in food safety. Int J Microbiol 2012:863945

Singh AP, Gouda S (2024) Utilizing environmental DNA/RNA for pathogen detection & ecology. Food Sci Rep 5(5):27–32

Singh M, Bindal G, Misra CS, Rath D (2022) The era of Cas12 and Cas13 CRISPR-based disease diagnosis. Crit Rev Microbiol 48(6):714–729

Solow BT, Cloak OM, Fratamico PM (2003) Effect of temperature on viability of Campylobacter jejuni and Campylobacter coli on Raw chicken or pork skin. J Food Prot 66(11):2023–2031

Soro AB, Whyte P, Bolton DJ, Tiwari BK (2020) Strategies and novel technologies to control Campylobacter in the poultry chain: A review. Compr Rev Food Sci Food Saf 19(4):1353–1377

Soroushianfar M, Asgari G, Afzali F, Falahat A, Soroush M, Baghahi M, Haratizadeh MJ, Khalili-Tanha G, Nazari E (2025) Application of Bioinformatics and Machine Learning Tools in Food Safety. Curr Nutr Rep 14(1):67

Stevens MP, Frankel GM (2015) The locus of enterocyte effacement and associated virulence factors of enterohemorrhagic *Escherichia coli*. Enterohemorrhagic *Escherichia coli* and Other Shiga Toxin-Producing *E. coli*, pp.97–130

Swaminathan B, Gerner-Smidt P (2007) The epidemiology of human listeriosis. Microbes Infect 9(10):1236–1243

Taskila S, Tuomola M, Ojamo H (2012) Enrichment cultivation in detection of food-borne Salmonella. Food Control 26(2):369–377

Towfek SK, Elkanzi M (2024) A review on the role of machine learning in predicting the spread of infectious diseases. Metaheuristic Optimiz Rev 2(1):14–27

Tzouros NE, Arvanitoyannis IS (2000) Implementation of hazard analysis critical control point (HACCP) system to the fish/seafood industry: A review. Food Reviews Int 16(3):273–325

Unnevehr LJ (2022) Addressing food safety challenges in rapidly developing food systems. Agric Econ 53(4):529–539

Urgancı NN, Yılmaz N, Alaşalvar GK, Yıldırım Z (2022) Pseudomonas aeruginosa and its pathogenicity. Turkish J Agriculture-Food Sci Technol 10(4):726–738

Valenti M, Ranganathan N, Moore LS, Hughes S (2021) Listeria monocytogenes infections: presentation, diagnosis and treatment. Br J Hosp Med 82(10):1–6

van de Merwe C, Simpson DJ, Qiao N, Otto SJ, Kovacevic J, Gänzle MG, McMullen LM (2024) Is the persistence of Listeria monocytogenes in food processing facilities and its resistance to pathogen intervention linked to its phylogeny? Appl Environ Microbiol 90(6):e00861–e00824

Vashisht V, Vashisht A, Mondal AK, Farmaha J, Alptekin A, Singh H, Ahluwalia P, Srinivas A, Kolhe R (2023) Genomics for emerging pathogen identification and monitoring: prospects and Obstacles. BioMedInformatics 3(4):1145–1177

Vázquez-Boland JA, Krypotou E, Scortti M (2017) Listeria placental infection. MBio 8(3):10–1128

Venkatasubbu GD, Baskar R, Anusuya T, Seshan CA, Chelliah R (2016) Toxicity mechanism of titanium dioxide and zinc oxide nanoparticles against food pathogens. Colloids Surf B 148:600–606

Venkateswaran K, Vaishampayan P, Probst AJ (2023) Metabolomic signatures and ATP bioluminescence assays for assessing microbial viability in complex matrices. Appl Environ Microbiol 89(2):e01523–e01522. https://doi.org/10.1128/aem.01523-22

Viazis S, Akhtar M, Feirtag J, Diez-Gonzalez F (2011) Reduction of *Salmonella enterica* and *Listeria monocytogenes* on lettuce using a bacteriophage cocktail. J Food Prot 74(11):1821–1830

Viazis S, Bazaco MC, Blessington T, Federman SLS, Lindsay M, Minor T, Nork B, Mattioli MC, Marshall KE, Wise ME, Weed B (2025) An overview of farm investigation findings associated with outbreaks of shiga toxin-producing *Escherichia coli* infections linked to leafy greens: 2009–2021. J Food Prot 88(7):100542

Vikram A, Tokman JI, Woolston J, Sulakvelidze A (2020) Phage biocontrol improves food safety by significantly reducing the level and prevalence of Escherichia coli O157: H7 in various foods. J Food Prot 83(4):668–676

Vizzini P, Braidot M, Vidic J, Manzano M (2019) Electrochemical and optical biosensors for the detection of campylobacter and listeria: an update look. Micromachines 10(8):500

Wang H (2016) *Factors contributing to biofilm formation of Yersinia enterocolitica* (Doctoral dissertation, Massey University)

Wang L, Li Y, Mustapha A (2007a) Rapid and simultaneous quantitation of Escherichia coli O157: H7, Salmonella, and Shigella in ground beef by multiplex real-time PCR and immunomagnetic separation. J Food Prot 70(6):1366–1372

Wang XW, Zhang L, Jin LQ, Jin M, Shen ZQ, An S, Chao FH, Li JW (2007b) Development and application of an oligonucleotide microarray for the detection of food-borne bacterial pathogens. Appl Microbiol Biotechnol 76(1):225–233

Wang Z, Tao X, Liu S, Zhao Y, Yang X (2021) An update review on Listeria infection in pregnancy. Infection and drug resistance, pp.1967–1978

Werner RK, Werner JR, Pinter E (2024) Escherichia coli O157: H7 (Enterohemorrhagic *E. coli*). Ciottone's disaster medicine. Elsevier, pp 782–784

Wideman NE, Oliver JD, Crandall PG, Jarvis NA (2021) Detection and potential virulence of viable but non-culturable (VBNC) Listeria monocytogenes: A review. Microorganisms 9(1):194

Wiktorczyk-Kapischke N, Skowron K, Grudlewska-Buda K, Wałecka-Zacharska E, Korkus J, Gospodarek-Komkowska E (2021) Adaptive response of Listeria monocytogenes to the stress factors in the food processing environment. Front Microbiol 12:710085

Wilson TK (2003) Development of a streamlined, selective-enrichment culture, one-tube (RT-) PCR-enzyme hybridization assay to detect bacterial fish pathogens in covertly infected farmed salmonids (Doctoral dissertation, University of Tasmania)

Wolff N, Hendling M, Schroeder F, Schönthaler S, Geiss AF, Bedenic B, Barišić I (2021) Full pathogen characterisation: species identification including the detection of virulence factors and antibiotic resistance genes via multiplex DNA-assays. Sci Rep 11(1):6001

World Health Organization (2018) Shiga toxin-producing Escherichia coli (STEC) outbreak surveillance report. WHO Press.

World Health Organization global estimates and regional comparisons of the burden of foodborne disease in 2010. PLoS Med, 12(12):e1001923

World Health Organization (2023) Whole genome sequencing as a tool to strengthen foodborne disease surveillance and response. Module 3: whole genome sequencing in foodborne disease routine surveillance. World Health Organization

Worley MJ (2025) Salmonella type III secretion system effectors. Int J Mol Sci 26(6):2611

Xiao X, Fu L, Zhang Z, Tu Z, Shen N, Fan S 2025 Recent Advances in Integrating Machine Learning with Omics Approaches in Food Science Nutrition Research. J Agric Food Chem 73(47)

Xu YG, Liu ZM, Zhang BQ, Qu M, Mo CS, Luo J, Li SL (2016) Development of a novel target-enriched multiplex PCR (Tem-PCR) assay for simultaneous detection of five foodborne pathogens. Food Control 64:54–59

Xu C, Kuang H, Xu L (2019) Pathogen immunoassay in food. Food immunoassay. Springer Singapore, Singapore, pp 255–319

Yang SC, Lin CH, Sung CT, Fang JY (2014) Antimicrobial peptides of food animals and their applications in food preservation. J Food Drug Anal 22(1):1–6

Yaqub MO, Joseph CE, Jain A, Edison LK (2024) Resistome mapping in foodborne pathogens: Understanding role in the transmission dynamics of resistance genes. Appl Microbiol 4(4):1476–1492

Ye K, Zhang Q, Jiang Y, Xu X, Cao J, Zhou G (2012) Rapid detection of viable Listeria monocytogenes in chilled pork by real-time reverse-transcriptase PCR. Food Control 25(1):117–124

Yin W, Zhuang J, Li J, Xia L, Hu K, Yin J, Mu Y (2023) Digital recombinase polymerase amplification, digital loop-mediated isothermal amplification, and digital CRISPR-Cas assisted assay: current status, challenges, and perspectives. Small 19(49):2303398

Yoon JY, Kim B (2012) Lab-on-a-chip pathogen sensors for food safety. Sensors 12(8):10713–10741

Zhao X, Kuipers OP (2021) Nisin-and ripcin-derived hybrid lanthipeptides display selective antimicrobial activity against Staphylococcus aureus. ACS Synth Biol 10(7):1703–1714

Zhou Z, Alikhan NF, Mohamed K, Fan Y, Achtman M (2020) The EnteroBase user's guide, with case studies on Salmonella transmissions and genomic epidemiology. Microb Genomics 6(10):e000333

Zhou Y, Ren M, Zhang P, Jiang D, Yao X, Luo Y, Yang Z, Wang Y (2022) Application of nanopore sequencing in the detection of foodborne microorganisms. Nanomaterials 12(9):1534