



Major foodborne zoonotic bacteria and their role in antimicrobial resistance

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ARTICLE INFO

Keywords:

Antimicrobial resistance
Foodborne zoonotic bacteria
Global disease burden
One Health

ABSTRACT

Foodborne zoonotic bacteria present a major public health concern worldwide, responsible for hundreds of millions of infections and hundreds of thousands of deaths annually. These organisms not only cause severe illness but are increasingly exhibiting resistance to critically important antimicrobials, limiting treatment options and complicating outbreak control. The rise of antimicrobial-resistant (AMR) strains, particularly in low- and middle-income countries, is closely linked to the misuse of antibiotics in both human medicine and food-producing animals. Resistance arises through multiple mechanisms, including enzymatic drug inactivation, target site modification, reduced membrane permeability, efflux pump activation, and the horizontal transfer of resistance genes via mobile genetic elements.

This paper presents an overview of the global burden of foodborne zoonoses, highlighting the prevalence and AMR patterns of major zoonotic bacterial pathogens (*Campylobacter* spp., *Salmonella*, Shiga toxin-producing *Escherichia coli*, *Listeria monocytogenes*, and methicillin-resistant *Staphylococcus aureus*) across different regions. It also addresses the substantial economic costs associated with these infections. Drawing on recent data from WHO, EFSA, ECDC, CDC, and OECD, the paper underscores the urgent need for coordinated, cross-sectoral strategies. Emphasis is placed on the One Health approach as a comprehensive framework to address the interconnected risks to human, animal, and environmental health. Strengthening surveillance, promoting responsible antimicrobial use, and improving food safety systems are essential to mitigate the growing threat of AMR along the food chain.

1. Introduction

Foodborne zoonotic bacteria pose a growing global public health concern, causing an estimated 600 million illnesses and 420,000 deaths annually (WHO, 2015). Among the most significant bacterial pathogens are *Campylobacter* spp., *Salmonella*, Shiga toxin-producing *Escherichia coli* (STEC),

Listeria monocytogenes, and methicillin-resistant *Staphylococcus aureus* (MRSA). These bacteria not only trigger acute infections but increasingly contribute to the spread of antimicrobial resistance (AMR), complicating treatment and disease control efforts (Vesković, 2025).

AMR is recognised as one of the most pressing global threats to human and animal health. Key

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Paper received July 28th 2025. Paper accepted September 10th 2025.

The paper was presented at the 63rd International Meat Industry Conference “Food for Thought: Innovations in Food and Nutrition” – Zlatibor, October 05th–08th 2025.

Published by Institute of Meat Hygiene and Technology – Belgrade, Serbia.

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drivers include the intensive use of antibiotics in animal production, inappropriate therapeutic and prophylactic use, and weak regulatory oversight (Nastasijević *et al.*, 2023; Milijašević *et al.*, 2024). The food chain acts as a major reservoir of resistant bacteria due to antibiotic use in food-producing animals, while global food trade accelerates the transboundary spread of resistance (Founou *et al.*, 2016). Additional factors such as inadequate hygiene practices, low biosecurity standards, and direct or indirect contact with contaminated food or animals contribute to human exposure (Mc Nulty *et al.*, 2016; Vesković, 2025). Resistance emerges through selection of naturally resistant strains, genetic mutations, and horizontal gene transfer, and may also be driven by antimicrobial residues in animal-derived foods (Serwecińska, 2020; Muteeb *et al.*, 2023). The confined conditions of intensive farming foster rapid spread of resistance genes within and between bacterial populations (Manyi-Loh *et al.*, 2018).

The burden of AMR is staggering. In 2019, an estimated 4.95 million deaths were associated with AMR globally, with 1.27 million directly attributable to resistant infections (Antimicrobial Resistance Collaborators, 2022). In the European Union (EU), AMR is responsible for more than 35,000 deaths and economic losses exceeding €11.7 billion each year (ECDC, 2024). Similar estimates apply to the United States (US), with over 2.8 million infections and 35,000 deaths annually linked to resistant bacteria, and healthcare costs exceeding US\$4.6 billion (CDC, 2019). Without effective mitigation, AMR could cause more than 10 million deaths annually by 2050, surpassing cancer, and lead to a cumulative economic loss of US\$100 trillion (O'Neill, 2016; OECD/WHO, 2022). In response, international organisations such as the World Health Organization (WHO), the Food and Agriculture Organization of the United Nations (FAO), the World Organisation for Animal Health (WOAH), and the United Nations Environment Programme (UNEP) advocate for a One Health approach that integrates human, animal, and environmental health. Core strategies include prudent antimicrobial use, improved animal husbandry, biosecurity, vaccination, and hygiene protocols (WHO, 2017).

This paper provides an overview of the major foodborne zoonotic pathogens—*Campylobacter* spp., *Salmonella* spp., STEC, *L. monocytogenes*, and MRSA—with emphasis on their prevalence, AMR patterns, and impact on public health. The aim is to contribute to understanding their role in AMR transmission through the food chain and support the

development of effective prevention and control strategies.

2. Literature search strategy

This review is based on peer-reviewed scientific literature and official reports addressing AMR in major foodborne zoonotic bacteria. Relevant publications were identified through a comprehensive search of electronic databases including PubMed, Scopus, Web of Science, and Google Scholar. In addition, documents and surveillance data from international organisations, such as the WHO, FAO, ECDC, and OECD were reviewed. The literature search focused on publications published between 2015 and 2025, using a combination of keywords such as “antimicrobial resistance”, “foodborne bacteria”, “zoonoses”, “One Health”, and specific bacterial names (e.g., *Campylobacter*, *Salmonella*, STEC, *L. monocytogenes*, MRSA). Sources were selected based on their scientific relevance, methodological quality, and alignment with the thematic scope of this review.

3. Overview of major foodborne bacteria and their role in AMR transmission

Foodborne zoonotic bacteria play a critical role in the transmission of AMR along the food chain. Their ability to persist throughout various stages of food production, processing, and distribution, as well as to colonise and cause infections in humans, makes them particularly relevant within the One Health framework. This section provides an overview of their prevalence, resistance patterns, and public health impact.

3.1. *Campylobacter* spp.

Campylobacter are leading bacterial causes of foodborne diarrhoea, responsible for an estimated 400–500 million cases of gastroenteritis annually (Igwaran and Okoh, 2019). In the US, approximately 1.5 million infections are reported each year, with an associated economic burden ranging from US\$1.3 to 6.8 billion (Kaakoush *et al.*, 2015), while annual costs in the EU are estimated at €2.4 billion (EFSA, 2024). Although most cases are mild and self-limiting, severe or systemic infections require antibiotic therapy, primarily macrolides and fluoroquinolones, with tetracyclines and aminoglycosides, such as gentamicin, occasionally used for invasive forms (Shen *et al.*, 2018). In the US, 29% of *Campylobacter* isolates

exhibit reduced susceptibility to these classes (CDC, 2019). Multidrug-resistant (MDR) strains are increasingly prevalent in low- and middle-income countries, where unregulated antibiotic use in animal production facilitates resistance spread through the food chain (Igwaran and Okoh, 2019; Gahamanyi et al., 2025). Ciprofloxacin resistance is particularly high in both humans and food-producing animals across the EU (EFSA/ECDC, 2025). In addition to *gyrA* point mutations, several MDR genes, *erm(B)*, *arsP*, *fosXCC*, and *cfr(C)*, have been identified (Tang et al., 2017; Shen et al., 2018). Horizontal gene transfer further complicates resistance monitoring and control (Guernier-Cambert et al., 2021).

3.2 *Salmonella*

Salmonella causes approximately 1.35 million infections annually in the US, leading to 26,500 hospitalisations and around 420 deaths (CDC, 2023). Of these, an estimated 212,500 cases are linked to antimicrobial-resistant strains, resulting in approximately 70 deaths and US\$400 million in treatment costs each year (CDC, 2019; 2023). Similarly, in the EU, 65,208 human salmonellosis cases were confirmed in 2022, with rising levels of AMR observed in isolates from humans, animals, and food, particularly against fluoroquinolones and third-generation cephalosporins (EFSA/ECDC, 2025), which complicates effective treatment. Commonly used antibiotic classes for treating *Salmonella* infections include β -lactams, fluoroquinolones, tetracyclines, aminoglycosides, and trimethoprim-sulfamethoxazole (Akinyemi and Ajoseh, 2017; San Millan, 2018). Resistance mechanisms in *Salmonella* involve alterations in antibiotic targets, overexpression of efflux pumps, and the acquisition of resistance genes, such as *bla*_{CTX-M}, *qnr*, and *aac(6')-Ib-cr*, which are also prevalent among other *Enterobacteriaceae* (WHO, 2023; Zhou et al., 2023; Monte et al., 2023). These resistance factors reduce therapeutic efficacy. The ability of *Salmonella* spp. to persist throughout the farm-to-fork continuum, along with its pronounced genetic adaptability, underscores its role as a critical vector in the spread of AMR under the One Health framework.

3.3 Shiga toxin-producing *Escherichia coli* (STEC)

STEC is a major foodborne pathogen responsible for severe gastrointestinal illness, including

haemorrhagic colitis and haemolytic uremic syndrome (HUS), particularly in children and the elderly. In 2022, 7,117 STEC cases were confirmed in the EU/EEA, with the highest rates in Ireland and Sweden (EFSA/ECDC, 2023). In the US, STEC causes an estimated 265,000 infections annually, leading to over 3,600 hospitalisations and 30 deaths (CDC, 2022). The most virulent serotype, *E. coli* O157:H7, is commonly linked to contaminated ground beef, raw milk, and fresh produce (Stager et al., 2023; Loor-Giler et al., 2025). Due to the risk of HUS, antibiotic treatment is generally avoided; however, AMR in STEC strains remains a significant public health concern. Resistance, particularly to ampicillin, tetracyclines, and trimethoprim-sulfamethoxazole, has been reported in both O157:H7 and non-O157 serogroups (Pan et al., 2021; EFSA/ECDC, 2025). Resistance genes, such as *bla*_{TEM}, *bla*_{CTX-M}, *tet(A/B)*, *sul*_{1/2}, and *dfrA*₁, are often plasmid- or integron-associated (Zhou et al., 2021; Chaudhary et al., 2023). MDR STEC strains have been detected in livestock, food, and the environment, with prevalence rates of 30–50%, particularly in areas with poor antibiotic regulation (Nada et al., 2023). While antimicrobial therapy is not standard for uncomplicated cases, MDR emergence poses risks in severe infections requiring treatment and contributes to the broader reservoir of resistance genes within the One Health interface.

3.4 *Listeria monocytogenes*

L. monocytogenes is a major zoonotic foodborne pathogen and the causative agent of listeriosis—a severe infection with high fatality rates among vulnerable populations. Though less common than other foodborne pathogens, it is associated with the highest hospitalisation and case-fatality rates in the EU. In 2022, 2,993 confirmed cases were reported across EU/EEA countries, with a case-fatality rate of 18.1% (EFSA/ECDC, 2023). In the US, approximately 1,600 cases and 260 deaths are recorded annually (CDC, 2024). While *L. monocytogenes* remains generally susceptible to first-line antibiotics like ampicillin and gentamicin, the emergence of resistant strains from food, clinical, and environmental sources is increasingly reported (Moura et al., 2023; Rippa et al., 2024; Soltysiuik et al., 2025). Key resistance mechanisms include plasmid- and transposon-mediated gene acquisition, biofilm and persister cell formation, and efflux pump activity (Bashiry et al., 2020; Nikolaou et al., 2025). These are often driven by antimicrobial use in both human and animal sectors (FAO/VMD,

2022). MDR strains have been detected in seafood, ready-to-eat meats, and dairy, complicating treatment and posing food safety risks (Menon *et al.*, 2021; Nikolaou *et al.*, 2025). *L. monocytogenes* can persist in food-processing environments and survive refrigeration, underscoring the need for stringent hygiene and AMR surveillance. Regional differences in resistance patterns, shaped by antibiotic use and regulatory practices, necessitate targeted monitoring strategies (Soltysiuk *et al.*, 2025). In the EU, Regulation (EC) No 2073/2005, as amended by Regulation (EU) 2024/2895 (applicable from July 2026), introduces a zero-tolerance requirement for *L. monocytogenes* in RTE foods supporting pathogen growth, aligning EU policy more closely with the US zero-tolerance approach.

3.5. Methicillin-resistant *Staphylococcus aureus* (MRSA)

MRSA plays a significant role in the transmission of AMR through the food chain. The emergence of livestock-associated MRSA (LA-MRSA) has further complicated AMR surveillance, especially in countries with intensive animal production systems (EFSA/ECDC, 2025). MRSA has been frequently detected in raw meat, milk, and dairy products, with contamination typically originating either from colonised animals or from infected food handlers (González-Machado *et al.*, 2024). Transmission can also occur via direct contact with infected animals or humans, as well as through contaminated food preparation surfaces (EFSA/ECDC, 2025). In the US, MRSA is responsible for over 323,700 infections and approximately 10,600 deaths annually, with associated healthcare costs exceeding US\$1.7 billion (CDC, 2019; Nelson *et al.*, 2022). In contrast, the EU recorded a decline in MRSA bloodstream infections, with an estimated 4.64 cases per 100,000 population in 2023, a 17.6% decrease compared to 2019 (ECDC, 2024). While recent EU cost estimates are limited, modelling studies suggest that MRSA infections affect around 150 000 patients yearly and impose an added burden of approximately €380 million on healthcare systems (Rocha *et al.*, 2020). Beyond the significant morbidity risk, particularly for immunocompromised

individuals, MRSA infections are very challenging and expensive to treat due to resistance to multiple antibiotic classes, including β -lactams, fluoroquinolones, and macrolides (Lade *et al.*, 2022; Abebe and Birhanu, 2023). Resistance is primarily mediated by the *mecA* gene, which encodes an altered penicillin-binding protein (PBP2a), conferring resistance to methicillin and other β -lactams. MRSA strains often carry additional resistance determinants, such as *erm* genes (macrolide resistance) and *norA*-associated efflux pumps (Abebe and Birhanu, 2023).

4. Mitigation of the AMR problem

The rising threat of AMR among major food-borne zoonotic bacteria underscores the need for an integrated and coordinated response. A sustainable solution to AMR requires the adoption of the One Health approach, which recognises the interconnection between human, animal, and environmental health. To address this complex challenge, the following elements are essential: *a*) rational use of antimicrobials in both human medicine and food-producing animals, supported by clear regulatory frameworks and stewardship programs; *b*) strengthening surveillance systems through harmonised monitoring protocols across sectors and countries, enabling early detection and timely intervention; *c*) investment in research focused on alternatives to antibiotics—such as vaccines, probiotics, phage therapy, and improved farming and hygiene practices; *d*) raising awareness and education of all stakeholders, including healthcare providers, veterinarians, farmers, policymakers, and consumers; *e*) implementation of national and regional action plans aligned with the Global Action Plan on AMR and adapted to local epidemiological realities; *f*) sustainable financing mechanisms, especially in resource-limited settings, to ensure continuity of AMR mitigation efforts; *g*) enhanced international collaboration and policy coherence across the human-animal-environment interface.

Only through a comprehensive and cross-disciplinary effort can we preserve the efficacy of life-saving antimicrobials and ensure a safer future for generations to come.

Disclosure Statement: No potential conflict of interest was reported by the authors.

Funding: The research results presented in this paper were funded by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, under the Agreement on the implementation and funding of scientific research work of scientific research organisations in 2025, No. 451-03-136/2025-03/200050 dated 4 February 2025.

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