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Review Paper

Major foodborne zoonotic bacteria and their role in antimicrobial resistance

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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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drivers include the intensive use of antibiotics in animal production, inappropriate therapeutic and prophylactic use, and weak regulatory oversight (*Nastasijevic 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 *blaCTX-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}, $bla_{\mathrm{CTX\text{-}M}}$, *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; *Sołtysiuk 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 (*Sołtysiuk 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 foodborne 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 lifesaving antimicrobials and ensure a safer future for generations to come.

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References

Abebe, A. A., & Birhanu, A. G. (2023). Methicillin-resistant *Staphylococcus aureus*: Molecular mechanisms underlying drug resistance development and novel strategies to combat. *Infection and Drug Resistance*, 16, 7641–7662. https://doi.org/10.2147/IDR.S428103

Akinyemi, K. O., & Ajoseh, S. O. (2017). Factors contributing to the emergence and spread of antibiotics resistance in *Salmonella* species. In *Current topics in Salmonella and Salmonellosis* (Chapter 6, pp. 97–114). https://doi.org/10.5772/67701

Antimicrobial Resistance Collaborators, (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *The Lancet*, 399(10325), 629–655. https://doi.org/10.1016/S0140-6736(21)02724-0

Bashiry, M., Javanmardi, F., Taslikh, M., Sheidaei, Z., Sadeghi, E., Abedi, A. S., Mirza Alizadeh, A., Hashempour-Baltork, F., Beikzadeh, S., Riahi, S. M., Hosseini, H., & Mousavi Khaneghah, A. (2022). *Listeria monocytogenes* in dairy products of the Middle East region: A systematic review, meta-analysis, and meta-regression study. *Iranian Journal of Public Health*, 51, 292. https://doi.org/10.18502/ijph.v51i2.8682

CDC, Centers for Disease Control and Prevention. (2019). *Antibiotic resistance threats in the United States, 2019*. https://www.cdc.gov/drugresistance/pdf/threats-report/2019-ar-threats-report-508.pdf (accessed May 29, 2025)

CDC, Centers for Disease Control and Prevention. (2022). *Annual reported cases of notifiable diseases and rates per 100,000, United States, 2020*. https://wonder.cdc.gov/nndss/static/2020/annual/2020-nndss.html

CDC, Centers for Disease Control and Prevention. (2023). *Salmonella*. https://www.cdc.gov/salmonella/index.html (accessed May 29, 2025)

CDC, Centers for Disease Control and Prevention. (2024). *Listeria (listeriosis)*. https://www.cdc.gov/listeria/index.html (accessed May 12, 2025)

Chaudhary, M. K., Jadhav, I., & Banjara, M. R. (2023). Molecular detection of plasmid mediated bla_{TEM}, $bla_{CTX-M,}$ and bla_{SHV} genes in Extended Spectrum β-Lactamase (ESBL) *Escherichia coli* from clinical samples. *Annals of Clinical Microbiology and antimicrobials*, 22(1), 33. https://doi.org/10.1186/s12941-023-00584-0

ECDC, European Centre for Disease Prevention and Control, (2024). *Antimicrobial resistance in the EU/EEA (EARS-Net) – Annual Epidemiological Report 2023*. Stockholm. https://www.ecdc.europa.eu/en/publications-data/antimicrobial-resistance-eueea-ears-net-annual-epidemiological-report-2023

EFSA, European Food Safety Authority, (2024). *Campylobacter*. Last reviewed: 2024. https://www.efsa.europa.eu/en/topics/topic/campylobacter (accessed May 12, 2025)

EFSA/ECDC, European Food Safety Authority, & European Centre for Disease Prevention and Control. (2023). The European Union One Health 2022 zoonoses report. *EFSA Journal*, 21, e08133. https://doi.org/10.2903/j.efsa.2023.8133

EFSA/ECDC, European Food Safety Authority, & European Centre for Disease Prevention and Control. (2025). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2022–2023. *EFSA Journal*, 23, 9237. https://doi.org/10.2903/j.efsa.2025.9237

European Commission, (2005). Commission Regulation (EC) No 2073/2005 of 15 November 2005 on microbiological criteria for foodstuffs. *Official Journal of the European Union*, L338, 1–26. Available: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX: 32005R2073 (accessed May 12, 2025)

European Commission, (2024). Commission Regulation (EU) 2024/2895 of 18 October 2024 amending Regulation (EC) No 2073/2005 as regards microbiological criteria for foodstuffs. *Official Journal of the European Union* L, 18–22. Available: https://eur-lex.europa.eu/legal-content/EN/TXT/?uri=CELEX:32024R2895 (accessed 12 May 2025)

FAO/VMD, Food and Agriculture Organization & Veterinary Medicines Directorate. (2022). Tackling antimicrobial use and resistance in food-producing animals—Lessons learned in the United Kingdom. FAO. https://www.fao.org/documents/card/en/c/cc1123en/

Founou, L. L., Founou, R. C., & Essack, S. Y. (2016). Antibiotic resistance in the food chain: A developing country-perspective. *Frontiers in Microbiology*, 7, 1881. https://doi.org/10.3389/fmicb.2016.01881

Gahamanyi, N., Habimana, A. M., Harerimana, J. P., et al. (2025). High prevalence of antibiotic resistant *Campylobacter* among patients attending clinical settings in Kigali, Rwanda. *BMC Infectious Diseases*, 25, 225. https://doi.org/10.1186/s12879-025-10626-x

González-Machado, C., Capita, R., & Alonso-Calleja, C. (2024). Methicillin-resistant *Staphylococcus aureus* (MRSA) in dairy products and bulk-tank milk (BTM). *Antibiotics* (Basel, Switzerland), 13(7), 588. https://doi.org/10.3390/antibiotics13070588

Guernier-Cambert, V., Trachsel, J., Maki, J., Qi, J., Sylte, M. J., Hanafy, Z., Kathariou, S., & Looft, T. (2021). Natural horizontal gene transfer of antimicrobial resistance genes in *Campylobacter* spp. from turkeys and swine. *Frontiers in Microbiology*, 12, 732969. https://doi.org/10.3389/fmicb.2021.732969

Igwaran, A., & Okoh, A. I. (2019). Human campylobacteriosis: A public health concern of global importance. *Heliyon*, 5(11), Article e02814. https://doi.org/10.1016/j.heliyon.2019.e02814

Kaakoush, N. O., Castaño-Rodríguez, N., Mitchell, H. M., & Man, S. M. (2015). Global epidemiology of *Campylobacter* infection. *Clinical Microbiology Reviews*, 28(3), 687–720. https://doi.org/10.1128/CMR.00006-15

Lade, H., Joo, H.-S., & Kim, J.-S. (2022). Molecular basis of non-β-lactam antibiotics resistance in *Staphylococcus aureus*. *Antibiotics*, 11, 1378. https://doi.org/10.3390/antibiotics11101378

Loor-Giler, A., Robayo-Chico, M., Puga-Torres, B., Hernandez-Alomia, F., Santander-Parra, S., Piantino Ferreira, A., Muslin, C., & Nuñez, L. (2025). *Escherichia coli* O157:H7, a common contaminant of raw milk from Ecuador: Isolation and molecular identification. *Foods*, 14(3), 410. https://doi.org/10.3390/foods14030410

Manyi-Loh, C., Mamphweli, S., Meyer, E., & Okoh, A. (2018). Antibiotic use in agriculture and its consequential resistance in environmental sources: Potential public health implications. *Molecules*, 23(4), 795. https://doi.org/10.3390/molecules23040795

Mc Nulty, K. M., Soon, J. M., Wallace, C. A., & Nastasijevic, I. (2016). Antimicrobial resistance monitoring and surveillance in the meat chain: A report from five countries in the European Union and European Economic Area. *Trends in Food Science and Technology*, 58, 1–13. https://doi.org/10.1016/j.tifs.2016.09.010

Menon, K. V., Sunil, B., & Latha, C. (2021). Prevalence and antibiotic resistance profile of *Listeria* spp. associated with seafoods from fish catchment areas in Kerala, India. *Veterinary World*, 14(3), 777–783. https://doi.org/10.14202/vetworld.2021.777-783

Milijašević, M., Vesković-Moračanin, S., Babić Milijašević, J., Petrović, J., & Nastasijević, I. (2024). Antimicrobial resistance in aquaculture: Risk mitigation within the One Health context. *Foods*, 13, 2448. https://doi.org/10.3390/foods13152448

Monte, D. F., Oliveira, S. D., Lopes, G. V., Nascimento, E. R., Pereira, V. L. A., & dos Santos, L. R. (2023). Resistance profile of *Salmonella* spp. to third generation cephalosporins and quinolones in chicken carcasses from Rio de Janeiro, Brazil. *Revista Brasileira de Ciência Avícola*, 25(1), eRBCA-2023-0010. https://doi.org/10.1590/1806-9061-2023-0010

Moura, A., Leclercq, A., Vales, G., Tessaud-Rita, N., Bracq-Dieye, H., Thouvenot, P., Madec, Y., Charlier, C., & Lecuit, M. (2023). Phenotypic and genotypic antimicrobial resistance of *Listeria monocytogenes*: An observational study in France. *The Lancet Regional Health – Europe*, 37, 100800. https://doi.org/10.1016/j.lanepe.2023.100800

Muteeb, G., Rehman, M. T., Shahwan, M., & Aatif, M. (2023). Origin of antibiotics and antibiotic resistance, and their impacts on drug development: A narrative review. *Pharmaceuticals*, 16(11), 1615. https://doi.org/10.3390/ph16111615

Nada, H. G., El-Tahan, A. S., El-Didamony, G., El-Gharabawy, R., El-Mokhtar, M. A., & Abdelaziz, M. A. (2023). Detection of multidrug-resistant Shiga toxin-producing *Escherichia coli* in some food products and cattle faeces in Al-Sharkia, Egypt: One Health menace. *BMC Microbiology*, 23, 127. https://doi.org/10.1186/s12866-023-02873-2

Nastasijevic, I., Proscia, F., Jurica, K., & Vesković-Moračanin, S. (2023). Tracking antimicrobial resistance along the meat chain: One Health context. *Food Reviews International*, 40(9), 2775–2809. https://doi.org/10.1080/87559129.2023.2279590

Nelson, R. E., Hyun, D., Jezek, A., & Samore, M. H. (2022). Mortality, length of stay, and healthcare costs associated with multidrug-resistant bacterial infections among elderly hospitalized patients in the United States. *Clinical Infectious Diseases*, 74(6), 1070–1080. https://doi.org/10.1093/cid/ciab696

Nikolaou, F. G., Colobatiu, L. M., Ciupescu, L. M., Tabaran, A., Hategan, A. R., Mihaiu, R., Tanasuica, R., Poenaru, M. M., & Mihaiu, M. (2025). Prevalence and antimicrobial resistance of *Listeria monocytogenes* isolated from dairy products in Romania. *Antibiotics*, 14(5), 482. https://doi.org/10.3390/antibiotics14050482

O'Neill, J. (2016). *Tackling drug-resistant infections globally: Final report and recommendations*. Review on Antimicrobial Resistance. https://amr-review.org/sites/default/files/160525_Final%20paper_with%20cover.pdf

OECD/WHO, Organisation for Economic Co-operation and Development, & World Health Organization. (2022). *Addressing the burden of infections and antimicrobial resistance associated with health care*. Paris/Geneva. https://www.oecd.org/health/Addressing-burden-of-infections-and-AMR-associated-with-health-care.pdf (accessed May 12, 2025)

Pan, Y., Hu, B., Bai, X., Yang, X., Cao, L., Liu, Q., Sun, H., Li, J., Zhang, J., Jin, D., & Xiong, Y. (2021). Antimicrobial resistance of non-O157 Shiga toxin-producing *Escherichia coli* isolated from humans and domestic animals. *Antibiotics*, 10(1), 74. https://doi.org/10.3390/antibiotics10010074

Rippa, A., Bilei, S., Peruzy, M. F., Marrocco, M. G., Leggeri, P., Bossù, T., & Murru, N. (2024). Antimicrobial resistance of *Listeria monocytogenes* strains isolated in food and food-processing environments in Italy. *Antibiotics*, 13(6), 525. https://doi.org/10.3390/antibiotics13060525

Rocha, L. E. C., Singh, V., Esch, M., Lenaerts, T., Liljeros, F., & Thorson, A. (2020). Dynamic contact networks of patients and MRSA spread in hospitals. *Scientific Reports*, 10, 9336. https://doi.org/10.1038/s41598-020-66270-9

San Millan, A. (2018). Evolution of plasmid-mediated antibiotic resistance in the clinical context. *Trends in Microbiology*, 26(12), 978–985. https://doi.org/10.1016/j.tim.2018.06.007

Serwecińska, L. (2020). Antimicrobials and antibiotic-resistant bacteria: A risk to the environment and to public health. *Water*, 12(12), 3313. https://doi.org/10.3390/w12123313

Shen, Z., Wang, Y., Zhang, Q., & Shen, J. (2018). Antimicrobial resistance in *Campylobacter* spp. *Microbiology Spectrum*, 6(2), eARBA-0013-2017. https://doi.org/10.1128/microbiolspec.ARBA-0013-2017

Sołtysiuk, M., Przyborowska, P., Wiszniewska-Łaszczych, A., Grabczak, M., & Kwit, R. (2025). Prevalence and antimicrobial resistance profile of *Listeria* spp. isolated from raw fish. *BMC Veterinary Research*, 21, 333. https://doi.org/10.1186/s12917-025-04792-y

Stager, C., Donovan, D., Edwards, L., Pereira, E., Williams, L., Freiman, J., Schwensohn, C., & Gieraltowski, L. (2023). Notes from the field: Multistate outbreak of *Escherichia coli* O157:H7 infections linked to a national fast-food chain – United States, 2022. *Morbidity and Mortality Weekly Reports*, 72(26), 732–733. https://doi.org/10.15585/mmwr.mm7226a6

Tang, Y., Dai, L., Sahin, O., Wu, Z., Liu, M., & Zhang, Q. (2017). Emergence of a plasmid-borne multidrug resistance gene *cfr*(C) in foodborne pathogen *Campylobacter*. *Journal of Antimicrobial Chemotherapy*, 6, 1581–1588. https://doi.org/10.1093/jac/dkx023

Vesković, S. (2025). In the global food system: Addressing food losses, waste, and safety. In S. Vesković (Ed.), *Natural food preservation: Controlling loss, advancing safety*. Springer. https://doi.org/10.1007/978-3-031-85089-9_2

WHO, World Health Organization, (2015). *WHO estimates of the global burden of foodborne diseases: Foodborne Disease Burden Epidemiology Reference Group 2007–2015*. https://apps.who.int/iris/handle/10665/199350

WHO, World Health Organization, (2017). *Guidelines on use of medically important antimicrobials in food-producing animals*. Geneva. https://www.who.int/publications/i/item/9789241550130

WHO, World Health Organization. (2023). *Antimicrobial resistance*. https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance (accessed May 29, 2025)

Zhou, K., Sun, L., Zhang, X., Xu, X., Mi, K., Ma, W., & Zhang, L. (2023). *Salmonella* antimicrobials inherited and the non-inherited resistance: Mechanisms and alternative therapeutic strategies. *Frontiers in Microbiology*, 14, 1176317. https://doi.org/10.3389/fmicb.2023.1176317

Zhou, W., Zhang, E., Zhou, J., Zhao, X., Chen, H., & Wang, Q. (2021). Characterization and comparative genomics analysis of IncFII multi-resistance plasmids carrying *bla*$_{\text{CTX-M}}$ and Type1 integrons from *Escherichia coli*. *Frontiers in Microbiology*, 12, 753979. https://doi.org/10.3389/fmicb.2021.753979

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