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Biological Hazard of antimicrobial resistant Foodborne pathogen

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Abstract
Antimicrobial resistance (AMR) remains of major interest for different types of food, antimicrobial-resistant bacteria, and/or antimicrobial resistance genes (transfer in pathogenic bacteria). The spread of pathogenic bacteria from food to consumers may occur by direct or indirect routes. Zoonotic microbes can spread through the environment, animals, humans, and the food chain. Antimicrobial drugs are used globally to treat infections in humans and animals and prophylactically in production agriculture. Research highlights that foods may become contaminated with AMR bacteria (AMRB) through the different stages that food goes through beginning and finally to the consumer. Multidrug -resistant foodborne microorganisms made the food safety situation more vulnerable to public health. Some microorganisms maintain their normal life functions in food and are used in food production, whereas others may cause food spoilage or food poising. Salmonella spp., *Campylobacter spp*., *Staphylococcus aureus*, *Escherichia coli,* and *Listeria monocytogenes* are the most pathogens causing health hazard. Approximately 1.8 million people die each year due to food-borne diarrheal infections in developing countries. The development of resistant bacteria in food animals can result from chromosomal mutations but is more commonly associated with the horizontal transfer of resistance determinants borne on mobile genetic elements. Food may represent a dynamic environment for the continuing transfer of antibiotic resistance determinants between bacteria.

Keywords: *Resistance; Antimicrobial; Foodborne; Microbes.*

Introduction

Recontamination of food during post-processing may be the cause of outbreaks of foodborne disease **Ansari, (2015).** The microbiological safety of food has become an important concern for consumers, various industries, and regulatory agencies because foodborne illness is one of the most significant public health problems worldwide **Bavisetty *et al.,* (2018).**

Antibiotic resistance was confirmed for all major foodborne pathogens: *Staphs, aureus.*, Salmonella spp., *Escherichia coli,* and *Listeria monocytogenes* **Jajere, (2019).** Many deaths accurse annually as a result of infection by antimicrobial-resistant pathogens, and the outlook is bleak, with premature mortality of nearly 300 million people by 2050 **Vikesland *et al.,* (2019)**. Swann was one of the first to sound the alarm about the problems linked to the indiscriminate use of antibiotics, suggesting that the enormous amount of antibiotics used without following norms could be unsafe for human health **Swann, (2020).**

The Food and Agriculture Organization **FAO, (2020)** the World Organization for Animal Health (WOIE), and WHO recommended the 'One Health' approach which supporting healthy animals, healthy people, and healthy environments

AMR has become a general threat to the prevention and management of bacterial infections **WHO, (2022)**. AMR threats are growing daily due to the occurrence of resistance in the bacterial strains for antibiotics **UNEP, (2022).** 600 million people are ill worldwide, and the resulting economic losses exceed USD 100 billion **WHO, (2022).**

The bacterial genera and species most commonly identified as emerging foodborne pathogens in scientific publications include *Escherichia coli*, Salmonella enterica*, Staph aureus.,* *Listeria monocytogenes* **Spernovasilis *et al.,* (2022)**. The indiscriminate usage of antimicrobials in human treatment and in animals of food production leads to the emerging and spread of antimicrobial-resistant bacteria (ARB) and AMR genes (ARGs) throughout the food supply chain **Kenyon, (2021).**

Foodborne Microbes Displaying Resistance:

Antibiotics are the most prescribed drugs that are used as antimicrobial substances during the production of foods such as meat and milk, and products derived from these are of major concern since antimicrobial residues may remain in foods intended for human consumption **CDC, (2020) and WHO, (2020).**

***Escherichia coli* Foodborne:**

Escherichia coli consider as food spoilage agent and is a is a foodborne pathogen **CDC, (2020) and WHO, (2020).** *E. coli* is widespread in the environment, and infections usually result from the consumption of fecally contaminated water or food. *E. coli* poisoning comes from contamination fruits , vegetables, poultry, pork, beef, fish, and milk **Enciso-Martínez *et al.,* (2022)**.

Shiga toxin produced by *E. coli* strains belonging to the EHEC pathotype, the cause of many foodborne outbreaks worldwide, may lead to bloody diarrhoea, haemorrhagic colitis, and haemolytic uremic syndrome **Asadi *et al.,* (2022).** *E. coli* O157:H7 in the 2011 outbreak led to 50 deaths. *E. coli* strains showed resistance to amoxicillin, tetracycline, cefotaxime, and ciprofloxacine **Smith & Fratamico (2018)**.

Methicillin Resistant *Staph. aureus* Foodborne:

Staph. aureus (MRSA) may resist methicillin and several other vital antibiotics. *Staph aureus* is a foodborne pathogen that causes food poisoning due to toxin production in food **Pourmand *et al.,* (2017)**. *Staph aureus* food poisoning is caused by enterotoxins produced in consumed food poisoning caused by *Staph. aureus* is characterized by a short incubation period (from 30 minutes to 8 hours), a rapid course, and frequent remission after 24 hours. The main symptoms include abdominal pain, nausea, vomiting, and diarrhoea. **Grispoldi *et al.,* (2021).**

Salmonella Foodborne:

Salmonella typhi and *S. paratyphi,* causing typhoid fever and paratyphoid fever, respectively, are responsible for infections only in humans. *Salmonella enteritidis* and *Salmonella. typhimurium* contribute to human digestive tract infections, with vomiting, diarrhoea, and fever; they are usually self-limiting but may also lead to extremely dangerous bacteraemia and intravascular and focal infections **(Marchello *et al.,* 2022)**. Infections caused by resistant strains of Salmonella may be more severe and result in higher rates of hospitalization. Almost all AMR Salmonella infections are foodborne and linked to the consumption of contaminated pork, turkey, beef, and chicken **Nair *et al.,* (2018).** The most common sources of infection are poultry meat, pork, eggs, dried food, infant formulas fruit and vegetable products **Krzyżewska-Dudek *et al.,* (2022)**.

***Listeria monocytogenes* Foodborne:**

The major sources of Listeria are milk raw fruits and vegetables, raw and smoked fish, raw meat, and ready-to-eat food. *Listeria monocytogenes* is tolerant to changing environmental conditions and can grow in a wide range of temperatures (0–45◦C), pH (4.3–9.6), and salinity (10.0% NaCl) **Skowron *et al.,* (2019).**

Due to its high adaptability, in recent years, there have been several major listeriosis outbreaks, including those associated with ready-to-eat processed meat products in 2017–2018 in the Republic of South Africa (200 deaths) **Smith *et al.,* (2019).**

Antimicrobial resistance:
AMR is defined as the inability or reduced ability of an antimicrobial agent to inhibit the growth of a bacterium, so that it can lead to therapy failure. Resistance to bacteria has occurred due to mutation, the uptake of exogenous genes by horizontal transfer from other bacterial strains, or the activation or triggering of a genetic cascade, thereby inducing the expression of resistance mechanisms **EFSA, (2008).**

The spread of AMR through relevant sectors occurs in two ways: first through the spread of the bacteria that carry resistance genes, and second through the spread of resistance genes between bacteria via horizontal gene transfer (HGT) **Patricia *et al.,* (2019); Wang *et al.,* (2012) and Wooldridge (2012).**

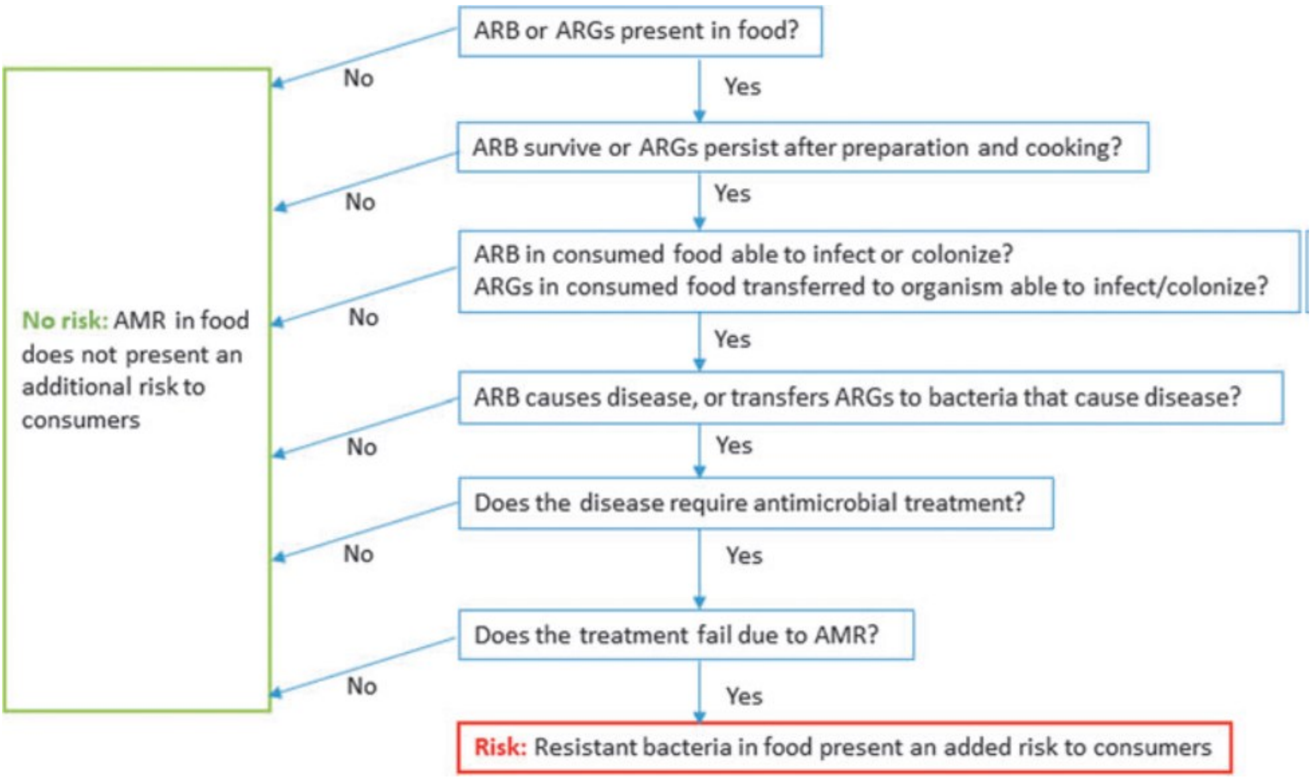

Fig. (1). Criteria required for the consideration of AMR as a distinct food safety risk. AMR, antimicrobial resistance; ARB, antimicrobial-resistant bacteria; ARGs, AMR genes. Adapted from **Smith & Fratamico, (2018).**

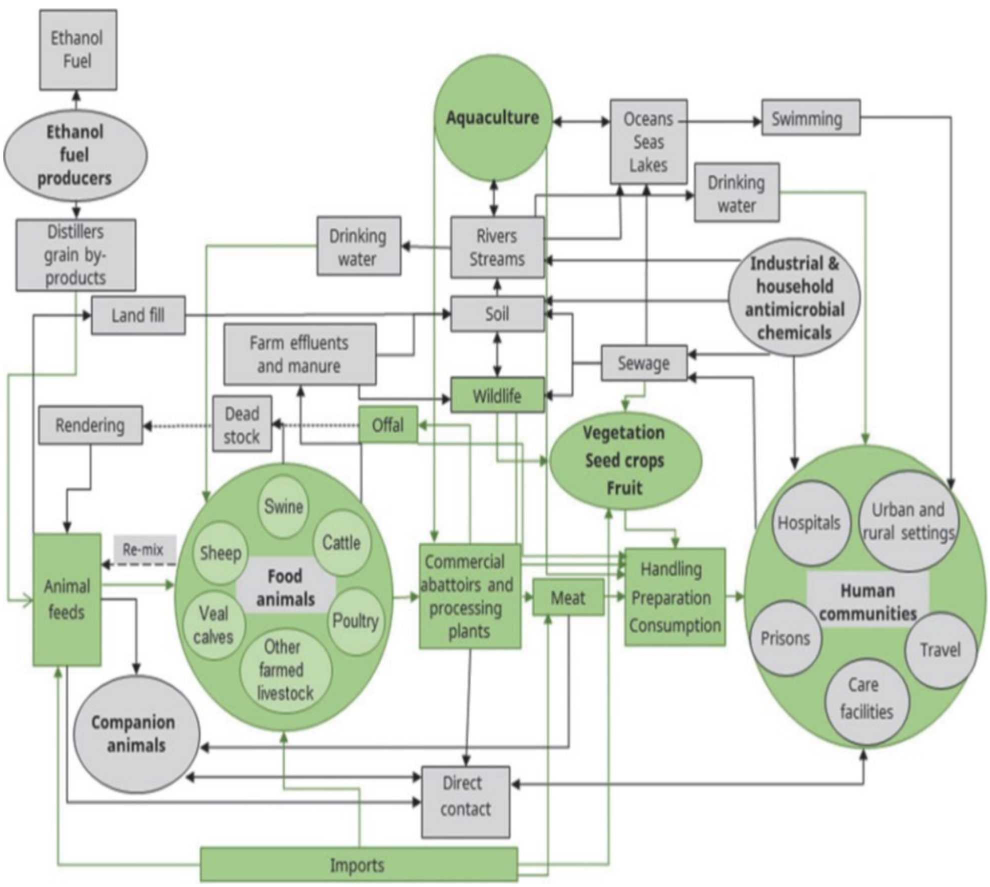

Fig. (2). AMR is a One-Health issue. Network diagram showing the settings where AMR may emerge, persist, or spread. The bold type indicates areas where antimicrobial use or exposure may occur. Green areas and arrows have a direct link to the foodborne pathway. Adapted from **Smith & Fratamico (2018).** AMR, antimicrobial resistance.

Mechanisms in Antimicrobial Resistance Bacteria (AMRB):

Microbes utilize various mechanisms to counteract antimicrobial agents, such as the breakdown of antibiotics or antibacterial agents by enzymes, modifications of antibiotic targets, changes in cell wall permeability, and the activation of alternative pathways **Verraes *et al.,* (2013).** Antimicrobial resistance (AMR) is a globally recognized threat and exemplifies the rapid adaptation of microbes to new environments. A prevalent mechanism of bacterial resistance is the enzymatic degradation of antimicrobial agents. Resistance to aminoglycosides is predominantly driven by enzymatic degradation through acetyltransferases, nucleotidyltransferases, and phosphotransferases **Grudlewska-Buda *et al.,* (2023) and Pires *et al.,* (2017)**.

Antimicrobial Resistance of food born bacteria:

Antimicrobial Resistance of *E. coli*

The wide variety of pathogenic *E. coli* strains and the emergence of multiple AMR mechanisms contribute to antibiotic resistance in E. coli, a frequently encountered issue. Currently, the most concerning isolates are those producing extended-spectrum β-lactamases and carbapenemases (such as KPC-2, NDM, and OXA -48-like), which often show resistance to cephalosporins, quinolones, and aminoglycosides **Alegría *et al.,* (2020) and Sivakumar *et al.,* (2021)**.

Antimicrobial Resistance of *Staphylococcus. aureus*

The antimicrobial resistance (AMR) in *Staph. aureus* has led to the emergence of methicillin-resistant *Staph. aureus* (MRSA) strains, which are resistant to almost all beta-lactam antibiotics and, in some cases, to many other antibiotic and chemotherapeutic groups. Due to *Staph. aureus* high survival rate outside a host (even for several months), multidrug-resistant strains present a significant issue not only in hospitals but also in the food production environment. *Staph. aureus* is a foodborne pathogen responsible for food poisoning due to its production of enterotoxins in food **Grispoldi *et al.,* (2021).**

Antibiotic Resistance of Salmonella spp.

Recently, the most pressing concern has been the increasing resistance of non-typhoidal *S. enteritidis* and *S. typhimurium* to antibiotics. Salmonella cells acquire mobile genetic elements, including plasmids with IncA/C, B/O, HI1, HI2, I1, N, F, and P replicons, which are often linked to multidrug resistance (MDR) **Chen *et al.,* (2016); Jacob *et al.,* (2022) and Nadi *et al.,* (2020).**

Antimicrobial Resistance of *Listeria monocytogenes:*

The preferred antibiotic therapy for treating listeriosis includes gentamicin or ampicillin, as well as rifampicin, vancomycin, linezolid, and carbapenem. If the patient is allergic to beta-lactam antibiotics, trimethoprim is used **Maury *et al.,* (2016).** In recent years, resistance to various antibiotics, including those used to treat listeriosis, has been observed in strains of *Listeria monocytogenes*. These strains have shown resistance to rifampicin, vancomycin, ampicillin, gentamycin, erythromycin, chloramphenicol, sulfamethoxazole, amoxicillin, and trimethoprim. The first multidrug-resistant strain of *Listeria monocytogenes* was identified in 1988 from a patient with meningitis in France **Unrath *et al.,* (2021)**.

Different Strategies to Control Antimicrobial Resistance Bacteria (AMRB):

Foodborne infections caused by AMR are among the most critical public health concerns. Infections caused by AMRB significantly increase morbidity and mortality rates, particularly in developing countries, while in developed nations, they lead to higher therapeutic costs **Harbarth *et al.,* (2015)**. The WHO established a 'Strategic and Technical Advisory Group' on AMR and recommended that WHO should play a leading role in forming the action plan. The FAO initiated its Plan for Antimicrobial Resistance to support WHO's global action plan in the food and agricultural sectors **FAO, (2020).**

The One Health approach was proposed by international organizations to mitigate AMR risks, forming an alliance between WHO, FAO, and OIE as a 'tripartite alliance.' WHO also launched a plan to address this global issue in collaboration with tripartite partners and released a 'Global Action Plan' on AMR **WHO, (2020).**

Highlighting possible strategies to address AMR concerns, WHO Global Action Plan outlines five strategic objectives as follows:

Increase Awareness: Awareness campaigns supported by mass and frequent messaging on social media about AMR can reduce antibiotic usage and mitigate the risks posed by AMR.

Promote Knowledge through Survillance: Governments, NGOs, industry, and academia can enhance their practical knowledge to tackle AMR issues

Hygiene, and Preventive Measures: Maintaining proper hygiene and cleanliness by adhering to recommended guidelines and good practices can help reduce AMR concerns.

Regulate Antimicrobials Use: Implementing mandatory guidelines, particularly for antibiotics used in treating infections in animals and humans, and banning the use of drugs as growth promoters in animals are essential.

Boost Economic Investment: There is a need for investments in the development of new antimicrobial treatments, green technology, analytical tools, and vaccines. A lack of such investments highlights the ongoing trend of persistent AMR **Samtiya *et al.,* (2022) and WHO (2023)**

World Antibiotic Awareness Week:

The objective of World Antibiotic Week is to emphasize the importance of using antibiotics prudently, promote education on proper usage, and encourage research for alternative antibiotics. World Antimicrobial Awareness Week has been renamed to World AMR Awareness Week (WAAW) after global consultations with participants from various sectors and regions. The decision to rename the campaign was driven by the need for a more accurate term that encompasses the concept of resistance, which is the primary challenge to be addressed. **Kujat Choy *et al.,* (2023) and WHO, (2023)**.

Conclusion

Foodborne bacteria, encompassing both pathogens and commensal bacteria, are showing a growing, extensive, and varied range of resistance to antimicrobial agents that are crucial for human and veterinary medicine. Preventing the spread of foodborne bacteria through food is vital for controlling the dissemination of antimicrobial-resistant pathogenic bacteria. Ensuring proper hygiene and cleanliness, along with reducing the use of antibiotics in humans and animals, can be achieved by using vaccines, probiotics, and vitamins to boost immunity, thereby minimizing the reliance on antibiotics

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The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests:

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References

Alegría, Á.; Arias-Temprano, M.; Fernández-Natal, I.; Rodríguez-Calleja, J.M.; García-López, M.L. and Santos, J.A. (2020). Molecular Diversity of ESBL-Producing *Escherichia coli* from Foods of Animal Origin and Human Patients. International Journal of Environmental Research and Public Health, 17(4),1312-1320. https://doi.org/10.3390/ijerph17041312

Ansari, C.B. (2015). Bacteriological examination of ready-to-eat foods (RTE) products of Tehran province, Iran. Adv. Food Sci. Technol, 3(7), 328–331.

Asadi, Z.; Ghanbarpour, R.; Kalantar-Neyestanaki, D. and Alizade, H. (2022). Determination of extended-spectrum β-lactamase producing and hybrid pathotypes of *Escherichia coli* isolates from diarrheic samples. Gene Reports, 27, 101583. https://doi.org/https://doi.org/10.1016/j.genrep.2022.101583

Bavisetty, S.C.B.; Vu, H.T.K.; Benjakul, S. and Vongkamjan, K. (2018). Rapid pathogen detection tools in seafood safety. Current Opinion in Food Science, 20, 92–99. https://doi.org/https://doi.org/10.1016/j.cofs.2018.05.013

Carl, N. and Otto, C. (2024). Antibiotic Resistance — Problems, Progress, and Prospects. New England Journal of Medicine, 371(19), 1761–1763. https://doi.org/10.1056/NEJMp1408040

CDC (2020). Antibiotic Resistance Threats in the United States; U.S. Department of Health and Human Services: Atlanta, GA, USA.

Chen, W.; Fang, T.; Zhou, X.; Zhang, D.; Shi, X. and Shi, C. (2016). IncHI2 Plasmids Are Predominant in Antibiotic-Resistant Salmonella Isolates. Frontiers in Microbiology, 7. https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2016.01566

European Food Safety Authority 'EFSA' (2008). Scientific Opinion of the Panel on Biological Hazards on a request from the European Food Safety Authority (EFSA) on overview of methods for source attribution for human illness from foodborne microbiological hazards. EFSA Journal, 764, 143.

Enciso-Martínez, Y.; González-Aguilar, G. A.; Martínez-Téllez, M.A.; González-

Pérez, C.J.; Valencia-Rivera, D.E.; Barrios-Villa, E. and Ayala-Zavala, J.F. (2022). Relevance of tracking the diversity of *Escherichia coli* pathotypes to reinforce food safety. International Journal of Food Microbiology, 374, 109736. https://doi.org/https://doi.org/10.1016/j.ijfoodmicro.2022.109736

Food and Agriculture Organization 'FAO' (2020). Action Plan on Antimicrobial Resistance. http://www.fao.org/3/a-i5996e.pdf

Grispoldi, L.; Karama, M.; Armani, A.; Hadjicharalambous, C. and Cenci-Goga, B.T. (2021). *Staphylococcus aureus* enterotoxin in food of animal origin and staphylococcal food poisoning risk assessment from farm to table. Italian Journal of Animal Science, 20(1), 677–690. https://doi.org/10.1080/1828051X.2020.1871428

Grudlewska-Buda, K.; Bauza-Kaszewska, J.; Wiktorczyk-Kapischke, N.; Budzyńska, A.; Gospodarek-Komkowska, E. and Skowron, K. (2023). Antibiotic Resistance in Selected Emerging Bacterial Foodborne Pathogens—An Issue of Concern?. Antibiotics, 12(5). https://doi.org/10.3390/antibiotics12050880

Harbarth, S.; Balkhy, H.H.; Goossens, H.; Jarlier, V.; Kluytmans, J.; Laxminarayan, R.; Saam, M.; Van Belkum, A.; Pittet, D. and participants, for the W.H.A.I.R.F. (2015). Antimicrobial resistance: one world, one fight!. Antimicrobial Resistance and Infection Control, 4(1), 49. https://doi.org/10.1186/s13756-015-0091-2

Jacob, J.J.; Solaimalai, D.; Rachel, T.; Pragasam, A.K.; Sugumar, S.; Jeslin, P.; Anandan, S. and Veeraraghavan, B. (2022). A secular trend in invasive non-typhoidal Salmonella in South India, 2000–2020: Identification challenges and antibiogram. Indian Journal of Medical Microbiology, 40(4), 536–540. https://doi.org/https://doi.org/10.1016/j.ijmmb.2022.07.015.

Jajere, S.M. (2019). A review of Salmonella enterica with particular focus on the pathogenicity and virulence factors, host specificity and antimicrobial resistance including multidrug resistance. Veterinary World, 12 (4), 504–521. https://doi.org/10.14202/vetworld.2019.504-521

Kenyon, C. (2021). Positive Association between the Use of Quinolones in Food Animals and the Prevalence of Fluoroquinolone Resistance in *E. coli* and *K. pneumoniae, A. baumannii* and *P. aeruginosa*: A Global Ecological Analysis. Antibiotics,10 (10). https://doi.org/10.3390/antibiotics10101193

Krzyżewska-Dudek, E.; Kotimaa, J.; Kapczyńska, K.; Rybka, J. and Meri, S. (2022). Lipopolysaccharides and outer membrane proteins as main structures involved in complement evasion strategies of non-typhoidal Salmonella strains. Molecular Immunology, 150, 67–77. https://doi.org/https://doi.org/10.1016/j.molimm.2022.08.009

Kujat Choy, S.; Neumann, E.M.; Romero-Barrios, P. and Tamber, S. (2023). Contribution of Food to the Human Health Burden of Antimicrobial Resistance. Foodborne Pathogens and Disease, 21(2), 71–82. https://doi.org/10.1089/fpd.2023.0099

Marchello, C.S.; Birkhold, M.; Crump, J.A.; Martin, L.B.; Ansah, M.O.; Breghi, G. Canals, R.; Fiorino, F.; Gordon, M.A.; Kim, J.H.; Hamaluba, M.; Hanumunthadu, B.; Jacobs, J.; Kariuki, S.; Malvolti, S.; Mantel, C.; Marks, F.; Medaglini, D. Mogasale, V. and Tack, B. (2022). Complications and mortality of non-typhoidal salmonella invasive disease: a global systematic review and meta-analysis. The Lancet Infectious Diseases, 22(5), 692–705. https://doi.org/10.1016/S1473-3099(21)00615-0

Maury, M.M.; Tsai, Y.H.; Charlier, C.; Touchon, M.; Chenal-Francisque, V.; Leclercq, A.; Criscuolo, A.; Gaultier, C.; Roussel, S.; Brisabois, A.; Disson, O.; Rocha, E.P.C.; Brisse, S. and Lecuit, M. (2016). Uncovering Listeria monocytogenes hypervirulence by harnessing its biodiversity. Nature Genetics, 48(3), 308–313. https://doi.org/10.1038/ng.3501

Nadi, Z.R.; Salehi, T.Z.; Tamai, I.A.; Foroushani, A.R.; Sillanpaa, M. and Dallal, M.M.S. (2020). Evaluation of antibiotic resistance and prevalence of common Salmonella enterica serovars isolated from foodborne outbreaks. Microchemical Journal, 155, 104660. https://doi.org/https://doi.org/10.1016/j.microc.2020.104660

Patricia, A.; Carla, N. and Luisa, P. (2020). Food-to-Humans Bacterial Transmission. Microbiology Spectrum, 8(1), 1–26. https://doi.org/10.1128/microbiolspec.mtbp-0019-2016

Pires, D.; de Kraker, M.E.A.; Tartari, E.; Abbas, M. and Pittet, D. (2017). Fight Antibiotic Resistance—It's in Your Hands: Call From the World Health Organization for 5th May 2017. Clinical Infectious Diseases, 64 (12), 1780–1783. https://doi.org/10.1093/cid/cix226

Pourmand, A.; Mazer-Amirshahi, M.; Jasani, G. and May, L. (2017). Emerging trends in antibiotic resistance: Implications for emergency medicine. The American Journal of Emergency Medicine, 35(8), 1172–1176. https://doi.org/https://doi.org/10.1016/j.ajem.2017.03.010

Samtiya, M.; Matthews, K.R.; Dhewa, T. and Puniya, A.K. (2022). Antimicrobial Resistance in the Food Chain: Trends, Mechanisms, Pathways, and Possible Regulation Strategies. Foods ,11(19). https://doi.org/10.3390/foods11192966

Sivakumar, M.; Abass, G.; Vivekanandhan, R.; Anukampa, Singh, D.K.; Bhilegaonkar, K.; Kumar, S.; Grace, M.R. and Dubal, Z. (2021). Extended-spectrum beta-lactamase (ESBL) producing and multidrug-resistant *Escherichia coli* in street foods: a public health concern. Journal of Food Science and Technology, 58(4), 1247–1261. https://doi.org/10.1007/s13197-020-04634-9

Skowron, K.; Wiktorczyk, N.; Grudlewska, K.; Wałecka-Zacharska, E.; Paluszak, Z.; Kruszewski, S. and Gospodarek-Komkowska, E. (2019). Phenotypic and genotypic evaluation of *Listeria monocytogenes* strains isolated from fish and fish processing plants. Annals of Microbiology, 69 (5), 469–482. https://doi.org/10.1007/s13213-018-1432-1

Smith, A.M.; Tau, N.P.; Smouse, S.L.; Allam, M.; Ismail, A.; Ramalwa, N.R.; Disenyeng, B.; Ngomane, M. and Thomas, J. (2019). Outbreak of *Listeria monocytogenes* in South Africa, 2017–2018: Laboratory Activities and Experiences Associated with Whole-Genome Sequencing Analysis of Isolates. Foodborne Pathogens and Disease, 16 (7), 524–530. https://doi.org/10.1089/fpd.2018.2586

Smith, J.L. and Fratamico, P.M. (2018). Emerging and Re-Emerging Foodborne Pathogens. Foodborne Pathogens and Disease, 15 (12), 737–757. https://doi.org/10.1089/fpd.2018.2493

Spernovasilis, N.; Tsiodras, S. and Poulakou, G. (2022). Emerging and Re-Emerging Infectious Diseases: Humankind's Companions and Competitors., 10 (1). https://doi.org/10.3390/microorganisms10010098

Swann, M.M. (2020). Use of Antibiotics in Animal Husbandry and Veterinary Medicine. Stationery Office.

United Nations Environment Programme 'UNEP' (2022). Environmental Dimensions of Antimicrobial Resistance: Summary for Policymakers. https://wedocs.unep.org/bitstream/handle/20.500.11822/38373/antimicrobial

Unrath, N.; McCabe, E.; Macori, G. and Fanning, S. (2021). Application of Whole Genome Sequencing to Aid in Deciphering the Persistence Potential of *Listeria monocytogenes* in Food Production Environments. Microorganisms, 9 (9). https://doi.org/10.3390/microorganisms9091856

Nair, V.T.D.; Venkitanarayanan, K. and Kollanoor Johny, A. (2018). Antibiotic-Resistant Salmonella in the Food Supply and the Potential Role of Antibiotic Alternatives for Control. Foods, 7(10). https://doi.org/10.3390/foods7100167

Verraes, C.; Van Boxstael, S.; Van Meervenne, E.; Van Coillie, E.; Butaye, P.; Catry, B.; De Schaetzen, M.A.; Van Huffel, X.; Imberechts, H.; Dierick, K.; Daube, G.; Saegerman, C.; De Block, J.; Dewulf, J. and Herman, L. (2013). Antimicrobial Resistance in the Food Chain: A Review., 10(7), 643–2669. https://doi. org/ 10. 3390/ijerph10072643

Vikesland, P.; Garner, E.; Gupta, S.; Kang, S.; Maile-Moskowitz, A. and Zhu, N. (2019). Differential Drivers of Antimicrobial Resistance across the World. Accounts of Chemical Research, 52(4), 916–924. https://doi.org/10.1021/acs.accounts.8b00643

Wang, H.; McEntire, J.C.; Zhang, L.; Li, X. and Doyle, M. (2012). The transfer of antibiotic resistance from food to humans: facts, implications and future directions. Revue Scientifique et Technique (International Office of Epizootics), 31(1), 249–260. https://doi.org/10.20506/rst.31.1.2117

World Health Origization 'WHO' (2020). Evolving Threat of Antimicrobial Resistance: Options for Action. World Health Organization (WHO), Geneva. http://apps. who. int/iris/bitstream/ 10665/ 44812/ 1/ 9789241503181

World Health Origization 'WHO' (2022). Food Safety. Key Facts. World Health Organization (WHO), Geneva. https://www.who.int/news-room/fact-sheets/detail/food-safety

World Health Origization 'WHO' (2023). Antibiotic Resistance. World Health Organization (WHO). https://www.who.int/news-room/fact-sheets/detail/antibiotic-resistance

Wooldridge, M. (2012). Evidence for the circulation of antimicrobial-resistant strains and genes in nature and especially between humans and animals. Revue Scientifique et Technique (International Office of Epizootics), 31(1), 231–247. https://doi.org/10.20506/rst.31.1.2109