

REVIEW ARTICLE

Antimicrobial-Resistant *Salmonella* at the Human–Animal–Environment Interface: A Critical One Health Review of Epidemiology, Genomic Surveillance, and Integrated Control Strategies

Abdulaziz M. Almuzaini*

Department of Veterinary Preventive Medicine, College of Veterinary Medicine, Qassim University, Buraydah, 51452, Saudi Arabia

*Corresponding author: ammzieny@qu.edu.sa

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ABSTRACT

Antimicrobial resistance in *Salmonella* is a key One Health issue because resistant lineages and AMR determinants occur across human, animal, food and environmental compartments. This important review article summarizes recent knowledge regarding the epidemiology, resistance mechanisms, integrated control and genomic surveillance of antimicrobial-resistant *Salmonella* at the human–animal–environment interface. There are significant differences in resistance patterns among serovars, geographic regions, host populations and surveillance systems. The epidemiology of several non-typhoidal *Salmonella* lineages includes food-producing animals and food chains, while the quantitative role of food-producing animals, wastewater and other environmental reservoirs in human infections is less well understood. Whole genome sequencing can be used to provide high resolution characterization of resistant lineages, mobile genetic elements, and potential epidemiological clusters, but cannot determine direction of transmission without temporal, spatial and exposure data. Significant restrictions are the use of different sampling approaches, antimicrobial resistance testing and methods and a lack of equal genomic-surveillance capacity, as well as the lack of representation for environmental and low-resource settings. Therefore, coordinated antimicrobial stewardship, food-safety measures, farm biosecurity, environmental surveillance and integration of phenotypic, genomic and epidemiological data across One Health sectors are all necessary to facilitate effective control.

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INTRODUCTION

Salmonella is one of the most significant bacterial foodborne pathogens causing illness globally which has a great burden on the public health, food security and economic development (Mkangara, 2023). It is a genus of Gram-negative, facultative intracellular bacteria and belongs to the family Enterobacteriaceae, which includes a wide variety of species that can infect almost any type of vertebrates and invertebrates (Munir *et al.*, 2025). Although there are many, only a few are responsible for the bulk of human infections and non-typhoidal *Salmonella* (NTS) are the major cause of food borne gastroenteritis worldwide (Zizza *et al.*, 2024). Typhoidal serovars, however, continue to cause systemic infections, especially in areas of poor sanitation and low-quality drinking water (Appiah *et al.*, 2022). *Salmonella* has a wide host range and is highly tolerant of food production

environments and natural habitats, allowing it to survive at the human, animal and environmental interfaces and hence perpetuate its spread (Yada, 2023).

In the last 20 years, antimicrobial resistance (AMR) has developed as one of the most challenging issues in the control of *Salmonella* infections (Lamichhane *et al.*, 2024). Resistance to several antimicrobials has caused their decreasing effectiveness in invasive cases of salmonellosis, such as in β -lactam, fluoroquinolone, third- and fourth-generation cephalosporin, aminoglycoside and polymyxin resistance (Grudlewska-Buda *et al.*, 2023). Multidrug-resistant (MDR) *Salmonella* is a *Salmonella* resistant to three or more classes of antimicrobials and has been growing more common in developed and developing countries (Onyeke and Bahman, 2025). The emergence of extended-spectrum β -lactamase (ESBL) producers, plasmid-mediated quinolone resistance (PMQR), and mobile genes for colistin resistance (mCR) has added to therapeutic

challenges and increased the risk of treatment failure (Shahzad *et al.*, 2023). These findings highlight the critical need for a coordinated surveillance and evidence-based intervention to help curb the spread of resistant *Salmonella* in interconnected ecosystems (Singh *et al.*, 2024).

The epidemiology of AMR *Salmonella* infections is very complicated, as the bacterium exists in a variety of ecological niches, which continuously interact with each other (Galán-Relaño *et al.*, 2023). Infections in humans mainly happen when they eat food that is contaminated, such as seafood, dairy, eggs, pork, beef, poultry and fresh produce (Ali and Alsayeqh, 2022). However, transmission of foodborne illness is just one aspect of a much larger epidemiological web (Hamaideh *et al.*, 2024). Resistant *Salmonella* are maintained and distributed by livestock, companion animals, wildlife, insects, irrigation water, wastewater, agricultural soils and food processing environments (Oludairo *et al.*, 2023). Ecological connectivity and potential exchange of resistance determinants is illustrated by the detection of resistant *Salmonella* and related resistance determinants across these compartments. The direction and frequency of cross-sector transmission must, however, be supported by supporting epidemiological, temporal, spatial, and molecular evidence (Despotovic *et al.*, 2023). This has resulted in interventions targeting only one sector, which are often ineffective at tackling the ecological drivers of antimicrobial resistance (Cocker *et al.*, 2024).

In recent years, the use of genomic technologies has transformed the surveillance and epidemiological investigation of antimicrobial-resistant *Salmonella* (Djordjevic *et al.*, 2024). The capacity for identifying outbreak-associated strains, characterizing antimicrobial resistance determinants, investigating the transmission route, and tracking the international spread of high-risk clones, has been greatly improved using whole genome sequencing (WGS), metagenomic sequencing, comparative genomics and advanced bioinformatics (Vashisht *et al.*, 2023). In contrast to traditional phenotypic surveillance, genomic surveillance allows for high-resolution analysis of the resistome, virulome and mobilome of *Salmonella* isolates as well as phylogenetic relationships, allowing for more precise source attribution and to identify emerging resistome and virulome threats earlier (Cardim Falcao *et al.*, 2024). The use of genomic data alongside of epidemiology and environment helped to enhance outbreak investigations and improved risk assessment, and genomic surveillance will be an essential part of future One Health surveillance systems (Struelens *et al.*, 2024).

There have been significant advances in the understanding of the molecular basis of antimicrobial resistance and national and international surveillance programs launched, but some challenges remain (Okeke *et al.*, 2024). There are huge inequities in the availability of surveillance systems, laboratory facilities and genomic sequencing tools, especially in low- and middle-income countries where salmonellosis is most prevalent (Olorunkosebi *et al.*, 2025). The role of environmental reservoirs, including wastewater, agricultural runoff, wildlife and natural ecosystems, in the persistence and dissemination of resistant *Salmonella* remains relatively under-studied, with only a partial understanding of its role (Elbehiry and Marzouk, 2025). In addition, the various

surveillance methods used, the methodologies of antimicrobial susceptibility testing, and the reporting of data on genomes still prevent global comparisons and coordinated risk assessments (Struelens *et al.*, 2024). To overcome these challenges, harmonized surveillance systems, standardized analytical tools, increased co-operation between international partners and increased investments in integrated One Health infrastructure are necessary (Pantuvo and Oluwarore, 2024).

Within this scope, the review summarizes four main questions: What are the distribution patterns of antimicrobial-resistant *Salmonella* and major resistance determinants of these strains in human, animal, food and environmental reservoirs? What epidemiological evidence supports the links or transmission of these strains between human, animal, food, and environmental reservoirs? What is the evidence to support the use of genomic surveillance for lineage characterization, the detection of resistance and the development of source attribution hypotheses? What is the evidence for integrated control measures and what are the key gaps?

Biology, virulence and antimicrobial resistance in *Salmonella*:

Salmonella is a facultative intracellular, gram-negative bacterium and is considered one of the most versatile bacterial pathogens of both human and animal hosts. It has an incredible ecological versatility, colonizing a variety of hosts, surviving in poor environmental conditions and persisting through the entire food production chain (Madhushan *et al.*, 2025). This adaptability is due to many virulence determinants, metabolic versatility and an extraordinary ability to obtain antimicrobial resistance genes via horizontal gene transfer (Hossain and Chowdhury, 2024). These features have allowed for the spread of antimicrobial resistant *Salmonella* to all continents, and it represents a big problem in both clinical and food safety settings (da Silva *et al.*, 2022). Thus, a fundamental understanding of *Salmonella* biology and pathogenic mechanisms is essential for interpreting *Salmonella* epidemiology, forecasting *Salmonella* evolution and implementing effective control measures in the One Health approach (Galán-Relaño *et al.*, 2023).

Salmonella includes two species, *Salmonella* (*S.*) *enterica* and *S. bongori* (Oludairo *et al.*, 2022). Of these, only *S. enterica* is responsible for many infections in humans and warm-blooded animals (Han *et al.*, 2024). According to the Kauffmann, White classification scheme, *S. enterica* is further divided into several subspecies and is known to have over 2,600 serovars, which vary in their somatic (O) and flagellar (H) antigens (Oludairo *et al.*, 2022). While only a small percentage of these serovars are of major importance in human disease, some are of global importance because of their broad host range, disease causing ability and the emergence of antimicrobial resistance (Aljeldah, 2022). *S. typhimurium* and *S. enteritidis* serovars make up a significant fraction of non-typhoidal salmonellosis in the world while *S. typhi* and *S. paratyphi* are the major causes of enteric fever (Gouda, 2024). The other serovars such as *S. heidelberg*, *S. newport*, *S. infantis*, *S. kentucky*, and *S. choleraesuis* have been very prominent due to their correlation with MDR and livestock and poultry production related foodborne outbreaks (Nichols *et al.*, 2022).

Salmonella has considerable ecological versatility and can colonize diverse host and environmental niches, including asymptomatic animal hosts (Galán-Relaño *et al.*, 2023). Poults, cattle, pigs, sheep and even aquatic animals, such as fish and shellfish, are often asymptomatic carriers and harbor and perpetuate bacteria into the environment with fecal shedding (Serbessa *et al.*, 2023). Companion animals, reptiles, amphibians, wild birds, rodents and insects are additional reservoirs which spread the disease into the environment (Gamble *et al.*, 2023). *Salmonella* is extremely hardy in the environment outside of living hosts and can persist in soil, water, manure, sediments, feed ingredients, food processing equipment and on industrial surfaces in the form of biofilms (Yada, 2023). This ecological persistence contributes significantly to the possibility of multiple contaminations in the food chain and cross species transmission.

Salmonella pathogenicity is dependent on the interplay between *Salmonella* virulence factors and the host immune system (Guo *et al.*, 2025). Infection usually occurs after ingestion of contaminated food or water, and bacteria can survive the acid environment of the stomach and colonize the distal ileum (Rossi *et al.*, 2023). The intestinal epithelial cell adhesion is carried out by fimbriae, outer membrane proteins and several adhesins which allow close contact with host tissues (Gierzyńska *et al.*, 2022). After attachment *Salmonella* actively invades epithelial cells, via the use of specific secretion systems, which inject *Salmonella* effector proteins directly into host cells to alter host cell signaling pathways that favor bacterial uptake (Li, 2022). This pathogen enters cells and resides in membrane-enclosed vacuoles in epithelial cells and macrophages, where it immune evades multiple components of innate immunity and allows it to disseminate systemically in susceptible hosts.

Central to *Salmonella* virulence are the *Salmonella* Pathogenicity Islands (SPIs) which contain many virulence factors central to invasion, intracellular survival, immune modulation and systemic infection (Sia *et al.*, 2025). Of these, SPI-1 and SPI-2 are thought to be the most important determinants of pathogenicity (Pico-Rodríguez *et al.*, 2024). SPI-1 is mainly responsible for bacterial invasion of intestinal epithelial cells by translocating effector proteins, which disrupt the cell's cytoskeleton and promote bacterial internalization, via a Type III secretion system (Zhou *et al.*, 2023). SPI-2 on the other hand, alters the intracellular milieu inside the macrophage, thereby enabling the intracellular survival of bacteria and evading the host antimicrobial defenses by preventing the degradation of bacteria in lysosomes (Xiong *et al.*, 2023). Other pathogenicity islands are involved in obtaining nutrients, toxin production, stress resistance and persistence in various host environments. Coordinated regulation of these virulence genes is important for *Salmonella* to alternate between extracellular and intracellular growth, and to adjust to changing conditions in the environment (Pokorzynski and Groisman, 2023).

In addition to the classical virulence factors, the formation of biofilms has proven to be an important survival mechanism that helps *Salmonella* survive in clinical and environmental conditions (Jahan *et al.*, 2022). Biofilms are organized microbial communities that are embedded in an extracellular polymeric matrix that they

produce, and which attach to abiotic and biotic surfaces (Flemming *et al.*, 2023). In food processing, biofilms form on stainless steel surfaces, plastic surfaces, conveyor belts, water lines and storage tanks and are known as “food” reservoirs because they are hard to kill with standard sanitation processes (Shineh *et al.*, 2023). Biofilm-associated bacteria are more resistant to these antimicrobial agents, oxidative stress, desiccation, ultraviolet radiation and disinfectants than their planktonic counterparts (Almatroudi, 2025). The horizontal transfer of resistance genes located on plasmids, integrons and transposons, which are carried by bacterial cells, is also accelerated by the close association of cells in a biofilm (Michaelis and Grohmann, 2023). Biofilms, therefore, can help drive environmental persistence as well as evolution and spread of MDR *Salmonella* (Aleksandrowicz *et al.*, 2023).

Salmonella's versatility is also reinforced by the existence of sophisticated regulatory networks, which allow it to respond quickly to environmental stress, as well as its capacity to adapt and survive in most environments (Sutar *et al.*, 2024). Global transcription regulators control the expression of genes for acid tolerance, osmotic adaptation, oxidative stress resistance, nutrient uptake and anaerobic metabolism. These adaptive mechanisms enable bacteria to survive the food processing and refrigerated storage, as well as transit through the stomach of the host and the presence of host immune defenses (Worley, 2023). The capacity to switch into “survival” modes (metabolically inactive or persistent) under stressful circumstances also enables bacterial populations to grow back when environment conditions improve, thus enhancing the survival when exposed to antimicrobial agents (Cotten and Davis, 2023).

A variety of chromosomal mutations and acquisition of mobile genetic elements containing resistance determinants have contributed to the development of antimicrobial resistance in *Salmonella* (Algarni *et al.*, 2022). Resistance mechanisms that are acquired through spontaneous mutation are only a small part of the arsenal, *Salmonella* can also obtain resistance genes through conjugative plasmids, integrons, transposons, insertion sequences and bacteriophages circulating among a variety of bacterial species living in humans, animals, and environmental reservoirs (Garrido *et al.*, 2024). These mobile genetic elements may carry multiple resistances allowing the emergence of multidrug-resistant strains that are able to resist to several antimicrobial classes at the same time (Noel *et al.*, 2022).

Resistance mechanisms range from a wide variety of molecular adaptations which make the antimicrobial less effective (Darby *et al.*, 2023). One of the most common is enzymatic inactivation, for example by the formation of β -lactamases that can break down penicillins, cephalosporins, and other β -lactam antibiotics (Kaderabkova *et al.*, 2022). The use of ESBL enzymes and AmpC β -lactamases is more common in food borne *Salmonella* isolates and significantly reduces the number of available treatment options (Saechue *et al.*, 2024). Fluoroquinolone resistance is generally due to chromosomal mutations which affect the action of DNA gyrase and topoisomerase IV and plasmid-mediated quinolone resistance genes have resulted in the spread of resistance worldwide (Hassen and Jouini, 2023). The

mechanisms of action of aminoglycoside resistance include aminoglycoside-modifying enzymes, while tetracycline resistance is often through efflux pumps and ribosomal protection proteins (Zhang *et al.*, 2023). Sulfonamide resistance occurs when the drug target enzymes are modified, which lowers the affinity with the drug and/or changes the target enzyme (Venkatesan *et al.*, 2023). The resistance to polymyxin (colistin) has been a growing concern, as plasmid-mediated *mcr* genes are important because mobile genetic elements can facilitate horizontal dissemination of colistin-resistance determinants among bacterial populations as depicted in Fig. 1 (Liu *et al.*, 2024; Mahmood *et al.*, 2025).

The combination of several resistance determinants in the individual isolates has led to a growing problem of multidrug resistant and, in some areas, extensively drug-resistant *Salmonella* lineages (Bisola Bello *et al.*, 2024). These resistant clones often have increased fitness, thus surviving under a decreased selection pressure for antimicrobials (Nair *et al.*, 2024). In contrast to previous thinking that resistance puts a significant biological cost on the pathogen, many current lineages have developed compensatory mutations that have kept them virulent and transmissible but still maintained resistance phenotypes (Lazar *et al.*, 2023). As a result, resistant strains have become well entrenched in livestock production systems, food processing, health and care facilities and natural environments (de Mesquita Souza Saraiva *et al.*, 2022). The eradication of resistant strains is becoming increasingly difficult and there is potential for widespread international trade, travel and migration to spread resistant strains as given in Table 1 (Endale *et al.*, 2023).

A major concern of *Salmonella* evolution is the development of virulence and antimicrobial resistance (Hassena *et al.*, 2022). Especially, more highly virulent strains contain multiple arrays of resistance genes, limiting the range of therapeutic drugs available and yet still having the potential to cause serious disease (Qin *et al.*, 2022). Described here is a notable convergence in the

globally disseminated epidemic clones of poultry, swine, cattle and international food trade (He *et al.*, 2022). Their ongoing emergence reinforces the need to build into a coordinated One Health surveillance system, that molecular epidemiology, genomic surveillance, and antimicrobial stewardship can all enable the detection of high-risk lineages before they spread in the population (Djordjevic *et al.*, 2024).

Global epidemiology of antimicrobial-resistant

***Salmonella*:** The epidemiology of antimicrobial-resistant *Salmonella* has radically transformed over the last 20 years, in part due to greater food production, trade, urbanization, antimicrobial usage, and the increasing mobility of humans, animals and food commodities (Bisola Bello *et al.*, 2024). Resistant *Salmonella* is now known to be a transboundary One Health problem in high income and LMIC countries, with varying levels, and different types of resistance present in different regions (Bisola Bello *et al.*, 2024). Multiple surveillance studies have repeatedly shown that MDR *Salmonella* is no longer just an occasional outbreak, but has become a part of human populations, livestock systems, food chains, wildlife reservoirs, and environmental compartments worldwide (Teklemariam *et al.*, 2023).

Salmonella non-typhoidal (SNT) is one of the common pathogenic bacteria responsible for bacterial foodborne illness worldwide, and accounts for millions of illness cases each year (Arya *et al.*, 2017). Even today, poultry products are the main source of human exposure in many countries, mainly because of the contamination of eggs, chicken meat and the environment of poultry processing. But there are also a few transmission vehicles, including beef, pork, dairy products, seafood, fresh produce and contaminated water (Bryan, 1988). With the emergence of high levels of resistant strains in food animals, there has been growing concern about the spread of resistant bacteria and resistance genes from agriculture to the human population via the food chain (Marshall and Levy, 2011).

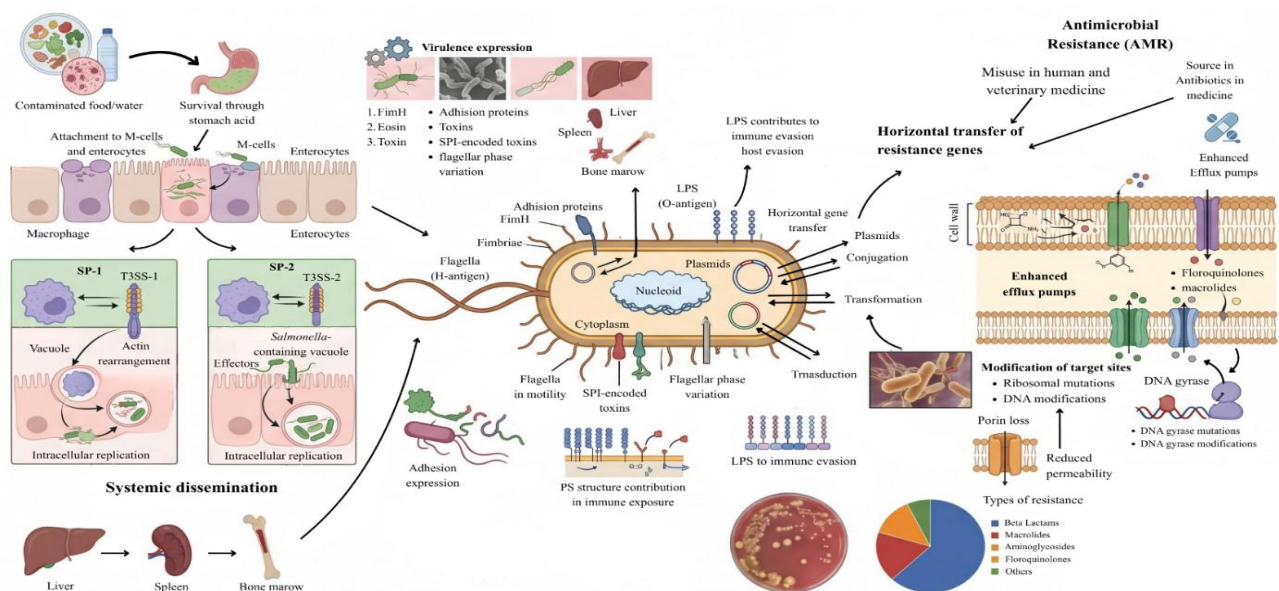


Fig. 1: Integrated overview of *Salmonella* pathogenesis and the most important mechanisms of antimicrobial resistance. The schematic summarizes the processes of intestinal invasion, intracellular survival and systemic dissemination, along with resistance mechanisms such as antimicrobial inactivation, modification of targets, decreased permeability, active efflux and horizontally acquired resistance determinants.

Table 1: Representative *Salmonella* serovars, principal reservoirs, exposure sources, clinical manifestations and major antimicrobial resistance characteristics

Serovar	Primary reservoirs	Common transmission sources	Major disease manifestations	AMR characteristics	References
<i>S. typhimurium</i>	Poultry, cattle, pigs, rodents, humans	Poultry meat, beef, pork, dairy products, contaminated produce	Gastroenteritis, bacteremia, invasive infections	Frequently multidrug resistant; resistance to ampicillin, tetracyclines, chloramphenicol, and fluoroquinolones	(Onyeke and Bahman, 2025)
<i>S. enteritidis</i>	Poultry, laying hens, eggs	Eggs, poultry meat, dairy products	Gastroenteritis, septicemia in vulnerable individuals	Increasing resistance to fluoroquinolones and third-generation cephalosporins	(Hinson et al., 2025)
<i>S. typhi</i>	Humans	Contaminated food and water	Typhoid fever	Extensively drug-resistant strains reported with resistance to fluoroquinolones, cephalosporins, and multiple first-line antibiotics	(Ahmad et al., 2024)
<i>S. paratyphi</i>	Humans	Contaminated food and water	Paratyphoid fever	Increasing fluoroquinolone resistance and multidrug resistance	(Browne et al., 2024)
<i>S. infantis</i>	Poultry	Chicken meat and poultry products	Gastroenteritis	Frequently harbors megaplasms carrying ESBL and multidrug resistance genes	(Kim et al., 2025)
<i>S. heidelberg</i>	Poultry and cattle	Poultry meat and beef	Gastroenteritis and invasive infections	and ESBL production and resistance to cephalosporins increasingly reported	(Mandujano-Hernández et al., 2024)
<i>S. newport</i>	Cattle, poultry, environment	Beef, dairy products, vegetables	Gastroenteritis and bloodstream infections	Multidrug resistance with plasmid-mediated resistance determinants	(McDermott et al., 2018)
<i>S. kentucky</i>	Poultry	Poultry meat	Gastroenteritis	High-level ciprofloxacin resistance reported globally	(Vakili et al., 2025)
<i>S. choleraesuis</i>	Swine	Pork products and direct animal contact	Septicemia and invasive disease	Frequent multidrug resistance including β -lactams and fluoroquinolones	(Gil Molino et al., 2020)
<i>S. dublin</i>	Cattle	Beef and raw milk	Invasive salmonellosis and bacteremia	Often multidrug resistant with increasing cephalosporin resistance	(Fritz et al., 2022)

Abbreviations: AMR, antimicrobial resistance; MDR, multidrug resistance; ESBL, extended-spectrum β -lactamase

MDR serovars *S. typhimurium*, *S. newport*, *S. heidelberg*, and *S. infantis* have been identified in surveillance programs in North America in a persistent manner (Ferrari et al., 2019). Recent surveillance from Southern Thailand has also documented the occurrence and antimicrobial resistance of *S. enterica* in sport animals and livestock (Narinthorn et al., 2025). Ampicillin, tetracyclines, sulfonamides and chloramphenicol resistance are common, and third generation cephalosporins and fluoroquinolones resistance has risen in some lineages (Nayeem et al., 2026). Cattle-associated *S. newport* and poultry-associated *S. heidelberg* are being important causes of invasive human infections (Chen et al., 2024). The diagnosis and treatment of infections caused by ESBL-producing *Salmonella* and *Salmonella* isolates harboring plasmid-mediated quinolone resistance genes have also become more complex (Shu et al., 2023).

Compared to some other countries, the prevalence of resistance in European countries is generally low, which may be due to stricter antimicrobial stewardship policies and regulations on antimicrobial usage in food animals (Beber et al., 2025). However, other monophasic variants of *S. typhimurium*, *S. enteritidis* and *S. infantis* are still serious issues (Montoro-Dasi et al., 2023). *S. infantis* with large-sized multidrug-resistance plasmids have been detected in the fast-growing multidrug-resistance dissemination of the bacterium in various poultry production systems in Europe (Farkas et al., 2025). Resistance to fluoroquinolones and third generation cephalosporins is present but not as common as in some areas and is being closely monitored because of the potential impact on public health.

The high population of humans, heavy livestock production in Asia, rapidly growing aquaculture industry, along with high antimicrobial consumption make it a big emerging hotspot for AMR *Salmonella* (Dewi et al., 2022). MDR is reported to have high prevalence in *S. typhimurium*, *S. enteritidis*, *S. kentucky* and *S.*

choleraesuis. Of particular concern is the spread of fluoroquinolone-resistant *S. kentucky*, and the development of extensively drug-resistant (XDR) *S. typhi* in areas of south Asia (Bisola Bello et al., 2024). Emergence of ESBL-producing strains and plasmid-mediated colistin resistance genes in clinical and animal isolates is indicative of the complexity of resistance in the region (Trongjit et al., 2022).

In Africa, invasive non-typhoidal *Salmonella* is an important cause of blood stream infection particularly in young children and immunocompromised patients (Fierer, 2022). Sequence type 313 (ST313) of MDR *S. typhimurium* is strongly associated with invasive disease in sub-Saharan countries (Van Puyvelde et al., 2023). Common resistance to first-line drugs like ampicillin, chloramphenicol and trimethoprim-sulfamethoxazole is prevalent and decreased susceptibility to fluoroquinolones and cephalosporins are increasingly reported (Nisa et al., 2022). The actual burden of the disease is probably underestimated in many countries due to poor laboratory infrastructure and surveillance capability (Ashenafi et al., 2024).

In addition, resistant *Salmonella* has been found in poultry, swine and cattle production and is becoming more prevalent in Latin America (Guerrero et al., 2022). Infection by serovars (*S. enteritidis*, *S. typhimurium*, *S. infantis*) is a common cause of disease in humans, and MDR profiles (β -lactams, tetracyclines & sulphonamides) are often reported (Algammal et al., 2023). A wider regional trade and food distribution network may allow for the spread of successful resistant clones internationally (Yartey et al., 2025). Resistant *Salmonella* is not just found in food animals and humans. MDR strains are increasingly being found in companion animals (dogs and cats), and there is potential for transmission within the home (Jin et al., 2023). *Salmonella* can be spread on agricultural production areas and in urban areas by wildlife, including wild birds, rodents, reptiles, and insects (Oludairo et al.,

2023). The aquatic ecosystems are attracting a special attention since the disposal of effluents, cultivation activities at and around the water bodies and agriculture activities have exposed the water bodies like rivers, lakes and coastal waters to antimicrobial residues and resistant bacteria (Chawla *et al.*, 2024). The links between environmental and food borne transmission are illustrated by the detection of resistant *Salmonella* in irrigation water, sediments, shellfish and aquaculture products (Table 2) (Pinamonti *et al.*, 2025).

One of the hallmarks of modern *Salmonella* epidemiology is the worldwide dissemination of high-risk clones of *Salmonella* that are multidrug resistant, virulent and highly environmentally resistant (Bisola Bello *et al.*, 2024). These lineages can be quickly spread across international boundaries through travel, migration, trade of food and live animals (Bhatia *et al.*, 2024). Local outbreaks are frequently the expression of larger international transmission networks, as evidenced by genomic studies that have shown that resistant strains found in different continents are very closely related (Struelens *et al.*, 2024). While the issue is becoming more evident, there are still some significant gaps in surveillance. There are few well-established surveillance systems to track the use of and resistance to antimicrobials in humans, animals and in the environment in many LMICs (Matee *et al.*, 2023). Environmental surveillance is especially poorly developed and thus this understanding is limited and restricted to the role of wastewater, agricultural runoff and natural ecosystems in maintaining and propagating resistant *Salmonella* (Ifedinezi *et al.*, 2024). Laboratory methods, data sharing, and genomic surveillance is not uniform in different geographic areas, making it difficult to make comparisons and assessments at a global level (Hill *et al.*, 2023).

To date, there is general agreement that antimicrobial-resistant *Salmonella* has been widely established throughout the human–animal–environment continuum (Dushayeva, 2025). The current trend of intensive farming, selection pressure of antimicrobials, environmental pollution and global mobility has set the stage for the emergence and global spread of increasingly resistant and widespread *Salmonella* lineages (Zhai *et al.*, 2025). The above trends highlight the importance of a joint One Health surveillance and integrated control measures approach to

tackle the pathogen in all inter-related reservoirs, not in individual sectors. The major drawback of the existing global epidemiology is geographic surveillance and publication bias. In areas where the lab infrastructure is not available, AMR prevalence could be underestimated because of the lack of data. Moreover, there is conflicting evidence about the relative importance of human and agricultural antimicrobial usage to clinical antimicrobial resistance; this means that there is a need to model antimicrobial resistance on a more local and context-specific basis rather than generalizing.

The Human–Animal–Environment Interface: A one health perspective: One Health is the best way to understand the epidemiology of AMR *Salmonella* due to the interconnection between human, animal and environmental health (Al-Khalaifah *et al.*, 2025). *Salmonella*, however, is a pathogen that has a greater reservoir of hosts and ecological niche, resulting in a complex transmission network that can allow the emergence and spread of resistant strains (Han *et al.*, 2024). The spread of resistant bacteria and antimicrobial resistance determinants in these interdependent sectors has turned *Salmonella* into an international ‘One Health’ problem and multidisciplinary and multidirectional efforts are needed to control it, not sector by sector (Perestrelo *et al.*, 2023).

Food-producing animals are still the main source of resistance bacteria, such as *Salmonella* (Almansour *et al.*, 2023). The organism is often found, and shed in the feces, without causing obvious disease in poultry, cattle, swine, and in aquaculture species, especially as they have become more common on farms (Serbessa *et al.*, 2023). Intensive livestock production allows animals to be in close contact with each other and stocking rates to be high, so that bacteria can be spread and resistant populations selected, particularly when animals are exposed to antimicrobials frequently (Stevenson, 2023). The contamination can happen at various points throughout the production chain, such as in feed, drinking water, housing facilities, transport vehicles, slaughterhouses and food processing plants (Ovuru *et al.*, 2024). Therefore, resistant *Salmonella* has the potential to enter and spread through the entire farm to fork chain, and ultimately ending up in consumers' hands in contaminated meat, eggs, milk, seafood or fresh produce (Mkangara, 2023).

Table 2: Global epidemiology of major antimicrobial-resistant *Salmonella* lineages

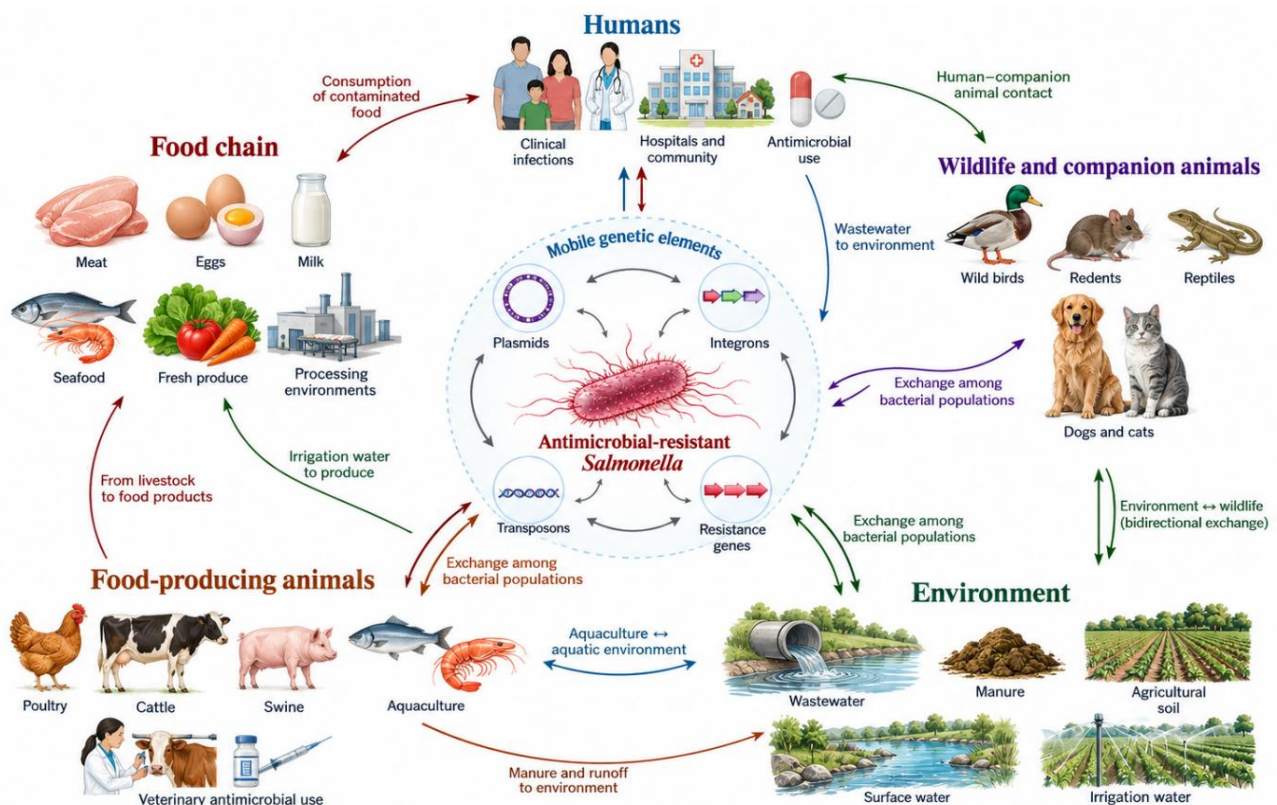
Region	Serovar lineage	/ Main source	Key AMR	Important trait	marker	/ Epidemiological importance	Evidence type	Reference
Europe	<i>S. enteritidis</i>	Poultry, eggs	FQ-R	Ciprofloxacin resistance		Major foodborne serovar	EU surveillance	(European Food Safety <i>et al.</i> , 2026)
Europe	<i>S. infantis</i>	Poultry	FQ-R, MDR	MDR poultry lineages		Persistent associated AMR	poultry- EU surveillance	(European Food Safety <i>et al.</i> , 2026)
Europe global	<i>S. kentucky</i>	Poultry, humans	FQ-R, MDR	ST198; ST314	emerging	International spread	clonal WGS	(Chen <i>et al.</i> , 2025)
South Asia	<i>S. typhi</i>	Humans	MDR, XDR	Genotype 4.3.1/H58		Major enteric fever lineage	AMR 13,000 genomes WGS	(Carey <i>et al.</i> , 2023)
Sub-Saharan Africa	<i>S. typhimurium</i>	Humans	MDR, FQ-R	ST313-L2		Invasive bloodstream infection		(Van Puyvelde <i>et al.</i> , 2023)
Americas	<i>S. heidelberg</i>	Poultry	MDR	β-lactam resistance		Poultry-associated AMR	Meta-analysis	(Diaz <i>et al.</i> , 2022)
Americas	<i>S. kentucky</i>	Poultry	MDR	Multiple resistance	drug	Poultry-chain dissemination	Meta-analysis	(Diaz <i>et al.</i> , 2022)
Americas	<i>S. typhimurium</i>	Poultry	MDR	AMP, TET, resistance	STR	Broad occurrence	poultry Meta-analysis	(Diaz <i>et al.</i> , 2022)
Southeast Asia	<i>S. enterica</i>	Livestock, sport	MDR	Multiple phenotypes	resistance	Animal-associated reservoir	AMR Field surveillance	(Narinthorn <i>et al.</i> , 2025)
Pakistan	<i>S. typhimurium</i>	Poultry, environment	Colistin-R	AMR profile	genes; WGS	Poultry–environment interface	Genomic study	(Mahmood <i>et al.</i> , 2025)

Close contact with infected animals or contaminated places plays a large role in the spread of disease and human infections are mainly caused by ingestion of contaminated food (Esposito *et al.*, 2023). Slaughterhouse workers, food handlers, laboratory workers, farmers and veterinarians are at higher risk of occupational exposure because they have more frequent contact with livestock and animal waste (Njoga *et al.*, 2023). Household reservoirs are also possible with companion animals, especially when they ingest raw animal products or are in environments where there is a high likelihood for exposure to contaminated surfaces (Martak *et al.*, 2024). Resistant *Salmonella* has been spreading between humans and companion animals, with numerous instances reported in recent years, confirming that agricultural is not the only environment for the presence of resistant *Salmonella* (Galán-Relaño *et al.*, 2023).

Environmental reservoirs are key to maintenance of the transmission cycle (Cocker *et al.*, 2024). Resistant bacteria and antimicrobial residues are released into rivers, lakes, irrigation systems and agricultural soils from agricultural runoff, untreated sewage, hospital effluents, pharmaceutical wastes and livestock manure (Akhter *et al.*, 2024). These contaminated environments create the potential for *Salmonella* to remain, interact with other bacteria and share the *Salmonella* resistance genes with other bacteria via horizontal gene transfer (Algarni *et al.*, 2022). Contamination of water for fresh produce has become a growing vehicle of infection and highlights the importance of environmental contamination affecting food safety and public health (Fig. 2) (Mititelu *et al.*, 2025).

Wildlife further helps to create ecological connectivity for *Salmonella* (Oludairo *et al.*, 2023). Resistant strains can be picked up in the contaminated agricultural or urban environment and could be spread over long distances by wild birds, rodents, reptiles, insects and other free-ranging animals (Kobuszewska and Wysok, 2024). Migratory birds are of special interest because they may be able to spread resistant *Salmonella* bacteria across continents; rodents and insects may spread resistant *Salmonella* within farms and food processing plants (Tawakol *et al.*, 2024). Wildlife have been recognized as a secondary reservoir but also play an important role in the persistence and long-distance spread of pathogens in One Health surveillance programs (Doyle *et al.*, 2025).

Horizontal gene transfer and the widespread occurrence of mobile genetic elements that can be spread between the bacterial populations that inhabit different ecological niches also contribute to the spread of antimicrobial resistance (Hossain and Chowdhury, 2024). Plasmids, integrons, transposons and bacteriophages allow for the easy transfer of resistance genes within a short time of just a few years between *Salmonella* and other enterobacteria in humans, animals and environmental ecosystems (Algarni *et al.*, 2022). Therefore, AMR should be considered as an ecological issue and not just a clinical issue (Okeke *et al.*, 2024). Concurrently, mitigation needs to take place through a combined effort that involves reduction in antimicrobial selection pressure, sanitation, good food safety practices and environmental reservoir monitoring as well as the usual human and veterinary surveillance (Milijasevic *et al.*, 2024).



Cross-sector detection indicates ecological connectivity. Transmission direction requires supporting epidemiological, temporal, spatial and genomic evidence.

Fig. 2: Transmission of antimicrobial resistant *Salmonella* between humans, animals, food and environment via One Health pathways. The framework provides a brief overview of key pathways of organism exposure, the spread and contamination of environmental antimicrobial resistance (EAMR) determinants.

Genomic surveillance and molecular epidemiology:

Widespread evolution of antimicrobial-resistant *Salmonella* has demonstrated the need to adopt new surveillance approaches (Dushayeva, 2025). These methods are still suitable for routine diagnosis but may not have the resolution to determine routes of transmission, identify resistant clones or differentiate between closely related outbreak strains (Liu *et al.*, 2023). The integration of recent developments in genomic technologies has revolutionized the surveillance of *Salmonella*, allowing high-resolution characterization of pathogen populations and new insights into the evolution, spread and maintenance of antimicrobial resistance in the One Health context (Djordjevic *et al.*, 2024).

Whole-genome sequencing (WGS) is increasingly used as a high-resolution approach for *Salmonella* surveillance because isolate genomes can provide information on serovar, sequence type, antimicrobial resistance determinants, virulence-associated genes, plasmid content, and phylogenetic relationships. WGS has the potential to enhance discrimination between related isolates and aid in investigating outbreaks or source attribution hypotheses when compared to traditional typing methods. But the similarity of the genomes does not automatically mean it is direct or whether it is transmitted from the orca to the dolphin, or vice versa. To be able to interpret epidemiological data reliably, genomics information needs to be combined with sampling date, geographical information, exposure history, and sampling density as well as other epidemiological metadata (Akinyemi *et al.*, 2023). WGS provides significantly more discriminatory power than traditional typing methods, which can be used to distinguish between human, animal, food product and environmental isolates to determine if they are linked to the same transmission chain (Dong *et al.*, 2025). As a result, WGS has been a crucial tool for outbreak investigations, source tracing and international surveillance programs (Gomes *et al.*, 2025).

One of the great strengths of genomic surveillance is that it can determine the full resistome, which refers to the set of antimicrobial resistance genes found in the genome of a bacterium (Matsumura *et al.*, 2025). Not only can genomic analysis detect genes encoding mobile colistin resistance, but also those encoding extended-spectrum β -lactamases (ESBLs), carbapenemases, aminoglycoside-modifying enzymes, tetracycline resistance proteins, plasmid-mediated quinolone resistance, and mobile colistin resistance, rather than relying exclusively on phenotypic resistance profiles (Shahzad *et al.*, 2023). This wide-ranging genetic data allows that resistance mechanisms that are beginning to occur can be detected early, before they are common in clinical practice (Muteeb *et al.*, 2023). In addition to the resistance genes, WGS can also be used for the characterization of the virulome, the set of genes involved in pathogenicity, host adaptation and evasion of immune system. Invasive disease and the ability to cause outbreaks worldwide has been linked to a combination of virulence and resistance determinants for several of the most successful global lineages of *Salmonella* (Bisola Bello *et al.*, 2024). Knowledge of the interaction of these characteristics is crucial for recognizing high-risk clones to be subjected to special monitoring and intervention (Fig. 3).

The genomic monitoring is also important to trace the movement of mobile genetic elements that can cause horizontal gene transfer (Tokuda and Shintani, 2024). Plasmids, integrons, transposons and genomic islands often carry several resistance genes, and these can be quickly transferred among bacterial populations that live in humans, animals, wild animals, and within the environment (Bhat *et al.*, 2023). Comparative genomic study of highly similar resistance plasmids isolated from different ecological sources strongly support the idea of cross-sector transmission, but the genomic similarity does not necessarily indicate the direction of transmission (Dushayeva, 2025). To calculate the directional spread, extensive epidemiology metadata is needed. These results highlight the need for human, veterinary, food and environmental genomic data to be collected and combined into a single One Health surveillance system (Oltean *et al.*, 2025).

The use of high-resolution molecular epidemiological techniques such as multi-locus sequence typing (MLST), core genome multi-locus sequence typing (cgMLST), and single nucleotide polymorphism (SNP) phylogenetic analysis, further extend our understanding of *Salmonella* population dynamics (Abdel-Gilil *et al.*, 2022). These techniques allow for accurate determination of genetic similarity amongst isolates and enable outbreak detection, source tracking and monitoring of the international spread of epidemic clones (Struelens *et al.*, 2024). In foodborne outbreaks, when the outbreak is under control, and the source of the contamination is a food product, genomic comparisons can help rapidly establish an epidemiological connection between the clinical cases and the contaminated food product, enabling public health officials to take timely action and carry out product recalls (Mather *et al.*, 2024).

New sequencing technologies, broadly known as metagenomics, have brought the scope of surveillance beyond cultured isolates of bacteria (Ko *et al.*, 2022). Metagenomics allows direct analysis of DNA extracted from wastewater, agricultural soils, food, and other environmental samples, even though the bacteria have not been isolated, for detection of *Salmonella* and associated resistance genes (Pennone *et al.*, 2022). This culture independent method is especially useful for environmental surveillance, a situation where bacterial levels can be low, or the bacteria cannot be cultured by conventional microbiological methods (Milligan *et al.*, 2023). Wastewater-based surveillance (WBSD) is a potentially useful approach for identifying the spread of resistant pathogens in the community and could help detect trends in resistance in the community before they are seen in clinical settings (Malcom and Bowes, 2025).

Although it has transformative potential, several challenges remain that continue to prevent the widespread adoption of genomic surveillance (Ling-Hu *et al.*, 2022). Despite the many advantages of sequencing, significant challenges remain such as the high cost of sequencing infrastructure, lack of bioinformatics expertise, lack of standardized pipelines for analysis, and unequal access to sequencing technologies (Nizamani *et al.*, 2023). Which are especially challenging in low- and middle-income countries, where the burden of salmonellosis is often highest and the need for sequencing is most acute (Grace,

2023). Furthermore, international data sharing agreements, standardization of metadata capture and harmonization of genomic databases is key to ensure the full potential of the genomic data for global surveillance and outbreak response (Ling-Hu *et al.*, 2022).

In summary, genomic surveillance has substantially improved the resolution with which salmonella populations, resistance determinants, and outbreak-associated clusters can be characterized. Ongoing linkage of genomic information and epidemiological, antimicrobial resistance surveillance and environmental data will reinforce One Health approaches focused on reducing the emergence and global spread of high-risk *Salmonella* lineages (Dushayeva, 2025). Genomic surveillance is hugely useful but has some limitations. Transmission pathways interpretation is very much dependent on sampling density, sequencing quality, bioinformatic pipeline standardization and the completeness of reference databases. In addition, there is a potential for unequal access to WGS technologies in low-resource settings, which can cause a major surveillance bias.

Integrated control strategies for antimicrobial-resistant *Salmonella*: Control of AMR *Salmonella* needs a coordinated approach that tackles the pathogen both within the human and animal sectors and between the two sectors, span the human–animal–environment interface (Dushayeva, 2025). Resistant *Salmonella* are not confined to any single reservoir but are spread throughout interconnected reservoirs and so a single population reduction in either human healthcare or animal production is unlikely to lead to long-term reductions in disease burden (Bisola Bello *et al.*, 2024). Promoting antimicrobial stewardship, farm biosecurity, food safety management, environmental protection and coordinated surveillance through a comprehensive One Health approach can help to break transmission cycles and diminish the selection pressure leading to antimicrobial resistance (Mudenda *et al.*, 2023).

Stewarding antimicrobials is still the basis of resistance mitigation (Khadse *et al.*, 2023). In human medicine, antibiotics should be used judiciously in response to clinical necessity and microbiological data and results, and

empirical therapy and inappropriate use of broad-spectrum antibiotics should be avoided (Chang *et al.*, 2022). The use of rapid diagnostic tools and antimicrobial susceptibility testing can help with evidence-based treatment decisions and minimize unnecessary use of antimicrobials that are vital to the treatment of patients (Schinas *et al.*, 2023). Public education on responsible use of antibiotics, and compliance with treatment protocols, is also important, to reduce the development of resistant bacterial populations (Adebisi, 2023).

Appropriate and responsible antimicrobial use is key for limiting the emergence and spread of antimicrobial resistant *Salmonella* among food-producing animals in the veterinary industry (Samtiya *et al.*, 2022). Routine use of antimicrobials should not be considered a best practice for disease management and should be replaced with preventative measures such as better husbandry, vaccination, nutrition and biosecurity (Guardabassi *et al.*, 2018). Adopting improved farm hygiene, restricting animal movement, using all-in/all-out production and effective cleaning and disinfection practices can significantly help to limit the spread of pathogens (Betiku *et al.*, 2025). As part of vaccination programs (especially in poultry), significant reductions in intestinal colonization and shedding of *Salmonella* have been shown, which decreases the contamination of animal food products (Shaji *et al.*, 2023).

Precautions needed for food safety are still essential at each stage of the farm-to-fork journey (Pierce *et al.*, 2022). Reducing contamination during production, processing, transportation and retail processes is made easier through the implementation of Good Agricultural Practices (GAP), Good Manufacturing Practices (GMP) and Hazard Analysis and Critical Control Point (HACCP) systems (Awuchi, 2023). Properly monitoring foods for microbiological safety, controlling the environment around processing equipment, maintaining proper temperature control while foods are being stored and transported, and controlling for cross-contamination are all important elements of foodborne disease prevention (Al-Sharif *et al.*, 2025). Educating consumers about safe handling of food and proper preparation and kitchen hygiene also minimizes the household risk of transmission (Saadat *et al.*, 2024).

Genomic surveillance workflow for antimicrobial-resistant *Salmonella*.

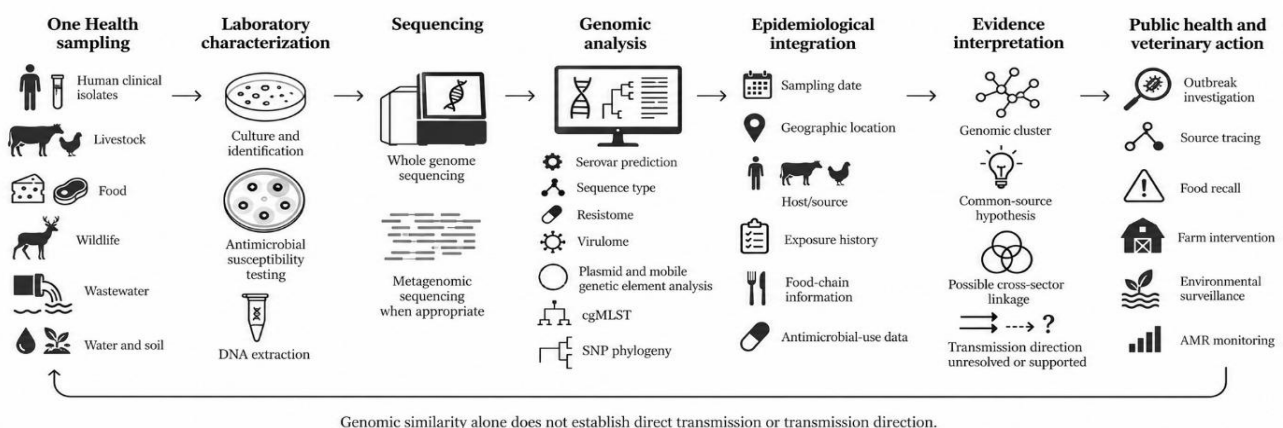


Fig. 3: A new workflow for genomic surveillance of antimicrobial-resistant *Salmonella*. Assessment of phenotypic, genomic and epidemiological data from humans, animals, food and environment to look for related lineages, resistance determinants and possible epidemiological clusters.

Another area that is important, but frequently overlooked, of One Health control strategies is environmental management (Pitt and Gunn, 2024). Prevention of agricultural runoff, safe disposal of hospital waste and pharmaceutical waste, wastewater treatment and proper disposal of manure, minimizes the input of resistant bacteria and antimicrobial residues into natural ecosystems (Abosse *et al.*, 2024). This is especially critical because good water quality is essential in preventing the transfer of resistant *Salmonella* into fresh produce and aquaculture systems via contaminated irrigation water and surface water (Gurtler and Gibson, 2022). Environmental surveillance, such as periodic monitoring of wastewater and surface water, can be an important source of information on the spread of resistant strains and is useful in addition to the standard clinical surveillance (Tiwari *et al.*, 2022).

It is critical to have integrated surveillance systems to identify the trend of emerging resistance and focus public health interventions (Jia *et al.*, 2023). When *Salmonella* isolates from human, animal, food, wildlife and environmental sources are monitored together, it can help identify potentially high-risk *Salmonella* clones which are responsible for outbreaks in the early stages and help determine the source of the outbreak (Bisola Bello *et al.*, 2024). The use of whole genome sequencing for national surveillance has significantly enhanced the capacity of national surveillance and provided more insights into transmission networks, monitoring the spread of resistance genes and evidence-based decision-making (Hasan *et al.*, 2025). International cooperation and common data sharing systems further enhance the global reaction to AMR *Salmonella*, especially with the growth in international trade and travel (Bisola Bello *et al.*, 2024).

Innovative, less conventional strategies should be used more frequently in future control measures to limit the use of traditional antibiotics (Cook and Wright, 2022). Various alternatives including bacteriophage therapy, probiotics, prebiotics, competitive exclusion cultures, antimicrobial peptides, immunomodulatory feed additives, and better vaccine technologies have proven to be very promising to decrease the colonization of *Salmonella* in livestock (Saleh *et al.*, 2025). While some of these strategies need to be further evaluated in commercial production, they are all sustainable techniques that could be used in tandem with antimicrobial stewardship and contribute to long term disease control (Pinto Ferreira *et al.*, 2022).

Finally, there is a need for continued communication between physicians, veterinarians, microbiologists, food safety officials, environmental scientists, and policy makers, as well as with the agricultural industry, to effectively manage the problem of antimicrobial-resistant *Salmonella* (Elbehiry *et al.*, 2025). Implementing evidence-based interventions across all the sectors of the One Health continuum will provide the best opportunity to minimize the emergence, persistence and global spread of resistant *Salmonella* (Elbehiry *et al.*, 2025).

Critical synthesis of one health evidence: The epidemiological link between compartments is strong, but varies significantly, with available evidence showing antimicrobial-resistant *Salmonella* present in all

compartments including human, animal, food, and environmental. Ecological overlap from detection of similar serovars, resistance phenotypes, resistance genes or mobile genetic elements in different sectors does not necessarily imply direct transmission. Focusing on stronger inference, the integration of temporal and geographical information, similar sampling strategies, epidemiological linkage, and adequate molecular or genomic discrimination are required.

Antimicrobial resistance patterns are also highly variable in different geographical regions, and These differences are likely to be real differences in antimicrobial use, circulating serovars, production systems, selection pressures, sampling intensity, laboratory capacity, and surveillance coverage, as well as differences in antimicrobial susceptibility testing methods and breakpoint interpretation. Therefore, apparent inter-regional differences should not be used to draw biological differences in the burden of resistance, especially in regions with limited surveillance. Genomic surveillance has made a significant impact on the capacity to detect related *Salmonella* strains, resistances, and mobile genetic elements. However, the direction of transmission and the time are still not definitively known from closely related genomes. The interpretation of whole genome sequencing data is dependent on sampling density, epidemiological metadata, temporal and spatial context, data quality, bioinformatic pipelines, and the completeness of existing comparison databases. Therefore, genome-based evidence should be used alongside traditional epidemiological investigations.

There is strong supporting evidence for the importance of a One Health approach for antimicrobial resistant *Salmonella*, but there is not equal evidence of the contribution of each of the compartments. While the food-animal and food-associated pathways are relatively well defined for several non-typhoidal serovars, the quantitative importance of wildlife, wastewater, agricultural environments, and other environmental reservoirs to human infection is less consistently defined. Such uncertainties should be considered when planning surveillance and control programs and in assessing the cross-sector detection of resistant organisms or resistance genes.

Research gaps and future perspectives: The field of epidemiology and molecular biology of antimicrobial-resistant *Salmonella* has made significant progress, but several gaps remain to be filled and will hamper the efforts towards effective prevention and control. Implementing surveillance programs for One Health is one of the greatest challenges, as there is significant variability in program implementation between different countries. Areas of low- and middle-income countries are still poorly monitored due to poor laboratory facilities, lack of funds, and lack of genomic sequencing technologies. These differences make it difficult to estimate the global burden of antimicrobial resistant *Salmonella* and to identify emerging HRSP clones. Comparatively little is known about environmental reservoirs either. Wastewater, agricultural soils, irrigation water, wildlife and aquaculture environments are now acknowledged as significant sources of resistant

Salmonella, but the role these sources play in the persistence and transmission of resistant *Salmonella* over time remains to be fully quantified. Long-term environmental surveillance of the movement of resistant strains and resistance genes in linked ecosystems should be extended and given more priority for future research. Combining the environmental and clinical and veterinary surveillance will give a better picture of the transmission dynamics and inform targeted interventions.

A priority is further harmonization of the genomic surveillance and antimicrobial resistance reporting systems. The consistency and reliability of the data is improved by standardized laboratory procedures, bioinformatics pipelines and worldwide available genomic databases which can facilitate rapid detection of outbreaks across borders. When paired with antimicrobial usage data, epidemiological and environmental information, the integration of whole genome sequencing data will further enhance source attribution and risk assessment, which will help to make prompt public health responses.

The need to continue researching sustainable alternatives to currently used antibiotics is also warranted. Vaccines, bacteriophage therapy, probiotics, antimicrobial peptides, and microbiomics (alteration of the microbiome) have shown potential to reduce colonization of *Salmonella* in animal production facilities, but further research is needed to address the long-term efficacy, economic feasibility, and large-scale implementation of these interventions. Moreover, the development of AI, machine learning, and predictive epidemiological modelling may help to better predict outbreaks, locate hotspots for emergence of resistance and devise surveillance strategies under One Health. More cooperation between countries, multidisciplinary partnerships and continued investment in integrated surveillance systems will be needed to address these research priorities. Enabling actions on the global level, linking science and evidence-based policy, will be critical to reducing the spread of antimicrobial-resistant *Salmonella* in the future.

Conclusions: AMR has become an intricate global health problem, with clinical, livestock production, food systems, wildlife and environmental reservoirs. It has persisted successfully across the human–animal–environment interface, a result of the interplay of antimicrobial selection pressure, microbial adaptation and complex transmission routes. Thus, antimicrobial-resistant *Salmonella* control needs a holistic approach by addressing antimicrobial stewardship, farm biosecurity, food safety, environmental management and coordinated surveillance. The recent progress in genomics technologies has greatly enhanced the ability to identify, characterize and monitor resistant *Salmonella* lineages, which has shed light on the evolution and transmission of pathogens. Progress is, however, hampered by the need for further improvements in surveillance capacity, and the need to make genomic data more comparable, as well as the lack of recognition of the contribution of environmental reservoirs. The importance of environmental reservoirs is clear, but important issues surrounding the exact influence of environmental reservoirs remain. New methods, still under development but not yet widely used, like machine learning for

predictive epidemiological modelling, other antimicrobials, and globally standardized genomic surveillance will become more important for future control measures. Two-way collaboration between countries, including through the sharing of knowledge and evidence, can improve global preparedness and help control one of the most important foodborne bacterial pathogens in the long-term in the world through One Health approaches.

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