TITLE PAGE
- Food Science of Animal Resources -
Upload this completed form to website with submission

ARTICLE INFORMATION	Fill in information in each box below
Article Type	Review article
Article Title	Antibiotic-Resistant Salmonella in Animal Products Jeopardize Human Health
Running Title (within 10 words)	Threat of Antibiotic-Resistant Salmonella
Author	Hyemin Oh[1,2] [First author], Yukyung Choi[3] [First author], Jeeyeon Lee[4]
Affiliation	[1] Risk Analysis Research Center, Sookmyung Women's University, Seoul 04310, Korea [2] Department of Food and Nutrition, Sookmyung Women's University, Seoul 04310, Korea [3] Chong Kun Dang Bio Research Institute, Ansan 15604, Korea [4] Department of Food & Nutrition, Dong-eui University, Busan 47340, Korea
Special remarks – if authors have additional information to inform the editorial office	
ORCID (All authors must have ORCID) https://orcid.org	Hyemin Oh (https://orcid.org/0000-0002-8073-7242) Yukyung Choi (https://orcid.org/0000-0002-7994-9862) Jeeyeon Lee(https://orcid.org/0000-0002-5885-6835)
Conflicts of interest List any present or potential conflict s of interest for all authors. (This field may be published.)	The authors declare no potential conflict of interest.
Acknowledgements State funding sources (grants, funding sources, equipment, and supplies). Include name and number of grant if available. (This field may be published.)	
Author contributions (This field may be published.)	Conceptualization: Oh H, Lee Y. Data curation: Oh H, Choi Y, Lee Y. Writing - original draft: Oh H, Choi Y, Lee Y. Writing - review & editing: Oh H, Choi Y, Lee Y.
Ethics approval (IRB/IACUC) (This field may be published.)	This article does not require IRB/IACUC approval because there are no human and animal participants.

CORRESPONDING AUTHOR CONTACT INFORMATION

For the corresponding author (responsible for correspondence, proofreading, and reprints)	**Fill in information in each box below**
First name, middle initial, last name	Jeeyeon Lee
Email address – this is where your proofs will be sent	jylee@deu.ac.kr
Secondary Email address	fmjylee02@gmail.com
Postal address	47340
Cell phone number	+82-10-4171-0716
Office phone number	+82-51-890-1596
Fax number	+82-505-182-6873

Abstract

Despite the significance of antibiotics in treating bacterial infections, antibiotic resistance is continuously increasing, thus posing a significant threat. In addition to strains resistant to individual drugs, multidrug-resistant (MDR) and pandrug resistant strains, which are resistant to all antibiotics, are emerging. *Salmonella*, a primary cause of global foodborne illness, is often transmitted through animal products. Antibiotic treatment is crucial for immunocompromised individuals, such as older adults and patients with weakened immune systems, due to their increased susceptibility to severe effects. MDR *Salmonella*, which can arise following antibiotic use in food animals, may transfer to humans, leading to significant health challenges. The emergence of *Salmonella* strains resistant to carbapenems, often considered a last-resort antibiotic class, is particularly concerning. *Salmonella* neutralizes antibiotics through mechanisms, such as horizontal gene transfer via plasmids, efflux/influx system regulation, and enzyme production that deactivate or alter antibiotics. The rise of mega plasmids in *Salmonella* is particularly alarming, as it may enable resistance to a broader range of antibiotics. This review summarizes the current state of the growing threat of MDR *Salmonella* and underscores the urgent need for a coordinated response.

Keywords: *Salmonella*, multidrug-resistance, outbreaks, resistance pattern, resistance mechanisms

Introduction

Since Alexander Fleming discovered penicillin in 1928, antibiotics have been widely used in human and veterinary medicine to control bacterial infections (Kasimanickam et al., 2021; Tan et al., 2015). In livestock production, antibiotics not only treat bacterial diseases to safeguard animal health but also promote growth in species, such as poultry, beef cattle, and swine, thus enhancing animal welfare and food safety (Marshall and Levy, 2011; Kasimanickam et al., 2021). However, the misuse and overuse of antibiotics have led to the emergence of antibiotic-resistant pathogens, rendering some infections untreatable (Hutchings et al., 2019). Antibiotic resistance refers to the ability of bacteria to survive and multiply despite antibiotic treatment, rendering these drugs ineffective (Chinemerem et al., 2022). When bacteria become resistant to three or more antibiotic classes, they are categorized as multidrug-resistant (MDR) (Li et al., 2023); resistance to all but one or two classes is classified as extensively drug-resistant (XDR) and resistance to all classes is termed pandrug-resistant (PDR) (Magiorakos et al., 2012). Antibiotic resistance has escalated to a global health crisis, complicating bacterial infection treatment and threatening public health (Chinemerem Nwobodo et al., 2022). Antibiotic-resistant bacteria can easily spread through transmission between animals, animal-derived foods, and humans, resulting in severe infections.

The Centers for Disease Control and Prevention (CDC) reports multiple foodborne *Salmonella* outbreaks in the US between 2013 to 2024, primarily linked to contaminated animal products (CDC, 2024). Notably, in 2024, an outbreak of *Salmonella* Enteritidis linked to contaminated eggs caused 65 illnesses and 24 hospitalizations, with investigations ongoing. Similarly, in 2021, outbreaks linked to raw frozen breaded stuffed chicken and ground turkey contaminated with *S.* Enteritidis and *Salmonella* Hadar caused 36 illnesses (12 hospitalizations) and 3 illnesses (4 hospitalizations), respectively. Other vehicles of *Salmonella* infection have included ground beef, raw chicken products, chicken salad, shell eggs, raw cookie dough, and charcuterie meats (CDC, 2024). In South Korea, *Salmonella* was the leading cause of foodborne outbreaks from 2019 to 2023, affecting 6,449 patients across 163 outbreaks. Other pathogens responsible for foodborne outbreaks included *Escherichia coli*, *Clostridium perfringens*, *Campylobacter jejuni*, *Staphylococcus aureus*, *Bacillus* spp., and *Vibrio* spp. (MFDA, 2024). According to Batz et al. (2011), *Salmonella* infections in the United States result in an estimated loss of approximately 17,000 quality-adjusted life years annually and incur costs of around $3.3 billion due to medical expenses and reduced productivity.

The persistence of *Salmonella*-derived foodborne outbreaks has heightened concerns about antibiotic-resistant *Salmonella* strains. Chloramphenicol-resistant *Salmonella* strains were first reported in the early 1950s, followed by resistance to antibiotics such as tetracycline, ampicillin, kanamycin, and trimethoprim (Jamilah et al., 2020; Van Leeuwen et al., 1982). MDR *Salmonella* strains originating from livestock and animal products can be transmitted to humans. For instance, during 2021-2022 in the US, 87% (1,110 out of 1,281 samples tested positive) of MDR *Salmonella* Newport were linked to beef products (Ford et al., 2023). To manage foodborne outbreaks effectively, it is essential to investigate the transmission routes of MDR *Salmonella*. Moreover, given that the efficacy of antibiotics is based on targeting specific bacterial functions, elucidating the mechanisms underlying antibiotic resistance is vital for ensuring the effective application of antibiotics (Abushaheen et al., 2020). Identifying critical transmission pathways can guide the development of prevention and control strategies. This review examines *Salmonella* detection cases in animal products, analyses antibiotic resistance patterns, outlines mechanisms of resistance acquisition, and proposes solutions to control antibiotic-resistant *Salmonella* outbreaks.

Prevalence of *Salmonella* in animal products

Salmonella species are among the leading bacterial causes of foodborne gastroenteritis globally (Sanchez et al., 2002). These gram-negative, facultative anaerobic bacteria belong to the

Enterobacteriaceae family and are commonly found in the gastrointestinal tracts of humans and animals (Agbaje et al., 2011). There are two *Salmonella* species, *S. bongori* (V) and *S. enterica*, with *S. enterica* divided into six subspecies: *enterica* (I), *salamae* (II), *arizonae* (IIIa), *diarizonae* (IIIb), *houtenae* (IV), and *indica* (VI) (Popoff and Minor, 1997; Giammanco et al., 2002). Among these, the *Salmonella enterica* subspecies is most associated with human infections, with *S.* Typhimurium and *S.* Enteritidis being the most significant serotypes of the more than 1,530 identified (Giammanco et al., 2002; Grimont and Weill, 2007).

Animal products, such as poultry (duck, chicken, and turkey), pork, and eggs, are primary sources of *Salmonella* infections. However, other food sources, including vegetables and fruits, have also been implicated (Sanchez et al., 2002). A meta-analysis by Ferrari et al. (2019) detected diverse *Salmonella* serovars, including *S.* Enteritidis, *S.* Typhimurium, *S.* Kentucky, and *S.* Sofia, as well as in pork, including *S.* Typhimurium, *S.* Hadar, *S.* Derby, and *S.* Meleagridis in pork, across all five continents. Below, we summarize global data on *Salmonella* prevalence and serovar distribution in animal products reported from 2013 to 2024 (Table 1).

Salmonella prevalence in poultry has been widely documented. Mazengia et al. (2014) analyzed 1,322 poultry samples, including whole chickens, ground chicken, and ground turkey, collected from US retail stores and USDA-approved processing facilities between 2011–2012, reporting a *Salmonella* prevalence of 11.3%. The most common serotypes identified were *S.* Heidelberg, *S.* Enteritidis, and *S.* Kentucky. In South Korea, Yoon et al. (2014) reported *Salmonella* in 51.3% of ducks and 3.7% of chickens sold at various market types, including supermarkets, traditional markets, internet outlets, and wholesale stores, in 2013. Common serotypes included, *S.* Typhimurium and *S.* Enteritidis with serotypes such as *S.* Stanley, *S.* Regent, *S.* Winterthur, and *S.* Westhampton detected only in ducks. La et al. (2021) focused on *S.* Enteritidis and isolated *Salmonella* in 61% of retail ducks and 14.1% of chickens between 2019 to 2020. Similarly, Kang et al. (2024) reported a *Salmonella* prevalence of 28.2% in ducks and 17.5% in chickens, while beef samples showed no *Salmonella* contamination. In the US, Guran et al. (2017) detected *Salmonella* in 32.4% of chicken samples, with serovars including *S.* Heidelberg, *S.* Kentucky, *S.* Typhimurium, *S.* Infantis, *S.* Seftenberg, *and S.* Thompson. Donado-Godoy et al. (2015) identified *S.* Paratyphi, *S.* Heidelberg, *S.* Lome, *and S.* Muenster in 26% of chicken meats. In Japan, Sasaki et al. (2021) detected *Salmonella* in 85.1% of chicken products (minced meat, breast, neck skin, thigh, and liver) purchased from processing plants and retail stores between 2018 and 2021. The most frequently detected serovars included *S.* Schwarzengrund, *S.* Infantis, *and S.* Manhattan.

Eggs are another significant vector for *Salmonella* infections. In South Korea, eggs and egg-based foods, such as kimbab, are major sources of *Salmonella* outbreaks. Hong et al. (2015) classified eggs and processed egg products, including whole egg liquid and egg powders, as high-risk (Group I) due to their frequent *Salmonella* contamination. Jung and Lee (2024) found *Salmonella* in 18.3% of eggshells and 20% of egg contents sampled from 60 grading and packing plants, with *S.* Infantis as the predominant serovar. Similarly, in Europe, eggs and egg-based products are leading sources of *Salmonella* outbreaks, followed by pork and bakery products (EFSA and ECDC, 2021). Tîrziu et al. (2020) reported a 6.3% prevalence of *S.* Enteritidis and *S.* Infantis in eggshells in Romania.

Pork and beef also pose risks for *Salmonella* transmission. In South Korea, Kang et al. (2024) found a 1.4% prevalence of *Salmonella* in pork samples. In Italy, *S. Brandenburg*, *S.* Typhimurium, *S.* Rissen, and *S.* London were detected in ready-to-eat (RTE) pork salami at a 4.8% prevalence, while in Romania, raw pork had a 22.6% prevalence, with RTE pork (primarily sausages) showing a 4.7% prevalence of various serovars, including *S.* Typhimurium (Tîrziu et al., 2020). In beef, *Salmonella* serovars such as *S.* Newport, *S.* Typhimurium, *S.* Enteritidis, *S.* Braenderup, *S.* Dublin, *S.* Uganda, *S.* Idikan, *S.* Infantis, *and S.* Muenchen were detected in ground beef, intact raw beef, and RTE beef. These findings were linked to 27 *Salmonella* outbreaks in the US between 2012 and 2019 (Canning et al., 2023).

In summary, animal products are significant vectors for *Salmonella* transmission to humans. The diversity of serovars, particularly *S.* Typhimurium *and S.* Enteritidis, highlights the potential for varied antibiotic resistance profiles, emphasizing the need for robust monitoring.

Status of antibiotic-resistant *Salmonella*

Although antibiotics are not always necessary for treating *Salmonella* infections, they are crucial for immunocompromised patients and those with severe cases. However, the overuse and misuse of antibiotics have accelerated the emergence of antibiotic-resistant *Salmonella*. Historically, chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole were the primary treatments for salmonellosis (Stoycheva and Murdjeva, 2006). As resistance to these drugs emerged, third-generation fluoroquinolones, including ciprofloxacin, became the preferred treatment (Bhandari et al., 2023). Increasing resistance among *Salmonella* strains has made managing salmonellosis more challenging (Argimon et al., 2022; CDC, 2023). The use of antibiotics in food animal production has significantly contributed to the emergence of resistant *Salmonella* strains.

The primary classes of antibiotics to which *Salmonella* has developed resistance are summarized in Table 2. Aminoglycosides, mainly effective against gram-negative bacteria, exert antibacterial effects by binding to the bacterial 30S ribosomal subunit and inhibiting protein synthesis (Gonzalez and Spencer, 1998; Hermann, 2005). Tetracyclines and amphenicols similarly inhibit protein synthesis by binding to bacterial ribosomes, with amphenicols specifically acting on the 50S ribosomal subunit (Hermann, 2005; Frye and Jackson, 2013). Sulfonamides, often combined with trimethoprim, interfere with bacterial folic acid synthesis, impairing DNA replication (Brumfitt et al., 1973; Eliopoulos and Huovinen, 2001). Fluoroquinolones inhibit bacterial DNA replication by targeting DNA gyrase but are prone to rapid resistance development (Drlica and Zhao, 1997; Redgrave et al., 2014). β-Lactams, the most widely used antibiotic class, inhibit bacterial cell wall synthesis by binding to penicillin-binding proteins, primarily targeting gram-positive bacteria but are also effective against some gram-negative bacteria (Tipper and Strominger, 1965). Carbapenems, a subset of β-lactams, exhibit strong resistance to β-lactamase and extended-spectrum β-lactamase (ESBL), enzymes that can inactivate many β-lactam antibiotics (Vardakas et al., 2012).

1. *Prevalence of antibiotic-resistant Salmonella in animal products*

In animal husbandry, antibiotics are widely used for disease control and growth promotion. This practice contributes to the development of antibiotic resistance in commensal and opportunistic bacteria in food animals (Cameron et al., 2016). Antibiotic-resistant *Salmonella* is frequently detected in poultry, such as chicken and duck, as well as in pork, and is a major source of human infection through contaminated raw meat (Borges et al., 2019). Pavelquesi et al. (2013) reported high levels of antibiotic resistance in *Salmonella* isolates from 53 contaminated chicken samples in Brazil. Among 78 *Salmonella* strains, resistance rates were 83.3% for amoxicillin/clavulanic acid, 64.1% for sulfonamide, and 46.2% for tetracycline. Additionally, 65.4% of the strains showed either resistance or intermediate susceptibility to ciprofloxacin.

Similarly, Perin et al. (2020) analyzed 98 *Salmonella* strains isolated from frozen chicken samples and found that all strains were resistant to chloramphenicol, imipenem, meropenem, and amikacin. High resistance rates were also observed for nalidixic acid (95.9%), tetracycline (93.9%), amoxicillin/clavulanic acid (83.7%), and ciprofloxacin (75.5%). In the US, Punchihewage-Don et al. (2024) reported that 27.2% of the 213 *Salmonella* isolates from chicken were resistant to tetracycline and minocycline, the highest among antibiotics tested. Likewise, Lv et al. (2024) found tetracycline (49.1%), ampicillin (48.2%), and streptomycin (35.1%) were the most frequently observed resistant antibiotics in China, where tetracycline and streptomycin are commonly used as growth promoters (McDermott et al., 2016).

In Korea, the highest resistance rates were showed for nalidixic acid (75.9%), ampicillin (63.2%), streptomycin (61.3%), tetracycline (59.3%), and sulfisoxazole (57.3%). *Salmonella* spp. isolation rates were higher in poultry [chickens (n=278) and ducks (n=177)] compared to cattle (n=0) and swine (n=2). These results represent a marked increase compared to 2021, when resistance rates were lower: 64.5% for nalidixic acid, 30.2% for ampicillin, 25.0% for tetracycline, 23.0% for streptomycin, and 23.4% for sulfisoxazole (APQA and NIFDS, 2024). Notably, resistance profiles differ between *Salmonella* isolated from pork and poultry. Gomes et al. (2022) reported that *Salmonella* isolated from pork had the highest resistance to azithromycin (95.0%), followed by ampicillin (51.7%), oxytetracycline (40.0%), and chloramphenicol (40.0%). In contrast, *Salmonella* isolates from poultry showed high resistance to quinolones, such as nalidixic acid (82.8%) and ciprofloxacin (74.1%), as well as sulfamethoxazole (81.0%), oxytetracycline (79.3%), and β-lactams (>69%).

Most studies reported antibiotic resistance data for *Salmonella* serotypes collectively as *Salmonella* spp. (Vaez et al., 2000; Thung et al., 2016); however, differences in antibiotic resistance have also been observed among individual serotypes. The antibiotic resistance patterns of *S.* Typhimurium frequently included the ASSuT profile (ampicillin, streptomycin, sulphonamides, and tetracycline) (Liu et al., 2023; Mellor et al., 2019). Resistance rates in *S.* Typhimurium were higher compared to other serotypes (Busani et al., 2004; Listorti et al., 2022). In Italy, Busani et al. (2004) reported that *S.* Typhimurium isolates from animal and animal-derived foods showed higher resistance to ampicillin, chloramphenicol, nalidixic acid, tetracycline, and streptomycin. *S.* Enteritidis strains frequently showed resistance to ampicillin, streptomycin, and sulphonamides in animal-derived food isolates. Additionally, *S.* Infantis strains showed higher resistance to sulphonamides and kanamycin. These observations highlight that *S.* Typhimurium consistently exhibits higher resistance rates across multiple antibiotics compared to *S.* Enteritidis or *S.* Infantis (Busani et al., 2004). Contrastingly, Abou Elez et al. (2021) reported that *S.* Enteritidis isolates had higher resistance rates than *S.* Typhimurium isolates to chloramphenicol, nalidixic acid, and imipenem in Egypt. The antimicrobial resistance patterns of *Salmonella* may differ regionally depending on antibiotic usage practices or the sources from which they are isolated.

Given these high resistance rates highlighted in these studies emphasize the urgent need for international collaboration to address antibiotic resistance, particularly in food animal production, where extensive antibiotic use promotes resistance in zoonotic pathogens such as *Salmonella*. Furthermore, these data indicate that antibiotic resistance in *Salmonella* from animal products is a global concern, with significant regional variations influenced by antibiotic usage practices. These illustrate how antibiotic use directly impacts resistance development in food-producing animals. A summary of antibiotic-resistant *Salmonella* isolated from animal products is presented in Table 3.

2. Emergence of antibiotic resistance due to antibiotic use

In 2015, the World Health Organization undertook efforts to improve global monitoring systems for antibiotic use, recognizing antibiotic resistance as a critical public and animal health issue. The World Organization for Animal Health (OIE) similarly acknowledged the impact of antibiotic use on resistance development (OIE, 2015; Jibril et al., 2021). Multiple studies have demonstrated a correlation between antibiotic use - especially of critically important antibiotics - and resistance rates in *Salmonella* from farms and products. For instance, chickens treated with ceftiofur for *Salmonella* infections exhibited resistance to ceftiofur (Dutil et al., 2010). In Nigerian poultry farms, widespread use of tetracycline and sulfonamides was significantly associated with resistance to these antibiotics in *Salmonella* strains isolated from poultry meat (Igbinosa et al., 2023).

In the US, between 2018 and 2019, MDR *Salmonella* Newport with reduced susceptibility to azithromycin caused 255 illnesses and 60 hospitalizations. These cases were linked to Mexican-style soft cheese and beef, contaminated with azithromycin- and ciprofloxacin-resistant *S.* Newport (Plumb et al., 2019). In Pakistan, significant resistance levels were detected in antibiotics commonly used as growth promoters and therapeutic agents in livestock and poultry, including erythromycin (100%), colistin (94.7%), tetracycline (87.7%), ciprofloxacin (84.2%), and ampicillin (64.9%). Resistance to clinically important antibiotics, such as azithromycin, was notably high at 93.0%, potentially linked to the widespread use of azithromycin for the treatment of COVID-19 in Pakistan (Fatima et al., 2023; Saeed et al., 2021). These findings underscore the substantial relationship between antibiotic use in livestock and the emergence of resistant *Salmonella* strains, highlighting the urgent need for strengthened antibiotic stewardship in animal agriculture to mitigate public health risks.

3. Co-resistant and MDR Salmonella in animal products

Antibiotic resistance in *Salmonella* from animal products arises primarily through two mechanisms: co-resistance, where a single gene imparts resistance to multiple antibiotics, and the presence of multiple genes conferring resistance to different antibiotics (Huo et al., 2024). Co-resistance allows *Salmonella* to resist various antibiotics, contributing to the prevalence of MDR strains, which are resistant to three or more antibiotic classes. The spread of MDR *Salmonella* represents a significant public health threat, as these strains are often resistant to critical antibiotics, including fluoroquinolones, third-generation cephalosporins, and even carbapenems (Hussain et al., 2020; Ejo et al., 2016). Co-resistance is particularly common in *Salmonella* strains resistant to both nalidixic acid and fluoroquinolone antibiotics (Oteo et al., 2000). Nalidixic acid, a first-generation quinolone, has historically been used to treat human and animal infections and as a growth promoter in food-producing animals. However, excessive use has led to an increase in quinolone-resistant *Salmonella* strains and reduced susceptibility to fluoroquinolones (Cho et al., 2019; Tamang et al., 2011).

Kapil et al. (2002) found that 56 nalidixic acid-resistant *Salmonella* strains exhibited significantly lower susceptibility to ciprofloxacin compared to 34 nalidixic acid-sensitive strains. Similarly, Ryan et al. (2011) demonstrated reduced ciprofloxacin susceptibility in 19 nalidixic acid-resistant *Salmonella* strains, while nalidixic acid-sensitive strains showed no change in susceptibility. In 2024, Kang et al. reported that 61.9% of *S.* Infantis isolates (253/409) from food animals (chickens, swine, cattle, and ducks) were resistant to ceftiofur, an important cephalosporin antibiotic. Notably, most resistant isolates obtained from chickens (249/253, 98.4%). Ceftiofur-resistant isolates also showed increased resistance to non-beta-lactam antibiotics, including nalidixic acid, streptomycin, tetracycline, and trimethoprim/sulfamethoxazole (Kang et al., 2024; Yarar et al., 2023). Resistance to third-generation cephalosporins, such as ceftiofur, is primarily driven by the bacterial synthesis of ESBL and/or AmpC β-lactamases, which inactivate cephalosporins (Burke et al., 2014). ESBL-producing *Salmonella* strains from animal products frequently display resistance to cephalosporins and multiple other antibiotic classes, including aminoglycosides, tetracycline, and fluoroquinolones, further contributing to MDR (Jeon et al., 2019; Zhao et al., 2001).

Jeon et al. (2019) observed that ESBL/pAmpC-positive *Salmonella* strains exhibited resistance to four or more antibiotics, including cephalosporins as well as non-cephalosporin antibiotics such as amoxicillin/clavulanic acid, tetracycline, ampicillin, ciprofloxacin, nalidixic acid, and gentamicin. The rising prevalence of MDR *Salmonella* in animal products presents a significant global health concern, emphasizing the need for international cooperation and stricter controls on agricultural antibiotic use to protect public health.

How *Salmonella* becomes antibiotic resistant?

Salmonella employs several mechanisms to neutralize antibiotic action. The first is the acquisition of antibiotic resistance genes, the second is the neutralization of antibiotics through enzymes, and the third is the control of the efflux and influx of antibiotics into and out of bacterial cells (Fig. 1).

1. Acquisition of antibiotic resistance

Salmonella primarily acquires resistance through the transfer of plasmids or resistance islands carrying antibiotic-resistance genes (Okaiyeto et al., 2024). Plasmids maintain stability within bacterial populations by employing post-segregational killing systems, which eliminate daughter cells lacking the plasmid (Aviv et al., 2014). The *Salmonella tetA* gene, responsible for tetracycline resistance, resides on a plasmid, facilitating its transfer among other *Salmonella* strains (Alcaine et al., 2007). Additionally, some *Salmonella* isolates carry multiple plasmids encoding resistance to antibiotics such as ampicillin, kanamycin, streptomycin, and tetracycline, leading to the development of MDR strains (Gebreyes and Altier, 2002; Rozwandowicz et al., 2018).

The IncHI1 plasmid, which carries ESBL genes and resistance genes for aminoglycosides and tetracyclines, has been detected in humans and animals across Europe (Rozwandowicz et al., 2018). IncHI1 has been notably implicated in MDR in *S.* Typhi (Holt et al., 2011). Ferreira et al. (2024) demonstrated that *Salmonella* strains (*S.* Enteritidis, *S.* Typhimurium, and *S.* Heidelberg) acquired resistance by artificial conjugation with a plasmid carrying resistance genes, resulting in a 4,096-fold increase in the minimum inhibitory concentration (MIC) for β-lactams.

The AmpC β-lactamase enzyme, encoded by plasmids, is particularly robust against inhibitors such as clavulanic acid and sulbactam (Jacoby, 2009; Le Terrier, 2024). For example, 16 *Salmonella* isolates from US food animals were found to possess IncA/C plasmids encoding

AmpC β-lactamase (Glenn et al., 2011). Megaplasmids, identified by Rosenerg et al. (1981), are significantly larger than standard plasmids, carry diverse resistance and virulence genes. The pESI megaplasmid, identified primarily in *S.* Infantis, is approximately 280 kb in size and confers resistance to various antibiotics while enhancing virulence (Aviv et al., 2014). Recent studies have documented the emergence of similar pESI-like megaplasmids globally (Cohen et al., 2020; Hall et al., 2021). For example, pESI-like plasmids in Russian broiler *Salmonella* isolates encoded resistance genes for spectinomycin (*aadA1*), doxycycline (*tetA/tetR*), tetracycline (*tetM*), trimethoprim (*dfrA14*), and sulfonamides (*sul1*). In Korea, *Salmonella* isolates from poultry farms classified as pESI-positive exhibited a 99.2% MDR rate, significantly higher than the 6.7% MDR rate of pESI-negative isolates (Kim et al., 2024).

2. *Antibiotic decomposition and modification using enzyme*

Salmonella produces enzymes that neutralize antibiotics by breaking them down or chemically modifying them. Chloramphenicol resistance arises from chloramphenicol acetyltransferase (CAT) an enzyme that attaches an acetyl group to chloramphenicol, preventing it from binding to the A-site on the bacterial ribosome and thereby inhibiting its ability to disrupt protein synthesis (Goodale et al., 2020). Brunelle et al. (2015) demonstrated that *Salmonella* isolates harboring the cat gene, which encodes CAT, displayed high resistance to chloramphenicol (MIC >512 μg/mL). Additionally, exposure to chloramphenicol has been linked to increased cellular invasion in *Salmonella*, suggesting that resistance may enhance infection risk. Guerra et al. (2002) indicated that integron-mediated cat transmission provides *Salmonella* with chloramphenicol resistance.

Carbapenems, critical last-resort antibiotics, are rendered ineffective by carbapenemase-producing non-typhoidal *Salmonella*, with resistant isolates reported from food, human, and animal sources (Fernández et al., 2018; Wang et al., 2017*). S.* Infantis from minced pork and *S.*

Indiana from chicken carcasses showed carbapenem resistance (Borowiak et al., 2017; Fischer et al., 2013; Wang et al., 2018). In Europe, *S.* Infantis, is considered a major carrier of carbapenem resistance (Borowiak et al., 2017), with the first carbapenem-resistant isolates detected in German livestock (Fischer et al., 2013).

β-Lactams, enzymes produced by gram-negative bacteria including *Salmonella*, hydrolyze the β-lactam ring, neutralizing β-lactam antibiotics. ESBL are more potent than standard β-lactamase and target third-generation- and fourth-generation β-lactams including cephalosporins and aztreonam, complicating treatment (Chaudhary and Aggarwal, 2004). ESBL-producing *Salmonella* isolated from the stool samples of patients with acute gastroenteritis, were significantly more resistant to quinolones underscoring the need for regular monitoring and management of ESBL-producing *Salmonella*.

Additionally, *Salmonella* inactivates aminoglycosides through enzymatic modification by acetyltransferase and phosphotransferase. These enzymes alter the conformation of the 30S ribosomal subunit, preventing aminoglycosides from binding to their target ribosome and rendering them ineffective (Frye and Jackson, 2013).

3. Controlling of the efflux and influx of antibiotics

Salmonella reduces the intracellular concentration of antibiotics by actively using efflux pumps and controlling membrane permeability. As a gram-negative bacterium, *Salmonella* requires antibiotics to penetrate its outer membrane to reach intracellular targets (Delcour, 2009). The outer membrane contains channels such as efflux pumps and porins that mediate the entry and exit of substances, including antibiotics. Efflux pumps like AcrAB-TolC, which are regulated by specific transporters, actively expel antibiotics from the cell, while porins such as OmpF selectively regulates antibiotic entry (Mahendran et al., 2010; Piddock, 2019). Overexpression of efflux pumps limits drug access, contributing to resistance (Blair et al., 2014). Inhibiting this overexpression, might make it possible to render *Salmonella* more sensitive to drugs. Siew et al. (2009) demonstrated that *Salmonella,* highly resistant to ciprofloxacin (256 μg/mL), exhibited a substantial decrease in resistance (to 0.25 μg/mL) when the AcrB component of the AcrAB-TolC efflux system was inactivated. Dowd et al. (2008) created a *Salmonella* strain (referred to as 2a) that developed resistance following continuous exposure to nalidixic acid. Comparative gene expression analysis indicated upregulation of efflux pump-related genes and downregulation of porin genes. Collectively, these findings suggest that *Salmonella* can develop antibiotic resistance by inducing efflux pump activity and reducing antibiotic influx. Furthermore, as efflux pump genes can reside on plasmids, antibiotic resistance can also be disseminated via horizontal gene transfer (Nishino, 2016).

Antibiotic alternatives

As part of the effort to manage MRD bacteria, alternative methods are emerging to replace antibiotics. In the long term, alternatives to antibiotics could reduce the use of antibiotics and slow the emergence of MRD bacteria. Antibiotic alternatives that are gaining attention include phage-based, antimicrobial oligonucleotides, and immunological approaches (e.g., monoclonal antibodies [mAb]) (Streicher, 2021). Phages are viruses that use bacteria as their hosts Lytic phages, which replicate and immediately destroy bacterial cells, are particularly promising as they lack the ability to transfer genetic elements to host cells, unlike lysogenic phages (Ly-Chatain, 2014; Sulakvelidze et al., 2001).They are also easy to genetically modify, isolate, and mass-produce, making them simpler to develop than new antibiotics (Khan and Rahman, 2022). Antimicrobial oligonucleotide are short base sequences that bind to specific bacterial mRNA, leading to mRNA degradation or inhibition of ribosomal binding (Chi et al., 2017; Streicher, 2021; Watts and Corey, 2011). The binding target mRNA can be a gene essential for the bacterial survival or an antibiotic resistance gene. It can also bind to a mRNA related to virulence (Streicher, 2021).

mAbs neutralize bacterial exotoxins by preventing their binding to ligands, reducing their pathogenic effects (Hansel et al., 2010). It is usually used as an adjuvant for antibiotics or as a preventive measure for high-risk groups (Sparrow et al., 2017). FDA-approved mAbs are already in use for treating various diseases, including cancer, infectious diseases, and autoimmune disorders (Elgundi et al., 2017).

Conclusion

Antibiotic resistance in *Salmonella* is increasingly concerning as resistance levels rise and MDR strains become increasingly prevalent. Megaplasmids carrying multiple resistance genes exacerbate. Despite regulations on antibiotic use in food animals in many countries, past antibiotic residues, as well as ongoing overuse and misuse, contribute to the persistence of MDR *Salmonella* in food animals, which poses a significant public health risk. MDR *Salmonella* infections are a serious concern, especially as resistance emerges to last-resort antibiotics, such as carbapenems. Alternative therapies, such as phage-based treatments and immunotherapies offer promising solutions and should be rapidly developed and applied in real-world settings. Also, prevention requires stringent measures, including regular monitoring and limiting the misuse of antibiotics in food animals. Collaboration between governments, industries, academia, and consumers is essential to address the severity of antibiotic resistance and implement effective solutions.

Conflict of Interest

The authors declare no potential conflict of interest.

Author Contributions

Conceptualization: Hyemin Oh, Lee J. Data curation: Oh H, Choi Y, Lee J. Writing - original draft: Oh H, Choi Y, Lee J. Writing - review & editing: Oh H, Choi Y, Lee J.

Ethics Approval

This article does not require IRB/IACUC approval because there are no human and animal participants.

References

Abou Elez RMM, Elsohaby I, El-Gazzar N, Tolba HMN, Abdelfatah EN, Abdellatif SS, Mesalam AA, Tahoun ABMB. 2021. Antimicrobial resistance of *Salmonella enteritidis* and *Salmonella typhimurium* isolated from laying hens, table eggs, and humans with respect to antimicrobial activity of biosynthesized silver nanoparticles. Animals (Basel) 11:3554.

Abushaheen MA, Fatani AJ, Alosaimi M, Mansy W, George M, Acharya S, Rathod S, Divakar DD, Jhugroo C, Vellappally S, Khan AA, Shaik J, Jhugroo P. 2020. Antimicrobial resistance, mechanisms and its clinical significance. Dis Mon 66:100971.

Agbaje M, Begum RH, Oyekunle MA, Ojo OE, Adenubi OT. 2011. Evolution of *Salmonella* nomenclature: a critical note. Folia Microbiol. 56:497-503.

Alcaine SD, Warnick LD, Wiedmann M. 2007. Antimicrobial resistance in nontyphoidal *Salmonella*. J Food Prot 70:780-790.

Animal and Plant Quarantine Agency [APQA] and National Institute of Food and Drug Safety Evaluation [NIFDS]. 2024. A survey of antimicrobial resistance in animals and retail livestock products in 2023. Animal and Plant Quarantine Agency, Gimcheon, Korea. pp 107-110.

Argimon S, Nagaraj G, Shamanna V, Sravani D, Vasanth AK, Prasanna A, Poojary A, Bari AK, Underwood A, Kekre M, Baker S, Aanensen DM, Lingegowda RK. 2022. Circulation of third- generation cephalosporin resistant *Salmonella* Typhi in Mumbai, India. Clin Infect Dis 74:2234-2237.

Aviv G, Tsyba K, Steck N, Salmon-Divon M, Cornelius A, Rahav G, Grassl GA, Gal-Mor O. 2014. A unique megaplasmid contributes to stress tolerance and pathogenicity of an emergent *Salmonella enterica* serovar Infantis strain. Environ Microbiol 16:977-994.

Batz MB, Hoffmann S, Morris JG. 2011. Ranking the risks: The pathogen-food combinations with the greatest burden on public health. Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA. p 12.

Bhandari M, Poelstra JW, Kauffman M, Varghese B, Helmy YA, Scaria J, Rajashekara G. 2023. Genomic diversity, antimicrobial resistance, plasmidome, and virulence profiles of *Salmonella* isolated from small specialty crop farms revealed by whole-genome sequencing. Antibiotics 12:1637.

Blair JM, Richmond GE, Piddock LJ. 2014. Multidrug efflux pumps in Gram-negative bacteria and their role in antibiotic resistance. Future Microbiol 9:1165–1177.

Bonardi S, Morganti M, Pupillo G, Brindani F. 2018. *Salmonella* Brandenburg in the pork chain in Italy: Genetic comparison with human isolates. Ital J Food Saf 7:1-7.

Borges KA, Martelo EB, Dos Santos LA, Furian TQ, Cisco IC, Manto L, Dos Santos LR. 2019. Detection and quantification of *Salmonella* spp. in poultry slaughterhouses of southern Brazil. J Infect Dev Ctries 13:455-460.

Borowiak M, Szabo I, Baumann B, Junker E, Hammerl JA, Kaesbohrer A, Malorny B, Fischer, J. 2017. VIM-1-producing *Salmonella* Infantis isolated from swine and minced pork meat in Germany. J Antimicrob Chemother 72:2131-2133.

Brumfitt W, Hamilton-Miller JMT, Kosmidis J. 1973. Trimethoprim-sulfamethoxazole: the present position. J Infect Dis 128:S778-S791.

Brunelle BW, Bearson BL, Bearson SM. 2015. Chloramphenicol and tetracycline decrease motility and increase invasion and attachment gene expression in specific isolates of multidrug-resistant *Salmonella enterica* serovar Typhimurium. Front Microbiol 5:801.

Busani L, Graziani C, Battisti A, Franco A, Ricci A, Vio D, Digiannatale E, Paterlini F, D'Incau M, Owczarek S, Caprioli A, Luzzi I. 2004. Antibiotic resistance in *Salmonella enterica* serotypes Typhimurium, Enteritidis and Infantis from human infections, foodstuffs and farm animals in Italy. Epidemiol Infect 132:245-251.

Burke L, Hopkins KL, Meunier D, De Pinna E, Fitzgerald-Hughes D, Humphreys H, Woodford N. 2014. Resistance to third-generation cephalosporins in human non-typhoidal *Salmonella enterica* isolates from England and Wales, 2010–12. J Antimicrob Chemother 69:977-981.

Cameron A, McAllister TA. 2016. Antimicrobial usage and resistance in beef production. J Anim Sci Biotechnol 7:68.

Canning M, Birhane MG, Dewey-Mattia D, Lawinger H, Cote A, Gieraltowski L, Schwensohn C, Tagg KA, Watkins LKF, Robyn MP, Marshall KE. 2023. *Salmonella* outbreaks linked to beef, United States, 2012–2019. J Food Prot 86:100071.

Centers for Disease Control and Prevention [CDC]. 2023. Information for healthcare professionals and laboratories. Available from: https://www.cdc.gov/salmonella/general/technical.html Accessed at Oct 10. 2024.

Chaudhary U, Aggarwal R. 2004. Extended spectrum β-lactamases (ESBL)–an emerging threat to clinical therapeutics. Indian J Med Microbiol 22:75-80.

Chinemerem Nwobodo D, Ugwu MC, Oliseloke Anie C, Al-Ouqaili MT, Chinedu Ikem J, Victor Chigozie U, Saki M. 2022. Antibiotic resistance: The challenges and some emerging strategies for tackling a global menace. J Clin Lab Anal 36:e24655.

Cho JK, Son KH, Kim KH, Kim JM, Park DH, Lee JW. 2019. Mutation in gyrA gene of nalidixic acid-resistant *Salmonella* isolates isolated from poultry slaughterhouse. Korean J Vet Serv 42:153-159.

Cohen E, Rahav G, Gal-Mor O. 2020. Genome sequence of an emerging *Salmonella enterica* Serovar Infantis and genomic comparison with other *S.* Infantis strains. Genome Biol Evol 12:151-159.

Delcour AH. 2009. Outer membrane permeability and antibiotic resistance. Biochim Biophys Acta 1794:808.

Donado-Godoy P, Byrne BA, Castellanos R, Vanegas C, Coral A, Arevalo A, Clavijo V, Vargas M, Zuňiga JJR, Tafur M, Pérez-Gutierrez E, Smith WA. 2015. Prevalence, resistance patterns, and risk factors for antimicrobial resistance in bacteria from retail chicken meat in Colombia. J Food Prot 78:751-759.

Drlica K, Zhao X. 1997. DNA gyrase, topoisomerase IV, and the 4-quinolones. Microbiol Mol Biol Rev 61:377-392.

Dutil L, Irwin R, Finley R, Ng LK, Avery B, Boerlin P, Bourgault AM, Cole L, Daignault D, Desruisseau A, Demczuk W, Hoang L, Horsman GB, Ismail J, Jamieson F, Maki A, Pacagnella A, Pillai DR. 2010. Ceftiofur resistance in *Salmonella enterica* serovar Heidelberg from chicken meat and humans, Canada. Emerg Infect Dis 16:48-54.

European Food Safety Authority [EFSA] and European Centre for Disease Prevention and Control [ECDC]. 2021. The European Union one health 2020 zoonoses report. EFSA J 19:e06971.

Ejo M, Garedew L, Alebachew Z, Worku W. 2016. Prevalence and antimicrobial resistance of *Salmonella* isolated from animal-origin food items in Gondar, Ethiopia. BioMed Res Int 2016:4290506.

Eliopoulos GM, Huovinen P. 2001. Resistance to trimethoprim-sulfamethoxazole. Clin Infect Dis 32:1608-1614.

Eng SK, Pusparajah P, Ab Mutalib NS, Ser HL, Chan KG, Lee LH. 2015. *Salmonella*: a review on pathogenesis, epidemiology and antibiotic resistance. Front Life Sci 8:284-293.

Fatima A, Saleem M, Nawaz S, Khalid L, Riaz S, Sajid I. 2023. Prevalence and antibiotics resistance status of *Salmonella* in raw meat consumed in various areas of Lahore, Pakistan. Sci Rep 13:22205.

Fernández J, Guerra B, Rodicio MR. 2018. Resistance to carbapenems in non-typhoidal *Salmonella enterica* serovars from humans, animals and food. Vet Sci 5:40.

Ferrari RG, Rosario DK, Cunha-Neto A, Mano SB, Figueiredo EES, Conte-Junior CA. 2019. Worldwide epidemiology of *Salmonella* serovars in animal-based foods: a meta-analysis. Appl Environ Microbiol 85:e00591-19.

Ferreira VA, Saraiva MM, Campos IC, da Silva MPS, Benevides VP, Almeida AM, Codognoto TA, Nascimento CF, de Lima TS, Rodrigues Ales, LB, Berchieri Junior A. 2024. *In vitro* conjugation of IncB/O-plasmid: Minimum inhibitory concentration of β-lactams increases 16-fold in *Salmonella enterica* compared with *Escherichia coli*. Microbial Pathog 193:106788.

Fischer J, Rodríguez I, Schmoger S, Friese A, Roesler U, Helmuth R, Guerra B. 2013. *Salmonella enterica* subsp. enterica producing VIM-1 carbapenemase isolated from livestock farms. J Antimicrob Chemother 68:478-480.

Ford L, Ellison Z, Schwensohn C, Griffin I, Birhane MG, Cote A, Fortenberry GZ, Tecle S, Higa J, Spencer S, Patton B, Patel J, Dow J, Maroufi A, Robbins A, Donovan D, Fitzgerald C, Burrell S, Tolar B, Folster JP, Cooley LA, Watkins LKF. 2023. Strain of multidrug-resistant *Salmonella* Newport remains linked to travel to Mexico and U.S. beef products — United States, 2021–2022. MMWR Morb Mortal Wkly Rep. 72:1225-1229.

Frye JG, Jackson CR. 2013. Genetic mechanisms of antimicrobial resistance identified in *Salmonella enterica*, *Escherichia coli*, and *Enteroccocus* spp. isolated from US food animals. Front Microbiol 4:135.

Gebreyes WA, Altier C. 2002. Molecular characterization of multidrug-resistant *Salmonella enterica* subsp. *enterica* serovar Typhimurium isolates from swine. J Clin Microbiol 40:2813-2822.

Giammanco GM, Pignato S, Mammina C, Grimont F, Grimont PA, Nastasi A, Giammanco G. 2002. Persistent endemicity of *Salmonella* bongori 48:z35:− in southern Italy: molecular characterization of human, animal, and environmental isolates. J Clin Microbiol 40:3502-3505.

Gomes VTM, Moreno LZ, Silva APS, Thakur S, La Ragione RM, Mather AE, Moreno AM. 2022. Characterization of *Salmonella enterica* contamination in pork and poultry meat from São Paulo/Brazil: Serotypes, genotypes and antimicrobial resistance profiles. Pathogens 11:358.

Goodale A, Michailidis F, Watts R, Chok SC, Hayes F. 2020. Characterization of permissive and non-permissive peptide insertion sites in chloramphenicol acetyltransferase. Microb Pathog 149:104395.

Gonzalez US III, Spencer JP. 1998. Aminoglycosides: a practical review. Am Fam Physician 58:1811-1820.

Grimont PAD, Weill FX. 2007. Antigenic formulae of the *Salmonella* serovars. WHO collaborating centre for reference and research on *Salmonella*. 9th ed. Institut Pasteur, Paris, France. p. 6-10.

Guerra B, Soto S, Cal S, Mendoza MC. 2000. Antimicrobial resistance and spread of class 1 integrons among *Salmonella* serotypes. Antimicrob Agents Chemother 44:2166-2169.

Guran HS, Mann D, Alali WQ. 2017. *Salmonella* prevalence associated with chicken parts with and without skin from retail establishments in the Atlanta metropolitan area, Georgia. Food Control 73:462-467.

Hall JP, Botelho J, Cazares A, Baltrus DA. 2022. What makes a megaplasmid?. Philos Trans R Soc B 377:20200472.

Hermann T. 2005. Drugs targeting the ribosome. Curr Opin Struct Biol 15:355-366.

Holt KE, Phan MD, Baker S, Duy PT, Nga TVT, Nair S, Turner AK, Walsh C, Fanning S, Farrell-Ward S, Dutta S, Kariuki S, Weill FX, Parkhill J, Dougan G, Wain J. 2011. Emergence of a globally dominant IncHI1 plasmid type associated with multiple drug resistant typhoid. PLoS Negl Trop Dis 5:e1245.

Hong SH, Park NY, Jo HJ, Ro EY, Ko YM, Na YJ, Yoon KS. 2015. Risk ranking determination of combination of foodborne pathogens and livestock or livestock products. J Food Hyg Saf 30:1-12.

Huo M, Xu X, Mi K, Ma W, Zhou Q, Lin X, Cheng G, Huang L. 2024. Co-selection mechanism for bacterial resistance to major chemical pollutants in the environment. Sci Total Environ 912:169223.

Hussain MA, Wang W, Sun C, Gu L, Liu Z, Yu T, Ahmad Y, Jiang Z, Hou J. 2020. Molecular characterization of pathogenic *Salmonella* spp. from raw beef in Karachi, Pakistan. Antibiotics 9:73.

Hutchings MI, Truman AW, Wilkinson B. 2019. Antibiotics: past, present and future. Curr Opin Microbiol 51:72-80.

Igbinosa IH, Amolo CN, Beshiru A, Akinnibosun O, Ogofure AG, El-Ashker M, Gwida M, Okoh AI, Igbinosa EO. 2023. Identification and characterization of MDR virulent *Salmonella* spp isolated from smallholder poultry production environment in Edo and Delta States, Nigeria. PLoS One 18:e0281329.

Jacoby G. 2009. AmpC Β-lactamases. Clin. Microbiol Rev 22:161-182.

Jamilah J, Hatta M, Natzir R, Umar F, Sjahril R, Agus R, Junita AR, Dwiyanti R, Primaguna MR, Sabir M. 2020. Analysis of existence of multidrug-resistant H58 gene in *Salmonella enterica* serovar Typhi isolated from typhoid fever patients in Makassar, Indonesia. New Microbes New Infect 38:100793.

Jeon HY, Kim YB, Lim SK, Lee YJ, Seo KW. 2019. Characteristics of cephalosporin-resistant *Salmonella* isolates from poultry in Korea, 2010–2017. Poult Sci 98:957-965.

Jibril AH, Okeke IN, Dalsgaard A, Olsen JE. 2021. Association between antimicrobial usage and resistance in *Salmonella* from poultry farms in Nigeria. BMC Vet Res 17:234.

Jung HR, Lee YJ. 2024. Prevalence and characterization of non-typhoidal *Salmonella* in eggs from grading and packing plants in Korea. Food Microbiol 120:104464.

Kang HS, Ali MS, Na SH, Moon BY, Kim JI, Hwang YJ, Yoon SS, Park SC, Lim SK. 2024. Nationwide surveillance and characterization of the third-generation cephalosporin-resistant *Salmonella enterica* serovar infantis isolated from chickens in South Korea between 2010 and 2022. Heliyon 10:e37124.

Kapil A, Renuka, Das B. 2002. Nalidixic acid susceptibility test to screen ciprofloxacin resistance in *Salmonella* typhi. Indian J Med Res 115:49-54.

Kasimanickam V, Kasimanickam M, Kasimanickam R. 2021. Antibiotics use in food animal production: escalation of antimicrobial resistance: where are we now in combating AMR? Med Sci 9:14.

Khan MAS, Rahman SR. 2022. Use of phages to treat antimicrobial-resistant *Salmonella* infections in poultry. Vet Sci 9:438.

Kim MB, Jung HR, Lee YJ. 2024. Emergence of *Salmonella* Infantis carrying the pESI megaplasmid in commercial farms of five major integrated broiler operations in Korea. Poultry Sci 103:103516.

Kim MS, Lim TH, Jang JH, Lee DH, Kim BY, Kwon JH, Choi SW, Noh JY, Hong YH, Lee SB, Yang SY, Lee HJ, Lee JB, Park SY, Choi IS, Song CS. 2012. Prevalence and antimicrobial resistance of *Salmonella* species isolated from chicken meats produced by different integrated broiler operations in Korea. Poult Sci 91:2370-2375.

Kim YJ, Chon JW, Lim JS, Song BR, Seo KH, Heo EJ, Park H-J, Wee S-H, Oh DH, Moon JS. 2015. Traceback investigation for *Salmonella* contamination at egg processing plants in South Korea: prevalence, antibiotic resistance, and epidemiological tracing by rep-PCR fingerprinting. J Food Sci 80:M759-M764.

Kim YJ, Song BR, Lim JS, Heo EJ, Park HJ, Wee SH, Oh SM, Moon JS. 2013. First report on isolation of *Salmonella* enteritidis from eggs at grocery stores in Korea. Food Sci Anim Resour 33:239-243.

Koh Y, Bae Y, Lee YS, Kang DH, Kim SH. 2022. Prevalence and characteristics of *Salmonella* spp. isolated from raw chicken meat in the Republic of Korea. J Microbiol Biotechnol 32:1307.

La TM, Kim T, Lee HJ, Lee JB, Park SY, Choi IS, Lee SW. 2021. Whole-genome analysis of multidrug-resistant *Salmonella* Enteritidis strains isolated from poultry sources in Korea. Pathogens 10:1615.

Lee SK, Chon JW, Song KY, Hyeon JY, Moon JS, Seo KH. 2013. Prevalence, characterization, and antimicrobial susceptibility of *Salmonella* Gallinarum isolated from eggs produced in conventional or organic farms in South Korea. Poult Sci 92:2789-2797.

Le Terrier C, Mlynarcik P, Sadek M, Nordmann P, Poirel L. 2024. Relative inhibitory activities of newly developed diazabicyclooctanes, boronic acid derivatives, and penicillin-based sulfone β-lactamase inhibitors against broad-spectrum AmpC β-lactamases. Antimicrob Agents Chemother 68:e00775-24.

Li L, Ma J, Yu Z, Li M, Zhang W, Sun H. 2023. Epidemiological characteristics and antibiotic resistance mechanisms of *Streptococcus pneumoniae*: An updated review. Microbiol Res 266:127221.

Listorti V, Garcia-Vozmediano A, Pitti M, Maurella C, Adriano D, Ercolini C, Dellepiane M, Guardone L, Razzuoli E. 2022. Antimicrobial resistance of *Salmonella* strains isolated from human, wild boar, and environmental samples in 2018-2020 in the Northwest of Italy. Pathogens 11:1446.

Liu M, Zhu K, Li X, Han Y, Yang C, Liu H, Du X, Xu X, Yang H, Song H, Qiu S, Xiang Y. 2023. Genetic characterization of a *Salmonella enterica* serovar Typhimurium isolated from an infant with concurrent resistance to ceftriaxone, ciprofloxacin and azithromycin. J Glob Antimicrob Resist 35:252-256.

Ly-Chatain MH. 2014. The factors affecting effectiveness of treatment in phages therapy. Front Microbiol 5:51.

Lv J, Geng L, Ye W, Gong S, Wu J, Ju T, Li L, Liu L, Zhang Y. 2024. Antimicrobial resistance and genetic relatedness of *Salmonella* serotypes isolated from food, asymptomatic carriers, and clinical cases in Shiyan, China. PLoS One 19:e0301388.

Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT, Monnet DL. 2012. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect 18:268-281.

Mahendran KR, Kreir M, Weingart H, Fertig N, Winterhalter M. 2010. Permeation of antibiotics through *Escherichia coli* OmpF and OmpC porins: screening for influx on a single-molecule level. J Biomol Screen 15:302-307.

Marshall BM, Levy SB. 2011. Food animals and antimicrobials: Impacts on human health. Clin Microbiol Rev 24:718-733.

Mazengia E, Samadpour M, Hill HW, Greeson K, Tenney K, Liao G, Huang X, Meschke JS. 2014. Prevalence, concentrations, and antibiotic sensitivities of *Salmonella* serovars in poultry from retail establishments in Seattle, Washington. J Food Prot 77:885-893.

McDermott PF, Tyson GH, Kabera C, Chen Y, Li C, Folster JP, Ayers SL, Lam C, Tate HP, Zhao S. 2016. Whole-genome sequencing for detecting antimicrobial resistance in nontyphoidal *Salmonella*. Antimicrob Agents Chemother 60: 5515-5520.

Mellor KC, Petrovska L, Thomson NR, Harris K, Reid SWJ, Mather AE. 2019. Antimicrobial resistance diversity suggestive of distinct *Salmonella* Typhimurium sources or selective pressures in food-production animals. Front Microbiol 10:708.

Ministry of Food and Drug Safety [MFDS]. Food safety Korea: foodborne outbreaks statistics. Available from: https://foodsafetykorea.go.kr/portal/healthyfoodlife/foodPoisoningStat. Accessed at Oct 09. 2024.

Moon JY, Kim WK, Lee KH, Na BJ, Go JC, Sim KS, Trypti AP, Hur J. 2016. Characteristics of antimicrobial resistant *Salmonella* Typhimurium isolates from chicken and pigs. Korean J Vet Serv 39:51-57.

Nishino K. 2016. Antimicrobial drug efflux pumps in *Salmonella*. In Efflux-Mediated Antimicrobial Resistance in Bacteria. 1st ed. Li XZ, Elkins C, Zgurskaya H. (ed). Springer, Cham, Switzerland. pp 261-279.

Oh H, Yoon Y, Yoon JW, Oh SW, Lee S, Lee H. 2023. *Salmonella* risk assessment in poultry meat from farm to consumer in Korea. Foods 12:649.

Okaiyeto SA, Sutar PP, Chen C, Ni JB, Wang J, Mujumdar AS, Zhang JS, Xu MQ, Fang XM, Zhang C, Xiao HW. 2024. Antibiotic resistant bacteria in food systems: Current status, resistance mechanisms, and mitigation strategies. Agriculture Communications 2:100027.

Organization for Animal Health [OIE]. 2015. OIE standards, guidelines and resolution on antimicrobial resistance and the use of antimicrobial agents. International Office of Epizootics, Paris, France. pp 137-146.

Oteo J, Aracil B, Alós JI, Gómez-Garcés JL. 2000. High rate of resistance to nalidixic acid in *Salmonella enterica*: its role as a marker of resistance to fluoroquinolones. Clin Microbiol Infect 6:273-276.

Pavelquesi SLS, Ferreira ACAO, Rodrigues LFS, Silva CMS, Silva ICR, Orsi DC. 2023. Prevalence and antimicrobial resistance of *Salmonella* spp. isolated from chilled chicken meat commercialized at retail in federal district, Brazil. J Food Prot 86:100130.

Perin AP, Martins B, Barreiros M, Yamatogi RS, Nero LA, Bersot DS. 2020. Occurrence, quantification, pulse types, and antimicrobial susceptibility of *Salmonella* sp. isolated from chicken meat in the state of Paraná, Brazil. Braz J Microbiol 51:335-345.

Piddock LJ. 2019. The 2019 Garrod lecture: MDR efflux in gram-negative bacteria—How understanding resistance led to a new tool for drug discovery. J Antimicrob Chemother 74: 3128-3134.

Plumb ID, Schwensohn CA, Gieraltowski L, Tecle S, Scheneider ZD, Freiman J, Cote A, Noveroske D, Kolsin J, Brandenburg J, Chen JC, Tagg KA, White PB, Shah HJ, Watkins LKF, Wise ME, Friedman CR. 2019. Outbreak of *Salmonella* Newport infections with decreased susceptibility to azithromycin linked to beef obtained in the United States and soft cheese obtained in Mexico - United States, 2018-2019. MMWR Morb Mortal Wkly Rep 68:713-717.

Popoff MY, Le Minor L. 1997. Antigenic formulas of the Salmonella serovars. WHO collaborating centre for reference and research on Salmonella. 7th rev. Institut Pasteur, Paris, France. p 56-87.

Punchihewage-Don AJ, Schwarz J, Diria A, Bowers J, Parveen S. 2024. Prevalence and antibiotic resistance of *Salmonella* in organic and non-organic chickens on the Eastern Shore of Maryland, USA. Front Microbiol 14:1272892.

Redgrave LS, Sutton SB, Webber MA, Piddock LJ. 2014. Fluoroquinolone resistance: mechanisms, impact on bacteria, and role in evolutionary success. Trends Microbiol 22:438-445.

Rosenberg C, Boistard P, Dénarié J, Casse-Delbart F. 1981. Genes controlling early and late functions in symbiosis are located on a megaplasmid in *Rhizobium meliloti*. Mol Gen Genet 184:326-333.

Rozwandowicz M, Brouwer MSM, Fischer J, Wagenaar JA, Gonzalez-Zorn B, Guerra B, Mevius DJ, Hordijk J. 2018. Plasmids carrying antimicrobial resistance genes in Enterobacteriaceae. J Antimicrob Chemother 73:1121-1137.

Ryan MP, Dillon C, Adley CC. 2011. Nalidixic acid-resistant strains of *Salmonella* showing decreased susceptibility to fluoroquinolones in the midwestern region of the Republic of Ireland due to mutations in the gyrA gene. J Clin Microbiol 49:2077-2079.

Sanchez S, Hofacre CL, Lee MD, Maurer JJ, Doyle MP. 2002. Animal sources of salmonellosis in humans. J Am Vet Med Assoc 221:492-497.

Saeed U, Rizwan US, Zahid PZ, Uppal R. 2021. Azithromycin treatment for SARS-CoV-2-related COVID-19 pandemic could worsen extensively drug resistant (XDR) typhoid: A risk of losing the last bullet against *Salmonella enterica* serovar typhi. Jundishapur J Microbiol 14:e113874.

Sasaki Y, Kakizawa H, Baba Y, Ito T, Haremaki Y, Yonemichi M, Ikeda T, Kuroda M, Ohya K, Hara-Kudo Y, Asai T, Asakura H. 2021. Antimicrobial resistance in *Salmonella* isolated from food workers and chicken products in Japan. Antibiotics 10:1541.

Siew C, Strock S, Ristic H, Kang P, Chou HN, Chen JW, Frantsve-Hawley J, Meyer DM. 2009. Assessing a potential risk factor for enamel fluorosis: a preliminary evaluation of fluoride content in infant formulas. J Am Dent Assoc 140:1228-1236.

Stoycheva MV, Murdjeva MA. 2006. Antimicrobial therapy of salmonelloses—Current state and perspectives. Folia Med 48:5-10.

Streicher LM. 2021. Exploring the future of infectious disease treatment in a post-antibiotic era: A comparative review of alternative therapeutics. J Glob Antimicrob Resist 24:285-295.

Sulakvelidze A, Alavidze Z, Morris Jr JG. 2001. Bacteriophage therapy. Antimicrob Agents Chemother 45:649-659.

Sully EK, Geller BL. 2016. Antisense antimicrobial therapeutics. Curr Opin Microbiol 33:47-55.

Tagar S, Qambrani NA. 2023. Bacteriological quality assessment of poultry chicken meat and meat contact surfaces for the presence of targeted bacteria and determination of antibiotic resistance of *Salmonella* spp. in Pakistan. Food Control 151:109786.

Tamang MD, Nam HM, Kim A, Lee HS, Kim TS, Kim MJ, Jang GC, Jung SC, Lim SK. 2011. Prevalence and mechanisms of quinolone resistance among selected nontyphoid *Salmonella* isolated from food animals and humans in Korea. Foodborne Pathog Dis 8:1199-1206.

Tan SY, Tatsumura Y. 2015. Alexander Fleming (1881–1955): Discoverer of penicillin. Singap Med J 56:366-367.

Tipper DJ, Strominger JL. 1965. Mechanism of action of penicillins: a proposal based on their structural similarity to acyl-D-alanyl-D-alanine. Proc Natl Acad Sci USA 54:1133-1141.

Thung TY, Mahyudin NA, Basri DF, Wan Mohamed Radzi CWJ, Nakaguchi Y, Nishibuchi M, Radu S. 2016. Prevalence and antibiotic resistance of *Salmonella* Enteritidis and *Salmonella* Typhimurium in raw chicken meat at retail markets in Malaysia. Poultry Sci 95:1888-1893.

Uma B, Prabhakar K, Rajendran S, Lakshmi Sarayu Y. 2010. Prevalence of extended spectrum beta lactamases in *Salmonella* species isolated from patients with acute gastroenteritis. Indian J Gastroenterol 29:201-204.

Vaez H, Ghanbari F, Sahebkar A, Khademi F. 2020. Antibiotic resistance profiles of *Salmonella* serotypes isolated from animals in Iran: a meta-analysis. Iran J Vet Res 21:188-197.

Vardakas KZ, Tansarli GS, Rafailidis PI, Falagas ME. 2012. Carbapenems versus alternative antibiotics for the treatment of bacteraemia due to Enterobacteriaceae producing extended-spectrum β-lactamases: a systematic review and meta-analysis. J Antimicrob Chemother 67:2793-2803.

Van Leeuwen WJ, Voogd CE, Guinée PAM, Manten A. 1982. Incidence of resistance to ampicillin, chloramphenicol, kanamycin, tetracycline and trimethoprim of *Salmonella* strains isolated in The Netherlands during 1975–1980. Antonie Leeuwenhoek 48:85-96.

Viana C, Sereno MJ, Pegoraro K, Yamatogi RS, Call DR, Bersot LS, Nero LA. 2019. Distribution, diversity, virulence genotypes and antibiotic resistance for *Salmonella* isolated from a Brazilian pork production chain. Int J Food Microbiol 310:108310.

Wang W, Baloch Z, Peng Z, Hu Y, Xu J, Fanning S, Li F. 2017. Genomic characterization of a large plasmid containing a *bla*$_{\text{NDM-1}}$ gene carried on *Salmonella enterica* serovar Indiana C629 isolate from China. BMC Infect Dis 17:1-8.

Xue XY, Mao XG, Zhou Y, Chen Z, Hu Y, Hou Z, Li MK, Meng JR, Luo XX. 2018. Advances in the delivery of antisense oligonucleotides for combating bacterial infectious diseases. Nanomed: Nanotechnol Biol Med 14:745-758.

Yarar MB, Turkyilmaz MK, Turkeyilmaz S. 2023. Investigation of integron, antimicrobial resistance and virulence gene profiles of *Salmonella enterica* subspecies enterica serovar Infantis isolates obtained from broiler chickens. Isr J Vet Med 78:4.

Yoon RH, Cha SY, Wei B, Roh JH, Seo HS, Oh JY, Jang HK. 2014. Prevalence of *Salmonella* isolates and antimicrobial resistance in poultry meat from South Korea. J Food Prot 77:1579-1582.

Zhao S, White DG, McDermott PF, Friedman S, English L, Ayers S, Meng J, Maurer JJ, Holland R, Walker RD. 2001. Identification and expression of cephamycinase *bla*$_{\mathrm{CMY}}$ genes in *Escherichia coli* and *Salmonella* isolates from food animals and ground meat. Antimicrob Agents Chemother 45:3647-3650.

Table legends

Table 1. Prevalence of *Salmonella* in animal products reported from 2013 to 2024 worldwide

Table 2. Class of antibiotics to which *Salmonella* is primarily resistant

Table 3. Antimicrobial resistance of *Salmonella* isolates and the ratio of MDR *Salmonella* from animal products

Figure legend

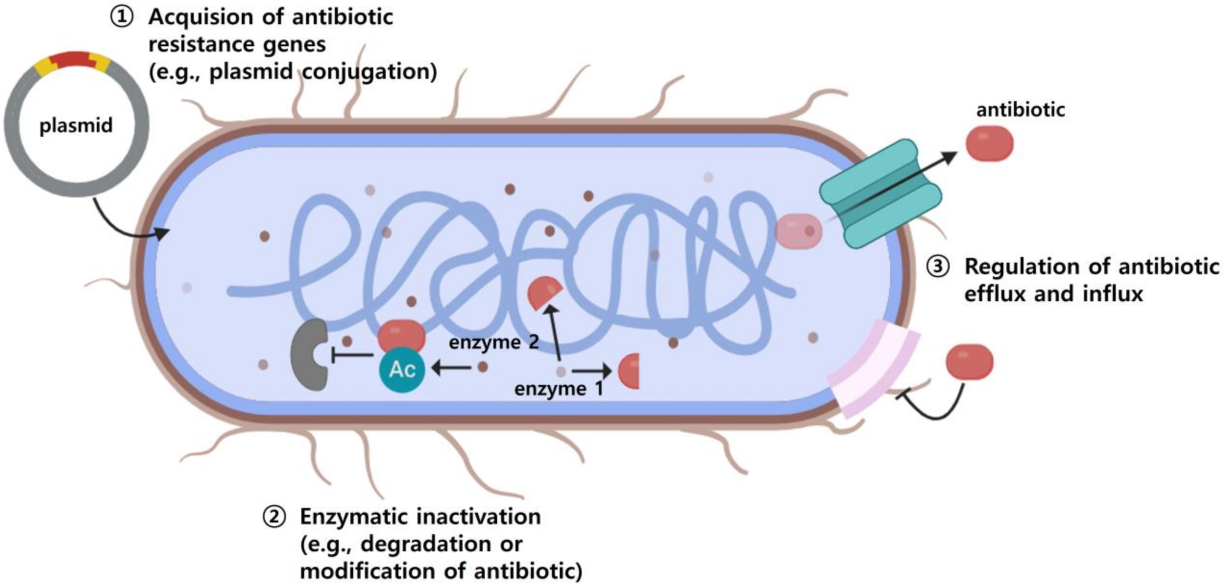

Fig. 1. Mechanisms by which antibiotic resistance can develop

This figure is created in BioRender.com (https://BioRender.com/a64s325).

Table 1. Prevalence of *Salmonella* in animal products reported from 2013 to 2024 worldwide

Food animals	Sample	No. of positive samples/no. of samples tested (% positive)	Serovars of *Salmonella*	Place of purchase	Country	Reference
Poultry	Poultry	150/1,322 (11.3) *Top two product types - Ground chicken 18/97 (15.6) - Ground turkey 23/180 (13.3)	*S*. Heidelberg, *S*. Enteritidis, *S*. Kentucky, *S*. Hadar, *S*. Schwarzengrund, *S*. Agona, *S*. Senftenberg, *S*. Berta, *S*. Litchfield, *S*. Mbandaka, *S*. Typhimurium	Retail chain stores, USDA-permitted processing establishments	United States	Mazengia et al. (2014)
	Duck	56/109 (51.3)	*S*. Typhimurium, *S*. Enteritidis, *S*. Stanley, *S*. Regent, *S*. Winterthur, and *S*. Westhampton	Supermarkets, traditional markets, internet shopping, wholesale market	South Korea	Yoon et al. (2014)
		11/18 (61)	*S*. Enteritidis	Supermarkets, traditional market	South Korea	La et al. (2021)
		87/309 (28.2)	*S*. Enteritidis	Retail markets	South Korea	Kang et al. (2024)
	Chicken	3/80 (3.7)	*S*. Typhimurium, *S*. Enteritidis	Supermarkets, traditional markets, internet shopping, wholesale market	South Korea	Yoon et al. (2014)
		51/200 (26)	*S*. Paratyphi, *S*. Heidelberg, *S*. Heidelberg, *S*. Lome, *S*. Muenster	Independent stores, main chain distributor	United States	Donado-Godoy et al. (2015)
		170/525 (32.4)	*S*. Heidelberg, *S*. Kentucky, *S*. Typhimurium, *S*. Infantis, *S*. Seftenberg, *S*. Thompson	Supermarket stores	United States	Guran et al. (2017)
		41/291 (14.1)	*S*. Enteritidis	Local supermarkets, traditional markets, the internet	South Korea	La et al. (2021)

		200/235 (85.1)	*S.* Schwarzengrund, *S.* Infantis, *S.* Manhattan	Retail stores and chicken processing plants	Japan	Sasaki et al. (2021)
		97/555 (17.5)	*S.* Enteritidis	Retail markets	South Korea	Kang et al. (2024)
	Raw chicken	12/132 (9.1%)	*S.* Infantis	Private production units	Romania	Tîrziu et al. (2020)
Eggs	Egg contents	42/650 egg pools (20 eggs per pool) (6.5)	*S.* Gallinarum	Conventional farm, organic farms	South Korea	Lee et al. (2013)
	Eggshells, egg contents	2 strains from eggshell, 1 strain from egg contents	*S.* Enteritidis	Grocery stores	South Korea	Kim et al. (2013)
	Liquid egg	9/195 (4.6)	*S.* Typhimurium, *S.* Bareilly, *S.* Tennessee, *S.* Richmond	Egg-breaking plants, a farm	South Korea	Kim et al. (2015)
	Eggshells	3/48 (6.3)	*S.* Enteritidis, *S.* Infantis	Private production units	Romania	Tîrziu et al. (2020)
	Eggshells, egg contents	Eggshells 11/60 (18.3), Egg contents 12/60 (20.0)	*S.* Infantis, *S.* Bareilly, *S.* Agona, *S.* Enteritidis, *S.* Montevideo, *S.* Enteritidis, *S.* Agona, *S.* Newport, *S.* Senftenberg, *S.* Derby	Grading and packing plant	South Korea	Jung & Lee (2024)
Pork	Ready-to-eat (RTE) pork (salami)	6/100 (6)	*S.* Brandenburg, *S.* Typhimurium, *S.* Rissen, *S.* London	Retail	Italy	Bonardi et al. (2018)
	Raw pork	33/146 (22.6)	*S.* Typhimurium, S. Rissen, S. Infantis, S. Bredeney, S. Derby, S. Brandenburg, S. Enteritidis, S. Gloucester, S. Goldcoast, S. Kottbus, S. Ruziz	Private production units	Romania	Tîrziu et al. (2020)
	RTE Pork (sausages)	3/62 (4.8)	*S.* Typhimurium	Retail markets	Romania	Tîrziu et al. (2020)
	Pork	7/503 (1.4)	Not analyzed	Retail markets	South Korea	Kang et al. (2024)

Table 2. Class of antibiotics to which *Salmonella* is primarily resistant

How to work	Class	Examples of drugs
Inhibition of protein synthesis	Aminoglycosides	Amikacin, gentamicin, kanamycin, streptomycin, tobramycin
	Tetracyclines	Doxycycline, minocycline, tetracycline
	Amphenicols	Chloramphenicol, thiamphenicol
Inhibition of folic acid synthesis	Trimethoprim-sulfonamides combinations	Sulfamethizole/trimethoprim, Sulfamethoxazole/trimethoprim
Inhibition of DNA replication	Fluoroquinolones	Ciprofloxacin, levofloxacin, norfloxacin, moxifloxacin
Inhibition bacterial cell wall synthesis	β-Lactams (β-lactamase inhibitor)	Amoxicillin/clavulanic acid, ampicillin/sulbactam, sultamicillin, carbapenems (meropenem, imipenem, doripenem)

Table 3. Antimicrobial resistance of *Salmonella* isolates and the ratio of MDR *Salmonella* from animal products

Food animals		Resistant antibiotics	Resistance %		MDR %	Reference
Raw meat	Chicken	Ampicillin	100%	(38/38)	65.7% (25/38)	Tagar and Qambrani, 2023
		Sulfamethoxazole	52.6%	(20/38)		
		Neomycin	44.7%	(17/38)		
		Erythromycin	39.4%	(15/38)		
		Erythromycin	100%	(47/47)	87.2% (41/47)	Kim et al., 2012
		Cephalothin	87.2%	(41/47)		
		Nalidixic acid	87.2%	(41/47)		
		Streptomycin	70%	(33/47)		
	Poultry	Nalidixic acid	76.0%	(346/455)	61.3% (279/455)	APQA and NIFDS, 2024
		Ampicillin	63.1%	(287/455)		
		Streptomycin	61.3%	(279/455)		
		Tetracycline	59.3%	(270/455)		
		Sulfisoxazole	57.3%	(261/455)		
		Cefotaxime	55.8%	(254/455)		
		Nalidixic acid	82.8%	(48/58)	79.3% (46/58)	Gomes et al., 2022
		Sulfamethoxazole	81.0%	(47/58)		
		Oxytetracycline	79.3%	(46/58)		
		Ciprofloxacin	74.1%	(43/58)		
		Ceftiofur	70.7%	(41/58)		
		Ampicillin	70.7%	(41/58)		
	Pork	Azithromycin	95.0%	(57/60)	50.0% (30/60)	
		Ampicillin	51.7%	(31/60)		
		Oxytetracycline	40.0%	(24/60)		
		Chloramphenicol	40.0%	(24/60)		
		Nalidixic acid	38.3%	(23/60)		
		Streptomycin	90.5%	(38/42)	80.9% (34/42)	Viana et al., 2019
		Tetracycline	88.1%	(37/42)		
		Ampicillin	81.0%	(34/42)		
		Chloramphenicol	71.4%	(30/42)		
		Ciprofloxacin	50.0%	(21/42)		

	Poultry Buffalo Cow Goat	Erythromycin	100%	(57/57)	19.3% (11/57)	Fatima et al., 2023
		Cefepime	98.2%	(56/57)		
		Colistin	94.7%	(54/57)		
		Azithromycin	93.0%	(53/57)		
		Tetracycline	87.7%	(50/57)		
		Ciprofloxacin	84.2%	(48/57)		
	Beef	Ampicillin	91.0%	(51/56)	69.6% (39/56)	Hussain et al., 2020
		Oxytetracycline	89.2%	(50/56)		
		Amoxicillin	82.1%	(46/56)		
		Neomycin	80.4%	(45/56)		
		Tetracycline	76.7%	(43/56)		
		Ciprofloxacin	60.7%	(34/56)		
		Cefepime	48.2%	(27/56)		
Chilled meat	Chicken	Amoxicillin/clavulanic acid	83.3%	(65/78)	53.8% (42/78)	Pavelquesi et al., 2023
		Sulfonamide	64.1%	(50/78)		
		Tetracycline	46.2%	(36/78)		
		Meropenem & Imipenem	100%	(98/98)	85.7% (84/98)	Perin et al., 2020
		Chloramphenicol	100%	(98/98)		
		Amikacin	100%	(98/98)		
		Nalidixic acid	95.9%	(94/98)		
		Tetracycline	93.9%	(92/98)		
		Amoxicillin/clavulanic acid	83.7%	(82/98)		
		Ciprofloxacin	75.5%	(74/98)		
Carcass	Chicken	Tetracycline	82.6%	(176/213)	45.5% (97/213)	Punchihewage-Don et al., 2024
		Minocycline	42.3%	(90/213)		
		Nitrofurantoin	40.3%	(86/213)		
		Cefazolin	38.0%	(81/213)		
		Ampicillin	32.4%	(69/213)		
		Sulphafurazole	92.0%	(46/50)	92.0% (46/50)	Moon et al., 2016
		Streptomycin	74.0%	(37/50)		
		Nalidixic acid	68.0%	(34/50)		

Swine	Tetracycline	95.2%	(40/42)	88.1% (37/42)
	Streptomycin	90.5%	(38/42)	
	Sulphafurazole	88.1%	(37/42)	