P-ISSN: 2304-3075; E-ISSN: 2305-4360
International Journal of Veterinary Science
www.ijvets.com; editor@ijvets.com

Research Article https://doi.org/10.47278/journal.ijvs/2025.097

Prevalence of *Salmonella* spp. on Poultry Farms in Kazakhstan and Analysis of Antimicrobial Resistance of the Isolates

Sergey Borovikov [1,*], Marat Kuibagarov [2], Dina Shirobokova [1], Zhannara Akanova [1], Anna Muranets [1] and Raushan Rychshanova [3]

[1]Department of Microbiology and Biotechnology, Faculty of Veterinary and Animal Husbandry Technology, S. Seifullin Kazakh Agrotechnical Research University, 010011, Astana, Kazakhstan
[2]Laboratory of Applied Genetics, National Center for Biotechnology, 010000, Astana, Kazakhstan
[3]Research Institute of Applied Biotechnology, Akhmet Baitursynov Kostanay Regional University, Kazakhstan
***Corresponding author:** nicsb_katu@mail.ru

Article History: 25-197 Received: 21-Jul-25 Revised: 28-Aug-25 Accepted: 02-Sep-25 Online First: 11-Sep-25

ABSTRACT

Salmonella infections are a significant public health concern worldwide, with poultry and poultry products being the primary sources of transmission. In Kazakhstan, data on the prevalence of *Salmonella* in poultry farms and the antimicrobial resistance of the isolates remain limited. In this study, we isolated and identified *Salmonella* strains from samples collected from poultry farms in the northern region of Kazakhstan and assessed their antimicrobial resistance profiles. The samples were cultured on differential diagnostic media, and the resulting isolates were identified using biochemical tests and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. From the 246 samples examined, 9 pure cultures were isolated and identified as *Salmonella enterica* subsp. *enterica*. The following *Salmonella* serotypes were identified: four isolates of *S. enteritidis*, one of *S. paratyphi C*, one of *S. moscow*, two of *S. infantis*, and one of *S. mbandaka*. These isolates exhibited multidrug resistance to several antibiotics including rifampicin, azithromycin, erythromycin, vancomycin, cefadroxil, cefuroxime, cefaclor, cephalothin, clarithromycin, doxycycline, cefazolin, clindamycin, kanamycin, streptomycin, nitrofurantoin, and piperacillin. In addition, all the isolates demonstrated moderate resistance to penicillin and tetracycline. These results provide insights into the species composition of circulating strains and their resistance patterns, which can contribute to the development of effective antimicrobial therapeutic strategies in poultry farming.

Key words: *Salmonella*, avian salmonellosis, isolate, identification, antibiotic resistance.

INTRODUCTION

A high prevalence of salmonellosis has been reported in many countries worldwide (Kongsanan et al. 2021; Mascitti et al. 2021; Chousalkar and Wilson 2022; Ayuti et al. 2024; Lu et al. 2025; Okpalaji at al. 2025; Bakishev at al. 2025), with the infection most frequently detected in samples from poultry farms or products (Ximenes et al. 2019; Wang et al. 2020; Rubio et al. 2021; Abayneh et al. 2023; Kim et al. 2024), including those in Kazakhstan (Barmak et al. 2023; Melnikova et al. 2024). Avian salmonellosis is an infectious disease that primarily affects the gastrointestinal tract and can lead to septicemia. In its subacute and chronic forms, the disease may also present with pneumonia and arthritis. The causative agents of infection include *S. enteritidis*, *S. typhimurium* and *S. pullorum-gallinarum*. Regardless of the serovar involved, salmonellosis imposes a significant socioeconomic burden on the poultry industry and society, including decreased egg production in laying hens, reduced weight gain, high mortality rates in embryos and young birds, and increased costs associated with diagnostic, therapeutic, and preventive measures (Lv et al. 2023). The primary source of infection is diseased birds, which shed large quantities of the pathogen through their feces and eggs. Transmission can occur via the gastrointestinal tract (contaminated feed and water), transovarially (to embryos), or via airborne particles and the conjunctival mucosa. Adult birds often remain asymptomatic but can become long-term carriers of *Salmonella*, with the pathogen being primarily localized in the ovaries, leading to prolonged shedding. Newly hatched chicks are the most susceptible to salmonellosis. *Salmonella* can invade the muscles and internal organs of birds, as well as contaminate eggs — not only on the

Cite This Article as: Borovikov S, Kuibagarov M, Shirobokova D, Akanova Z, Muranets A and Rychshanova R, 2025. Prevalence of *Salmonella* spp. on poultry farms in Kazakhstan and analysis of antimicrobial resistance of the isolates. International Journal of Veterinary Science 14(6): 1084-1092. https://doi.org/10.47278/journal.ijvs/2025.097

surface of the shell but also internally, primarily accumulating in the yolk (Bessarabov et al. 2009; Lu et al. 2025). The traditional causative agent of pullorum disease in chickens is *Salmonella pullorum-gallinarum*. However, in many cases, chickens are infected with *S. enteritidis* and other serovars that do not cause clinical symptoms or mortality, which complicates the assessment of the health status of a farm (Staroselsky 2010). Statistical analyses of salmonellosis outbreaks have indicated an increased frequency of *Salmonella* detection in domestic poultry, including chickens (Ansari-Lari et al. 2022; Shen et al. 2023). According to World Health Organization experts, the absence of clinical signs in infected birds and the challenges associated with detecting asymptomatic carriers make them persistent sources of environmental and poultry product contamination (Geneva: World Health Organization 1991).

In Kazakhstan, studies have confirmed the presence of salmonellosis in selected poultry farms in several regions (Nuraliev and Kochish 2017; Mendybayeva 2022). However, many regions remain unexplored and the geographical distribution of the isolates has not been adequately addressed.

Research on the antimicrobial resistance of *Salmonella* spp. is currently highly relevant for several reasons. *Salmonella* remains a major pathogen responsible for foodborne poisoning and infectious diseases in humans. Additionally, the constant emergence of new *Salmonella* strains with antimicrobial resistance presents serious challenges in both veterinary and human medicine, potentially rendering standard treatment regimens ineffective (Jajere 2019; Rodrigues et al. 2020; Alikhan et al. 2022).

This study aimed to examine samples collected from poultry farms in the northern regions of the Republic of Kazakhstan, isolate and identify *Salmonella* spp., and investigate their microbiological and biochemical characteristics as well as their level of resistance to antimicrobial agents.

MATERIALS AND METHODS

Location and study material

The study material consisted of biological and pathological samples collected from poultry farms in the Kostanay, Akmola, and Karaganda regions of Kazakhstan. The samples included feces, feed, equipment swabs, organs from deceased birds, and contents of the gastrointestinal tract. Samples were placed in sterile containers containing transport medium (Ames medium) and transported to the laboratory under cold-chain conditions.

Microbiological and bacteriological analyses were performed in accordance with GOST 31659-2012 (2013). The following culture media were used for pathogen isolation: buffered peptone water (LLC "Scientific and Production Center Biokompas-S," Russia); Rappaport-Vassiliadis soya broth (LLC "Scientific and Production Center Biokompas-S"); bismuth sulfite agar, Ploskirev medium, Endo medium, and Violet Red Bile Lactose (VRBL) agar (Federal State Research Center for Applied Microbiology and Biotechnology, Russia); Hiss medium with sucrose and mannitol (LLC "Scientific and Production Center Biokompas-S"); and Mueller-Hinton agar (HiMedia Laboratories, India). Colony morphologies were recorded after incubation in a thermostat for 24–48h.

Biochemical identification included tests for glucose, lactose, mannitol, and sucrose fermentation, hydrogen sulfide and indole production and catalase and oxidase activities. Additionally, an OF-test (Erba Mannheim, Czech Republic) and Voges–Proskauer reaction were performed.

Serotyping was carried out using an agglutination assay with a set of *Salmonella*-specific antisera ("PETSAL," Russia) following the Kauffmann–White classification scheme. Species-level identification was performed using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) with the Bruker Real-Time Classification software (Bruker Daltonics). A score ≥2.0 was considered a reliable identification. Antibiotic susceptibility was determined by the disk diffusion method on Mueller-Hinton agar using 33 antibiotic discs (NICF, Russia). The results were interpreted based on the EUCAST criteria (versions 8.0 [2018] and 9.0 [2019]). Statistical analysis was performed using Microsoft Excel 2010, applying Student's *t*-test with a significance level of $\alpha < 0.05$.

RESULTS

The collected clinical samples were delivered to the Kazakhstan–China Laboratory for Biosafety at S. Seifullin Kazakh Agrotechnical Research University (Astana) for further analysis. After incubation in a thermostat for 24 or 48h, colonies grown on various differential diagnostic media (Ploskirev agar, Endo medium, and bismuth sulfite agar) were evaluated (Fig. 1). On Ploskirev agar, the growth of Salmonella spp. was observed as colorless round colonies with black centers (Fig. 1A). On Endo medium, *Salmonella* spp. appeared as round, colorless or slightly pink colonies (Fig. 1B). On bismuth sulfite agar, *Salmonella* spp. formed black colonies with a characteristic metallic sheen or greenish colonies with a dark green halo (Fig. 1C).

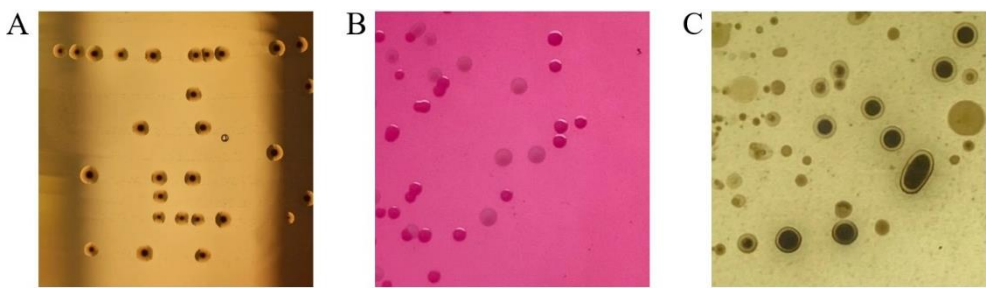

Fig. 1: Growth pattern of *Salmonella* bacteria on Ploskirev medium (A), Endo medium (B) and bismuth sulfite agar (C).

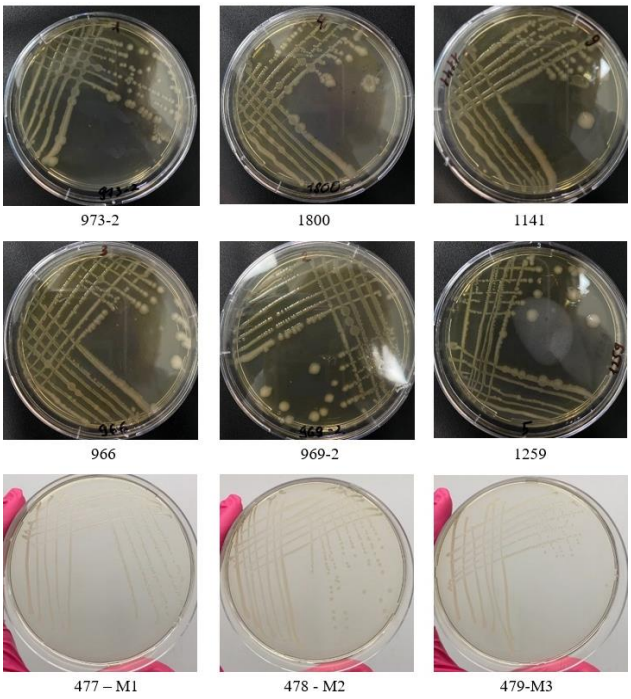

Fig. 2: Growth of typical *Salmonella* colonies on LB agar.

Streak plating was performed on LB agar using the quadrant dilution method (Fig. 2).

In the analyzed samples, typical colonies of *Salmonella* spp. and other bacteria, such as *Escherichia coli*, *Klebsiella oxytoca*, and *Klebsiella pneumoniae* were detected; however, the later three were not of interest in this study.

To identify the causative agents of salmonellosis, Gram staining and microscopy of typical *Salmonella* colonies were performed. The results clearly showed Gram-negative rod-shaped bacteria that measured 3 to 7µm in length and 0.3 to 0.7µm in width.

Biochemical testing of *Salmonella* isolates on VRBL agar indicated hydrogen sulfide production but no lactose fermentation. On Hiss medium with sucrose and mannitol, the isolates were capable of fermenting mannitol but not sucrose. The OF-test indicated the ability of *Salmonella* isolates to ferment glucose, as evidenced by a color change from green to yellow. Additional biochemical tests confirmed catalase production and the absence of oxidase activity in the isolated *Salmonella* strains. Thus, biochemical identification showed that the isolated cultures were capable of producing hydrogen sulfide and fermenting glucose and mannitol, lacked indole production, and had a positive catalase reaction, all of which are characteristic features of *Salmonella* spp.

Furthermore, the affiliation of the isolates with the genus *Salmonella* was confirmed via MALDI-TOF MS (Fig. 3).

Ion detection and comparison of their mass, structure, and abundance with the reference database available on the mass spectrometer confirmed the affiliation of all nine studied isolates with the genus *Salmonella* was confirmed.

Having analyzed the biochemical properties of *Salmonella* spp. and confirmed their taxonomic identities, the antimicrobial susceptibilities of the isolates were then assessed (Fig. 4).

Analyte Name	Analyte ID	Organism (best match)	Score Value	Organism (second best match)	Score Value
A6 (+++) (A)	A6	Salmonella sp	2.421	Salmonella sp	2.338
B6 (+++) (A)	B6	Salmonella sp	2.392	Salmonella sp	2.296
C6 (+++) (A)	C6	Salmonella sp	2.404	Salmonella sp	2.14
D6 (+++) (A)	D6	Salmonella sp	2.348	Salmonella sp	2.141
E6 (++) (A)	E6	Salmonella sp	2.277	Salmonella sp	2.077
F6 (+++) (A)	F6	Salmonella sp	2.438	Salmonella sp	2.351
G6 (+++) (A)	G6	Salmonella sp	2.415	Salmonella sp	2.314
A8 (+) (B)	A8	Salmonella sp	1.96	Salmonella sp	1.941
A9 (++) (C)	A9	Salmonella sp	2.143	Salmonella sp	2.141
B8 (-) (C)	B8	no peaks found	< 0	no peaks found	< 0
B9 (++) (A)	B9	Niallia circulans	2.255	Niallia circulans	2.037
C8 (-) (C)	C8	not reliable identification	1.087	not reliable identification	1.081
C9 (+) (B)	C9	Niallia circulans	1.889	Niallia circulans	1.826
D8 (++) (A)	D8	Salmonella sp	2.152	Salmonella sp	2.14
D9 (+) (B)	D9	Niallia circulans	1.84	Niallia circulans	1.727
E8 (++) (A)	E8	Salmonella sp	2.272	Salmonella sp	2.264
E9 (+) (B)	E9	Niallia circulans	1.822	Niallia circulans	1.76
F8 (-) (C)	F8	not reliable identification	1.543	not reliable identification	1.542
F9 (++) (A)	F9	Niallia circulans	2.051	Niallia circulans	2.034
G8 (++) (A)	G8	Salmonella sp	2.265	Salmonella sp	2.235
G9 (+) (B)	G9	Niallia circulans	1.926	Niallia circulans	1.766
H8 (++) (C)	H8	Salmonella sp	2.237	Salmonella sp	2.225
H9 (++) (A)	H9	Niallia circulans	2.004	Niallia circulans	1.927

Fig. 3: Identification of isolates belonging to the genus Salmonella using mass spectrometry method.

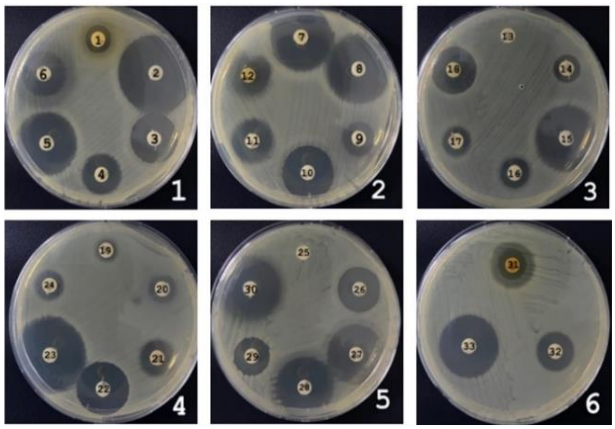

Fig. 4: Determination of the sensitivity of isolates of Salmonella bacteria to antimicrobial agents.

The results of the bacteriological analyses are presented in Table 1. Based on the results of the antimicrobial resistance study, a heat map of the isolated Salmonella strains was created (Fig. 5).

Table 1: Antimicrobial resistance of *Salmonella* strains isolated from samples collected at poultry farms in the Republic of Kazakhstan

№	Name and concentration of antimicrobial agents	Isolate No. 973-2	Isolate No. 1259	Isolate No. 1800	Isolate No. 1141	Isolate No. 969-2	Isolate No. 966	Isolate No. 477 - M1	Isolate No. 478 -M2	Isolate No. 479 -M3
		Serotype *S.enteritidis*	Serotype *Paratyphy C*	Serotype *S.enteritidis*	Serotype *S.moscow*	Serotype *S.enteritidis*	Serotype *S.enteritidis*	Serotype *S. infantis*	Serotype *S.infantis*	Serotype *S.mbandaka*
1	Rifampicin (5µg)	R	R	R	R	R	R	R	R	R
2	Co-trimoxazole (Sulfamethoxazole/Trimethoprim) (25µg [23.75/1.25µg])	R	S	S	S	S	S	R	R	S
3	Amikacin (30µg)	S	S	S	S	S	S	S	S	S
4	Amoxiclav (Amoxicillin/Clavulanic acid) (30µg [20/10µg])	R	R	R	R	S	R	R	S	S
5	Ampicillin (10µg)	S	S	S	S	S	S	S	S	S
6	Azithromycin (15µg)	R	R	R	R	R	R	R	R	S
7	Cefotaxime (30µg)	R	S	S	S	S	S	S	S	S
8	Ceftriaxone (30µg)	S	S	S	S	S	S	S	S	S
9	Erythromycin (15µg)	R	R	R	R	R	R	R	R	R
10	Gentamicin (10µg)	S	S	S	S	S	S	S	S	S
11	Penicillin G (10units)	R	R	R	S	S	S	R	R	S
12	Tetracycline (30µg)	R	R	R	R	S	R	R	R	S
13	Vancomycin (30µg)	R	R	R	R	R	R	R	R	R
14	Cefadroxil (30µg)	R	R	R	R	R	R	R	R	R
15	Cefoperazone (75µg)	S	R	S	S	S	S	S	S	S
16	Ampicillin/Sulbactam (20µg [10/10µg])	R	R	R	R	R	R	R	R	S
17	Cefuroxime (30µg)	R	R	R	R	R	R	R	R	R
18	Cefaclor (30µg)	R	R	R	R	R	R	R	R	R
19	Cephalothin (30µg)	R	R	R	R	R	R	R	R	R
20	Clarithromycin (15µg)	R	R	R	R	R	R	R	R	R
21	Doxycycline HCl (30µg)	R	R	R	R	R	R	R	R	R
22	Tobramycin (10µg)	R	R	S	S	S	S	S	S	R
23	Amoxicillin (10µg)	S	S	S	S	S	S	S	S	S
24	Cefazolin (30µg)	R	R	R	R	R	R	R	R	R
25	Clindamycin (2µg)	R	R	R	R	R	R	R	R	R
26	Kanamycin (30µg)	R	R	R	R	R	R	R	R	R
27	Lomefloxacin (10µg)	R	R	R	S	S	S	S	S	S
28	Ofloxacin (5µg)	R	R	S	S	S	S	S	S	S
29	Streptomycin (10µg)	R	R	R	R	R	R	R	R	R
30	Chloramphenicol (30µg)	R	R	S	S	S	S	S	S	S
31	Nitrofurantoin (300µg)	R	R	R	R	R	R	R	R	R
32	Piperacillin (100µg)	R	R	R	R	R	R	R	R	R
33	Ciprofloxacin (5µg)	R	S	S	S	S	S	S	S	S

Note: R, resistant; S, susceptible

Int J Vet Sci, 2025, 14(6): 1084-1092.

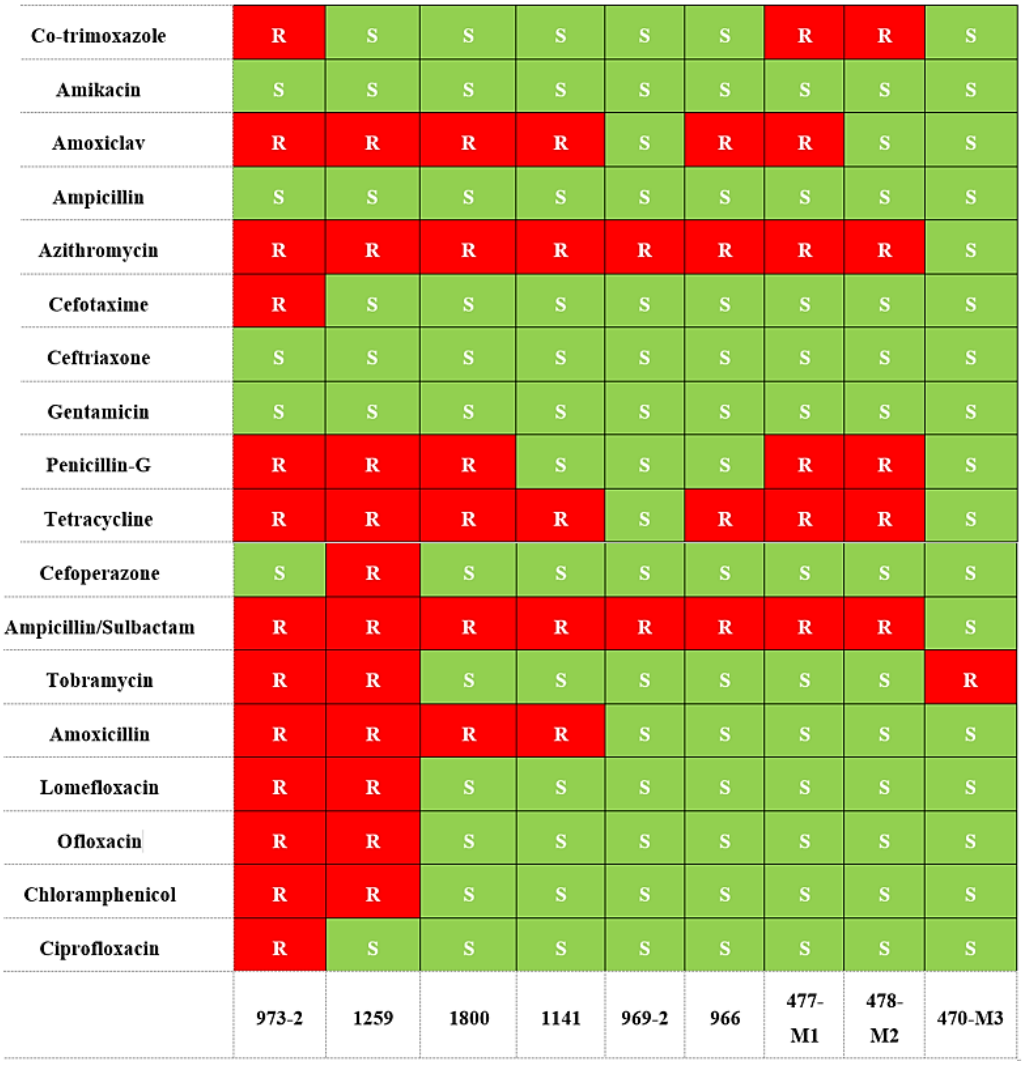

Fig. 5: Heatmap of antimicrobial susceptibility of *Salmonella* isolates from poultry farms in Kazakhstan. The X-axis represents the isolates, and the y-axis lists the antibiotics tested. Colors indicate assessment of susceptibility: green indicates sensitivity and red indicates resistance. Antibiotics to which all isolates showed resistance were excluded to ensure objectivity.

Analysis of the antimicrobial susceptibility profiles of the isolated *Salmonella* strains showed evidence of multidrug resistance (MDR). The isolates demonstrated susceptibility to antibiotics, such as amikacin, ceftriaxone, gentamicin, amoxicillin, and ciprofloxacin. However, they also exhibited resistance to a broad range of antibiotics, including rifampicin, azithromycin, erythromycin, vancomycin, cefadroxil, cefuroxime, cefaclor, cephalothin, clarithromycin, doxycycline, cefazolin, clindamycin, kanamycin, streptomycin, nitrofurantoin, and piperacillin. Moderate resistance to certain antibiotics was observed in some isolates.

The differences between the isolates of various serotypes are also noteworthy. *Salmonella infantis* exhibited particularly high resistance to antibiotics, which remained effective against most other serovars. In contrast, *Salmonella mbandaka* was found to be susceptible to a broad range of antibiotics, including amoxicillin/clavulanic acid and co-trimoxazole. Of particular concern was the *S. paratyphi C* isolate, which demonstrated the highest level of resistance, whereas *S. enteritidis* isolates showed the greatest susceptibility to antimicrobial agents.

DISCUSSION

Salmonella is a major cause of foodborne disease outbreaks worldwide. In the European Union, the number of confirmed cases of salmonellosis was 87,923 in 2019 and 57,702 in 2020, the lowest figure recorded since 2007 (Gambino et al. 2022). In Portugal, the incidence of salmonellosis has remained low in recent years due to vaccination programs targeting laying hens and breeder flocks, in combination with strict biosecurity compliance. Among poultry, particularly broilers and layers, *Salmonella enterica* subsp. *enterica* serovar Enteritidis remains the leading cause of foodborne infections. Examination of 102 *S. Enteritidis* isolates resulted in the identification of 170 virulence genes. Phylogenetic analysis demonstrated genetic heterogeneity among the isolates, varying by sample type, collection date, and genetic composition. These findings expand the current dataset and support more accurate characterization of the circulating strains (Leão et al. 2024).

Nevertheless, despite ongoing control measures, salmonellosis continues to occur at a high frequency within the European Union. In 2020 alone, 694 outbreaks were recorded. To assess and pinpoint the main factors associated with the occurrence of *Salmonella* spp. in the Spanish food chain (2015–2020), Rodríguez et al. (2023) compared three categorical variables: product type, geographical region, and production stage. Meat products were found to be the most relevant in terms of *Salmonella* prevalence, with the slaughterhouse stage representing the most critical point. The highest levels of contamination

were observed in pork and poultry meat. Importantly, the detection of *Salmonella* at the final stages of the food chain, particularly at the retail level, poses a direct risk for human infection.

In Romania, the characteristics of prevalent pathogenic *Salmonella* serovars, their antimicrobial susceptibility, and antimicrobial resistance genes were investigated in 112 isolates recovered from raw poultry meat between 2011 and 2021. The most common serotypes identified were *Salmonella enterica* serovar Enteritidis and Typhimurium (56% and 25%, respectively). Most isolates were resistant to at least three antimicrobial agents. The findings of this study demonstrated the presence of multidrug-resistant *Salmonella* serovars in poultry meat products (Forgaciu et al. 2022).

According to Drauch et al. (2022), the most prevalent serovar in broilers within the European Union is *Salmonella infantis*. The study evaluated infection dynamics and immune responses in four chicken lines following exposure to *S. infantis*. Particular attention was given to bacterial shedding, cecal colonization, and both humoral and cellular immunity. The results demonstrated line-dependent differences: laying hens exhibited lower levels of fecal shedding and cecal colonization than broilers. Thus, fast-growing broilers pose the greatest risk of transmission of infection to humans.

Another study reported the isolation of *Salmonella* from various raptor species kept in aviaries at an Italian wildlife center. All *S. infantis* strains identified in both feed and raptors were multidrug-resistant and classified into different clusters, suggesting either persistent infection or the involvement of additional sources. Considering the substantial risk of zoonotic transmission, regular monitoring and decontamination of feed for captive birds are strongly recommended (Corradini et al. 2024).

In Asian countries, non-typhoidal salmonellosis remains the leading cause of foodborne zoonoses. A total of 300 samples of chicken products and human feces were examined for *Salmonella enterica* in Wasit Province, Iraq. The pathogen was detected in 8.66% of poultry samples and 4.6% of human samples. Antimicrobial susceptibility testing was conducted with 19 antibiotics, while serotyping relied on standard PCR and sequencing of a specific rRNA gene. The study further identified genetic mutations in *S. enterica*, which were associated with altered molecular traits and the development of multidrug resistance (Al-Shafee and Abdulwahid 2024).

A study conducted in Singapore investigated the prevalence, antimicrobial resistance, and sequence types of *Salmonella* isolates obtained from poultry products and wild birds. *Salmonella* was detected in 0.08 and 0.99% of food and wild bird samples, respectively. None of the isolates from wild birds (n=15) exhibited phenotypic antimicrobial resistance, whereas the isolates from food products showed a high percentage of phenotypic resistance to at least one antimicrobial agent. These findings indicate that the *Salmonella* isolates obtained from wild birds may have been exposed to lower levels of antimicrobial pressure (Aung et al. 2019). However, these results contradict those of another study conducted in Bangladesh, wherein multidrug-resistant non-typhoidal *Salmonella* was detected in migratory birds (Card et al. 2023).

Antibiotic resistance of *Salmonella* strains is a major obstacle in controlling avian salmonellosis, with several studies reporting MDR in *Salmonella* isolates. For example, a study conducted on isolates from poultry farms in Ethiopia revealed that 32.7% of the strains were resistant to at least one antimicrobial agent, particularly streptomycin (75%) and ampicillin (59.4%) (Basazinew et al. 2025). In Sudan, antimicrobial resistance was examined in 64 *Salmonella* isolates, representing 28 different serovars of *Salmonella enterica* subsp. enterica. Most of these isolates (98.4%) were resistant to at least one antimicrobial agent. The most common MDR patterns include resistance to ampicillin and cephalexin (Elmadiena et al. 2013). In the present study, all *Salmonella* isolates (n=9) obtained from biological and pathological samples collected from poultry farms exhibited resistance to multiple antimicrobial agents. Additionally, all the isolates demonstrated moderate resistance to penicillin and tetracycline.

In Vietnam, the uncontrolled use of antibiotics for disease prevention and as growth promoters in livestock has led to the development of antibiotic resistance. A review of three major electronic databases (PubMed, Web of Science, and ScienceDirect) covering the period from January 2013 to December 2020 revealed that bacterial isolates, including *Salmonella*, *Escherichia coli*, and *Enterococcus* spp. obtained from pigs and poultry, exhibited multidrug resistance to antimicrobials. The authors emphasize the need to restrict the use of antibiotics in food-producing animals (Di et al. 2021).

Our findings are consistent with those of previous studies by scientists from Kazakhstan, who isolated *Salmonella* spp. from retail outlets and livestock enterprises in the Kostanay and North Kazakhstan regions and evaluated their resistance to antibacterial drugs. Phenotypic analysis of the antimicrobial resistance of *Salmonella* isolates revealed strong resistance to tetracycline (82/137) and nitrofuran (81/137) (Mendybayeva et al. 2022). In a more recent investigation, Mendybayeva et al. (2023) analyzed 398 poultry product samples from Northern Kazakhstan and reported the recovery of 46 *Salmonella* isolates, the majority of which were identified as *S. enteritidis* (80.4%). Antimicrobial susceptibility testing revealed that 64.3% of the isolates were resistant to three or more classes of antimicrobial agents, indicating a significant prevalence of multidrug resistance in poultry-derived *Salmonella* in the region.

Taken together, these results suggest that the high level of multidrug resistance observed in *Salmonella enterica* subsp. *enterica* isolates from Kazakhstan is associated with the indiscriminate use of antimicrobial agents in the treatment of farm animals, which has contributed to the development of resistance in certain *Salmonella* serovars (Coyne et al. 2018; Di et al. 2021).

Conclusion

Analysis of samples collected from poultry farms in the Republic of Kazakhstan confirmed the presence of *Salmonella enterica* subsp. *enterica*, which was identified as *S. enteritidis*, *S. paratyphi*, *S. moscow*, *S. infantis*, and *S. mbandaka*. These findings raise concern because the isolates were obtained directly from poultry farm samples and may be potential sources of contamination in poultry

products.

Antimicrobial susceptibility testing of the isolated strains revealed their sensitivity to several antibiotics, including amikacin, ceftriaxone, gentamicin, amoxicillin, and ciprofloxacin. However, the isolates exhibited MDR, including resistance to rifampicin, azithromycin, erythromycin, vancomycin, cefadroxil, cefuroxime, cefaclor, cephalothin, clarithromycin, doxycycline, cefazolin, clindamycin, kanamycin, streptomycin, nitrofurantoin, and piperacillin. In addition, all the isolates showed moderate resistance to penicillin and tetracycline.

Differences in antimicrobial susceptibility at the serotypic level should be considered when evaluating the efficacy of antibiotic therapies. Overall, a high degree of similarity in resistance profiles was observed among *Salmonella* isolates from geographically distant farms, suggesting a widespread distribution of resistant strains.

Therefore, we recommend that veterinary professionals carefully select effective antimicrobial agents. Furthermore, we emphasize the need for broad-scale surveillance studies on poultry farms across all regions of the country to identify circulating *Salmonella* strains and to determine their resistance profiles.

DECLARATIONS

Funding: This study is funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (No. AP23490406).

Acknowledgement: This study is funded by the Science Committee of the Ministry of Education and Science of the Republic of Kazakhstan (No. AP23490406).

Conflict of Interest: The authors declare no competing interests.

Data Availability: The data supporting this study's findings are available in this article. There is no other supporting data.

Ethics Statement: The research protocols of this study were approved by the Ethics Committee of S. Seifullin Kazakh Agrotechnical Research University (Protocol No. 1, dated November 15, 2023). All procedures were carried out in accordance with biosafety regulations and ethical standards for animal handling.

Author's Contribution: SB Design and management of the study, MK Mass spectrometry, DS Bacteriological studies and species identification of bacterial cultures, ZA and RR Sampling of biological material, SB and AM Data analysis and manuscript writing. All authors have read and approved the final manuscript.

Generative AI Statement: The authors declare that no Gen AI/DeepSeek was used in the writing/creation of this manuscript.

Publisher's Note: All claims stated in this article are exclusively those of the authors and do not necessarily represent those of their affiliated organizations or those of the publisher, the editors, and the reviewers. Any product that may be evaluated/assessed in this article or claimed by its manufacturer is not guaranteed or endorsed by the publisher/editors.

REFERENCES

Abayneh E, Goba H and Shurbe M, 2023. Salmonellosis prevalence and risk factors in chicken breeding farms in and around Arba Minch town, Gamo Zone, Ethiopia. Journal of Infection in Developing Countries 17(2): 226-235. https://doi.org/10.3855/jidc.17553

Alikhan NF, Moreno LZ, Castellanos LR, Chattaway MA, McLauchlin J, Lodge M, O'Grady J, Zamudio R, Doughty E, Petrovska L, Cunha MPV, Knöbl T, Moreno AM and Mather AE, 2022. Dynamics of *Salmonella enterica* and antimicrobial resistance in the Brazilian poultry industry and global impact on public health. PLoS Genetics 18(6): e1010174. https://doi.org/10.1371/journal.pgen.1010174

Al-Shafee AAJ and Abdulwahid MT, 2024. Occurrence, antimicrobial resistance, and molecular characterization of Salmonella enterica from chicken products and human in Wasit Governorate of Iraq. Open Veterinary Journal 14: 1117-1129. https://doi.org/10.5455/OVJ.2024.v14.i5.5

Ansari-Lari M, Hosseinzadeh S, Manzari M and Khaledian S, 2022. Survey of *Salmonella* in commercial broiler farms in Shiraz, southern Iran. Preventive Veterinary Medicine 198: 105550. https://doi.org/10.1016/j.prevetmed.2021.105550

Ayuti SR, Khairullah AR, Al-Arif MA, Lamid M, Warsito SH, Moses IB, Hermawan IP, Silaen OSM, Lokapirnasari WP, Aryaloka S, Ferasyi TR, Hasib A and Delima M, 2024. Tackling salmonellosis: A comprehensive exploration of risks factors, impacts, and solutions. Open Veterinary Journal 14(6): 1313-1329. https://doi.org/10.5455/OVJ.2024.v14.i6.1

Bakishev T, Amirgazin A, Kuibagarov M, Shevtsov A, Bakisheva Z, Yessembekova G, Kairzhanova A, Kadyrov A, Guo K, Wang X, Abdrakhmanov S and Borovikov S, 2025. Genome-wide characterization and comparative phylogenomics of three *Salmonella Abortusequi* strains isolated from equine abortions in Kazakhstan. Veterinary World 18(6): 1571-1580. https://doi.org/10.14202/vetworld.2025.1571-1580

Aung KT, Chen HJ, Chau ML, Yap G, Lim XF, Humaidi M, Chua C, Yeo G, Yap HM, Oh JQ, Manogaran V, Hapuarachchi HC, Maiwald M, Tee NWS, Barkham T, Koh TH, Gutiérrez RA, Schlundt J and Ng LC, 2019. *Salmonella* in retail food and wild birds in Singapore: prevalence, antimicrobial resistance, and sequence types. International Journal of Environmental Research and Public Health 16(21): 4235. https://doi.org/10.3390/ijerph16214235

Barmak S, Sultankulova G and Zholdybaeva E, 2023. Detection of Salmonella enterica in food products. Global Biological Journal 3(72): 246–255

Basazinew E, Dejene H, Dagnaw GG, Lakew AZ and Gessese AT, 2025. A systematic review and meta-analysis of salmonellosis in poultry farms in Ethiopia: prevalence, risk factors, and antimicrobial resistance. Frontiers in Veterinary Science 12: 1538963. https://doi.org/10.3389/fvets.2025.1538963

Bessarabov BF, Melnikova II and Sushkova NK, 2009. *Diseases of Poultry: A Textbook* (2nd ed., reprint). Lan Publishing, St. Petersburg, pp. 220–229

Card RM, Chisnall T, Begum R, Sarker MS, Hossain MS, Sagor MS, Mahmud MA, Uddin ASMA, Karim MR, Lindahl JF and Samad MA, 2023. Multidrug-resistant nontyphoidal *Salmonella* of public health significance recovered from migratory birds in Bangladesh. Frontiers in Microbiology 14: 1162657. https://doi.org/10.3389/fmicb.2023.1162657

Di KN, Pham DT, Tee TS, Binh QA and Nguyen TC, 2021. Antibiotic usage and resistance in animal production in Vietnam: a review of existing literature. Tropical Animal Health and Production 53(3): 340. https://doi.org/10.1007/s11250-021-02780-6

Drauch V, Mitra T, Liebhart D, Hess M and Hess C, 2022. Infection dynamics of *Salmonella* Infantis vary considerably between chicken lines. Avian Pathology 51(6): 561-573. https://doi.org/10.1080/03079457.2022.2108373

Chousalkar KK and Willson NL, 2022. Nontyphoidal *Salmonella* infections acquired from poultry. Current Opinion in Infectious Diseases 35(5): 431-435. https://doi.org/10.1097/QCO.0000000000000876

Corradini C, De Bene AF, Russini V, Carfora V, Alba P, Cordaro G, Senese M, Terracciano G, Fabbri I, Di Sirio A, Di Giamberardino F, Boria P, De Marchis ML and Bossù T, 2024. Detection of *Salmonella* Reservoirs in Birds of Prey Hosted in an Italian Wildlife Centre: Molecular and Antimicrobial Resistance Characterisation. Microorganisms 12(6): 1169. https://doi.org/10.3390/microorganisms12061169

Coyne LA, Latham SM, Dawson S, Donald IJ, Pearson RB, Smith RF, Williams NJ and Pinchbeck GL, 2018. Antimicrobial use practices, attitudes, and responsibilities in UK farm animal veterinary surgeons. Preventive Veterinary Medicine 161: 115-126. https://doi.org/10.1016/j.prevetmed.2018.10.021

Elmadiena MM, El Hussein AA, Muckle CA, Cole L, Wilkie E, Mistry K and Perets A, 2013. Antimicrobial susceptibility and multi-drug resistance of *Salmonella enterica* subspecies enterica serovars in Sudan. Tropical Animal Health Production 45(5): 1113-8. https://doi.org/10.1007/s11250-012-0334-7

Forgaciu A, Tabaran A, Colobatiu L, Mihaiu R, Dan SD and Mihaiu M, 2022. Concerning Increase in Antimicrobial Resistance Patterns of Pathogenic Strains of *Salmonella* Isolated in Poultry Meat Products. Antibiotics (Basel) 11(11): 1469. https://doi.org/10.3390/antibiotics11111469

Gambino D, Gargano V, Butera G, Sciortino S, Pizzo M, Oliveri G, Cardamone C, Piraino C, Cassata G, Vicari D and Costa A, 2022. Food is a reservoir of MDR Salmonella: prevalence of ESBLs profiles and resistance genes in strains isolated from food. Microorganisms 10(4):780.

Geneva: World Health Organization, 1991. Control of Salmonella Infections: The Role of Veterinary and Food Hygiene. Report by the WHO Expert Committee. 83 p

GOST 31659–2012, 2013. Food products. Methods for detection of bacteria of the genus *Salmonella*. Standardization, Moscow

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

Kim M, Barnett-Neefs C, Chavez RA, Kealey E, Wiedmann M and Stasiewicz MJ, 2024. Risk Assessment Predicts Most of the Salmonellosis Risk in Raw Chicken Parts is Concentrated in Those Few Products with High Levels of High-Virulence Serotypes of Salmonella. Journal of Food Protection 87(7): 100304. https://doi.org/10.1016/j.jfp.2024.100304

Kongsanan P, Angkititrakul S, Kiddee A and Tribuddharat C, 2021. Spread of Antimicrobial-Resistant *Salmonella* from Poultry to Humans in Thailand. Japanese Journal of Infectious Diseases 74(3): 220-227. https://doi.org/10.7883/yoken.JJID.2020.548

Leão C, Silveira L, Usié A, Gião J, Clemente L, Themudo P, Amaro A and Pista A, 2024. Genetic Diversity of *Salmonella enterica* subsp. *enterica* Serovar Enteritidis from Human and Non-Human Sources in Portugal. Pathogens 13(2): 112. https://doi.org/10.3390/pathogens13020112

Lu J, Wu H, Wu S, Wang S, Fan H, Ruan H, Qiao J, Caiyin Q and Wen M, 2025. *Salmonella*: Infection mechanism and control strategies. Microbiological Research 292: 128013. https://doi.org/10.1016/j.micres.2024.128013

Lv P, Zhang X, Song M, Hao G, Wang F and Sun S, 2023. Oral administration of recombinant *Bacillus subtilis* expressing a multi-epitope protein induces strong immune responses against *Salmonella Enteritidis*. Veterinary Microbiology 276: 109632. https://doi.org/10.1016/j.vetmic.2022.109632

Mascitti AK, Kipper D, Dos Reis RO, da Silva JS, Fonseca ASK, Ikuta N, Tondo EC and Lunge VR, 2021. Retrospective whole-genome comparison of Salmonella enterica serovar Enteritidis from foodborne outbreaks in Southern Brazil. Brazilian Journal of Microbiology 52(3): 1523-1533. https://doi.org/10.1007/s42770-021-00508-0

Melnikova T, Bakirova G, İzmuqan A, Musina G and Dzhamalova G, 2024. Monitoring the resistance of industrial chicken farming in the Almaty region of Kazakhstan to salmonellosis. Experimental Biology 101(4): 67-82. https://doi.org/10.26577/bb.2024.v101.i4.a5

Mendybayeva AM, 2022. Study of phenotypic and genotypic resistance characteristics of Salmonella enterica strains circulating in the Northern region of Kazakhstan (PhD dissertation). Kostanay, 173

Mendybayeva AM, Aliyeva GK, Chuzhebayeva GD, Tegza AA and Rychshanova RM, 2022. Antibiotic resistance of enterobacterial pathogens isolated on the territory of the Northern Kazakhstan. Comparative Immunology, Microbiology & Infectious Diseases 87: 101854. https://doi.org/10.1016/j.cimid.2022.101854

Mendybayeva A, Abilova Z, Bulashev A and Rychshanova R, 2023. Prevalence and resistance to antibacterial agents in *Salmonella enterica* strains isolated from poultry products in Northern Kazakhstan. Veterinary World 16(3): 657-667. https://doi.org/10.14202/vetworld.2023.657-667

Nuraliev ER and Kochish II, 2017. Pullorum-salmonellosis in backyard poultry as a natural reservoir of the pathogen for industrial poultry farming. Agrarian Science Journal 24–29.

Okpalaji NC, Okonkwo AP, Okonkwo JC, Ezenyilimba BN, Ejivade OM, Okafor EC, Ezejesi HC and Nwankwo CA, 2025. Pathogen profile of poultry industries in Oyi local government area of Anambra State, Nigeria. Agrobiological Records 19: 24-34. https://doi.org/10.47278/journal.abr/2025.004

Shen X, Yin L, Zhang A, Zhao R, Yin D, Wang J, Dai Y, Hou H, Pan X, Hu X, Zhang D and Liu Y, 2023. Prevalence and Characterization of *Salmonella* Isolated from Chickens in Anhui, China. Pathogens 12(3): 465. https://doi:10.3390/pathogens12030465

Rodríguez A, Sacristán C, Iglesias I and de la Torre A, 2023. Salmonella assessment along the Spanish food chain: Likelihood of Salmonella occurrence in poultry and pig products is maintained across the food chain stages. Zoonoses and Public Health 70(8): 665-673. https://doi.org/10.1111/zph.13076

Rodrigues GL, Panzenhagen P, Ferrari RG, Paschoalin VMF and Conte-Junior CA, 2020. Antimicrobial resistance in non-typhoidal *Salmonella* Isolates from Human and Swine Sources in Brazil: A Systematic Review of the Past Three Decades. Microbial Drug Resistance 26(10): 1260-1270. https://doi.org/10.1089/mdr.2019.0475

Rubio MDS, Rodrigues Alves LB, Viana GB, Benevides VP, Spina de Lima T, Santiago Ferreira T, Almeida AM, Barrow PA and Berchieri Junior A, 2021. Heat stress impairs egg production in commercial laying hens infected by fowl typhoid. Avian Pathology 50(2): 132-137. https://doi.org/10.1080/03079457.2020.1845302

Staroselsky A, 2010. Problems and solutions for salmonellosis in

modern poultry farming. Veterinaria (2): 13–15

Wang X, Wang H, Li T, Liu F, Cheng Y, Guo X, Wen G, Luo Q, Shao H, Pan Z and Zhang T, 2020. Characterization of Salmonella spp. isolated from chickens in Central China. BMC Veterinary Research 16(1): 299. https://doi.org/10.1186/s12917-020-02513-1

Ximenes E, Ku S, Hoagland L and Ladisch MR, 2019. Accelerated sample preparation for fast *Salmonella* detection in poultry products. Methods in Molecular Biology 1918: 3-20. https://doi.org/10.1007/978-1-4939-9000-9_1