



Original Research Paper/Review Paper

Salmonella Enterica Isolated from Different Poultry Species in Eastern Algeria: Serotype Diversity and Antibiotic Resistance Profile

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Key Words

Salmonella enterica, Poultry, Serotyping, Antimicrobial Resistance, Multidrug Resistance, MAR Index, Eastern Algeria.

Abstract

Salmonella enterica remains a major pathogen causing severe economic losses in the poultry sector and posing significant public health risks globally. This study aimed to determine the prevalence, serotypic diversity, and antimicrobial resistance profiles of Salmonella enterica isolated from various commercial poultry production lines across eastern Algeria.

A multi-center survey was conducted between April 2013 and May 2025 across 137 poultry farms located in eight provinces of eastern Algeria (Sétif, Bordj Bou Arreridj, M'sila, Batna, Constantine, Mila, Skikda, and Oum El-Bouaghi). A total of 321 biological organ samples (liver, heart, and oviducts) were collected from birds exhibiting clinical signs or suspicious necropsy lesions. Isolation and identification were carried out in accordance with ISO 6579-1:2017 guidelines and the API 20E system. Serotyping was performed per ISO/TR 6579-3 recommendations. Antibiotic susceptibility testing against 12 molecules was conducted using the disk diffusion method following CLSI/CA-SFM guidelines.

An overall farm prevalence of 51.82% (71/137) was observed, with marked variation across production lines. The highest prevalence occurred in layer breeders (100%, 3/3) and laying hens (80.00%, 44/55), followed by turkeys (40.00%, 4/10), broilers (29.82%, 17/57), and broiler breeders (25.00%, 3/12). Among the 71 isolated strains, five serotypes were identified, dominated by Salmonella Gallinarum (56.34%, n = 40) and Salmonella Enteritidis (35.21%, n = 25), alongside Salmonella Pullorum (4.22%, n = 3), partially serotyped strains (2.82%, n = 2; S. spp. O:6,7 and S. spp. O:1,2), and one non-typeable isolate (1.41%). Antimicrobial profiling demonstrated total susceptibility (100%) to cefotaxime, gentamicin, colistin, and chloramphenicol, as well as high efficacy for amoxicillin-clavulanic acid (90.14% susceptible), trimethoprim-sulfamethoxazole (90.14%), and enrofloxacin (97.08%). Conversely, alarmingly high resistance was detected against nalidixic acid (98.54%), followed by moderate resistance to tetracycline (23.94%), nitrofurantoin (22.53%), and ampicillin (15.44%). Multidrug resistance (MDR, ≥ 3 classes) was observed in 14.08% (n = 10) of isolates, yielding a Multiple Antibiotic Resistance Index (MARI) of 0.27. Statistical analysis revealed a highly significant association between poultry species and serotype distribution (p < 0.01), whereas MDR profiles were uniformly distributed across species (p > 0.05).

The elevated prevalence of host-adapted (S. Gallinarum) and zoonotic (S. Enteritidis) serotypes, coupled with high quinolone resistance and a elevated MAR index, underscores critical gaps in biosecurity and antimicrobial stewardship in Algerian poultry production. Stricter hygiene measures and prudent antibiotic monitoring are urgently needed.

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Received: 25th May, 2026; Revised: 6th June, 2026; Accepted: 8th June, 2026; Available Online: 19th August, 2026

(DOI): 10.70102/AEJ.2026.18. 6

Introduction

Salmonella enteric is an anaerobic, Gram-negative, facultative intracellular pathogen that can invade and replicate within animal host cells, causing systemic and enteric diseases in a wide range of avian and mammalian species, including *Salmonella enteritis* and typhoid fever (Raut et al., 2023; Mkangara, 2023). The capacity of these bacteria to adapt rapidly to the biological features of new hosts facilitates interspecies transmission and leads to considerable epidemiological shifts; this adaptability is exemplified by non-typhoidal salmonellosis leads to considerable economic losses in animal production and constitutes a major cause of morbidity and mortality worldwide, with approximately 93.8 million cases of gastroenteritis and 155,000 deaths annually (Sanni et al., 2023; Oludairo et al., 2022). The poultry-processing sector, including poultry meat and eggs, constitutes a particularly significant route of infection for consumers (Mkangara, 2023; Chowdhury et al., 2023; Attia et al. 2022; Wessels et al., 2021).

Despite the existence of a large number of serovars of this species (about 2,500 serovars) are recognized, only a few *S. enterica* serotypes are responsible for the majority of infections in poultry. They are generally serovars adapted to particular host species and normally asymptomatic (Kipper et al., 2022; Khan & Shamim 2022; Akinyemi et al., 2023; Zakaria et al., 2022)

The three most common *Salmonella enteric* serovars with zoonotic potential in poultry worldwide are *Salmonella Enteritidis*, *Salmonella Gallinarum*, and *Salmonella Pullorum*. *S. Enteritidis* is a highly virulent, non-

host-specific pathogen that causes enteritis in poultry and poses a threat to humans. *S. Gallinarum* exclusively infects birds and is the causal agent of avian typhoid, whereas *S. Pullorum* also specifically infects birds and is responsible for pullorosis (Kipper et al., 2022; Li et al., 2022; Hossain et al., 2021; Farhat et al., 2023). Avian typhoid and pullorosis are severe systemic diseases attributable to strictly avian-adapted strains (*Salmonella Gallinarum* and *Salmonella Pullorum*, respectively) (Julianingsih, 2023; Lublin et al., 2021).

All the above strains result in enormous losses for poultry producers due to high mortality, reduced zootechnical performance, and constraints on international trade (Attia et al., 2022; Ravikumar et al., 2023; Ravikumar et al., 2022; Ahmad et al. 2023). The risk of toxigenic human food infection constitutes an additional consequence for consumers, rendering poultry an object of permanent biosafety vigilance and challenge (Elbehiry et al., 2023; Ricke, 2021; Raut et al., 2023). At the same time, the growing emergence of multi-resistant strains of critical antibiotics for human medicine such as quinolones, 3rd generation cephalosporins and, more recently, polymyxins is now a worrying reality, for both veterinarians and public health authorities. This situation is aggravated by the excessive use, often unregulated, of antimicrobials in livestock where treatments are administered preventively or empirically (Nguyen et al., 2021; Ghimpețeanu et al., 2022; Caneschi et al., 2023; Tian et al. 2021; Kasimanickam et al., 2021).

In Algeria, the poultry sectors have experienced considerable development over the past two decades, making an essential contribution to national food security (Bouziane et al., 2024; Al Shukri 2022; Lazereg et al., 2024). However, recent epidemiological data in Algeria highlight the

persistent and worrying circulation of the main serotypes of *Salmonella* spp in poultry farming, such as *S. Enteritidis*, *S. Typhimurium* and *S. Infantis* (Belabed et al., 2025; Sebaa et al., 2022; Samia et al.2021; Bellil et al.2024). In parallel, the survey by Djeflal et al. (2018) on farms in the north-eastern region of Algeria reveals that *Salmonella* isolates mainly belong to the Kentucky and Heidelberg serovars, followed to a lesser extent by *Enteritidis*, *Virginia*, and *Newport*. Very high rates of multiresistance reaching in some cases 60% were observed in studies conducted on *Salmonella* spp in poultry in Algeria, these findings highlight a significant concern for public health and food safety related to antibiotic resistance in this important sector (Guechtouli et al.2024). For this reason, the present study aims to determine the prevalence, isolate and identify *Salmonella enterica* strains from organ samples of different avian species in eastern Algeria and evaluate their resistance profiles to the main antibiotics used in veterinary medicine.

Material and Method

2.1 Study area and samples

The present survey was conducted from April 2013 to May 2025 in eight localities in eastern Algeria: Sétif, Bordj Bou Arreridj, Msila, Batna, Constantine, Mila, Skikda and Oum El-Bouaghi (tab list).

The target population consisted of 136 poultry farms, including 57 broiler farms, 55 layer farms, 10 turkey farms, 12 broiler breeder farms, and 02 layer breeder farms. The selection of farms was based on voluntary consent of the farm managers

to participate in the study. Out of 321 biological samples (organs: 137 liver, 137 heart, and 47 oviduct) were collected from suspected farms (table 1), the selection based on clinical signs and necropsy findings (Madjo et al .2012). Samples were collected individually, placed in sterile containers, and stored at +4°C in a cooler during transport to the laboratory.

2.2 Laboratory analysis

2.2.1 Isolation, preliminary characterization and identification of pathogenic bacteria

The procedure based on guidelines of the revised standard protocol for salmonella isolation ISO 6579.1:2017 Amendment 1: Annex D.

2.2.1.1 Pre-enrichment

One gram of each organ(liver, heart muscle and ovary) was sampled per subject. Deep tissue extraction was performed following a surface cauterization to avoid contamination. Each sample was suspended in a sterile vial containing 9 ml of buffered peptonic water and incubated at 37°C for 18 hours.

2.2.1.2 Enrichment

The enrichment was carried out simultaneously in two selective enrichment broths. Using steril Pasteur pipettes, 0.1 ml and 1ml of the pre-enrichment broth were respectively inoculated into 10 ml of Rappaport Vassiliadis Soja (RVS) broth and Mueller Kauffman Tetrathionate Novobiocine (MKTTn) broth. The MKTTn tubes were incubated at 37°C for 18 to 24 hours, while the RVS tubes at 42°C for 18- 24 hours.

2.2.1.3 Plating

Following enrichment, samples were streaked onto two different selective agar media mainly xylose

lysine deoxycholate (XLD) agar and Hecht Enteric agar, then incubated at 37°C for 24 hours. All colonies suspected *Salmonella* spp. were subcultured for purification and retained for identification.

2.2.1.4 Identification using API 20 E

Presumptive *Salmonella* colonies were identified using the API 20 E system (BioMérieux, France) designed for enterobacteria. Preparation of the test strips and inoculum was performed according to the manufacturer's instructions. After incubation at 37°C for 24 hours, the resulting biochemical profiles were analyzed using the APIWEB® identification software.

The biochemical characteristics obtained via the API 20 E system for various *Salmonella* enteric serotypes (*S. Gallinarum*, *S. Pullorum*, *S. Enteritidis* and other *Salmonella* spp.) are summarized in supplementary 1.

2.2.2 Antibiotic sensitivity tests

Antibiotic susceptibility testing was performed using the disk diffusion method on Mueller Hinton agar (Bio-Rad), following the guidelines of the clinical and laboratory standards institute (CLSI, 2021).

The diameters of the inhibition zones were measured, and the results were interpreted according to the criteria established by the of the

antibiogram committee of the French society of microbiology (CA-SFM).

The following antibiotic discs were tested: Ampicillin (AMP), Amoxicillin/clavulanic acid (AUG), Cefotaxim (CTX), Pefloxacin (PEF), Tetracycline (TE), Trimethoprim-Sulfamethoxazole (SXT), Gentamicin (CN), Chloramphenicol (C), Colistin (CT), Nalidixic Acid (NAL), Enrofloxacin (ENR) and Nitrofurantoin (FUR).

2.2.3 Serotyping

Strains confirmed as *Salmonella* spp. were further serotyped according to the guidelines described in ISO/TR 6579-3.

Before testing for specific antigens (O-antigens, H-antigens, and Capside-antigens), the strains must first test negative for self-agglutination. If agglutination occurs upon the addition of the appropriate antisera, the reaction is considered positive, indicating the presence of the corresponding antigen.

2.2.4 Statistical analysis

The chi-square (χ^2) test was utilized to initially analyze and explore the relationship that exists between different poultry species and various *Salmonella* serotypes. Additionally, the test was employed to examine the connection between the multidrug resistance profiles and the poultry species in this study.

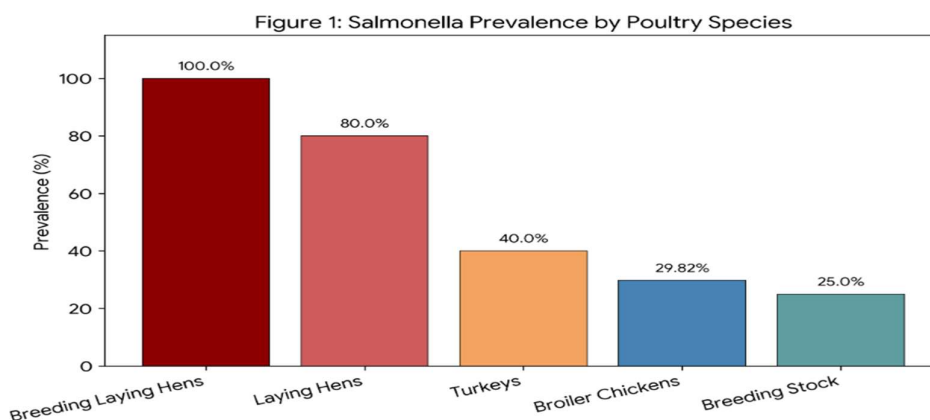
Results

3. Results

3.1 Frequency of Isolation and Overall Prevalence

Out of a total of 137 investigated poultry farms, 71 *Salmonella enterica* strains were isolated, corresponding 43

to an overall prevalence of 51.82%. A detailed breakdown by production type reveals significant disparities in prevalence rates (Figure 1). The highest prevalence was observed in the breeding of laying hens, where 100% of the sampled farms ($n = 3$) were confirmed positive. This was closely followed by laying hen flocks, which exhibited an 80% positivity rate (44 out of 55 farms). In contrast, meat-producing birds showed comparatively lower rates: turkey farms recorded a 40% prevalence ($n = 4$ out of 10), broiler chickens showed 29.82% ($n = 17$ out of 57), and broiler breeding stock had the lowest prevalence at 25% ($n = 3$ out of 12).



3.2 Serotyping of Isolated Strains

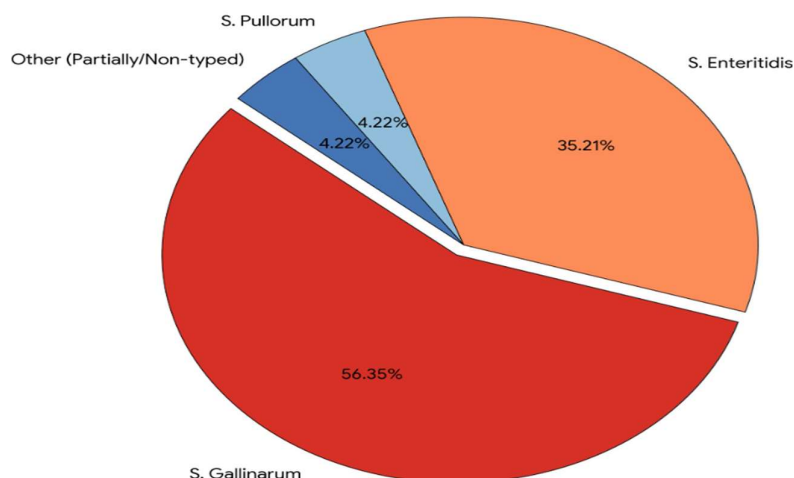
Serological characterization of the 71 isolates identified five distinct *Salmonella* serotypes, with a marked predominance of host-adapted and zoonotic strains (Figure 2). *Salmonella* Gallinarum was the most frequently isolated serotype, accounting for 56.34% ($n = 40$) of the isolates, followed by *Salmonella* Enteritidis at 35.21% ($n = 25$). *Salmonella* Pullorum was identified in 4.22% ($n = 3$) of cases. The remaining 4.22% consisted of partially serotyped strains (*Salmonella* spp. O:6,7 and O:1,2, 1.41% each) and one non-typeable strain (1.41%).

Regarding host specificity, broiler chickens displayed the highest serotypic diversity (*S. Enteritidis*, *S.*

Gallinarum, *S. Pullorum*, *Salmonella* spp. O:6,7, and non-typeable). In laying hens and their breeding stock,

S. Gallinarum, *S. Enteritidis*, and *S. Pullorum* were dominant. Notably, all isolates originating from broiler breeders were strictly identified as *S. Enteritidis*.

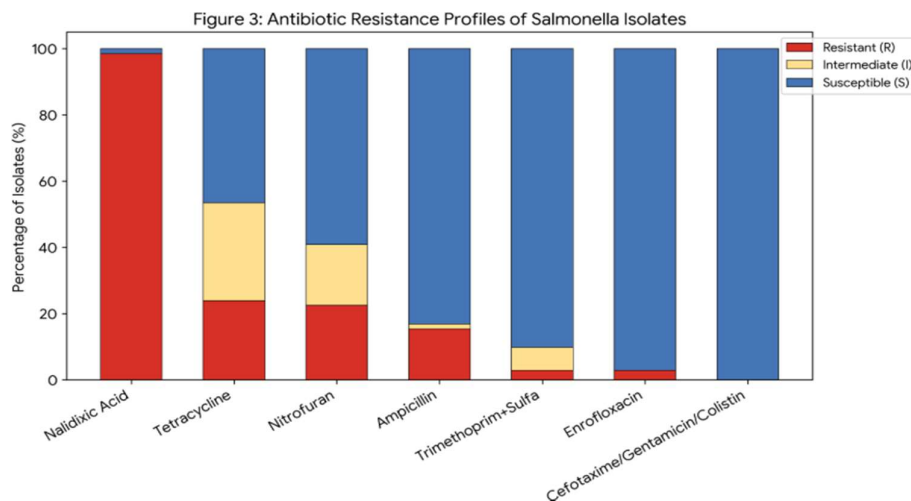
Figure 2: Distribution of Salmonella Serotypes



1.3 Antibiotic Resistance Profile

Antimicrobial susceptibility testing against 12 molecules revealed highly variable resistance profiles among the isolates (Figure 3). Complete efficacy (100% susceptibility) was observed for Cefotaxime, Gentamicin, Colistin, and Chloramphenicol, with no resistant strains detected. High efficacy was also noted for Amoxicillin-clavulanic acid (90.14% susceptible; 1.46% resistant), Trimethoprim-sulfamethoxazole (90.14% susceptible; 2.92% resistant), and Enrofloxacin (97.08% susceptible; 2.92% resistant).

Conversely, a critically high resistance rate was recorded against Nalidixic acid, with 98.54% of the isolates displaying resistance. Moderate resistance was observed for Tetracycline (23.94% resistant, 29.58% intermediate), Nitrofurantoin (22.53% resistant, 18.32% intermediate), and Ampicillin/Amoxicillin (15.44% resistant, 1.46% intermediate).



1.4 Multi-Drug Resistance (MDR) Phenotypes

Analysis of multi-drug resistance phenotypes showed that 14.08% (n = 10) of the isolates were resistant to at least three different antimicrobial classes. These MDR isolates exhibited four distinct resistance profiles and recorded a high Multiple Antibiotic Resistance Index (MARI) of 0.27, exceeding the high-risk threshold of 0.20. The most prevalent MDR phenotypes were the combinations of Ampicillin–Nalidixic Acid–Nitrofurantoin (predominantly in broilers) and Nalidixic Acid–Tetracycline–Nitrofurantoin (observed in both broilers and laying hens).

1.5 Statistical Associations

Statistical evaluation indicated a highly significant association between the poultry species and the isolated *Salmonella* serotypes ($p < 0.01$), underscoring the strong host-adaptation of certain strains, such as

S. Gallinarum in laying flocks. However, no statistically significant difference was observed regarding the distribution of multi-antibiotic resistance profiles among the different poultry species ($p > 0.05$). This suggests that selective antimicrobial pressures and multi-drug resistance acquisition are widely distributed across the investigated poultry sectors.

Discussion

In 137 studied farms, 71 strains of *Salmonella enterica* were isolated, corresponding to an overall farm prevalence of 51.82%. The serotypical distribution showed a predominance of *S. Gallinarum* (n = 40; 56.3%), followed by *S.*

Enteritidis (n = 25; 35.2%) and *S. Pullorum* (n = 3; 4.2%). The partially serotyped strains accounted for 2.8% (n = 2), including *Salmonella* spp. O:6,7 (n = 1; 1.4%) and *Salmonella* spp. O:1,2 (n = 1; 1.4%). And a non-serotyped strain (n = 1; 1.4%). Furthermore a strong representation of *S. Gallinarum* in laying lines and a predominance of *S. Enteritidis* in broilers ($p < 0.01$) were observed.

S. Gallinarum has been observed with similar prevalence rates in Nigeria (39%) (Sunmonu et al 2025). While it is rare in European countries applying eradication programmes (about 8.54%) (Zhou et al., 2022). 25% (Djemaïoune et al, 2025) on poultry farm and Turkey flocks

Previous studies in Algeria, Morocco and Argentina have shown similar prevalence of *S. Enteritidis* ranging from 6.4 % up to 51.25% (Djemaïoune et al 2025; Belabed et al. 2025; Heleili et al., 2025; Ayachi et al., 2025; Chergui et al., 2025; Bennoune et al., 2025; Hoffmann et al., 2025; Djeghout et al., 2020; Mezali et al., 2024, 2020; El Allaoui et al., 2023). While others In Ethiopia, China and Mongolia have reported a high prevalence of *S. Enteritidis* in poultry meat, ranging from 23.65% up to 45.28% (Waktole et al., 2024; Wang et al., 2024; Chen et al., 2025; Wang et al. (2023); Song et al., 2025). Guechtouli et al. (2024) in Algeria, noted lower levels of *S. Enteritidis*.

S. Enteritidis and *S. Gallinarum* remain predominant circulating serotypes in poultry farms, posing a significant epidemiological threat to both poultry production and public health (Kipper et al. 2022) (Farhat et al. 2023)

. This Maybe be attributed to their ability to undergo vertical transmission from breeder flocks, as well as the potential for horizontal contamination at the hatchery level (Shang et al. 2021) (Shterzer et al. 2023)

Regarding *S. Pullorum* serotype prevalence in poultry farms, similar rates were observed in Algeria, Morocco, (Guechtouli et al., 2024 ; Mezali et al., 2020; Djeflal et al., 2018; El Allaoui et al., 2023). Chen et al. (2025) in China observed a predominance of *S. Pullorum* in unvaccinated herds, with rates of 22,64 % significantly higher than those recorded in Algeria. Barrow & Freitas Neto (2011) report, in various poultry contexts, isolation rates generally varying between 5% and 20%, with higher peaks during acute episodes. In Shandong province, Chen et al. (2025) documented the presence of *S. Pullorum* in chicken, duck, and goose farms, with prevalences higher than ours. In Mongolia, Song et al. (2025) highlighted a notable prevalence in poultry meat, again higher than our results. Finally, Hoffmann et al. (2025) in Argentina highlight the rarity of *S. Pullorum* with rates lower than ours. The low occurrence of *S. Pullorum* (three cases) observed in this work can be explained by the predominance of adult birds among the samples collected ($p < 0.01$). Indeed, this bacterium is mainly involved in the infections of young subjects, while adults tend to remain asymptomatic carriers (Chappell, 2007).

Researchers have reported similar prevalence rates of the partially serotyped strains in Algeria, Morocco (3–6%) (El Allaoui et al., 2017; Mezali et al., 2020).

Grimont & Weill (2007) specify that the O:6,7 and O:1,2 antigens are shared by several serovars, which explains the limits of classical serotyping in the absence of specific sera. Generally, some O antigens are shared by several serovars, O:6,7 is common to *S. Virchow*, *S. Infantis* and *S. Panama*, while O:1,2 may

correspond to *S. Paratyphi A*, *S. Sendai* or other serotypes uncommon in poultry (Grimont & Weill, 2007). The use of whole genome sequencing (WGS) allows to confirm the identity of partially typed strains and reveal distinctive genetic characteristics, thus improving the understanding of infection sources and transmission routes, with greater efficiency than conventional approaches (Chen et al., 2025; Song et al. 2025; Zhang et al., 2025; Wang et al., 2023).

The antibiogram showed that all strains of *Salmonella enterica* in our study were fully (100%) sensitive to cefotaxime, gentamicin, colistin and chloramphenicol. In Algeria, Tunisia and Morocco recent studies have shown similar results reporting very high rates of sensitivity to gentamicin, cefotaxime and colistin (Mezali et al., 2020; Guechtouli et al., 2024; Kout et al., 2025; El Allaoui et al., 2023; Oueslati et al., 2022). The EFSA & ECDC reports (2025) indicated that, throughout the European Union, resistance to gentamicin and colistin in avian *Salmonella* remains generally low, therefore similar to our results. Some regions of Latin America and Asia show higher resistance levels to colistin and aminoglycosides, particularly in China (Chen et al., 2025) and Argentina (Hoffmann et al., 2025), as reported by recent studies (Rau et al., 2021). These resistances mainly affect *Salmonella* isolates in poultry, especially the *S. Enteritidis* and *S. Infantis* serovars. However, other regions manage to maintain lower resistance rates through enhanced surveillance and stricter antimicrobial usage policies (Georganas et al., 2024; Song et al., 2025; Wang et al., 2024; Zhang et al., 2018; Waktole et al., 2024). A high resistance to nalidixic acid (98.5%) was observed in our study. In Algeria, several studies confirm this trend in avian products such as meat and egg, where they reported rates ranged from 90% up to 98% (Mezali et al., 2020; Guechtouli et al., 2024; Djeflal et al., 2018). Chen et

al. (2025) documented rates above 50% in chicken, duck and goose farms in Shandong province (China). In Argentina, the work of Hoffmann et al. (2025) shows that resistance rates to nalidixic acid are similar to our data for the *S. Enteritidis* and *S. Infantis* serovars. likely reflects excessive quinolone use and frequent underdosing in poultry farming is associated with cross-resistance with modern fluoroquinolones.

Previous studies have shown comparable rates of tetracycline resistance (23.9%) in the meat and egg sectors (Guechtouli et al., 2024; Kout et al., 2025; El Allaoui et al., 2023). while Djeflal et al. (2018) in the North-East reported lower values (15%). Other researchers have reported higher values in poultry farms (>40%) (Mezali et al., 2020; Chen et al., 2025; Hoffmann et al., 2025). This situation can be partly explained by the fact that, in the laying hen, tetracycline is often preferred because it does not require any waiting period before the consumption of eggs. Globally, tetracyclines remain among the most widely used antibiotics in poultry farming, particularly in low- and middle-income countries, which maintains selection pressure and promotes the emergence and spread of resistant strains (WHO-GLASS, 2024). Regarding nitrofurans resistance (22.5%). Several studies have reported resistance rates in poultry farms ranging from 21% upto 35% (Chen et al., 2025; Hoffmann et al., 2025; Rau et al., 2021; Guechtouli et al., 2024). Our result could reflect ancient uses or cross-selection although their use is prohibited in Algeria.

The resistance to ampicillin observed in our study was 15.4%, in Algeria, several authors have documented this issue and the higher observed rate was (>25%) (Kout et al., 2025 ;

Mezali et al., 2020; Djeflal et al., 2018; Guechtouli et al., 2024). Several studies conducted worldwide on ampicillin resistance in the poultry sector have reported rates equal to or even higher than ours, with some, such as those in China (Chen et al., 2025), Mongolia (Song et al., 2025), Morocco (El Allaoui et al., 2017) and Argentina (Hoffmann et al., 2025) reaching levels above 50%, highlighting a global trend of concern.

In our study, only 2.9% of the strains exhibited resistance to trimethoprim-sulfamethoxazole (SXT). This favorable profile joins the observations of several Algerian authors which reported prevalences ranged from 2% upto 4% (Mezali et al., 2020; Djeflal et al., 2018; Kout et al., 2025), confirming that this molecule overall retains good effectiveness. Other studies reported different rates of SXT resistance in poultry and poultry products which sometimes exceeded 40% (Song et al., 2025; Hoffmann et al., 2025; Wang et al., 2024; Georganas et al., 2024; Waktole et al., 2024). These results reflected heterogeneous selection pressures and antimicrobial use practices on a global scale (EFSA & ECDC, 2025). The resistance to enrofloxacin (ENR) in our series was low (2.9%), representing one of the most favorable profiles and aligning with findings from Algeria (Mezali et al., 2020; Guechtouli et al., 2024; Kout et al., 2025), though slightly higher than in the Northeast (Djeflal et al., 2018). In contrast, significantly higher rates were reported in Morocco (El Allaoui et al., 2023), China (Wang et al., 2024), Argentina (Hoffmann et al., 2025), and other non-European countries (Georganas et al., 2024; Waktole et al., 2024), as also highlighted by EFSA & ECDC (2025). The amoxicillin-clavulanic acid (AMC) combination showed high efficacy in our study, with only 1.4% resistance, consistent with low rates reported in Algeria (Mezali et al., 2020; Djeflal et al., 2018; Guechtouli et al.,

2024; Kout et al., 2025) and Morocco (El Allaoui et al., 2017). Internationally, WHO-GLASS (2024) confirms AMC's effectiveness against non-ESBL-producing *Salmonella*, but EFSA & ECDC (2025) warn of rising resistance due to enzymatic mechanisms. Higher resistance rates have been noted in China (Wang et al., 2024), Mongolia (Song et al., 2025), and Argentina (Hoffmann et al., 2025), with global concerns echoed by Georganas et al. (2024) and Waktole et al. (2024).

In our study, we noted a 14% rate of multiresistance among avian *Salmonella enterica* isolates, which remains relatively moderate. In addition, no significant difference was observed between the multidrug resistance profiles of different poultry species ($p>0.05$). The multidrug resistance (MDR) rate in our study (14%) is lower than those reported in Algeria by Guechtouli et al. (2024) and Douif et al. (2018), as well as in neighboring countries like Tunisia (Oueslati et al., 2021), Nigeria (Ahmed et al., 2019), and Egypt (Hassan et al., 2016). It is, however, similar to rates observed in Morocco (El Allaoui et al., 2017) and slightly lower than that reported by Bounar-Kechih et al. (2012), and in Algeria (22,72%) by Djemaïoune et al. (2025). These findings reflect considerable regional variability in MDR prevalence. Globally, rates of multiresistance in *Salmonella* vary widely, and the results observed in our study are lower than those reported in many regions. Globally, multidrug resistance (MDR) rates in *Salmonella* vary significantly, with our study reporting lower rates than many regions, especially in Asia and sub-Saharan Africa. Higher MDR levels have been documented in China (Wang et al., 2024), Mongolia (Song et al., 2025), Malaysia (Syed

Abu Thahir et al., 2023), and Pakistan (Asif et al., 2017), often linked to poor antibiotic regulation. In Latin America, extremely high rates were found in Chile (Lapierre et al., 2020) and Argentina (Hoffmann et al., 2025). Conversely, MDR rates in the EU remain generally lower than ours (EFSA & ECDC, 2025).

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