Research Article

Isolation, Identification, and Genetic Characterization of Antibiotic Resistance of *Salmonella* Species Isolated from Chicken Farms

Ahmed Shalaby, Mahmoud M. Ismail, and Hanem El-Sharkawy

Department of Poultry and Rabbit Diseases, Faculty of Veterinary Medicine, Kafrelsheikh University, Kafrelsheikh 33511, Egypt

Correspondence should be addressed to Hanem El-Sharkawy; hanem_amin@yahoo.com

Received 26 October 2022; Revised 14 November 2022; Accepted 15 November 2022; Published 29 November 2022

Academic Editor: Lawrence Sheringham Borquaye

Copyright © 2022 Ahmed Shalaby et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

*Salmonella* is a major cause of foodborne outbreaks. It causes gastroenteritis in humans and animals. This micro-organism causes severe illness in chickens and has a major impact on chicken productivity and the poultry industry. This study aimed to address the prevalence of *Salmonella* infection in broiler chicken farms in Kafrelsheikh, Gharbia, and Menofeya provinces in Egypt during 2020–2022. This work also aimed to evaluate the genetic characterization and antibiotic resistance of the isolated *Salmonella* strains. Clinical signs and mortalities were observed and recorded. In total, 832 samples were collected from 52 broiler flocks, including 26 from both one-week-old and 6-week-old chicken farms from different organs (liver, intestinal content, spleen, and gallbladder). The prevalence of *Salmonella* infections was reported in the study region to be 36.54%. Of the 26 one-week-old farms surveyed, 11 (42.31%) and 8/26 (30.77%) of the six-week-old broiler chicken farms had *Salmonella* infections. Recovered isolates were serotyped as 9 (47.37%) *S. enteritidis* O 1,9,12, ad monophasic H: g: m: -, 6 (31.58%) *S. shangani* 2, (10.53%) *S. gueuletapee* 1, (5.26%) *S. I(salamae)*, and 1 (5.26%) untypable. The results showed that *Salmonella* infection was predominant in one-week-old chicks compared to infection in six-week-old and uninfected flocks. All *Salmonella* isolates were resistant to ampicillin and erythromycin, while all isolates were sensitive to ciprofloxacin, chloramphenicol, and levofoxacin. The isolates also contained 10.53% (2/19) streptomycin, 10.53% (2/21) gentamicin, 15.79% (3/19) doxycycline, and 26.32% (5/19) lincomycin and colistin. The phenotypically resistant *Salmonella* samples against ampicillin, erythromycin, and macrolide harbored *bla*<sub>TEM</sub>, *bla*<sub>SHV</sub>, *ermB*, *ereA*, *mphA*, and *ermB*, respectively. This baseline data on *Salmonella* spp. prevalence, serotyping, and antibiotic profiles are combined to define the antimicrobial resistance to this endemic disease. Elucidation of the mechanisms underlying this drug resistance should be of general importance in understanding both the treatment and prevention of *Salmonella* infection in this part of Egypt.

1. Introduction

Chicken is a significant source of eggs and meat. The poultry production-related industry is one of the economically important agro-industry components [1]. *Salmonella* spp. is one of the most causative agents of diseases in poultry and avian species [2]. It causes heavy economic losses because of its high mortality rate and reduced production rate in poultry [3]. The economic cost of the *Salmonella* spp. outbreak has been estimated to be $11.6 billion in the USA [4] and more than €3 billion in the European Union [5].

Poultry is one of the most preferable reservoirs for *Salmonella* spp., which will allow it to transmit to humans through food [6]. Poultry meat is thought to be the most common source of *Salmonella* infection in humans, accounting for roughly 40% of clinically reported cases [7]. *Salmonella* spp. is a Gram-negative bacteria that belongs to the family Enterobacteriaceae [8]. *Salmonella* spp. is an
opportunistic zoonotic organism that infects human and animal cells through contaminated food and the environment [9]. It infects a wide variety of cells, such as M cells, epithelial cells, dendritic cells, and macrophages [10]. It can survive both in the absence and presence of oxygen [11].

Salmonella spp. chickens are usually divided into three classes based on the diseases they cause [12]. The first class comprises nonmotile, chicken-adapted Salmonellae, which include S. gallinarum, which causes fowl typhoid, and S. pullorum, which causes pullorum disease in chickens [13]. Fowl typhoid (FT) and pullorum disease (PD) are septicemic, which causes pullorum disease in chickens [13].

The second class of Salmonella that affects birds is the invasive, nonhost-specific Salmonella, which can infect more than one host, including animals and humans, and is called paratyphoid Salmonella in birds. This type of bacteria causes paratyphoid in birds, and it is of zoonotic concern. The paratyphoid Salmonella includes 10–20 serovars. S. enteritidis, S. typhimurium, S. shangani, S. gueuletapee, and S. I. salamae are the most important serovars [15].

Salmonella enteritidis, S. typhimurium, S. shangani, S. gueuletapee, and S. I. salamae have been reported to be the most common salmonellae isolated from Egyptian poultry farms [16]. They are transmitted horizontally between farms and vertically to the progeny through trans-ovarian infection [16]. The clinical manifestations of paratyphoid infections are most predominant in young chickens, especially in the first few weeks of life. The most common symptoms associated with paratyphoid disease in broilers include depression, anorexia, and diarrhea, with high mortalities, especially in the first week of life. While in adult birds, the infection is asymptomatic, and the infected birds are considered carriers, which are the most dangerous source for the shedding of bacteria in meat and eggs of zoonotic concern (Tiwari, Swamy, et al.).

The third class of Salmonella is neither host-adapted nor invasive and may cause disease in humans and other animals [14].

The widespread use of antibiotics on poultry farms as growth promoters or prophylaxis as well as for treatment can raise concerns about antibiotic resistance, which has been reported in many Salmonella spp. serovars [17]. During the second half of the twentieth century, there were two significant breakthroughs in the epidemiology of nontyphoidal salmonellosis throughout the world [18]. First, multidrug-resistant Salmonella typhimurium strains, such as S. typhimurium DT104, have arisen, and second, Salmonella enteritidis has emerged as a prominent poultry and egg pathogen [19].

Amoxicillin (β-lactam antibiotic) competitively inhibits penicillin-binding protein 1. By producing an enzyme called a β-lactamase, which attacks the β-lactam ring; bacteria frequently become resistant to β-lactam antibiotics. Prophylactic β-lactam resistance develops through four main mechanisms: the production of a β-lactamase enzyme (primarily in Gram-negative bacteria), low expression of external membrane proteins, alterations in the dynamic site of penicillin-binding proteins (PBPs), and active efflux [20].

There are genes that are associated with resistance to β-lactamase blaTEM-1, blaTEM-2, and blaSHV-1. The β-lactam ring of penicillin is hydrolyzed by blaTEM β-lactamases, which is how they work. There are three types of SHVs (sulfhydryl variables): 2b, 2be, and 2ber. Penicillin and first- and second-generation cephalosporins are hydrolyzed by type 2b; third-generation cephalosporins are hydrolyzed by type 2be; while clavulanic acid and tazobactam are resistant to type 2br. Every year, new β-lactamase variants are recorded, and this poses a challenge to the medical field [21].

Erythromycin stops bacteria from producing their protein by attaching to the bacterial cell membrane and the 50S subunit of the ribosome. A small 30S subunit and a large 50S subunit make up the bacteria’s ribosome. The latter has at least 30 proteins and 23S rRNA. Erythromycin inhibits protein synthesis by attaching to the 50S subunit. Erythromycin ribosomal methylase is a ribosomal enzyme that modifies the 50S subunit’s binding site for erythromycin. It is encoded by the ermB gene. The modification gene markedly reduces the affinity of erythromycin for its target [22]. Macrolides, including erythromycin, inhibit bacterial protein synthesis by binding at the exit tunnel of the 50S ribosomal subunit. They do this by preventing peptidyl transferase from adding the growing peptide attached to tRNA to the next amino acid. It also inhibits bacterial ribosomal translation [23]. Macrolide inactivation also occurs by phosphotransferases encoded by mphA and mphB [24]. A resistance enzyme that preferentially inactivates 14-membered macrolides (such as erythromycin, telithromycin, and roxithromycin) over 16-membered macrolides is encoded by the mphA gene (e.g., tylosin and spiramycin). It phosphorylates macrolides in a GTP-dependent manner at the 2'-OH hydroxyl group of the desosamine sugar of macrolides [25]. Resistance to macrolides may also be due to the ereA gene (erythromycin resistance esterase type I) [26]. This encodes the erythromycin esterase enzyme, which causes enzymatic hydrolysis of the macrolactone ring [23].

Serotyping is a basic biomarker for investigating the epidemiology status of Salmonella infections, and it’s frequently used to allocate the source of contamination during epidemics [27]. This method was established by White and Kauffmann based on the detected phase-shift flagella antigen and flagella H, somatic O antigen [2]. The method addressed is considered the reference one for the serotyping of Salmonella spp. Serotyping of Salmonella spp. has many advantages, including details regarding the disease’s severity, the source of contamination, and the pattern of resistance. Molecular characterization methods have been used to identify differences between Salmonella strains. These methods include PCR, pulsed-field gel electrophoresis (PFGE), random amplification of polymorphic DNA (RAPD), etc. [28].

This study aimed to isolate and identify Salmonella spp. from different provinces in Egypt. The study also concludes the investigation of antimicrobial resistance against 11 different clinically relevant antimicrobials and the molecular characterization of resistance-attributed genes.
2. Methods

2.1. Sampling Strategy and Salmonella Isolation. This study has conveniently targeted 52 broiler chicken flocks (Avian 48, Abdelsalam Hegazy Company), of which 26 were one-week-old chick flocks and 26 were six-week-old birds. These farms were investigated for Salmonella infections. The broiler chicken flocks were surveyed in Kafrelsheikh, Gharbia, and Menofeya provinces in Egypt during 2020–2022. The birds showed different clinical signs, including reluctance to move, pasty diarrhea, huddling near the source of the heat, ruffling feathers, dehydration, decreased body weight gain, droopy wings, lameness, and high mortalities of 9.64% ± 1.72 in one-week-old chicks from each broiler chicken farm. Four living, diseased birds were selected randomly and sacrificed. At postmortem, sections from the liver, gallbladder, spleen, and intestinal contents were collected under aseptic conditions for Salmonella isolation. Within five hours of collection, samples were delivered to the lab and stored on ice until then. Selenite-F broth (SFB) (Oxoid, UK) was combined with one gramme of tissue from each organ and incubated statically at 37°C for an overnight period. The enrichments were applied to XLD agar (Oxoid, UK) using a swap, and they were then incubated at 37°C overnight. One colony from each plate that appeared to be Salmonella spp. was chosen for additional examinations based on appearance [29].

2.2. Biochemical Identification. The pure pink colonies on XLD agar with black centre colouration were taken as suspected colonies of Salmonella spp. According to Lamboro et al. [30], these bacterial colonies were confirmed biochemically as Salmonella spp. [30]. The biochemical tests used for Salmonella spp. detection were IMViC reactions that included indole, methyl red, Vogues Proskauer, oxidase, and citrate utilization tests [31]. Urease hydrolysis and hydrogen peroxide production were also tested [31].

2.3. Serological Identification of Salmonella Isolates. Serotyping of suspected Salmonella strains was conducted at the Animal Health Research Institute, Dokki, Giza, Egypt, according to the manufacturer’s instructions (Denka Seiken Co., Tokyo, Japan). Briefly, the isolates were examined with an eminential A–67. The positive isolates were tested with anti-Salmonella A-E and anti-Salmonella F-67. The samples were identified by using anti-Salmonella antibodies grouped by specific O antigens (2, 4, 7, 8, etc.). The samples were tested for grouped anti-Salmonella H antigen phases 1 and 2.

2.4. Genomic DNA Extraction and Purification. A single colony was collected from each plate and inoculated into five ml of selenite-F broth SFB (Oxoid, UK) throughout the course of an overnight period at 37°C. One minute of 13000 rpm centrifugation was performed on one milliliter of bacterial culture broth in a microcentrifuge tube. After removing the supernatant, the bacterial pellets were heated at 95°C for 10 minutes while being homogenized with water devoid of nucleases. Finally, the boiled lysates were centrifuged, and the supernatant was removed to create DNA templates that were stored at −80°C until use [32].

2.5. Molecular Detection of the Salmonella Genus and Antimicrobial Resistance-Associated Genes. The ompC gene was used as a specific determinant for Salmonella spp. detection [33]. The amplification of ompC PCR was performed using primers, as shown in Table 1, according to the method described by the authors of [33]. Salmonella isolates were screened for five genes known to be associated with antibiotic resistance to ampicillin, erythromycin, and macrolides. These genes are blatem, blasvi, and ermb, eraA, and mphA, respectively, as shown in Table 1 according to the methods described by [34, 35].

Briefly, primers were utilized in a 25 μl of uniplex PCR mix, comprising 12.5 μl of EmeraldAmp Max PCR Master Mix (Takara, Japan), 1 μl of each primer (20 pmol), 5.5 μl of water, and 5 μl of DNA template. The reaction was performed in an Applied Biosystems 2720 thermal cycler. The cycling condition started with primary denaturation at 94°C for 5 min, followed by 35 cycles and a final extension at 72°C for 10 min. The specific annealing of each gene is shown in Table 1. The positive controls were represented by field samples that were previously confirmed to be positive by PCR for the antimicrobial resistance-related genes in the reference laboratory for veterinary quality control on poultry production, an Animal Health Research Institute. The Salmonella ATCC 9184 strain was used as a control positive for ompC gene detection, while sterile water was added to the PCR mix with each primer pair as a control negative.

2.6. The Antimicrobial Susceptibility Test. Antimicrobial susceptibility testing (AST) was carried out using the Kirby–Bauer disc diffusion method as recommended by the CLSI [36]. E. coli ATCC25922 and E. coli NCTC10418 were used as quality control strains during AST. The AST for Salmonella isolates was conducted against 11 antimicrobial agents that are clinically used in the Egyptian poultry industry. This includes ciprofloxacin (CIP 5 μg), chloramphenicol (C 30 μg), streptomycin (STR 10 μg), gentamicin (CN 10 μg), erythromycin (E 15 μg), doxycycline (DO 30 μg), levofloxacin (LEV 5 μg), ampicillin (AM 10 μg), lincomycin (L 2 μg), norfloxacin (NOR 10 μg), and colistin (CT 10 μg). The tested Salmonella inoculum was prepared by direct saline suspension of a nutrient broth culture from an isolated colony on selective XLD agar plates that had been incubated for 18 to 24 hours. The bacterial suspension of tested Salmonella was adjusted in sterile saline by adding approximately one ml of overnight bacterial suspension to 4 ml of sterile saline to match the 0.5 McFarland standard (containing approximately 1–2x10^8 CFU/ml for American Type Culture Collection (ATCC) 2592 E. coli) by using a McFarland densitometer (Biomerieux Biotechnology, UK). Using a sterile swab, the saline suspension was applied to the Mueller–Hinton Agar plate (Oxoid, UK). Antibiotic-containing antimicrobial discs were strewn throughout the
Mueller–Hinton agar surface after it had been inoculated. Overnight, the agar plates were incubated at 37°C. Using sliding calipers and interpretation, the diameters of the inhibited zones, including the diameter of the discs, were measured and observed according to the Clinical Laboratory Standards Institute (Table 2) [37].

2.7. Statistical Analysis. Student’s t-tests were employed using Microsoft Excel software for the percentage of mortalities related to Salmonella infection and the rate of isolation of Salmonellae from internal organs, according to the method described by [38].

3. Results

3.1. Clinical Signs, Incidence, and Mortalities of Salmonella spp. Samples were collected from 52 broiler chicken farms from the study regions, and clinical symptoms of Salmonella infection were gathered at the time of sampling. The symptoms, which included diarrhea, dehydration, decreased body weight gain, lameness, and significant mortalities, were primarily seen in one-week-old broiler chicks. Hepatitis, hepatomegaly with necrotic foci, arthritis, typhlitis, omphalitis, myocarditis, and pneumonia were the predominant postmortem pathologies. However, the symptoms were less severe in older birds at the 6th week of age.

Out of 832 clinical samples collected from 52 broiler flocks from different organs (liver, intestinal content, spleen, and gallbladder), 19 (2.28%) putative Salmonella spp. were isolated from individual birds (one isolate per bird) (Table 3).

Of all the 26 surveyed one-week-old farms, 11 (42.31%) and 8/26 (30.77%) of the six-week-old broiler chicken farms had Salmonella infection. In the first-week-old birds, Salmonella infection caused a significantly higher (P < 0.01) mortality rate in the Salmonella-positive flocks (9.64% ± 1.72) compared to the negative flocks (2.5% ± 0.99). However, the mortality rates of the infected and uninfected 6-week-old flocks did not significantly differ (P = 0.15). The rates of isolation of Salmonellae from the liver 7/208 (3.6%) and gallbladder 6/208 (2.88%) were significantly (P < 0.05) higher than those isolated from the spleen and intestinal content, with an isolation rate of 3/208 (1.44%) for both of them (Table 3).

3.2. Molecular Identification of Salmonella Isolates. The isolates were confidently identified as Salmonella spp. by amplification of the ompC gene (Figure 1). The PCR con- firmed 19 of the Salmonella isolates that were identified phenotypically and biochemically.

3.3. Results of Serological Identification of Salmonella Isolates. The isolated Salmonellae (n = 19) were serotyped. Our finding showed that S. enteritidis 9 (47.37%) with O antigen 1,9,12 and H antigen phase one g, m: S. shangani 6 (31.58%) with O antigen 3,10,15 and H antigen, phase one d, and phase two 1, 5. S. gueuletapee 2 (10.53%) with O antigen 9,12, and H antigen phase 1 g,m,s; S. II (salamae) 1 (5.26%) with O antigen 6,8 and H antigen phase one g,s,t; and H antigen phase two e,n,x; and untypable Salmonella 1 (5.26%) (Table 4).

3.4. Antimicrobial Resistance Profiles. Salmonella spp. resistance to β-lactamase ampicillin was 100% (19/19), ciprofloxacin 0% (0/19), erythromycin 100% (19/19), chloramphenicol 0% (0/19), streptomycin 10.53% (2/19), gentamicin 10.53% (221), doxycycline 15.79% (3/19), levofloxacin 0% (0/19), lincomycin 26.32% (5/19) resistant, and 73.68% (14/19) intermediate (Table 5).

3.5. Molecular Detection of Antimicrobial Resistant Associated Genes. All the phenotypically resistant Salmonella isolates against ampicillin, harbored blaTEM, but 18/19 of them carried blaSHV, (Table 4 and Figure 1). Erythromycin and lincomycin-resistant strains harbored ermB 6/19 (31.58%), ereA 2/19 (10.53%), and mphpA 19/19 (100%), respectively, as shown in Table 5 and Figure 2.

4. Discussion

Salmonella species are members of the Enterobacteriaceae family. They are nonspore-forming, facultatively anaerobic, and Gram-negative rods [8]. They pose a significant challenge in our lives nowadays. Salmonella spp. can be found in all poultry products that are consumed by humans, including meat and eggs. However, it can contaminate other food products and infect humans, so it is considered a health-threatening organism [39]. It is responsible for a variety of poultry diseases, including fowl typhoid, pullorum, and paratyphoid diseases. Our results showed that the clinical signs of paratyphoid Salmonellae including, S. enteritidis, S. typhimurium, S. shangani, S. gueuletapee, and S. II salamae, were more severe in young birds than in older ones. This may be due to a deficiency of beneficial microflora in the intestine of young chicks obtained from hatcheries, which makes them susceptible to infection with Salmonella. These results were consistent with [14]. In this study, 832 samples were collected from 52 poultry flocks, and we found that 19 (2.28%) of them were positive for Salmonella spp., and the young age was more affected by the disease than the old age, as the clinical signs and mortalities were higher at the young age than others. The isolation of Salmonella from the liver (3.36%) and gallbladder (2.88%) was significantly (P < 0.05) higher compared to that of the spleen and intestinal content (1.44%). These findings could be explained by the high invasive ability of these motile Salmonellae. The results found in this study were close to those of El-Sharkawy et al. [16]. Our results indicated that the isolates were serotyped as 9 (47.37%) S. enteritidis O 1,9,12, ad monophasic H: g: m: -, 6 (31.58%) S. shangani 2, (10.53%) S. gueuletapee 1, (5.26%) S. II (salamae) and 1 (5.26%) untypable. Our results were in the same line as described by the authors of [40]. In this study, Salmonella spp. can be considered a major pathogen and an important hazard for the poultry industry, particularly young broilers due to the
### Table 2: Breakpoint values of each antimicrobial agent according to [36].

<table>
<thead>
<tr>
<th>Antimicrobial agent(s) tested</th>
<th>Disc concentration</th>
<th>Resistant ≤ mm</th>
<th>Salmonella isolates</th>
<th>Intermediate (mm)</th>
<th>Sensitive ≥ mm</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ampicillin (AM)</td>
<td>10 μg</td>
<td>13</td>
<td>14:16</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>Ciprofloxacin (CIP)</td>
<td>5 μg</td>
<td>15</td>
<td>16:20</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td>Chloramphenicol (C)</td>
<td>30 μg</td>
<td>12</td>
<td>13:17</td>
<td>18</td>
<td></td>
</tr>
<tr>
<td>Streptomycin (STR)</td>
<td>10 μg</td>
<td>11</td>
<td>12:14</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>Gentamycin (CN)</td>
<td>10 μg</td>
<td>12</td>
<td>13:14</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>Erythromycin (E)</td>
<td>15 μg</td>
<td>13</td>
<td>14:22</td>
<td>23</td>
<td></td>
</tr>
<tr>
<td>Doxycycline (Do)</td>
<td>30 μg</td>
<td>10</td>
<td>11:13</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td>Levofloxacin (LEV)</td>
<td>5 μg</td>
<td>13</td>
<td>14:16</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>Lincomycin (L)</td>
<td>2 μg</td>
<td>9</td>
<td>10:14</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>Norfloxacin (NOR)</td>
<td>10 μg</td>
<td>12</td>
<td>13:16</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>Colistin (CT)</td>
<td>10 μg</td>
<td>10</td>
<td>11:13</td>
<td>14</td>
<td></td>
</tr>
</tbody>
</table>

### Table 3: Putative *Salmonella* spp. that was isolated from the organs of individual chickens.

<table>
<thead>
<tr>
<th>Organ</th>
<th>Liver</th>
<th>Gall bladder</th>
<th>Spleen</th>
<th>Intestine</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of collected samples</td>
<td>208</td>
<td>208</td>
<td>208</td>
<td>208</td>
<td>832</td>
</tr>
<tr>
<td><em>S. enteritides</em></td>
<td>3 (1.44%)</td>
<td>3 (1.44%)</td>
<td>2 (0.96%)</td>
<td>1 (0.48%)</td>
<td>9 (1.08%)</td>
</tr>
<tr>
<td><em>S. shangani</em></td>
<td>2 (0.96%)</td>
<td>2 (0.96%)</td>
<td>1 (0.48%)</td>
<td>1 (0.48%)</td>
<td>6 (0.72%)</td>
</tr>
<tr>
<td><em>S. gueuletapee</em></td>
<td>1 (0.48%)</td>
<td>1 (0.48%)</td>
<td>0</td>
<td>0</td>
<td>2 (0.24%)</td>
</tr>
<tr>
<td><em>S. II (salamae)</em></td>
<td>1 (0.48%)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1 (0.12%)</td>
</tr>
<tr>
<td>Unconformity</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1 (0.48%)</td>
<td>1 (0.12%)</td>
</tr>
<tr>
<td>TOTAL</td>
<td>7 (3.36%)</td>
<td>6 (2.88%)</td>
<td>3 (1.44%)</td>
<td>3 (1.44%)</td>
<td>19 (2.28%)</td>
</tr>
</tbody>
</table>

### Figure 1: *Salmonella* spp. and beta-lactam resistance genes are diagnostic. PCR amplification of the (a) *ompC* (representative), the (b–c) beta-lactam resistance genes *bla*TEM and *bla*SHV are found in *Salmonella* spp. Electrophoresis was carried out on a 1.5% agarose gel. Lane L 100 bp DNA ladder, lane P for positive control, and lane N for negative control. Samples were run on a 1.5% TAE agarose gel.
high mortalities, which showed levels of (9.64% ± 1.72) in one-week-old chicken farms compared to the none infected flocks (2.5% ± 0.99). This may be due to diarrhea dehydration, and severe lesions in the liver and other vital organs caused by infection with these motile and invasive Salmonellae. Our findings also showed that there was no significant difference in mortality rates between infected and uninfected 6-week-old flocks (P = 0.15). Our results were compatible with the study conducted by El-Sharkawy et al. [16].

In the study area, ampicillin and erythromycin are the recommended first-line agents used for the treatment of poultry infections. However, these antibiotics are misused because they are not used in the right doses and durations, given the high burden of developing antimicrobial resistance strains of bacteria against these agents. This study discovered

<table>
<thead>
<tr>
<th>Antibiotic disk sample no.</th>
<th>Serotype CIP NOR C S L E AM CN LEV DO CT ereA ermB mphA blaTEM blaSHV</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>S. S S S I R R R R S I I J J − − + + + +</td>
</tr>
<tr>
<td>2</td>
<td>S. S S S I I R R R S S R R − − + + + +</td>
</tr>
<tr>
<td>3</td>
<td>S. S S S R R R R S S R R + + + + + +</td>
</tr>
<tr>
<td>4</td>
<td>S. S S S S R R R R S I S − + + + + +</td>
</tr>
<tr>
<td>5</td>
<td>S. S S S I R R R S S S R I − − + + + +</td>
</tr>
<tr>
<td>6</td>
<td>S. S S S I I R R R S S I R − − + + + +</td>
</tr>
<tr>
<td>7</td>
<td>S. S S S S I R R R S S S S − − + + + +</td>
</tr>
<tr>
<td>8</td>
<td>S. S S S S I I R R R S S I − − + + + +</td>
</tr>
<tr>
<td>9</td>
<td>S. S S S I S I R R R S S − + + + + +</td>
</tr>
<tr>
<td>10</td>
<td>S. S S S S I R R I S S I R + + + + + +</td>
</tr>
<tr>
<td>11</td>
<td>S. S S S S I R R I S S I S + + + + + +</td>
</tr>
<tr>
<td>12</td>
<td>S. S S S S I R R R S S S S − − + + + +</td>
</tr>
<tr>
<td>13</td>
<td>S. S S S S I R R R S S S S − − + + + +</td>
</tr>
<tr>
<td>14</td>
<td>S. S S S S I R R R S S S I − − + + + +</td>
</tr>
<tr>
<td>15</td>
<td>S. S S s S I R R R S s S S − − + + + +</td>
</tr>
<tr>
<td>16</td>
<td>S. S S s R I R R R S s s R − − + + + +</td>
</tr>
<tr>
<td>17</td>
<td>S. S S s S I R R R S S S S − − + + + +</td>
</tr>
<tr>
<td>18</td>
<td>S. S S S I I R R R S S I S − − + + + +</td>
</tr>
<tr>
<td>19</td>
<td>S. S S S S S I R R R S S S I − − + + + +</td>
</tr>
</tbody>
</table>

Figure 2: Molecular identification of macrolide resistance genes. PCR amplification of (a–c) macrolide resistance genes ermB, ereA, and mphA on an ethidium bromide-stained 1.5% TAE agarose gel. L 100 bp DNA ladder, lane P for positive control, and lane N for negative.
that all detected Salmonella strains were erythromycin- and ampicillin-resistant. Indeed, these antibiotics were the most commonly prescribed without AST. They were also the most easily available on the market without a prescription because they were also very cheap. A similar study revealed that Salmonella spp. was more sensitive to levofloxacin, norfloxacin, ciprofloxacin, chloramphenicol, gentamycin, streptomycin, doxycycline, and colistin, while it was more resistant to ampicillin, erythromycin, and lincomycin [41, 42].

Genes responsible for extended-spectrum β-lactamases (ESBL) production arise by a point mutation at the active site of the earlier β-lactamases and are usually plasmid-mediated. In addition, ESBL-positive Gram-negative bacteria often carry genes that confer high resistance levels to many other antibiotics [43]. This can limit the chemotherapeutic options for ESBL-producing pathogens and facilitate the interspecies and intraspecies dissemination of ESBLs. Therefore, phenotypic detection of ESBLs among Enterobacteriaceae species is important for epidemiological purposes and for limiting the spread of resistance mechanisms.

In this study, ampicillin resistance of Salmonella spp. was dependent on the presence of blTEM 18/19 (94.7%) and bl酰2/19 (100%) of isolated Salmonella. Our finding agreed with the results described in a previously reported study by the authors of [44]. Furthermore, we found that the erythromycin resistance of Salmonella isolates was attributed to ermb 6/19 (31.58%), erA 2/19 (10.53%), and mphA 19/19 (100%), which harbored by resistant Salmonella isolates. Similar results were observed by [44]. The presence of at least one of these resistance mechanisms in all resistant strains may have been responsible for an increasing number of mortalities in one-week-old broiler chicken farms.

5. Conclusion

This study has been focused on giving a clear pattern of the current situation of Salmonella spp. infection in broiler chickens, especially in Egypt. Salmonella spp., including prevalence, serotyping, and an antimicrobial resistance profile. As a result, it is prudent for farmers to develop and share knowledge about salmonellosis diagnosis, treatment, and prevention protocols in order to reduce economic losses and human health risks. Limiting disease burdens would not only improve the well-being of managed broilers but also provide new avenues for achieving the WHO’s global development goal of eliminating poverty and famine.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon reasonable request.

Ethical Approval

All experimental protocols were approved by the Committee on Research, Publication, and Ethics of the Faculty of Veterinary Medicine, Kafrelsheikh University, Egypt, which complies with all relevant Egyptian legislation in research and publications.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors’ Contributions

All authors were involved in the conception of the research idea, the design of the methodology, supervision, data analysis, and interpretation. All authors drafted and prepared the manuscript for publication and revision. All authors read and approved the final manuscript.

Acknowledgments

This work was funded by the authors, who worked at the Kafrelsheikh University

References


