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Prevalence and antibiotic resistance profiles of *Salmonella* spp. in chicken meat

Rabia TELSAÇ, Rabia Mehtap TUNCAY

1Department of Food Hygiene and Technology, Health Sciences Institute, Van Yüzüncü Yıl University, Van, Turkey
2Department of Food Hygiene and Technology, Faculty of Veterinary Medicine, Van Yüzüncü Yıl University, Van, Turkey

**Abstract:** This study aimed to determine the *Salmonella* spp. presence in 100 chicken meat samples (25 breasts and 25 drumsticks with skin and 25 breasts and 25 drumsticks without skin) that were collected between February and April, 2021, in Van, Türkiye and investigate the antibiotic resistance profiles of the isolates. The results of the cultivation and PCR analysis revealed that a total of 17 samples comprising four drumstick with skin (16%), five drumstick without skin and breast without skin (20%), and three breast with skin (12%) samples were positive for *Salmonella* spp. The analysis of 17 chicken meat samples yielded a total of 33 *Salmonella* spp. isolates. *S. Enteritidis* and *S. Typhimurium* were not detected in the serotyping of *Salmonella* isolates using PCR. According to the disc diffusion test, the isolates were resistant to amoxicillin/clavulanic acid and streptomycin (33.33%), ampicillin (36.36%), gentamicin and ceftriaxone (24.24%), chloramphenicol (42.42%), cefotaxime (12.12%), tetracycline (30.30%), and trimethoprim-sulfamethoxazole (81.82%). The isolates were intermediately resistant to streptomycin (18.18%) and tetracycline (9.09%). PCR analysis for the detection of resistance genes revealed that 77.78% and 62.96% of the trimethoprim-sulfamethoxazole-resistant isolates harbored *sul1* and *sul2* genes, respectively. The *pse-1* gene was detected in 66.67% of the ampicillin-resistant isolates while the *tetA* and *tetB* genes were detected in 20% and 10% of the tetracycline-resistant isolates, respectively. The *ant(3’)-la* gene was detected in all (100%) gentamicin-resistant isolates. In conclusion, the absence of *S. Typhimurium* and *S. Enteritidis* in the *Salmonella* spp. isolates from the chicken meats that were obtained from the Van market indicated the compliance of the products with the Turkish Food Codex while the presence of *Salmonella* spp. indicated the poor hygienic quality of the meats. The high antimicrobial resistance of the isolates and the presence of the resistance genes can result in the transmission of resistant species to humans, which may require complicated treatments and cause the emergence of a serious public health issue.

**Key words:** Antibiotic resistance, chicken meat, foodborne pathogen, *Salmonella* spp.

1. Introduction

*Salmonella* spp. is an important pathogen of the family *Enterobacteriaceae* and causes foodborne infections. Among different contaminated foods, poultry meat and eggs are important sources of transmission of *Salmonella* to humans [1,2]. *Salmonella* spp. are gram-negative, facultative anaerobic bacteria that are typically 0.7–1.5 × 2.0–5.0 μm in diameter, rod-shaped, catalase-positive, oxidase-negative, generally motile by means of peritrichous flagella, nonspore-forming, and found in the intestines of animals. They grow at temperatures of 5–45 °C with an optimum temperature of 35–37 °C, and at a values of 0.95 or greater [3–6].

The resistance to basic antibiotics is increasing in *Salmonella* infections, which has become a major health threat worldwide. This can limit the treatment options for people with severe infections. The appropriate use of antibiotics is among the most important ways of slowing the growing rates of resistance to antibiotics. The appropriate use of antibiotics in humans and animals, especially their timely use and use as specified, can help prevent antibiotic resistance and the spread of resistant bacteria [7,8].

The factors such as the excessive and inappropriate use of antimicrobial agents in the production of food animals, the misuse of antibiotics, irregular antibiotic sales, inappropriate antibiotic prescriptions, the presence of mobile genetic elements (plasmid DNA, transposons, and integrons) lead to the exacerbation of antimicrobial resistance and its spread among *Salmonella* species [9–11].

This study aims to detect the presence of *Salmonella* spp. in chicken meats that are sold in the Van market, identify the isolates, and determine their antimicrobial resistance.

2. Materials and methods

2.1. Sample collection

The material of the research was determined by selecting a total of 100 chicken meat samples, 25 breast (skin) and 25...
thigh (skin), 25 breast (skinside), and 25 thigh (skinside). In order to increase the diversity of the samples, taking into account the product information packed using foam board and stretch film were taken at different times (2 for each) from 50 different sales points consisting of markets, butchers, and delicatessens. Samples were collected under aseptic conditions between February and April, 2021, brought to the laboratory in refrigerated thermos boxes set to +4 °C, and analyzed immediately.

2.2. Bacterial strains
Reference *Salmonella enterica* serovar Typhimurium (S. Typhimurium) ATCC 14028 and *Salmonella enterica* serovar Enteritidis (S. Enteritidis) ATCC 13076 that were obtained from the Food Hygiene and Technology Department of the Veterinary Faculty of Van Yüzüncü Yıl University were used as positive control for cultural cultivation and PCR analyses.

2.3. The isolation and identification of *Salmonella* spp.
The TS EN ISO 6579-1 [12] and EN ISO 6579-1:2017/A1 [13] standards were referred to for the detection of *Salmonella* spp. The purity of the suspicious colonies was examined using Gram staining. Additionally isolates were identified by certain biochemical assays (oxidase, urease, sulfur, indole, glucose, lactose, sucrose fermentation, and lysin decarboxylase) and agglutination test using polyvalent *Salmonella* antiserum (Microgen Salmonella Latex M42, England) as *Salmonella* spp. [14]. The agglutination-positive colonies were kept at −20 °C until PCR analysis.

2.4. The confirmation of the presence of *Salmonella* spp. using PCR
A commercial kit (GeneAll, South Korea) was used for the DNA extraction of the *Salmonella* spp. colonies that were isolated from the chicken meats. Following the instructions of the manufacturer, the pure genomic DNA samples were kept at −20 ± 1 °C until analyses. The specific primer pair (5′-AAACGTTGAAAAACTGAGGA-3′; 5′-TCGTCATTCCATTACCTACC-3′) that was developed by Hoofar et al. [15] for the Styinva-JHO-2 gene region was used for the PCR confirmation of the *Salmonella* spp. isolates. For the preparation of the PCR mixture, 12.5 µL mastermix (A.B.T™, Türkiye), 1.5 µL (10 µM) of each primer, and 5 µL genomic DNA were added and the total volume was brought to 25 µL using PCR water. For the PCR-confirmation of the isolates, 1.5 µL of (10 µM) of each primer, and 5 µL genomic DNA were added and the total volume was brought to 25 µL using PCR water. For *S. Enteritidis*, after pre-denaturation at 94 °C for 5 min, a 35-cycle amplification procedure comprising denaturation at 94 °C for 60 s, annealing at 57 °C for 90 s, extension at 72 °C for 60 s, and final extension at 72 °C for 5 min was employed while the same procedure except for the temperature and duration of annealing, which was set to 52 °C for 60 s, was employed for *S. Typhimurium*. Next, gel electrophoresis of the amplicons was carried out as mentioned above.

2.5. The identification of *S. Enteritidis* and *S. Typhimurium* using PCR
The specific primer pairs for Sdf-ENT (5′-AAATGTGTTTATCTGATGCAAGGG-3′; 5′-GTTGTCTCTTCTGTTACGATGCAG-3′, 299 bp) and TYPH (5′-TTGTTACTTTTTTACCCCTGAA-3′; 5′-CCCTGACAGCCGTTAGATAAT-3′, 401 bp) for *S. Enteritidis* [16] and *S. Typhimurium* [17] were used, respectively, for the PCR-confirmation of the isolates. For the preparation of the PCR mixture, 12.5 µL mastermix (A.B.T™, Türkiye), 1.5 µL (10 µM) of each primer, and 5 µL genomic DNA were added and the total volume was brought to 25 µL using PCR water. For *S. Enteritidis*, after pre-denaturation at 94 °C for 5 min, a 35-cycle amplification procedure comprising denaturation at 94 °C for 60 s, annealing at 57 °C for 90 s, extension at 72 °C for 60 s, and final extension at 72 °C for 5 min was employed while the same procedure except for the temperature and duration of annealing, which was set to 52 °C for 60 s, was employed for *S. Typhimurium*. Next, gel electrophoresis of the amplicons was carried out as mentioned above.

2.6. The determination of antibiotic resistance
The antibiotic resistance of the isolates was examined using the disk diffusion method that was proposed by European Committee on Antimicrobial Susceptibility Testing (EUCAST)¹ and Clinical & Laboratory Standards Institute (CLSI) [18]. The amoxicillin/clavulanic acid (AUG), ampicillin (AMP), gentamicin (CN), chloramphenicol (C), cefotaxime (CTX), ceftiraxone (CRO), streptomycin (S), tetracycline (TE), and trimethoprim-sulfamethoxazole (SXT) antibiotic disks were used in the study. As a result of the test, the zone diameters were measured and compared with the values specified in the EUCAST and CLSI to determine the resistance profiles of the isolates (Table 1).

2.7. The genotypic characterization of antibiotic resistance
The presence of the ampicillin, gentamicin, tetracycline, and sulfamethoxazole resistance genes in the *Salmonella* spp. isolates, which were determined to be phenotypically resistant using the disk diffusion method, was examined. For this purpose, the specific primer pairs that were developed by Bacci et al. [19] for ampicillin, gentamicin, and tetracycline and by Zishiri et al. [20] for sulfamethoxazole were used (Table 2). For the preparation of the PCR mixture, 10 µL of mastermix (A.B.T™, Türkiye), 1.5 µL (10 µM) of each primer, and 5 µL of genomic DNA were added and the total volume was brought to 25 µL using PCR water. Table 2 shows the primer pairs used in the PCR analyses.

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The protocol initiated a predenaturation process at 94 °C for 5 min, followed by a 35-cycle amplification procedure comprising denaturation at 94 °C for 60 s, annealing at the appropriate temperatures for each gene (Table 2) for 60 s, extension at 72 °C for 60 s, and final extension at 72 °C for 5 min. The presence of antibiotic resistance genes was determined by the detection of gene-specific bands (Table 2) in the electrophoresis gel.

### 2.8. Statistical analysis
In the study, SPSS 13.0 package program [21] was used to calculate the analysis results as a percentage.

### 3. Results
#### 3.1. Results for the isolation and identification of *Salmonella* spp.
*Salmonella* spp. was isolated from 17 samples (17%) among the 100 samples with or without skin that were procured from the markets, grocery stores, and butchers in Van, Türkiye. *S. Enteritidis* and *S. Typhimurium* were not identified in any sample. Among the samples, four drumstick samples with skin (16%), five drumstick and breast samples without skin (20%), and three breast samples with skin (12%) tested positive for *Salmonella* spp.
Figure 1 shows the PCR results for the positive strains. In the study, a total of 33 Salmonella colonies were isolated from 17 chicken meat samples that were detected as Salmonella spp.-positive.

3.2. The antibiotic resistance of the Salmonella spp. isolates

Table 3 shows the antibiotic resistance and susceptibility of the 33 Salmonella spp. isolates that were obtained from 17 chicken meat samples.

In the study, a total of 33 Salmonella spp. isolates were obtained from 17 chicken meat samples. Of these isolates, 11 were resistant to amoxicillin/clavulanic acid and streptomycin (33.33%), 12 to ampicillin (36.36%), 8 to gentamicin and ceftriaxone (24.24%), 14 to chloramphenicol (42.42%), 4 to cefotaxime (12.12%), 10 to tetracycline (30.30%), and 27 to trimethoprim/sulfamethoxazole (81.82%). Of the isolates, 22 were susceptible to amoxicillin/clavulanic acid (66.67%), 21 to ampicillin (63.64%), 25 to gentamicin (75.76%), 19 to chloramphenicol (57.58%), 29 to cefotaxime (87.88%), 24 to ceftriaxone (72.73%), 11 to streptomycin (33.33%), 14 to tetracycline (42.42%), and 5 to trimethoprim-sulfamethoxazole (15.15%). It was observed that intermediate to streptomycin (18.18%) and tetracycline (9.09%) developed. It was also determined that 16 of the 30 isolates (53.33%) obtained were phenotypically resistant to two or more antibiotics.

3.3. The presence of the antibiotic resistance genes in the Salmonella spp. isolates

Table 3 shows the resistance genes and their distribution in 33 Salmonella spp. isolates with respect to the antibiograms. Table 4 shows the profile of the antibiotic resistance genes in the antibiotic-resistant Salmonella spp. isolates. In addition, Figure 2 shows the agarose gel image of the antibiotic-resistant Salmonella spp. isolates that were identified using PCR.

According to the antibiogram results of 33 Salmonella spp. isolates obtained in the study; The pse-1 gene was detected in 8 of the 12 isolates (66.67%) resistant to ampicillin, the ant(3″)-la gene was detected in all of the 8 isolates (100%) resistant to gentamicin, the tetA gene was detected in 2 of the 10 isolates (20%) resistant to tetracycline, and the tetB gene was detected in one (10%). It was determined that of 27 isolates resistant to trimethoprim-sulfamethoxazole, 21 of them carried the sul1 gene (77.78%) and 17 of them sul2 (62.96%). It was observed that the isolates containing tetA and tetB genes were different from each other, and 16 of the 27 trimethoprim-sulfamethoxazole-resistant isolates carried both sul1 and sul2 genes (59.26%).

4. Discussion and conclusion

The Salmonella serotypes are regarded as important causes of foodborne diseases worldwide. The infection is usually transmitted through the consumption of contaminated waters and foods of animal origin. Fruits and vegetables that are contaminated with human and animal feces can also cause Salmonella outbreaks [22]. The salmonellosis cases in Europe were reported to be the second most common zoonosis in humans in 2018 [23].

A total of 100 chicken meat samples (breasts and drumsticks with and without skin with 25 samples for each) that were procured from the markets, groceries, and butchers in Van were examined, which revealed that 17 of the samples (17%) contained Salmonella spp. This value was lower than those reported by Domínguez et al. [24], Yang et al. [25], Fearnley et al. [26], Süzme [27], Yıldırım et al. [28], Thung et al. [29], Aydin [30], Asal-Ulus [31], and Çadırcı et al. [32] and higher than those reported by Beli et al. [33], Telli [34], and Acaröz et al. [35]. Although it is not in the scope of this study, the differences in the prevalence of Salmonella spp. may be attributed to various factors.
such as sample size, applications during production, the hygiene of the personnel, tools in the sales outlets, and seasonal differences.

According to the Turkish Food Codex Regulation on Microbiological Criteria\(^2\), 25-g raw chicken meat and chicken meat preparations should not contain S. Typhimurium and S. Enteritidis. S. Enteritidis and S. Typhimurium were not identified in any of the 17 Salmonella spp. isolates, thus complying with the regulation.

In another study from Türkiye, S. Enteritidis and S. Typhimurium were not identified on chicken meat [36], chicken meat/internal organs [37], and packaged organic chicken meat [31], which is in agreement with our results. Beli et al. [33] reported S. Enteritidis as the most common serotype but they also reported identifying S. Senftenberg, S. Newport, S. Abony, S. Agona, S. Banana, S. Brancaster, S. Infantis, and S. Oslo. Domínguez et al. [24] found S. Enteritidis, S. Hadar, and serotype 4,12:b:- (II) to be the most common serotypes in chicken meat samples; they also detected S. Mbandaka, S. Derby, S. Virchow, and S. Paratyphi B. Fearnley et al. [26] reported that S. Infantis and S. Typhimurium phage type 135a were the most common Salmonella serotypes in chicken meats. Agbaje et al. [38] found S. Haifa to be the most common serotype in chicken meats, followed by S. Chomedey, S. Saintpaul, S. Kaňji, S. Derby, and S. Blockley. The differences between the present study and others are attributable to the differences in the prevalence of the S. Enteritidis and S. Typhimurium serotypes, region, the number and type of samples, and methods used in bacterial isolation and identification.

According to the report of the Turkish Ministry of Health for the National Salmonella Control Program\(^3\), S. Enteritidis was the most isolated Salmonella species from human clinical samples between 2012 and 2016, followed by S. Typhimurium, S. Infantis, S. Paratyphi B, and S. Kentucky. Moreover, the three most dominant serovars in the poultry slaughterhouse samples (chicken carcasses) were reported to be S. Infantis, S. Kentucky, and S. Enteritidis, respectively. Similarly, S. Infantis was reported to be the most common serovar in chicken and chicken meats by the European Food Safety Authority (EFSA) and European Centre for Disease Prevention and Control (ECDC) [23].

Antimicrobials either kill infectious microorganisms or inhibit their growth. Antibiotics such as ciprofloxacin, azithromycin, and ceftriaxone may be needed for the treatment of the severe infections of Salmonella spp.\(^4\)

The excessive and inappropriate use of antimicrobials in medicinal and veterinary practices can cause antimicrobial resistance, which is an important public health issue. Furthermore, the resistance mechanisms of bacteria are

\(\text{Table 3. The antibiotic resistance, susceptibility of the Salmonella spp. isolates that were obtained from the chicken meat samples and the distribution of the antibiotic resistance genes.}\)

<table>
<thead>
<tr>
<th>Antibiotics</th>
<th>Resistant n (%)</th>
<th>Intermediate n (%)</th>
<th>Susceptible n (%)</th>
<th>Genes</th>
<th>n of genes (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amoxicillin/clavulanic acid</td>
<td>11 (33.33)</td>
<td>-</td>
<td>22 (66.67)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Ampicillin</td>
<td>12 (36.36)</td>
<td>-</td>
<td>21 (63.64)</td>
<td>pse-1</td>
<td>8 (66.67)</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>8 (24.24)</td>
<td>-</td>
<td>25 (75.76)</td>
<td>ant(3&quot;)-la</td>
<td>8 (100)</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>14 (42.42)</td>
<td>-</td>
<td>19 (57.58)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Cefotaxime</td>
<td>4 (12.12)</td>
<td>-</td>
<td>29 (87.88)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Ceftriazone</td>
<td>8 (24.24)</td>
<td>-</td>
<td>24 (72.73)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Streptomycin</td>
<td>11 (33.33)</td>
<td>6 (18.18)</td>
<td>11 (33.33)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>10 (30.30)</td>
<td>3 (9.09)</td>
<td>14 (42.42)</td>
<td>tetA</td>
<td>2 (20)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>tetB</td>
<td>1 (10)</td>
</tr>
<tr>
<td>Trimethoprim-sulfamethoxazole</td>
<td>27 (81.82)</td>
<td>-</td>
<td>5 (15.15)</td>
<td>sul1</td>
<td>21 (77.78)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>sul2</td>
<td>17 (62.96)</td>
</tr>
</tbody>
</table>

n: number of positive isolates


quite important in the development of antimicrobial resistance [22, 39]. For example, the genomic element in *S*. *Typhimurium* that causes resistance to ampicillin, chloramphenicol, streptomycin, sulfonamide, and tetracycline can horizontally spread among other serotypes and gain additional resistance-determining qualities [22].

In the present study, the positive *Salmonella* isolates were resistant to trimethoprim-sulfamethoxazole (81.82%), chloramphenicol (42.42%), ampicillin (36.36%), amoxicillin-clavulanic acid and streptomycin (33.33%), tetracycline (30.30%), gentamicin and ceftriaxone (24.24%), and cefotaxime (12.12%), respectively.

According to the report published by the National *Salmonella* Control Program⁵, among the *Salmonella* isolates from broiler houses, 18.5% were resistant to ampicillin, 4.8% were resistant to gentamicin, 7.7% were resistant to chloramphenicol, 0.9% were resistant to cefotaxime, 33.5% were resistant to streptomycin, 29.4% were resistant to tetracycline, 32.2% were resistant to trimethoprim, and 93.1% were resistant to sulfamethoxazole.

Table 4. The profile of the antibiotic resistance genes in the antibiotic-resistant *Salmonella* spp. isolates (AMP/CN/TE/SXT).

<table>
<thead>
<tr>
<th>Isolates</th>
<th>Antibiotic resistance</th>
<th><em>pse</em>-1</th>
<th><em>ant</em>(3°)-1a</th>
<th><em>tet</em>A</th>
<th><em>tet</em>B</th>
<th>sul1</th>
<th>sul2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isolate 1</td>
<td>TE/SXT</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 2</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 3</td>
<td>AMP/CN/TE/SXT</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 4</td>
<td>AMP/CN/TE/SXT</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 5</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 7</td>
<td>AMP/SXT</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 8</td>
<td>AMP/CN/SXT</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 11</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 12</td>
<td>CN/SXT</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 13</td>
<td>TE/SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 14</td>
<td>TE</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 15</td>
<td>AMP/TE/SXT</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 16</td>
<td>AMP/TE/SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 17</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 18</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Isolate 19</td>
<td>AMP/CN/TE</td>
<td>-</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 20</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 21</td>
<td>SX T</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 22</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 23</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 24</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 25</td>
<td>AMP/TE</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 26</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 27</td>
<td>AMP/SXT</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 28</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Isolate 29</td>
<td>SXT</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
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<td>Isolate 30</td>
<td>AMP/SXT</td>
<td>+</td>
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<tr>
<td>Isolate 31</td>
<td>CN/SXT</td>
<td>-</td>
<td>+</td>
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<tr>
<td>Isolate 32</td>
<td>AMP/CN/TE/SXT</td>
<td>+</td>
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<tr>
<td>Isolate 33</td>
<td>AMP/CN/SXT</td>
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In the present study, 11 Salmonella spp. isolates (33.33%) were determined to be resistant to amoxicillin-clavulanic acid. This is higher than the value reported by Yan et al. [40] (10.5%) but lower than that reported by Yang et al. [25] (36%). In their studies, Chaisatit et al. [41] and Acar [36] did not find any amoxicillin-clavulanic acid-resistant isolates. In the present study, 12 Salmonella spp. isolates (36.36%) were determined to be resistant to ampicillin (%36.36). This is higher than the values reported in some studies [36, 38, 42, 43] but lower than those reported in others [32, 40, 41, 44]. Among the examined Salmonella spp. isolates, eight were resistant to gentamicin (24.24%) in the present study, which differs from the numbers reported in other studies [32, 38, 40-43]. In the present study, 14 Salmonella spp. isolates (42.42%) were resistant to chloramphenicol, which is higher than some values reported by other researchers [36, 38, 42, 43], close to those reported by Yan et al. [40] (42.1%) and Çadırcı et al. [32] (40.78%), and lower than the value reported by Miranda et al. [44] (89.3%). In the present study, four isolates (12.12%) were resistant to cefotaxime. Elkenany et al. [46] reported that 13.13% of the isolates from broiler chicken farms and wholesale points were resistant to cefotaxime while Çadırcı et al. [32] reported the value to be 14.47%. Miranda et al. [44] found no isolates that were resistant to cefotaxime. Eight of the Salmonella spp. isolates were resistant to ceftriaxone (24.24%) while Yang et al. [25] and Sirken et al. [43] found this value to be 19% and 11.9%, respectively. Yan et al. [40] and Asal-Ulus [31] found no isolates that were resistant to ceftriaxone. In the present study, 11 Salmonella spp. isolates (33.33%) were resistant to streptomycin, which is close to the values reported in some studies [38] and different from those in other studies [32, 33, 38, 42, 44]. Ten of the Salmonella spp. isolates (30.30%) were resistant to tetracycline, which is higher than those reported by Chaisatit et al. [41] (21.4%) and Çadırcı et al. [32] (18.42%) and lower than those reported by Van et al. [42] (38.9%), Miranda et al. [44] (78%), Yan et al. [40], Sirken et al. [43] (91.66%), Babacan and Karadeniz [45] (82.85%), and Agbaje et al. [38] (89.3%). In the present study, 27 Salmonella spp. isolates (81.82%) were determined to be resistant to trimethoprim-sulfamethoxazole, which is higher than those reported in some studies [32, 36, 40, 41, 43-45].

The analyses revealed that 8 of the 12 ampicillin-resistant isolates (66.67%) harbored the pse-1 gen, 8 gentamicin-resistant isolates (100%) harbored the ant(3")-la gen, 2 of the 10 tetracycline-resistant isolates (20.00%) harbored the tetA gene while 1 tetracycline-resistant isolate (10.00%) harbored the tetB gen, and 21 of the 27 trimethoprim-sulfamethoxazole-resistant isolates (77.78%) harbored the sul1 gene while 17 (62.96%) harbored the sul2 gene. In other studies, Bacci et al. [19] reported the presence of the pse-1, ant(3")-la, tetA, tetB, and sul1 genes in 2%, 12%, 34%, and 16% of the isolates. Agbaje et al. [38] reported the presence of the tetA gene in all isolates (100%), the presence of the sul1 gene in 78.9% of the isolates, and the presence of the sul2 gene in 10.5%.

Figure 2. The agarose gel image of the antibiotic-resistant Salmonella spp. isolates that were identified using PCR M: 100 bp DNA marker; 1-3: sul1 gene (350 bp); 4-7: sul2 gene (720bp); 7-9: pse-1 gene (419 bp); 10-12: the ant(3")-la gene (526 bp); 13: the tetA gene (210 bp); 14: tetB gene (659 bp).

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of the isolates. Acar [36] found that 9% of the isolates harbored the tetA gene while 81% harbored the sul1 gene. Cortes-Vélez et al. [47] reported that 42.5% of the isolates harbored the tetB gene while 57.4% harbored the sul2 gene. However, Acar [36] did not identify the tetB and sul2 genes in the isolates.

The examination of antibiotic resistance revealed that 30 of the Salmonella spp. isolates (90.90%) were resistant to two or more antibiotics and 20 isolates (66.66%) carried two or more antibiotic resistance genes. Van et al. [42] found that 88.9% of the chicken meat isolates were resistant to at least one antibiotic; Yan et al. [40] reported that 89.47% of the chicken meat isolates were resistant to multiple antibiotics; and Sirken et al. [43] determined that 92.85% of the isolates were resistant to at least 4 different antibiotics. Bacci et al. [19] found that 52.0% of the 50 Salmonella spp. isolates were resistant to multiple antibiotics and 22% of the isolates had multiple resistance genes. In their study in which 166 Salmonella spp. isolates were obtained from chicken meats and offal, Abd-Elghany et al. [48] found that 95.18% of the isolates were resistant to multiple antibiotics. Elkenany et al. [46] reported that all 120 isolates (100%) that were obtained from broiler chicken farms and wholesale points were resistant to multiple antibiotics.

The differences in the values reported in the present study and in other studies are attributable to serotype differences, regional and environmental differences, and the use of uncontrolled and inappropriate doses of antibiotics. Moreover, the lack of antibiotic resistance genes in bacteria that are phenotypically resistant to the same antibiotic indicated possibly different mechanisms of resistance to ampicillin, tetracycline, and sulfamethoxazole (such as integron, plasmid, and transposon).

In conclusion, although the analyses revealed that the Salmonella spp. isolates from the chicken meats in the market did not contain S. Typhimurium or S. Enteritidis, thus conforming to the Turkish Food Codex, the presence of Salmonella spp. indicated poor hygiene quality. Furthermore, the high antimicrobial resistance of the isolates and the presence of resistance genes in some isolates can cause the transmission of resistant species to humans and complicate treatment, which can lead to a great public health issue.

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Conflict of interest
The authors declare that they have no conflicts of interest.

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