Antibiotic Resistance in *Salmonella* from Retail Foods of Animal Origin and Its Association with Disinfectant and Heavy Metal Resistance

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This study aims to demonstrate the antibiotic resistance and its association with disinfectant and heavy metal resistance in 152 *Salmonella* isolates recovered from retail foods of animal origins. Susceptibility testing demonstrated that 92.8% isolates were resistant to at least one antibiotic, and the resistance was highest to oxytetracycline (80.9%), followed by trimethoprim (64.5%), amoxicillin (28.9%), ampicillin (28.3%), levofloxacin (21.7%), ciprofloxacin (16.4%), and gentamicin (10.5%), respectively. The *bla*TEM and *tet*A genes (44.7%) were commonly present. The *qacF* and *qacE*D1 genes were detected in 18.4% and 8.6% of all isolates. The Cu-resistance genes *pco*R, *pco*C, and *pco*A were the most prevalent (20.4–40.8%), followed by Hg-resistance gene *mer*A (17.8%) and As-resistance genes *ars*B (6.6%). The antibiotic resistance was highly associated with disinfectant or certain heavy metal resistance genes. Most notably, the association among Cu-resistance genes (*pco*C, *pco*R), disinfectant resistance genes (*gacF*, *gacED*), and tetracycline and sulfonamide resistance genes (*tet*, *sul*) was significant (*p* < 0.05). Pulsed-field gel electrophoresis revealed that *Salmonella* isolates was associated with supermarkets indicating the possibility of crosscontamination in farms or processing environment. This study indicated that retail meats may be a reservoir for the dissemination of antibiotic-resistant *Salmonella* and using disinfectants for decontamination or metals in livestock may provide a pressure for coselecting strains with acquired resistance to other antimicrobials.

**Keywords:** antibiotic, disinfectant, heavy metal, resistance, *Salmonella*

**Introduction**

*Salmonella* is recognized as a common bacterial cause of foodborne diarrheal illness worldwide.1–3 Every year, ~42,000 cases of salmonellosis are reported through the Centers for Disease Control and Prevention in the United States; these cases have resulted in high morbidity and economic costs.4,5 In China, the increase in consumption of food products of animal origin also increased potential exposure to *Salmonella*.6,7 The genus *Salmonella* encompasses a large taxonomic group with more than 2,600 different serotypes.8 Although all serotypes of *Salmonella* may be regarded as potential human pathogens, the vast majority of infections are caused by a limited number of serotypes, of which *Salmonella* Enteritidis and *Salmonella* Typhimurium are the two most common serotypes associated with gastrointestinal disease in humans.9,10

Approaches to prevent and control salmonellosis in livestock have been dependent on the use of antibiotics for many years. However, numerous antibiotic-resistant bacteria have been reported in different countries.11–13 Most of the antibiotic-resistant *Salmonella* are of zoonotic origin and acquire their resistance in food animal hosts, which might cause human infections through the food chain.14 Therefore, antibiotic resistance in pathogenic bacteria from animals can be a serious threat to public health.15
Disinfectants are extensively used to control infection and/or microbial contamination in food manufacturing facilities and environments. Among the different disinfectants currently available, quaternary ammonium compounds (QACs), such as benzalkonium chloride (BC) and cetlypyridinium chloride (CTPC), are used extensively because these compounds are nonirritating and noncorrosive with little toxicity and high antimicrobial efficacy over a wide pH range. The wide use and misuse of QACs in food environments can impose a selective pressure for bacteria and contribute to the emergence of disinfectant-resistant microbes.

Metal-containing compounds with antimicrobial or growth-promoting activity are also widely used as feed additive in food animals. Copper sulfate and organic arsenicals (e.g., phenylarsonic acid) are agents for therapy and growth, and mercury compounds have been usually used as disinfectants in food animal-producing environment for a number of years. Due to its stable and persistent features, when heavy metals accumulate to critical concentrations, they potentially trigger resistance to emerge within the food animal hosts. The heavy metal resistance genes (HMRGs) have also been identified in different environments. The genes that are responsible for resistance to arsenic (arsA), copper (copB), and zinc (czrC) have been observed in methicillin-resistant *Staphylococcus aureus* isolated from livestock. Meanwhile, the genes czrA and arsB for cobalt and arsenic resistance, respectively, have been found in municipal wastewater treatment plants and associated with antibiotic resistance genes (ARGs). Furthermore, the HMRGs appear to be predominantly plasmid mediated.

Previously studies demonstrated that a relationship between the acquisition of HMRGs and ARGs, and antibiotic resistance may arise through coexistence or crossresistance to metals or coregulation of resistance pathways. The disinfestant resistance genes, as well as HMRGs, are commonly located in mobile genetic elements (MGEs). The widespread use of disinfectants has raised concerns about their possible involvement in the development of antimicrobial resistance, particularly coresistance to antibiotics. Therefore, under the pressure of concomitant use of antibiotics, heavy metals, and disinfectants, the potential coselection of resistance genes and the spread of acquired resistance is enhanced. However, little information was known about the occurrence of disinfectant and heavy metal resistance in *Salmonella* isolated from retail foods of animal origin. The current study investigated the prevalence of antibiotic, disinfectant, and heavy metal resistance in *Salmonella* isolates, determined the associations between antibiotic resistance and the presence of disinfectant (QACs) and/or HMRGs, and explored the genetic relatedness of *Salmonella* from retail foods of animal origin.

**Materials and Methods**

**Sampling**

A total of 327 raw meat samples, including pork (*n* = 137), chicken (*n* = 91), and beef (*n* = 99) were purchased from supermarkets in Sichuan Province between July 2013 and December 2014. The samples were aseptically collected in sterilized plastic bags and kept cold during transport from the supermarket to the laboratory. The tested antibiotics were as follows: amoxicillin (AMX), amoxicillin/clavulanic acid (AMC), ampicillin (AMP), cefiotur (EFT), oxytetracycline (OTC), ciprofloxacin (CIP), levo-floxacin (LEV), trimethoprim (TMP), and gentamicin (GEN), all of which were purchased from Hangzhou Microbial Reagent Co., Ltd. The minimum inhibitory concentrations (MICs) were determined by using the agar dilution method, and breakpoints for antibiotic susceptible and/or resistant were determined as recommended by the Clinical and Laboratory Standards Institute (CLSI). *Escherichia coli* ATCC 25922 and *E. coli* ATCC 35218 were used as the quality control strains. The resistance genes were examined through PCR using specific oligonucleotide primers as described previously. All results were confirmed by at least two independent experiments.
Chemical; ≥98% purity). The MICs of disinfectants were determined using the agar dilution method recommended by the CLSI. The range of concentrations used to determine the MICs of both disinfectants were 0.125 to 1,024 mg/L. E. coli ATCC 10536 was used as the quality control strain. The disinfectants’ resistance genes [sugE(p), qacED1, qacE, qacF, and qacG] were amplified and sequenced as previously described.

Detection of HMRGs

The 17 different HMRGs encoding for 9 heavy metal resistance were detected by PCR based on published methods. The positive controls that carried the resistance genes were confirmed using PCR followed by sequence analysis (Sangon Biotech, Shanghai, China).

Pulsed-field gel electrophoresis

All the isolates were selected for pulsed-field gel electrophoresis (PFGE) analysis using the PulseNet protocol (www.cdc.gov/pulsenet/PDF/ecoli-shigella-salmonella-pfge-protocol-508c.pdf). The XbaI-digested DNA fragments were analyzed using 1% agarose gels and a CHEF MAPPER electrophoresis system (Bio-Rad, Hercules, CA). The electrophoresis conditions were as previously described. Salmonella enterica serovar, Braenderup H9812, was used as a marker. PFGE results were analyzed by BioNumerics software, and banding patterns were compared using Dice coefficients with a 1.5% band position tolerance.

Data analysis

Chi-squared test of independence or Fisher’s exact test was performed to analyze data using SPSS v.12 (SPSS, Inc., 1989–2003). A p-value less than 0.05 was considered statistically significant for comparison.

Results

Prevalence and serotypes of Salmonella

Of the 327 retail meat samples, 46.5% (n = 152) were contaminated with Salmonella. The most common prevalence was observed in pork (n = 75, 54.7%), followed by chicken (n = 43, 47.3%) and beef (n = 34, 34.3%), respectively. Among the 152 Salmonella isolates, 21 Salmonella serotypes were detected. Salmonella Derby was the most prevalent (28.9%, n = 44), followed by Salmonella Typhimurium (15.8%, n = 24), Salmonella Rissen (15.8%, n = 24), Salmonella Enteritidis (9.9%, n = 15), and Salmonella London (5.9%, n = 9). The top five serotypes accounted for more than 75% of the strains.

The distribution of serotypes varied by meat types (Table 1). In chicken, the predominant serotypes were Salmonella Enteritidis (34.9%, n = 15), Salmonella Derby (18.6%, n = 8), and Salmonella Typhimurium (9.3%, n = 4). Six serotypes, including Salmonella Enteritidis, Salmonella Agona, Salmonella Corvallis, Salmonella Hadar, Salmonella Indiana, and Salmonella Kouka, were only isolated from chicken. For pork samples, most isolates were contaminated with Salmonella Derby (32.0%, n = 24), followed by Salmonella Rissen (24.0%, n = 18), and Salmonella Typhimurium (14.7%, n = 11). The Uganda and Waycross serotypes were only detected in pork. In beef samples, the top three serotypes were Salmonella Derby (35.3%, n = 12), Salmonella Typhimurium (26.5%, n = 9), and Salmonella Rissen (8.8%, n = 3), whereas Salmonella Albany and Salmonella Give were only detected in beef.

Phenotype and genotype of antibiotic resistance in Salmonella

In general, 92.8% (n = 141) Salmonella isolates demonstrated resistance to at least one antibiotic and 43.4% (n = 66) were multidrug resistant (MDR, resistance to at least three classes of antibiotics). As shown in Fig. 1, of all the resistant isolates, 80.9% (n = 123) were resistant to OTC, followed by TMP (64.5%, n = 98), AMX (28.9%, n = 44), AMP (28.3%, n = 43), LEV (21.7%, n = 33), CIP (16.4%, n = 25), and GEN (10.5%, n = 16). Moreover, 48 resistance profiles were observed in the resistant isolates, and the top three frequent resistance profiles were OTC (17.7%, n = 25), OTC–TMP (17.7%, n = 25), and AMX–OTC–TMP (11.3%, n = 16). The frequency of antibiotic resistance varied depending on meat types (Fig. 1) and serotypes (Fig. 2). Notably, of the isolates from pork, 97.3% (n = 73) showed resistance to antibiotics, followed by 94.1% (n = 32) in beef, and 83.7% (n = 36) in chicken. The prevalence of MDR Salmonella also was highest in pork (49.3%, n = 37), followed by chicken (44.2%, n = 19) and beef (n = 10, 29.4%). Besides, the prevalence of

Table 1. Serotypes of Salmonella from Different Retail Meats

<table>
<thead>
<tr>
<th>Chicken</th>
<th>% (n)</th>
<th>Pork</th>
<th>% (n)</th>
<th>Beef</th>
<th>% (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salmonella Enteritidis</td>
<td>34.9 (15)</td>
<td>Salmonella Derby</td>
<td>32.0 (24)</td>
<td>Salmonella Derby</td>
<td>35.3 (12)</td>
</tr>
<tr>
<td>Salmonella Derby</td>
<td>18.6 (8)</td>
<td>Salmonella Rissen</td>
<td>24.0 (18)</td>
<td>Salmonella Typhimurium</td>
<td>26.5 (9)</td>
</tr>
<tr>
<td>Salmonella Typhimurium</td>
<td>9.3 (4)</td>
<td>Salmonella Typhimurium</td>
<td>14.7 (11)</td>
<td>Salmonella Rissen</td>
<td>8.8 (3)</td>
</tr>
<tr>
<td>Salmonella Agona</td>
<td>7.0 (3)</td>
<td>Salmonella London</td>
<td>9.3 (7)</td>
<td>Salmonella London</td>
<td>5.9 (2)</td>
</tr>
<tr>
<td>Salmonella Rissen</td>
<td>7.0 (3)</td>
<td>Salmonella Anatum</td>
<td>8.0 (6)</td>
<td>Salmonella Kumus</td>
<td>5.9 (2)</td>
</tr>
<tr>
<td>Salmonella Hadar</td>
<td>4.7 (2)</td>
<td>Salmonella Clackamas</td>
<td>4.0 (3)</td>
<td>Salmonella Clackamas</td>
<td>3.0 (1)</td>
</tr>
<tr>
<td>Salmonella Anatum</td>
<td>2.3 (1)</td>
<td>Salmonella Meleagridis</td>
<td>2.7 (2)</td>
<td>Salmonella Albany</td>
<td>3.0 (1)</td>
</tr>
<tr>
<td>Salmonella Indiana</td>
<td>2.3 (1)</td>
<td>Salmonella Norwich</td>
<td>1.3 (1)</td>
<td>Salmonella Bareilly</td>
<td>3.0 (1)</td>
</tr>
<tr>
<td>Salmonella Kouka</td>
<td>2.3 (1)</td>
<td>Salmonella Bareilly</td>
<td>1.3 (1)</td>
<td>Salmonella Kedougou</td>
<td>3.0 (1)</td>
</tr>
<tr>
<td>Salmonella Meleagridis</td>
<td>2.3 (1)</td>
<td>Salmonella Uganda</td>
<td>1.3 (1)</td>
<td>Salmonella Meleagridis</td>
<td>3.0 (1)</td>
</tr>
<tr>
<td>Salmonella Kedougou</td>
<td>2.3 (1)</td>
<td>Salmonella Waycross</td>
<td>1.3 (1)</td>
<td>Salmonella Give</td>
<td>3.0 (1)</td>
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<tr>
<td>Salmonella Norwich</td>
<td>2.3 (1)</td>
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<tr>
<td>Salmonella Corvallis</td>
<td>2.3 (1)</td>
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<tr>
<td>Salmonella Bareilly</td>
<td>2.3 (1)</td>
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</tbody>
</table>
FIG. 1. Antibiotic resistance of *Salmonella* isolated from different meat types. OTC, oxytetracycline; TMP, trimethoprim; AMX, amoxicillin; AMP, ampicillin; EFT, ceftiofur; AMC, amoxicillin/clavulanic acid; LEV, levofloxacin; CIP, ciprofloxacin; and GEN, gentamicin; MDR, multidrug resistance.

Resistance to OTC and TMP was observed significantly higher in pork isolates than in beef and chicken isolates \((p < 0.001)\), whereas a higher prevalence of resistance to AMP was observed in the isolates from chicken than from pork and beef isolates \((p < 0.001)\). Interestingly, all *Salmonella* Typhimurium \((n = 24)\) were resistant to at least one antibiotic, and high frequency of antibiotic resistance to LEV \((p < 0.001)\) and CIP \((p < 0.05)\) was observed in *Salmonella* London compared with the other serotypes.

As shown in Fig. 3a, the *blaTEM* \((44.7\%, n = 34)\) gene was most common in β-lactam-resistant isolates. Of the aminoglycoside-resistant isolates, the *ant(3’T)-Ia* gene was detected in highest frequency \((50\%, n = 8)\). In tetracycline-resistant isolates, *tetA* \((44.7\%, n = 55)\) was the most prevalent. Notably, the prevalence of *sul1*, *sul2*, and *sul3* were the same \((20.4\%, n = 20)\) in trimethoprim-resistant isolates. Only the *qnrA* gene was detected in 40\% \((n = 14)\) of quinolone-resistant isolates. Moreover, 68 ARGs combinations were observed in *Salmonella*, and the top three frequent resistance gene combinations were *tetA* (5.3\%, \(n = 8)\), *tetC* (4.6\%, \(n = 7)\), *tetG* (3.3\%, \(n = 5)\), and *tetA-tetG* (3.3\%, \(n = 5)\).

The prevalence of ARGs also varied by meat types and serotypes. The tetracycline-resistant genes, *tetA*, *tetG*, and *tetC*, were the most common genes in pork (46.7\%, \(n = 35\)), beef (35.3\%, \(n = 12\)), and chicken (37.3\%, \(n = 16\)) isolates. Among different meat types, the prevalence of trimethoprim resistance genes and aminoglycoside resistance genes in pork isolates was the highest. Among different serotypes, *Salmonella* Rissen contained all ARGs genes tested and the prevalence of *tetA*, *sul1*, *sul3*, *blaCTX-M*, and *ant(3’T)-Ia* were the highest. However, most ARGs were absent in the isolates of *Salmonella* Enteritidis.

**Phenotype and genotype of disinfectant resistance in Salmonella**

Figure 4 showed the distribution of the MICs of disinfectants in *Salmonella* isolates from different retail meats. Our results revealed that the MICs of CTPC were 8 to 256 mg/L and BC were 8 to 128 mg/L. Generally, most *Salmonella* isolates exhibited MICs of 128 mg/L for CTPC \((79.4\%, n = 102)\) and BC \((58.6\%, n = 89)\). The chicken isolates \((90.7\%, n = 39)\) had higher MICs \((128 mg/L)\) for BC than those from the beef \((79.4\%, n = 27)\) and pork \((48.0\%, n = 36)\) isolates \((p < 0.001)\). Meanwhile, 76.0\% \((n = 57)\) of the isolates that originated from pork had higher MICs \((128 mg/L)\) for CTPC than those from the chicken \((53.5\%, n = 23)\) from chicken and the 20.6\% \((n = 9)\) from beef \((p < 0.001)\). The MIC50 values and MIC90 values were the same in the isolates from different meat types \((128 mg/L)\). In addition, the MIC ranges varied in the top five serotypes.

The *qacF* and *qacEAl* gene was detected in 18.4\% \((n = 28)\) and 8.6\% \((n = 13)\) of all the isolates, whereas the *qacE*, *qacG*, and *sugE(p)* genes were not detected in any isolates (Fig. 3b). The *qacF* was found the highest frequency in pork \((24\%, n = 18)\) and *Salmonella* Rissen \((26.1\%, n = 6)\). The *qacEAl* gene was found the highest frequency in chicken \((16.3\%, n = 7)\) and *Salmonella* Rissen \((26.1\%, n = 6)\).

**Prevalence of HMRGs**

Totally, 58.55\% \((n = 89)\) of the isolates carried at least one HMRG. The Cu-resistance genes *pcor*, *pcoC*, and *pcoA* were the most common, accounting for 43.4\% \((n = 66)\), 40.8\% \((n = 62)\), and 20.4\% \((n = 31)\), respectively (Fig. 3c). Besides, 17.8\% \((n = 27)\) and 6.6\% \((n = 10)\) of the isolate...
carried the Hg-resistance gene merA, and As-resistance gene arsB, respectively. A total of 14 gene combinations were found in all isolates. The top three resistance gene combinations were pcoC (n = 14), pcoR (n = 14), and pcoC-pcoR (n = 14) (Supplementary Table S1; Supplementary Data are available online at www.liebertpub.com/mdr).

The distribution of the gene combinations varied by meat types and serotypes. The pork isolates possessed most types of the gene combinations, in which pcoC (14.7%, n = 11) and pcoC-pcoR (13.3%, n = 10) were the main genotypes. The pcoR (11.6%, n = 5) and pcoC-pcoR (7.0%, n = 3) were the top two gene combinations in chicken isolates. The pcoC (14.7%, n = 5) and pcoR-pcoA-pcoC (14.7%, n = 5) were the top two gene combinations in beef isolates. The pcoC and pcoR were found in high prevalence in Salmonella Rissen (75.0%, n = 18). The merA and arsB were found in a frequency of 34.9% (n = 8) in Salmonella Typhimurium, and pcoA was detected in 47.8% (n = 11) of Salmonella.
Typhimurium. In Salmonella Rissen, only Cu-resistance genes were found, and only one isolate of Salmonella Enteritidis had the merA gene.

Association between disinfectant and antibiotic resistance

Most notably, the presence of disinfectant resistance genes was significantly associated with the trimethoprim and the related resistance genes sul (p < 0.05) (Supplementary Table S2). Among the qacF- and qacEA1-positive isolates, 100% (n = 28) and 93.3% (n = 12) of the isolates were resistant to at least one antibiotic, and 64.3% (n = 18) and 46.2% (n = 6) of the isolates were MDR, respectively. All the qacF-positive isolates contained β-lactam resistance genes and 85.7% (n = 24) had trimethoprim resistance genes. Meanwhile, 84.6% (n = 11) and 61.5% (n = 8) of the qacEA1-positive isolates possessed β-lactam and sulfonamide resistance genes, respectively.

Association between HMRGs and antibiotic resistance

In general, we found association between the presence of HMRGs and antibiotic resistance or ARGs (p < 0.05 or <0.001) (Supplementary Table S2). The gene pcoA was significantly associated with antibiotic resistance and the genes, including β-lactam and blatem, tetracycline and tetA, tetB, tetC, and aminoglycosides and ant(3")-Ia. The pcoC gene was significantly associated with the resistance to trimethoprim and sul3, and tetracycline and tetG. The pcoR gene was associated with tetracycline resistance and the genes tetA, tetC, and tetG. Moreover, the association among merA and tetracycline resistance and the gene tetG was significant. No significant association was observed between the presence of arsb and antibiotic resistance.

More particularly, the association among tetracycline resistance genes, disinfectant resistance genes, and Cu-resistance genes pcoC or pcoR, and sulfonamide resistance genes, disinfectant resistance genes, and Cu-resistance genes, pcoC or pcoR, was significant (p < 0.05).

PFGE typing

Up to 41 distinct PFGE clusters (using a cutoff value of 70%) were identified among the 152 Salmonella isolates (Supplementary Fig. S1). The dendrogram showed that isolates of the same serotypes were clustered together, except for a few individual isolates. The most common cluster 21 was comprised of 16 isolates of Salmonella Derby. Similar results were obtained in cluster 9 (Salmonella Typhimurium) and cluster 6 (Salmonella Rissen). PFGE clusters were also associated with supermarkets. In cluster 41, two Salmonella Anatum isolates originated from the same supermarket (WH). Moreover, 75% (n = 12) of the Salmonella Derby isolates (cluster 21) were obtained from the same supermarket located in different areas (including QJ, CJ, JJ, JJ1, and WJ). Similarly, cluster 1, 12, 25, and 37 were clearly associated with the sampling supermarkets regardless of location. In addition, some PFGE clusters were also associated with meat types. For example, PFGE clusters 10, 22, and 40 were comprised of isolates recovering from pork, whereas clusters 1 and 28 were from chicken, and cluster 17 from beef. Thus, PFGE revealed that the Salmonella isolates were associated with the meat types and sampling supermarkets, indicating the possibility of crosscontamination in farms or processing environments. PFGE results also indicated that the resistance genes were widely distributed in isolates with different meat types and serotypes.

Discussion

Generally, Salmonella Derby, Salmonella Typhimurium, and Salmonella Rissen were the most common serotypes in our study, followed by Salmonella Enteritidis and Salmonella London. Salmonella Enteritidis and Salmonella Typhimurium were of the most common serotypes associated with human infections from food of animal origins and have been found among human isolates in Italy, Spain, and United States. Gantzhorn et al. reported that Salmonella Derby and Salmonella Typhimurium were the most prevalent serotypes in Danish pig slaughterhouses. Salmonella Enteritidis and Salmonella London were the common prevalent serotypes in retail meats as well. In our study, Salmonella Enteritidis was only identified with high frequency in chicken, which was also the most prevalent serotype in chicken meat in the Shandong and Shaanxi province, China. Higher carriage of these Salmonella serotypes by animals may contribute to the contamination of retail meats in human food supply.

The increase of antimicrobial resistance in Salmonella from retail meats has become a common problem worldwide. Antibiotic resistance was common among the Salmonella isolates, particularly a high level of resistance to tetracycline (80.9%) and trimethoprim (64.5%). Similarly, the most frequent resistance profile of Salmonella isolated from pork and chicken meats in North Vietnam was tetracycline (58.5%), followed by sulfonamides (58.1%). The Food and Drug Administration (FDA) has confirmed that Salmonella isolated from food animals showed highest resistance to tetracycline and sulfonamides. The globalization of trade in retail meats could allow resistant Salmonella spread to different countries, which might increase the risk of the emergence and accumulation of antibiotic resistance worldwide. The Salmonella isolates from pork in our study showed higher resistance to antibiotics than from beef and chicken. All Salmonella Typhimurium isolates were resistant to at least one antibiotic. The results showed that the frequency of antibiotic resistance may be related with meat types and serotypes.

The blatem, ant(3")-Ia, and tetA genes were the most common in β-lactam-, aminoglycoside-, and tetracycline-resistant genes in our isolates, respectively. A similar result was reported by Yahiaoui et al., in which blatem was the most frequent β-lactam-resistant gene in E. coli. Moreover, a high prevalence of tetA (55.6%), tetB (91.7%), and ant(3")-Ia (67.5%) genes were observed in the S. enterica isolated from chicken and quail carcasses. The distribution of ARGs varied by meat types. The genes tetA, tetG, and tetC were the most common genes in pork, beef, and chicken isolates, respectively. There was a higher prevalence of trimethoprim- and gentamicin-resistant genes found in pork isolates than in chicken and beef isolates. Bacci et al. also observed that a higher percentage of the ant(3")-Ia gene in Salmonella spp. isolated from quail and chicken carcasses than in those isolated from chicken meat, and the
tetA and tetB genes were more frequent in chicken meat and carcasses isolates, respectively.

The majority of the Salmonella isolates showed MICs of 128 mg/L for CTPC (79.4%) and BC (58.6%). Our previous study demonstrated that 67.5% and 52.6% of the E. coli isolated from retail meats exhibited MICs of 4 to 128 and 32 mg/L for CTPC and BC, respectively.61 Moreover, unlike antibiotics and copper in animal feeds were 15.9–2041.8 and undetected–0.3%, 23.4%, and 62.7% were positive for the genes pco, mer, and czc, respectively.65 The Cu-resistance genes potentially contributes to the development and maintenance of resistance to antibiotics and metals Cr and Co. The IncA/C plasmid isolated from Aeromonas salmonicida subsp. salmonicida carried mer and multiple ARGs. The association among Cu-resistant genes (pcoA and pcoR), disinfectant-resistant genes, and tetracycline- and sulfonamide-resistant genes was significant (p < 0.05). Both Hg-resistance genes (merTPCADE) and several antimicrobial-encoding genes (sul1, qacEAI, aadA1, and blaOXA-1) have been identified on plasmid pUO-StVR2 in Salmonella Typhimurium and these are linked with Transposon 21.27 Whole genome sequencing was performed in our study and will confirm the location of these genes in the near future.

Conclusions

In conclusion, this study demonstrated that antimicrobial resistance was common among the Salmonella isolates from retail food of animal origin. Antibiotic, disinfectant, and heavy metal resistance varied by meat types and serotypes. The antibiotic resistance was highly associated with disinfectant or HMRGs. The farms or processing environment may be a major source for crosscontamination with Salmonella. Therefore, the retail meats may be a reservoir for the dissemination of antibiotic-resistant Salmonella and using disinfectants for decontamination or metals in livestock may provide a pressure for coselecting strains with acquired resistance to other antimicrobials.

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Disclosure Statement

No competing financial interests exist.

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