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Research Note

Prevalence and Characteristics of Quinolone Resistance in *Salmonella* Isolated from Retail Foods in Lanzhou, China

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ABSTRACT

The aim of this study was to determinate the prevalence of *Salmonella* in retail foods and its resistance to quinolones in retail foods in Lanzhou, People's Republic of China. In this work, 2,182 food samples, collected from March 2015 to December 2018, were analyzed to detect *Salmonella* and then analyzed for serotype distribution, quinolone resistance, and quinolone-resistant gene detection. The findings demonstrate that the overall prevalence of *Salmonella* in these food categories was low. A total of 41 (1.9%) of 2,182 food samples were found to be positive for *Salmonella*. Ten distinct serovars were identified, and *Salmonella* Derby, *Salmonella* Anatum, and *Salmonella* Enteritidis were the most prevalent serovars. According to the broth microdilution test, the resistance percentages were 90.2% to nalidixic acid, 39.0% to enrofloxacin, 41.5% to ciprofloxacin, 29.3% to ofloxacin, and 26.8% to levofloxacin. Among the quinolone-resistant isolates, 12 strains had a single mutation in *gyrA* at codon 83 (Ser→Phe) or codon 87 (Asp→Asn or Asp→Gly). Five isolates had one *parC* mutation (Ser80→Arg) and one or two *gyrA* hot spot mutations. *qnr* genes were found in seven isolates (five *qnrB* and two *qnrD*), and the *aac(6′)-Ib* gene in seven isolates. Two isolates carry both *qnrB* and *aac(6′)-Ib-cr* genes. Based on these results, a low prevalence of *Salmonella* contamination in retail foods was found, but it might play a potential risk factor in the spread of quinolone-resistant *Salmonella* strains in the Lanzhou region.

HIGHLIGHTS

- *Salmonella* serovars Derby, Anatum, and Enteritidis were most prevalent from retail foods in Lanzhou.
- Certain strains harbored quinolone-resistant genes.
- Those strains may play an important role in disseminating drug resistance.
- Considering these points, those strains may represent a public health risk.

Key words: Plasmid-mediated quinolone resistance; Prevalence; Quinolone resistance–determining region mutation; Resistance; *Salmonella*

Salmonellosis is one of the most widespread foodborne diseases that is a serious public health problem in many parts of the world *(34, 35)*. *Salmonella* is a rod-shaped, gram-negative bacterium belonging to the *Enterobacteriaceae* family. This genus includes more than 2,600 serovars *(18, 45)*. In most cases, the various food sources—particularly foods of animal origin, such as pork, beef, poultry, mutton, egg, and milk—can lead to human infection *(47)*.

Antimicrobial resistance of *Salmonella* is still one of the major global health problems *(14, 15)*. In addition, multidrug resistance to *Salmonella (18, 25)* has rapidly evolved, posing a challenge for chemotherapy treatment and treatment of certain illnesses (e.g., *Salmonella gastroenteritis*) *(28)*. The increasing prevalence of multidrug resistance to *Salmonella* and resistance to clinically important antibiotics has been an emerging problem in the People's Republic of China and other countries *(24)*. Therefore, the severity of multidrug resistance to *Salmonella* is of particular concern *(1, 31)*. Antimicrobial-resistant *Salmonella* emerges from the uncontrolled use of antimicrobial drugs to treat or to prevent diseases and promote growth in large-scale animal production, such as poultry, pigs, sheep, and cattle. These matters have enhanced the need for epidemiological studies describing the prevalence and patterns of resistance in *Salmonella (21, 27)*.

In veterinary and human medicine, quinolones, particularly fluoroquinolones, are generally used for the treatment of multidrug-resistant *Salmonella* because of their spectrum antimicrobial activity in vivo *(33)*. In *Salmonella,* DNA gyrase (*gyrA* and *gyrB*) and topoisomerase IV gene (*parC*

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TABLE 1. *Prevalence of* Salmonella *in food samples collected in Lanzhou, northwest China, in 2015 to 2018*

Food type	No. of positive samples/total no. of samples (%)				
	2015	2016	2017	2018	4-Yr total
Raw meat					
Pork	3/92 (3.3)	2/46 (4.3)	2/63 (3.2)	1/23 (4.3)	8/224 (3.6)
Beef	2/41 (4.8)	2/82 (2.4)	1/30 (3.3)	0/62 (0)	6/215 (2.7)
Mutton	1/47 (2.1)	3/94 (3.2)	2/70 (2.9)	1/24 (4.2)	7/235 (2.9)
Chicken	3/25 (1.2)	5/75 (6.6)	3/100 (3)	1/75 (1.3)	12/275 (4.4)
Cooked meat products					
Roasted meats	1/40 (2.5)	1/39 (2.6)	0/58 (0)	0/29 (0)	2/166 (1.2)
Sauced meats	0/36 (0)	1/70 (1.4)	0/44 (0)	0/33 (0)	1/183 (0.5)
Sausage	0/29 (0)	0/60 (0)	0/56 (0)	0/42 (0)	0/187 (0)
Other products					
Yogurt	0/62 (0)	0/31 (0)	0/62 (0)	0/31 (0)	0/186 (0)
Raw milk	0/80 (0)	0/75 (0)	0/72 (0)	0/66 (0)	0/293 (0)
Egg	1/33 (3)	2/66 (3)	1/66 (1.5)	1/53 (1.9)	5/218 (2.3)
Total	11/485 (2.3)	16/638 (2.5)	9/621 (1.4)	4/438 (0.9)	41/2,182 (1.9)

and *parE*) point mutations are directly related to quinolone resistance. These target genes are called quinolone resistance–determining regions (QRDRs). Various determinants of plasmid-mediated quinolone resistance (PMQR) have been discovered. It is believed that resistance to quinolones is mediated by two mechanisms *(12)*. PMQR has three parts: resistance efflux pump (e.g., *qepA* and *oqxAB*), *qnr* gene families (*qnrA, qnrB, qnrC, qnrD,* and *qnrS*), and the *aac(6′)-Ib-cr* gene (modified aminoglycoside acetyltransferase gene) *(20)*. QRDR mutation isolates and PMQR-positive isolates present a different level of resistance to quinolones. Therefore, we emphasize the importance of studying these genes.

Lanzhou is an economic and political center in Gansu province, located in western China. This area is the core area of "One Belt and One Road" (a national strategy to eliminate trade barriers, establish a free-trade area, and promote investment and trade cooperation between the countries along the Silk Road); thus, it attracts a range of tourists and trading partners from around the world. Better monitoring of public health issues in food production is needed to reduce the high incidence of *Salmonella* isolates in food. There have been several studies on the antimicrobial resistance of foodborne *Salmonella* isolates in China *(5, 10, 21, 27, 48),* but the lack of data on the prevalence of *Salmonella* in the city of Lanzhou led us to undertake this study. Thus, the objective of this study was to determine prevalence and contamination levels, serotype distribution, quinolone resistance, and drug-targeted gene mutations of *Salmonella* in different food products obtained in Lanzhou to obtain data for quantitative risk assessments of *Salmonella* in these foods.

MATERIALS AND METHODS

Specimen collection and isolate identification. From March 2015 to December 2018, 2,182 samples of retail foods were collected monthly from open-air markets and supermarkets in four urban area in Lanzhou city. As shown in Table 1, these retail foods were raw meat (pork, beef, mutton, and chicken), cooked meat products (roasted meats, sauced meats, and sausages), yogurt, raw milk, and eggs. Samples were collected within the framework of the inspection procedures of the food authorities and official control by the health authorities. Each sample was marked, placed in a separate sterile tube, and transported to laboratories immediately in an ice chest.

Isolation of *Salmonella* was performed using standard procedures described in a national standard of the People's Republic of China (GB/T 4789.4-2003) *(29)*. Specific steps were as follows: each sample (25 g of solids and 5 mL of liquid) was placed in a separate sterile shaker flask and washed with 225 mL of buffered peptone water with vigorous shaking for 5 min. The rinse was incubated at 37°C in a water bath with shaking at 200 rpm for 8 h, and then 10 mL of buffered peptone water was added to 100 mL of selenite cystine broth at 37°C for 16 to 24 h. A loop of inoculum from the selenite cystine broth was streaked onto *Salmonella-Shigella* agar or xylose lysine deoxycholate agar (CHROMagar, Shanghai, China) and incubated for 16 to 24 h at 37°C. Presumptive strains were picked from each plate by testing in triple sugar iron and lysine-iron agar slants and incubated for 16 to 24 h at 36°C. Isolates with typical *Salmonella* phenotypes were confirmed using API 20E test strips (bioMerieuxVitek, Marcy l'Etoile, France). *Salmonella* isolates were stored in Luria-Bertani broth containing 10% glycerol at –80°C until used.

Serotyping. All *Salmonella* isolates were serotyped by the slide agglutination method using commercial O and H antisera (Difco, BD, Detroit, MI), according to the manufacturer's instructions.

Antimicrobial susceptibility testing. Antimicrobial susceptibility was evaluated using the broth microdilution method and according to Clinical and Laboratory Standards Institute guidelines *(7)*. As quality control, *Escherichia coli* ATCC 25922 was tested in each run. This test was performed using representatives of the quinolone class for veterinary therapeutic use, such as nalidixic acid (NAL), ciprofloxacin (CIP), enrofloxacin (ENO), ofloxacin (OFL), and levofloxacin (LVX). The isolates were classified as susceptible or resistant according to the interpretative standards recommended by the Clinical and Laboratory Standards Institute *(7)*.

TABLE 2. *Distribution of* Salmonella *serotypes in retail foods*

	No. of positive samples							
Salmonella serotype	Pork	Beef	Mutton	Chicken	Cooked meat products	Yogurt	Egg	Total no. (%)
Typhimurium	1	1	1	2				5 (12.2)
Enteritidis	1	2	1	2			1	7 (17.1)
Derby	2	1	2	2	2		2	11 (26.8)
Agona	1							1 (2.4)
Anatum		1	1	3			2	7 (17.1)
Kentucky				1				1 (2.4)
London			1					1 (2.4)
Senftenberg	3	1			1			5 (12.2)
Heidelberg				1				1 (2.4)
Stanley				1				1 (2.4)
Untypeable			1					1 (2.4)
Total	8	6	7	12	3	0	5	41 (100)

PCR amplification and DNA sequencing. All isolates were analyzed using PCR assays for the QRDRs of *gyrA, gyrB, parC,* and *parE (17, 38, 43, 49)* and PMQR determinants (*qnrA, qnrB, qnrD, qnrS,* and *aac(6′)-Ib-cr*). The primers have been described in previous studies *(11, 32, 38, 43, 47)*. To prepare genomic DNA, the bacterial suspension was collected and heated at 100°C for 10 min and then incubated on ice for 10 min. The samples were then centrifuged (Thermo Pico17, Thermo Scientific, Waltham, MA) at 13,800 × *g* for 5 min. The supernatants were collected and stored at 4°C until further use. The QRDRs genes were amplified by PCR under the following cycling conditions: 5 min for predenaturation at 95°C, followed by 35 cycles of 30 s at 95°C, 30 s at an annealing temperature of 56°C, a 30-s extension at 72°C, and a final extension step of 10 min at 72°C. The PMQR genes were amplified by PCR performed under the following conditions: one cycle of predenaturation at 95°C for 5 min, followed by 35 cycles at 95°C for 30 s; annealing at 54°C for *qnrA* and *qnrB*; annealing at 56°C for *qnrD* and *qnrS* and at 56°C for *aac(6′)-Ib-cr* for 30 s; an extension at 72°C for 30 s; and a final extension at 72°C for 10 min. All PCR products were sequenced by the Nanjing Genscript Biology Co. Sequence data were then analyzed by DNA Star, and the sequences were compared with reference sequences from the National Center for Biotechnology Information's GenBank.

Statistical analysis. The chi-square test was used for data analysis using SPSS software (SPSS Inc., Chicago, IL), and a P value less than 0.05 was considered significant.

RESULTS

Prevalence and serotyping of *Salmonella* in retail food products. Table 1 shows the prevalence of *Salmonella* in various food categories in Lanzhou from March 2015 to December 2018. A total of 2,182 food samples were taken from the Lanzhou food industry and at the retail level. During this 4-year period, 41 (1.9%) of 2,182 food samples were found to be positive for *Salmonella*. The annual overall prevalence of *Salmonella*-positive food samples differed significantly ($P < 0.05$) between years compared with 2018, varying between 0.9 and 2.5% yearly. The overall 4-year prevalence of *Salmonella* in raw meat products was 3.5% in the 949 investigated food samples and 0.5% in the 536 analyzed cooked meat samples. *Salmonella* was isolated from raw eggs (positive investigated samples, 2.3%), raw pork (3.6%), raw beef (2.7%), raw mutton (2.9%), raw chicken (4.4%), roasted meats (1.2%), and sauced meats (0.5%). All sausage, yogurt, and raw milk were *Salmonella* negative from 2015 to 2018. In short, in some single years (2018), the *Salmonella* prevalence was significantly ($P < 0.05$) lower in some food categories than the 4-year mean prevalence in that category (Table 1).

Ten serovars were identified among the 41 isolates, and 1 isolate from the mutton samples was untypeable (Table 2). The top five serovars were *Salmonella* Derby ($n = 11$, 26.8%), *Salmonella* Anatum ($n = 7$, 17.1%), *Salmonella* Enteritidis ($n = 7$, 17.1%), *Salmonella* Typhimurium ($n = 5$, 12.2%), and *Salmonella* Senftenberg ($n = 5$, 12.2%). *Salmonella* London was detected only in mutton samples. *Salmonella* Heidelberg and *Salmonella* Stanley were detected only in chicken samples. Various serovars were identified in other types of retail foods. In addition, *Salmonella* Derby and *Salmonella* Senftenberg were the serovars isolated from cooked meat samples.

Antimicrobial susceptibility. Among these 41 isolates, 4 isolates were sensitive to all tested quinolones (including NAL), 17 (41.5%) isolates were resistant to CIP, 16 (39.0%) isolates were resistant to ENO, 12 (29.3%) isolates were resistant to OFL, and 11 (26.8%) isolates were resistant to LVX in the broth microdilution test. A total of 37 (90.2%) isolates were resistant to NAL (data not shown). The broth microdilution test identified 58.5% (24 of 41) of isolates with decreased susceptibility to CIP (MICs between 0.125 and 0.5 mg/mL), 60.9% (25 of 41) with decreased susceptibility to ENO, 70.7% (29 of 41) with decreased susceptibility to OFL, and 73.2% (30 of 41) with decreased susceptibility to LVX (MICs between 0.25 and 1 mg/mL). The resistance profile obtained with the microdilution test showed that 11 (26.8%) isolates were resistant to all tested quinolones, 4 (9.7%) were resistant to CIP and NAL, 4

TABLE 3. *Distribution of PMQR genes and mutations in* gyrA, gyrB, parC, *and* parE *genes in* Salmonella *isolates recovered from retail foods with quinolone-resistant characteristics*[a]

Strain	Source	*Salmonella* serotype	QRDR mutation				PMQR	Resistance profile (MIC)
			gyrA	*gyrB*	*parC*	*parE*		
LZS003	Pork	Typhimurium	*D87N*	WT	WT	WT	*aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL
LZS011	Pork	Enteritidis	*D87N*	WT	WT	WT	*aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL
LZS023	Pork	Derby	WT	WT	WT	WT		CIP NAL
LZS025	Pork	Senftenberg	WT	WT	WT	WT	*qnrD*	CIP NAL ENO
LZS029	Beef	Enteritidis	WT	WT	WT	WT		NAL ENO
LZS033	Beef	Typhimurium	*D87G*	WT	WT	WT		CIP NAL
LZS035	Mutton	Typhimurium	*D87N*	WT	*S80R*	WT	*aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL
LZS099	Mutton	Derby	WT	WT	WT	WT		NAL ENO
LZS102	Mutton	Enteritidis	WT	WT	WT	WT		CIP NAL ENO
LZS103	Chicken	Kentucky	WT	WT	WT	WT		NAL ENO
LZS179	Chicken	Derby	*D87N*	WT	WT	WT	*qnrB*	CIP NAL ENO LVX OFL
LZS199	Chicken	Typhimurium	*S83F/D87N*	WT	*S80R*	WT	*qnrB/aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL
LZS204	Chicken	Typhimurium	*D87G*	WT	*S80R*	WT	*qnrD*	CIP NAL ENO LVX OFL
LZS211	Chicken	Anatum	WT	WT	WT	WT		CIP NAL
LZS214	Chicken	Enteritidis	*S83F*	WT	*S80R*	WT	*aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL
LZS217	Chicken	Enteritidis	*D87N*	WT	WT	WT	*qnrB*	CIP NAL ENO LVX OFL
LZS219	Chicken	Heidelberg	WT	WT	WT	WT		NAL ENO
LZS220	Chicken	Derby	*D87N*	WT	WT	WT	*qnrB*	CIP NAL ENO LVX OFL
LZS222	Egg	Enteritidis	*S83F/D87N*	WT	*S80R*	WT	*qnrB/aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL
LZS230	Egg	Anatum	WT	WT	WT	WT		CIP NAL
LZS233	Egg	Derby	*D87N*	WT	WT	WT	*aac(6′)-Ib-cr*	CIP NAL ENO LVX OFL

[a] QRDR, quinolone resistance–determining regions; PMQR, plasmid-mediated quinolone resistance; WT, wild type; CIP, ciprofloxacin; NAL, nalidixic acid; ENO, enrofloxacin; LVX, levofloxacin; OFL, ofloxacin.

(9.7%) were resistant to ENO and NAL, 1 (2.4%) was resistant to CIP, ENO, and NAL, and 1 (2.4%) was resistant to CIP, NAL, and OFL (Table 3).

Analysis of QRDR mutation and detection of PMQR. According to antimicrobial susceptibility, 21 isolates of *Salmonella* were selected for detection of the QRDR mutation (*gyrA, gyrB, parC,* and *parE*) and PMQR. The distributions of QRDR gene mutations and PMQR are listed in Table 3. Eight isolates had wild-type *gyrA, gyrB, parC,* and *parE*. Twelve isolates had a single mutation in *gyrA* at codon 83 (Ser→Phe) or codon 87 (Asp→Asn or Asp→Gly). Five isolates had one *parC* mutation (Ser80→Arg) and one or two *gyrA* hot spot mutations (Table 3). None of the mutations presented in the *gyrB* and *parE* genes. The detection of resistance genes showed seven isolates carrying the *aac(6′)-Ib-cr* gene, five carrying the *qnrB* gene, and two carrying the *qnrD* gene. Among these, 11 isolates were resistant to all tested quinolones; 6 strains were recovered from chicken samples, 2 were recovered from egg samples, 2 were recovered from pork samples, and 1 was recovered from mutton samples. The most prevalent *qnr*-positive serovars were *Salmonella* Typhimurium and *Salmonella* Enteritidis. None of the isolates presented the *qnrA, qnrC,* and *qnrE* genes. Seven *gyrA* mutation-positive and *qnr*-positive isolates presented the *aac(6′)-Ib-cr* gene in association (Table 3): three *Salmonella* Typhimurium, three *Salmonella* Enteritidis, and one *Salmonella* Derby.

DISCUSSION

Drug-resistant bacteria isolated from food has been considered a potential source of resistance in human pathogens, particularly *Salmonella*. It is possible for resistant bacteria from animals to be transmitted to a human subject. Surveillance of the resistance rates among foodborne pathogens of animal-based retail foods is clearly important in management and risk assessment.

In the present study, 41 (1.9%) *Salmonella*-positive samples were recovered from 2,182 retail food products in Lanzhou, China. This result was similar to previous reports showing *Salmonella* occurrence of 2.32% in 2000 *(40),* 3.32% in 2001, 3.55% in 2002 *(39),* 2.2% in 2014 *(26),* and 3.5% in 2016 *(47)* but lower than results from retail foods in Shaanxi province (9.6% *(36)*) and cooked meat products in Henan province (9.0% *(48)*). This rate is significantly lower than the prevalence of *Salmonella* in food products reported from other provinces in China, which was 20.9% in Hebei province *(5),* 36.8% in Shaanxi province *(46),* and 27.8% in Sichuan province *(27)*. *Salmonella* in retail food products was at a low or negative level in some areas of China *(6, 42)*. No *Salmonella* was isolated from yogurt, in agreement with previous reports *(45)*.

In this study, 10 serovars were isolated from retail foods, dominated by *Salmonella* Derby (26.8%), *Salmonella* Anatum (17.1%), *Salmonella* Enteritidis (17.1%), *Salmonella* Typhimurium (12.2%), and *Salmonella* Senftenberg (12.2%). Among them, *Salmonella* Enteritidis and *Salmonella* Anatum were the most common serovars isolated from

chicken samples. *Salmonella* Senftenberg was the most common serovar isolated from pork samples, and untypeable serovars were isolated from mutton samples. In China, a previous study reported that *Salmonella* Senftenberg and *Salmonella* Anatum were the common serovar from cooked meat products in Henan province; *Salmonella* Derby and *Salmonella* Enteritidis were also detected *(48)*. Another previous study reported that *Salmonella* Derby, *Salmonella* Meleagridis, *Salmonella* Enteritidis, and *Salmonella* Senftenberg were the dominant serovars from retail foods in China *(47)*. Other countries report *Salmonella* as well. In Thailand, *Salmonella* Enteritidis and *Salmonella* Derby were isolated as common serovars from retail foods *(2)*. In Estonia, only *Salmonella* Enteritidis and *Salmonella* Infantis were isolated as common serovars from retail foods *(22)*. In Myanmar, *Salmonella* Albany, *Salmonella* Kentucky, *Salmonella* Braenderup, and *Salmonella* Indiana were isolated as common serovars from retail foods *(30)*. In Brazil, 26 *Salmonella* serovars were identified. *Salmonella* Typhimurium was the predominant serovar, followed by *Salmonella* Enteritidis and *Salmonella* Muenchen *(33)*. However, *Salmonella* Derby, *Salmonella* Enteritidis, and *Salmonella* Anatum were the commonly identified serovars in the present study. In addition, these common serovars were frequently observed in clinical *Salmonella* in China, suggesting an association between *Salmonella* food poisoning and salmonellosis *(24, 47)*.

In the current study, *Salmonella* isolated from cooked meat showed a lesser degree of quinolone resistance than that from other samples, whereas *Salmonella* isolated from chicken and egg showed a greater degree of quinolone resistance than that from other samples (Table 3). It was observed that 11 isolates—4 *Salmonella* Typhimurium, 3 *Salmonella* Derby, and 4 *Salmonella* Enteritidis isolates—exhibited resistance to CIP, NAL, ENO, LVX, and OFL. These strains are of particular clinical concern, because quinolones are drugs of choice for treating salmonellosis *(10, 44)*. This finding reveals that these strains would not be disrupted by all commonly used antimicrobial agents during therapy, which indicates a potentially serious impact on human health. These findings may not be surprising, Since the 1980s, a large number of quinolones have been used broadly in veterinary medicine in China *(12, 18, 35)*. Previous research showed that *Salmonella* was primary in chickens and has been specifically resistant to quinolones since 2000 *(39)*.

The main mechanisms of quinolone resistance in *Salmonella* have been attributed to several point mutations in the QRDR genes (*gyrA, gyrB, parC,* and *parE*) and the PMQR genes. In *Salmonella,* similar to other bacteria species, the hot spot mutations associated with resistance to quinolones occur in the *gyrA* gene, resulting from substitutions of Ser83 with Tyr, Ala, or Phe and of Asp87 with Tyr, Gly, or Asn *(13)*. For *E. coli (16), Pseudomonas aeruginosa (4), Riemerella anatipestifer (36),* and *Actinobacillus pleuropneumoniae (41),* mutations of QRDR at different sites affect to different levels of resistance to quinolone, and coinstantaneous mutations in *gyrA* and *parC* genes produce high levels of quinolone resistance. In the present study, we found that two isolates had double mutations (Ser83→Phe or Asp87→Asn) in the *gyrA* gene and nine isolates had a single mutation (Asp87→Asn or Asp87→Gly) in the *gyrA* gene. For *parC,* five resistant strains had a mutation at Ser80→Arg, and there are one or two *gyrA* hot spot mutations. In agreement with previous studies, multiple mutants generally had higher MICs than mutants with a single mutation in the QRDR *(3, 9, 12)*.

In many previous studies, the *qnrA, qnrB, qnrS, qnrD,* and *aac(6′)-Ib-cr* PMQR had decreasing or limiting susceptibility to quinolone *(13, 16, 20)*. In this study, we found a high prevalence of isolates carrying PMQR genes (29.2%, 12 of 41). The most prevalent serovars associated with the presence of PMQR genes were *Salmonella* Typhimurium (4 of 12) and *Salmonella* Enteritidis (4 of 12). Two isolates presented an association between *qnrB* and *aac(6′)-Ib-cr* genes. A similar study has been reported by Park et al. *(32)* in the United States. Consistent with these findings, Xu et al. *(44)* investigated *qnr* and *aac(6′)-Ib* genes in *Enterobacter cloacae* in China. Kim et al. *(19)* studied enterobacterium isolated from clinical samples in Korea, and Pribul et al. *(33)* studied *Salmonella* isolates from the food chain in Brazil. The *qnrB, qnrD,* and *aac(6′)-Ib-cr* genes have been reported to be widely distributed among intestinal bacteria. Consequently, all these *Salmonella*-positive retail food products represented a high risk for the consumers *(8, 19)*. Therefore, the Chinese food safety management should implement further surveillance for retail food products. Insights into the resistance mechanism from this study will guide the development of proper therapy and countermeasures *(23)*.

In conclusion, our study is the first report of the prevalence of *Salmonella* in retail food products in Lanzhou city. Diversity was observed in the isolated serotypes, with *Salmonella* Derby, *Salmonella* Anatum, and *Salmonella* Enteritidis as the predominant serotypes. High resistance to quinolone was detected. The quinolone resistance of poultry products is particularly serious, indicating that numerous antimicrobial agents commonly used in chicken are ineffective. We also found that several hot spot mutations associated with resistance to quinolones occur in the *gyrA* and *parC* gene, and a high prevalence of isolates carrying PMQR genes was detected. The increased detection of QRDR mutation and PMQR in *Salmonella*, is a serious problem in public health and must be monitored constantly. This information may provide useful data for the development of public health policies and effective strategies to ensure the security of China's food products.

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