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# Antimicrobial resistance profiles of *Campylobacter jejuni* and *Salmonella* spp. isolated from enteritis patients in Japan

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**Running head:** *Campylobacter* and *Salmonella* from Humans

**ABSTRACT**

Understanding the antimicrobial resistance of *Campylobacter jejuni* and *Salmonella* spp. isolated from patients with enteritis will aid in therapeutic decision-making. This study aimed to characterize *C. jejuni* and *Salmonella* spp. isolates from patients with enteritis. For *C. jejuni*, the resistance rates against ampicillin, tetracycline, and ciprofloxacin were 17.2%, 23.8%, and 46.4%, respectively. All the *C. jejuni* isolates were susceptible to erythromycin, which is recommended as a first-choice antimicrobial if *Campylobacter* enteritis is strongly suspected. *C. jejuni* was classified into 64 sequence types (STs), and the five major STs were ST22, ST354, ST21, ST918, and ST50. The ciprofloxacin-resistance rate of ST22 was 85.7%. For *Salmonella*, the resistance rates against ampicillin, cefotaxime, streptomycin, kanamycin, tetracycline, and nalidixic acid were 14.7%, 2.0%, 57.8%, 10.8%, 16.7%, and 11.8%, respectively. All the *Salmonella* spp. isolates were susceptible to ciprofloxacin. Therefore, fluoroquinolones are the recommended antimicrobials against *Salmonella* enteritis. *S.* Thompson, *S.* Enteritidis, and *S.* Schwarzengrund were the three most prevalent serotypes. The two cefotaxime-resistant isolates were serotyped as *S.* Typhimurium and were found to harbor $bla_{\text{CMY-2}}$. The results of this study would help select antimicrobials for treating patients with *Campylobacter* and *Salmonella* enteritis.

**KEYWORDS:** antimicrobial resistance, *Campylobacter*, enteritis, *Salmonella*

## INTRODUCTION

*Campylobacter* spp. and non-typhoidal *Salmonella* spp. are bacterial pathogens causing foodborne illnesses globally. The World Health Organization has stated that these two genera are among the four key global causative agents of diarrhea [40, 42]. Although several *Campylobacter* spp. have been identified as pathogens in human campylobacteriosis, *Campylobacter jejuni* infections account for more than 80% of human campylobacteriosis [4, 8, 22, 46]. The annual number of food poisoning outbreaks in Japan caused by *Campylobacter* spp. was higher than 200 between 2014 and 2018 [44]. In Japan, chicken and beef are considered major sources of foodborne campylobacteriosis [4, 8]. *Salmonella* spp. are serotyped into more than 2,600 serotypes based on three structures, somatic (O), flagellar, and capsular surface antigens. Four O-serogroups (O:4, O:7, O:8, and O:9) are major contributors to human non-typhoidal salmonellosis [12, 19, 21, 27]. Following the Infectious Agents Surveillance Report (https://kansen-levelmap.mhlw.go.jp/Byogentai/Pdf/data81j.pdf), the top seven frequent *Salmonella* serotypes in patients in 2021 were *S*. Typhimurium, *S*. Schwrzengrund, *S*. Infantis, *S*. Thompson, *S*. Enteritidis, *S*. Braenderup and *S*. Corvallis. Although the annual number of food poisoning outbreaks in Japan caused by *Salmonella* spp. was less than 50 since 2011, the average number of patients per outbreak is 38 [44]. Eggs, vegetables, and chicken are considered major sources of foodborne salmonellosis in Japan [18].

*Campylobacter* and *Salmonella* infections typically cause acute self-limiting enteritis. Although antimicrobial therapy is not recommended in various cases, it may be lifesaving in patients with severe symptoms and health risk groups such as infants, the older population, and immunocompromised patients [16, 40, 42]. Fluoroquinolones,

such as ciprofloxacin and levofloxacin, and third-generation cephalosporins (TGCs), such as cefotaxime and ceftriaxone, have been classified as “critically important antimicrobials for human medicine” by the World Health Organization [41]. These antimicrobials, along with penicillins, tetracyclines, aminoglycosides, sulfonamides, and macrolides, are also used to treat bacterial infections in food-producing animals in Japan [24]. Since numerous Japanese studies have reported multidrug-resistant *C. jejuni* and *Salmonella* spp. isolated from broilers, cattle, and pigs [14, 15, 17, 28, 30, 33], humans can get infected with these multidrug-resistant species by consuming various foods derived from these animals. Furthermore, there are Japanese reports on the isolation of fluoroquinolone-resistant *Campylobacter* spp. and TGC-resistant *Salmonella* spp. from enteritis patients [26, 27]. Therefore, antimicrobial resistance in the two genera is an important issue in the chemotherapeutic treatment of patients with enteritis. This study aimed to determine the antimicrobial resistance profiles of the two genera isolated from patients with enteritis. Moreover, we characterized these isolates genotypically and serologically. The results of this study would help characterize *Campylobacter jejuni* and *Salmonella* spp. isolated from patients with enteritis and select antimicrobials for treating enteritis patients.

## MATERIALS AND METHODS

### *Isolates*

This study used 151 clinical isolates of *C. jejuni* and 102 clinical isolates of *Salmonella* spp. belonging to O:4 (36 isolates), O:7 (40 isolates), O:8 (7 isolates), and O:9 (19 isolates) serogroups. These isolates were obtained from the stool specimens of 253 different patients with enteritis between December 2019 and April 2022 at BML,

109 Inc., in Saitama, Japan. The stool specimens for *C. jejuni* and *Salmonella* spp. were
110 obtained from hospitals in 29 (61.7%) and 24 (51.1%) of the 47 prefectures in Japan,
111 respectively. For the isolation of *C. jejuni*, each specimen was streaked on a modified
112 charcoal cefoperazone deoxycholate agar plates containing a chromogenic substrate
113 (BD™ mCCDA Clear-HT; Nippon Becton Dickenson Company Ltd, Tokyo, Japan) and
114 incubated microaerobically at 42 °C for 48 hr using AnaeroPack-Microaero (Mitsubishi
115 Gas Chemicals, Tokyo, Japan). For the isolation of *Salmonella* spp. each specimen was
116 streaked onto a modified Salmonella–Shigella agar plate (Eiken Chemical Co., Tokyo,
117 Japan) and incubated at 37 °C for 24 hr. In this study, no human participants were
118 directly involved. Hence, clearance of human ethics is not required. We used isolates
119 routinely cultured from clinical specimens from hospitals. At the laboratory, these
120 isolates were collected in Microbank™ vials (Pro-Lab Diagnostics Inc., Round Rock,
121 TX, USA) and stored at −80 °C. To characterize these isolates, *C. jejuni* isolates were
122 grown on brain heart infusion agar containing 5% horse blood (Oxoid Ltd., Hampshire,
123 UK) microaerobically at 42 °C using AnaeroPack-Microaero (Mitsubishi Gas
124 Chemicals), while *Salmonella* spp. isolates were grown on brain heart infusion agar
125 (Oxoid) aerobically at 37 °C.
126 *Antimicrobial susceptibility testing*
127 Antimicrobial susceptibility testing of *C. jejuni* and *Salmonella* spp. isolates
128 was conducted using the broth microdilution method using dried plates (Eiken
129 Chemical). *C. jejuni* ATCC 33560 and *Escherichia coli* ATCC 25922 were used as
130 quality control strains for *C. jejuni* and *Salmonella* spp., respectively.
131 Antimicrobial susceptibility testing of *C. jejuni* isolates was conducted against
132 ampicillin (0.12–256 mg/L), streptomycin (0.12–128 mg/L), tetracycline (0.12–128

mg/L), chloramphenicol (0.12–256 mg/L), nalidixic acid (0.12–128 mg/L), ciprofloxacin (0.03–64 mg/L), erythromycin (0.12–128 mg/L), and gentamicin (0.12–256 mg/L). The breakpoints for ampicillin (32 mg/L), streptomycin (32 mg/L), erythromycin (32 mg/L), tetracycline (16 mg/L), nalidixic acid (32 mg/L), ciprofloxacin (4 mg/L), and chloramphenicol (16 mg/L) were adopted from the Clinical and Laboratory Standards Institute (CLSI) [6] and Japanese Veterinary Antimicrobial Resistance Monitoring (JVARM) system [24]. The breakpoint for gentamicin (2 mg/L) was specified by the Danish Integrated Antimicrobial Resistance Monitoring and Research Programme [9].

Antimicrobial susceptibility testing for *Salmonella* spp. isolates was conducted against ampicillin (1–128 mg/L), cefazolin (1–128 mg/L), cefotaxime (0.5–64 mg/L), streptomycin (1–128 mg/L), kanamycin (1–128 mg/L), tetracycline (0.5–64 mg/L), nalidixic acid (1–128 mg/L), ciprofloxacin (0.03–4 mg/L), colistin (0.12–16 mg/L), chloramphenicol (1–128 mg/L), gentamicin (0.5–64 mg/L), and trimethoprim (0.25–16 mg/L). The breakpoints for ampicillin (32 mg/L), cefazolin (8 mg/L), cefotaxime (4 mg/L), streptomycin (32 mg/L), kanamycin (64 mg/L), tetracycline (16 mg/L), nalidixic acid (32 mg/L), ciprofloxacin (1 mg/L), colistin (4 mg/L), chloramphenicol (32 mg/L), gentamicin (16 mg/L), and trimethoprim (16 mg/L) were adopted from the CLSI [7] and JVARM system [24].

*Multilocus sequence typing of* C. jejuni *isolates*

Multilocus sequence typing of *C. jejuni* isolates was performed following the seven-locus scheme for *Campylobacter*, employing the primer sets and experimental conditions suggested by the *Campylobacter* Multilocus sequence typing (MLST) database (http://pubmlst.org/campylobacter/).

157 *Sequencing of partial* gyrA *genes in ciprofloxacin-resistant* C. jejuni

158 In one *C. jejuni* isolate per sequence type determined by MLST, partial *gyrA*
159 genes of the isolates were amplified using polymerase chain reaction (PCR) [47], and
160 the PCR products were directly sequenced.

161 *Serotyping of* Salmonella *spp. isolates*

162 Somatic antigens of *Salmonella* spp. isolates were confirmed by slide
163 agglutination using O antisera (Denka Co., Tokyo, Japan). *Salmonella* isolates were
164 further tested for flagella antigens via tube agglutination using H antisera (Denka).
165 Serovars were determined based on the combinations of O and H group antigens
166 following the Kauffmann–White scheme [13]. Isolates agglutinated with anti-O:4 and
167 anti-H:i serum but not anti-H:1 or anti-H:2 serum were confirmed as monophasic
168 variants of *S*. Typhimurium using a previously reported PCR method [11].

169 *Determination of antimicrobial resistance genes and sequence types based on MLST in*
170 *cefotaxime-resistant* Salmonella *spp. isolates using whole-genome sequence analysis*

171 DNA was extracted from cefotaxime-resistant strains using the DNeasy®
172 UltraClean® Microbial Kit (Qiagen GmbH, Hilden, Germany). Whole-genome
173 sequence analysis was performed as previously described [34]. Sequencing libraries for
174 each isolate were prepared using the QIAseq FX Library Kit (Qiagen) to obtain paired-
175 end sequences (300 bp × 2) using the Illumina Miseq platform. The draft genome
176 sequence was assembled using A5-miseq with only Illumina short-read data. Gene
177 annotation was performed using DFAST version 1.2.3 with the following databases:
178 DFAST default database [39], ResFinder database [45], and Bacterial Antimicrobial
179 Resistance Reference Gene database (PRJNA313047). MLST was performed using the
180 "mlst" program version 2.16.2 (https://github.com/tseemann/mlst) with the PubMLST

database (https://pubmlst.org/).

## RESULTS

For *C. jejuni*, the resistance rates against ampicillin, streptomycin, tetracycline, nalidixic acid, and ciprofloxacin were 17.2%, 2.6%, 23.8%, 47.0%, and 46.4%, respectively (Table 1). All the *C. jejuni* isolates were susceptible to erythromycin, gentamicin, and chloramphenicol. In addition, *C. jejuni* was classified into 64 sequence types (STs) using MLST (Table 2). The five major STs were ST22 (14 isolates), ST354 (12 isolates), ST21 (9 isolates), ST918 (9 isolates), and ST50 (8 isolates). The ciprofloxacin resistance rates of ST22, ST354, ST21, ST918, and ST50 were 85.7% (12/14), 25.0% (3/12), 100.0% (9/9), 33.3% (3/9), and 0.0% (0/8), respectively. Ciprofloxacin resistance was observed in 32 (50.0%) of these 64 STs. Among the 32 STs, the Thr86Ile substitution (mediated by the C257T mutation in the *gyrA* genes) was detected in 31 STs. The remaining one ST (ST11491) had the Thr86Lys substitution (mediated by the C257A mutation). Moreover. ST8071 and ST10424 had the Asp90Asn substitution (mediated by the G268A mutation) and the Val149Ile substitution (mediated by the G508A mutation), respectively, in addition to the Thr86Ile substitution.

For *Salmonella* spp., the resistance rates against ampicillin, cefazolin, cefotaxime, streptomycin, gentamicin, kanamycin, tetracycline, nalidixic acid, colistin, chloramphenicol, and trimethoprim were 14.7%, 2.0%, 2.0%, 57.8%, 1.0%, 10.8%, 16.7%, 11.8%, 7.8%, 2.9%, and 9.8%, respectively. All the isolates were susceptible to ciprofloxacin. In the O:4 serogroup (36 isolates), *S.* Schwarzengrund was the most prevalent serovar (13 isolates), and nine (69.2%) isolates were resistant to kanamycin (Table 3). The *S.* Typhimurium monophasic variant was the second most prevalent

serovar (nine isolates), and five (55.6%) isolates were resistant to ampicillin and streptomycin. The two cefotaxime-resistant isolates obtained from two different prefectures were serotyped as *S*. Typhimurium, and they harbored the AmpC-type β-lactamase gene of $bla_{\text{CMY-2}}$ (Table 4). These two cefotaxime-resistant isolates also had seven genes encoding resistance to aminoglycoside (*aac(6')-Iaa*, *ant(3'')-Ib*, and *aph(6)-Id*), phenicol (*floR*), quinolone (*qnrB19*), sulfonamide (*sul2*), and tetracycline (*tet*(A)). In the O:7 serogroup (40 isolates), *S*. Thompson was the most prevalent serovar (22 isolates). Among these 40 isolates, 39 (97.5%) did not show multidrug resistance. In the O:8 serogroup (seven isolates), *S*. Manhattan was the most prevalent serovar, and two isolates were resistant to streptomycin and tetracycline. In the O:9 serogroup (19 isolates), *S*. Enteritidis was the most prevalent serovar (15 isolates), and seven (46.7%) isolates were resistant to ampicillin, streptomycin, and nalidixic acid.

## DISCUSSION

In Japan, fluoroquinolones are recommended as first-choice antimicrobials for empiric therapy of patients with diarrhea and *Salmonella* enteritis [16]. Moreover, macrolides are recommended as first-choice antimicrobials if *Campylobacter* enteritis is strongly suspected or patients have been exposed to regions where quinolone-resistant *Campylobacter* spp. is prevalent [16]. Ohishi *et al*. [26] reported that the ciprofloxacin-resistance rate in *C. jejuni* isolated from patients between 2007 and 2014 is 44.3%. Moreover, Yamada *et al*. [43] reported that the ciprofloxacin-resistance rate in *C. jejuni* isolated from patients between 2009 and 2017 was 41.9%, and the Thr86Ile substitution in GyrA was observed in 93.9% of ciprofloxacin-resistant *C. jejuni* isolates. The Thr86Ile point mutation in GyrA has been identified as the predominant mutation and

229 is associated with increased quinolone resistance [20]. In the present study, the
230 ciprofloxacin-resistance rate in *C. jejuni* was 46.4%, and the Thr86Ile substitution in
231 GyrA was observed in 96.9% of ciprofloxacin-resistant *C. jejuni* isolates, suggesting
232 that the fluoroquinolone-resistance rate has consistently been more than 40% in the last
233 decade, and macrolides must ideally be the first-choice antimicrobials if *Campylobacter*
234 enteritis is strongly suspected, given that erythromycin resistance was not observed in
235 *C. jejuni* isolates. The top five STs were ST22, ST354, ST21, ST918, and ST50 in the
236 present study. Among these, ST21 is one of the predominant STs in *C. jejuni* isolated
237 from cattle [33], and the remaining 4 STs are less abundant in *C. jejuni* isolated from
238 cattle and poultry [2, 26, 33]. We reported that seven (77.8%) of the nine ST21 isolates
239 from cattle are resistant to tetracycline, nalidixic acid, and ciprofloxacin [33]. Of the
240 nine ST21 isolates obtained in the present study, six (66.7%) were also resistant to these
241 three antimicrobials. Moreover, we reported that the two most abundant STs in *C. jejuni*
242 isolated from Japanese layer flocks are ST4389 (eight isolates) and ST6704 (seven
243 isolates), and 93.3% (14/15) of them are ampicillin-resistant [32]. In that study, two
244 ST354 and two ST918 isolates were obtained from layer flocks, of which 75.5% (3/4)
245 were susceptible to all the tested antimicrobials. These results suggest that some of the
246 STs adapted to cattle and poultry are likely to be pathogenic to humans, and the
247 causative foods of human *C. jejuni* infection can be identified using a combination of
248 MLST and antimicrobial resistance profiles of *C. jejuni* isolates. Asakura *et al.* [3]
249 reported ST22 as the most prevalent ST in *C. jejuni* isolated from human
250 campylobacteriosis cases in Osaka Prefecture, Japan, between 2010 and 2011. In
251 contrast, ST22 *C. jejuni* is less abundant in cattle and poultry [2, 30, 32, 33]. Thus,
252 humans might exhibit enteritis easily when infected with ST22, compared to that with

253 other STs. This may be the reason ST22 is the predominant ST isolated from stool
254 specimens of campylobacteriosis patients. Moreover, Takahashi *et al*. [38] reported that
255 serotype HS:19 isolates in Japan accounted for 67 out of 102 (65.7%) *C. jejuni* isolates
256 obtained from patients with Guillain-Barré syndrome (GBS), a severe post-infection
257 autoimmune disease. Akase *et al*. [1] reported 98.9% (87/88) of serotype HS:19 isolated
258 from patients with GBS, sporadic diarrheal patients, and poultry meat samples to be
259 ST22. To understand the relationship between ST22 isolates from humans and livestock,
260 further characterization of these ST22 isolates is needed.

261 To the best of our knowledge, there are no reports about the isolation of
262 fluoroquinolone-resistant *Salmonella* spp. from enteritis patients in Japan this decade.
263 In this study, ciprofloxacin resistance was not observed in *Salmonella* isolates.
264 Therefore, fluoroquinolones are the ideal first-choice antimicrobials against *Salmonella*
265 enteritis. In addition, ceftriaxone is recommended as a second-choice antimicrobial for
266 *Salmonella* enteritis [16]. Although the prevalence of TGC-resistant *Salmonella* spp. in
267 chicken products and broilers has increased since 2005 [5, 10, 25, 28], the prevalence
268 has decreased after withdrawing the use of TGC in broiler production in 2012 [5, 35].
269 We recently reported that 1.3% (4/309) of *Salmonella* isolates (three *S*. Infantis and one
270 *S*. Manhattan strains) isolated from chicken products sampled between January 2018
271 and October 2021 were resistant to cefotaxime and harbored $bla_{\text{CMY-2}}$ or $bla_{\text{TEM-52B}}$ [31].
272 In the present study, cefotaxime resistance was very low (2.0%, 2/102), and both the
273 TGC-resistant *Salmonella* isolates were *S*. Typhimurium harboring $bla_{\text{CMY-2}}$. Although
274 TGC-resistant *S*. Typhimurium has never been isolated from broilers, layers, or pigs in
275 Japan [5, 28, 29, 35, 36], it has been isolated from cattle, and all of them have been
276 found to harbor $bla_{\text{CMY-2}}$ [17]. Shimojima *et al*. [37] investigated the presence of

*Salmonella* in 993 imported meat products (281 chicken, 393 pork, and 319 beef products) between 2009 and 2017, but no TGC-resistant *S*. Typhimurium was isolated.

*Salmonella* Thompson, *S*. Schwarzengrund, *S*. Infantis, and *S*. Braenderup were the prevalent serotypes in this study. Most of the *S*. Schwarzengrund serotypes were multidrug resistant; however, *S*. Thompson, *S*. Infantis, and *S*. Braenderup were not. *S*. Schwarzengrund and *S*. Infantis are the two most prevalent serotypes in chicken meat in Japan, and more than 65% of them are multidrug-resistant [23, 31, 37]. *S*. Thompson, *S*. Infatnis, and *S*. Braenderup are the prevalent serotypes in layer breeding chains in Japan, and most of them are not multidrug-resistant [29, 36]. Meanwhile, in beef and pork, *S*. Typhimurium and its monophasic variant are the two most prevalent serotypes, while *S*. Thompson, *S*. Schwarzengrund, *S*. Infantis, and *S*. Braenderup are barely isolated [37].

In conclusion, the characteristics of human *C. jejuni* and *Salmonella* spp. isolates could represent the characteristics of these two bacterial isolates originating from contaminated food. Monitoring the antimicrobial resistance of *C. jejuni* and *Salmonella* spp. isolated from food-producing animals and food would thus aid in the selection of antimicrobials for treating *Campylobacter* and *Salmonella* enteritis patients.

## CONFLICT OF INTEREST

The authors declare no conflict of interest.

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Table 1. Antimicrobial resistance rates of *Campylobacter jejuni* and *Salmonella* spp. isolates.

| Antimicrobial | No. of resistant isolates (%) | |
|---|---|---|
| | *Campylobacter jejuni* | *Salmoella* spp. |
| Ampicillin | 26 (17.2) | 15 (14.7) |
| Cefazolin | NT | 2 (2.0) |
| Cefotaxime | NT | 2 (2.0) |
| Streptomycin | 4 (2.6) | 59 (57.8) |
| Erythromycin | 0 (0.0) | NT |
| Gentamicin | 0 (0.0) | 1 (1.0) |
| Kanamycin | NT | 11 (10.8) |
| Tetracycline | 36 (23.8) | 17 (16.7) |
| Nalidixic acid | 71 (47.0) | 12 (11.8) |
| Ciprofloxacin | 70 (46.4) | 0 (0.0) |
| Colistin | NT | 8 (7.8) |
| Chloramphenicol | 0 (0.0) | 3 (2.9) |
| Trimethoprim | NT | 10 (9.8) |

462 48. NT: not tested.

Table 2. Antimicrobial resistane profiles of 151 *Campylobacter jejuni* isolates.

| CC (No.) | ST | ARP | No. | CC (No.) | ST | ARP | No. |
|---|---|---|---|---|---|---|---|
| 21 (35) | 19 | NA+CPFX | 5 | 354 (17) | 354 | ABPC+NA+CPFX | 1 |
| | 21 | TC+NA+CPFX | 6 | | | TC+NA+CPFX | 1 |
| | | SM+NA+CPFX | 1 | | | NA+CPFX | 1 |
| | | NA+CPFX | 2 | | | ABPC | 1 |
| | 50 | ABPC | 2 | | | susceptible | 8 |
| | | TC | 2 | | 1723 | susceptible | 1 |
| | | susceptible | 4 | | 4091 | susceptible | 1 |
| | 53 | susceptible | 2 | | 5721 | susceptible | 1 |
| | 806 | TC+NA+CPFX | 1 | | 10010 | susceptible | 1 |
| | | TC | 1 | | 10432 | susceptible | 1 |
| | 883 | susceptible | 2 | 443 (6) | 51 | ABPC+NA+CPFX | 1 |
| | 4253 | susceptible | 3 | | 440 | NA+CPFX | 1 |
| | 4526 | TC+NA+CPFX | 2 | | | NA | 1 |
| | 5649 | NA+CPFX | 1 | | | susceptible | 2 |
| | 9776 | NA+CPFX | 1 | | 1904 | ABPC | 1 |
| 22 (14) | 22 | ABPC+NA+CPFX | 2 | 464 (7) | 4106 | TC | 1 |
| | | TC+NA+CPFX | 2 | | 4389 | ABPC | 1 |
| | | NA+CPFX | 8 | | 5731 | susceptible | 1 |
| | | ABPC | 1 | | 6704 | ABPC | 3 |
| | | susceptible | 1 | | 10424 | NA+CPFX | 1 |
| 42 (5) | 42 | TC+NA+CPFX | 1 | 508 (1) | 508 | susceptible | 1 |
| | | susceptible | 1 | 574 (1) | 9996 | susceptible | 1 |
| | 447 | NA+CPFX | 2 | 607 (5) | 607 | NA+CPFX | 3 |
| | 459 | TC+NA+CPFX | 1 | | 4600 | ABPC | 1 |
| 45 (7) | 11 | susceptible | 1 | | 10431 | susceptible | 1 |
| | 45 | ABPC+NA+CPFX | 2 | 658 (4) | 1044 | susceptible | 3 |
| | | TC+NA+CPFX | 2 | | 10443 | susceptible | 1 |
| | | ABPC | 1 | Unassigned (20) | 468 | susceptible | 1 |
| | | susceptible | 1 | | 922 | ABPC+TC+NA+CPFX | 2 |
| 48 (9) | 918 | NA+CPFX | 3 | | | NA+CPFX | 1 |
| | | susceptible | 6 | | 2274 | TC+NA+CPFX | 1 |
| 52 (3) | 52 | NA+CPFX | 2 | | | NA+CPFX | 1 |
| | 10440 | susceptible | 1 | | 2535 | ABPC+NA+CPFX | 1 |
| 61 (5) | 61 | susceptible | 2 | | 4325 | NA+CPFX | 1 |
| | 628 | susceptible | 1 | | | ABPC | 2 |
| | 1244 | TC | 1 | | 4622 | ABPC+TC | 1 |
| | 11491 | TC+NA+CPFX | 1 | | 6609 | TC+SM+NA+CPFX | 1 |
| 257 (4) | 257 | susceptible | 2 | | 8071 | TC+NA+CPFX | 1 |
| | 824 | susceptible | 1 | | | NA+CPFX | 2 |
| | 4022 | ABPC+SM+TC | 1 | | 10006 | NA+CPFX | 1 |
| 283 (3) | 4063 | susceptible | 2 | | 10437 | SM+TC+NA+CPFX | 1 |
| | 10486 | TC+NA+CPFX | 1 | | 11069 | ABPC+TC+NA+CPFX | 1 |
| 353 (5) | 400 | NA+CPFX | 1 | | 11080 | NA+CPFX | 1 |
| | 10425 | TC | 4 | | 11081 | ABPC+NA+CPFX | 1 |

Abbreviations: CC: clonal complex, ST: sequence type, ARP: antimicrobial resistance profile, ABPC: ampicillin, SM: streptomycin, TC: tetracycline, NA: nalidixic acid, CPFX: ciprofloxacin.

Table 3. Antimicrobial resisntace profiles of 102 *Salmonella* isolates.

| O serogroup (No.) | Serovar (No.) | ARP | No. |
|---|---|---|---|
| O:4 (36) | Schwarzengrund (13) | SM+KM+TC+NA+TMP | 1 |
| | | SM+KM+TC+TMP | 2 |
| | | SM+KM+TMP | 2 |
| | | SM+KM+TC | 1 |
| | | SM+TC+TMP | 1 |
| | | KM+TMP | 3 |
| | | Susceptible | 3 |
| | Typhimurium (5) | ABPC+CEZ+CTX+SM+TC+NA+CP | 2 |
| | | SM+GM+KM+TC+TMP | 1 |
| | | SM | 1 |
| | | Susceptible | 1 |
| | Typhimurium monophasic variant (9) | ABPC+SM+KM+TC+CL+CP | 1 |
| | | ABPC+SM+TC | 3 |
| | | ABPC+SM | 1 |
| | | SM+TC | 2 |
| | | SM | 1 |
| | | TC | 1 |
| | Agona (3) | SM | 3 |
| | Saintpoul (4) | SM | 1 |
| | | Susceptible | 3 |
| | Paratyphi B (1) | Susceptible | 1 |
| | Brandenburg (1) | Susceptible | 1 |
| O:7 (40) | Thompson (22) | SM+NA | 1 |
| | | SM | 10 |
| | | Susceptible | 11 |
| | Infantis (7) | SM | 4 |
| | | Susceptible | 3 |
| | Braenderup (7) | SM | 5 |
| | | Susceptible | 2 |
| | Virchow (2) | SM | 2 |
| | Oranienburg (1) | SM | 1 |
| | Montevideo (1) | Susceptible | 1 |
| O:8 (7) | Manhattan (3) | SM+TC | 2 |
| | | Susceptible | 1 |
| | Corvallis (2) | Susceptible | 2 |
| | Bovismorbificans (1) | SM | 1 |
| | Untypable (1) | Susceptible | 1 |
| O:9 (19) | Enteritidis (15) | ABPC+SM+NA+CL | 5 |
| | | ABPC+SM+NA | 2 |
| | | ABPC+NA | 1 |
| | | CL | 2 |
| | | Susceptible | 5 |
| | Panama (3) | SM | 2 |
| | | Susceptible | 1 |
| | Durban (1) | SM | 1 |

Abbreviations: ARP: antimicrobial resistance profile, ABPC: ampicillin, SM: streptomycin, TC: tetracycline, CL: colistin, CP: chloramphenicol, NA: nalidixic acid, TMP: trimetoprim.

Table 4. Antimicrobial resistance genes in cefotaxime-resistant isolates

| Serovar | Isolate | ST | Antimicrobial resistance profile | Antimicrobial resistance genes |
|---|---|---|---|---|
| Typhimurium | 202203 | 19 | ABPC+CEZ+CTX+SM+TC+NA+CP | *aac(6')-Iaa* , *ant(3'')-Ib* , *bla* $_{\text{CMY-2}}$, *aph(6)-Id* , *floR* , *qnrB19* , *sul2* , *tet* (A) |
| Typhimurium | 202204 | 19 | ABPC+CEZ+CTX+SM+TC+NA+CP | *aac(6')-Iaa* , *ant(3'')-Ib* , *bla* $_{\text{CMY-2}}$, *aph(6)-Id* , *floR* , *qnrB19* , *sul2* , *tet* (A) |

467 ST: sequence type.