Original Article

Genetic and Antibiotic Resistance Characteristics of *Campylobacter jejuni* Isolated from Diarrheal Patients, Poultry and Cattle in Shenzhen*

JU Chang Yan[1], ZHANG Mao Jun[2], MA Yan Ping[1], LU Jing Rang[3], YU Mu Hua[1], CHEN Hui[1], LIU Chu Yun[1], GU Yi Xin[2], FU Yan Yan[2], and DUAN Yong Xiang[1,#]

1. Nanshan Center for Disease Control and Prevention, Shenzhen 518054, Guangdong, China; 2. State Key Laboratory of Infectious Disease Prevention and Control, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing 102206, China; 3. ORD, Environmental Protection Agency, Cincinnati, Ohio 45220, United States

Abstract

Objective To investigate genetic and antibiotic resistance characteristics of *Campylobacter jejuni* (*C. jejuni*) isolated from Shenzhen.

Methods Multilocs sequence typing and agar dilution methods were used to define the genotype and antibiotic resistance of *C. jejuni,* respectively.

Results In total, 126 *C. jejuni* strains were isolated. The prevalence of *C. jejuni* was 5.3% in diarrheal patients. The prevalence in poultry meat (36.5%) was higher than that in cattle meat (1.1%). However, the prevalence in poultry cloacal swabs (27.0%) was lower than that in cattle stool (57.3%). Sixty-two sequence types were obtained, among which 27 of the STs and 10 alleles were previously unreported. The most frequently observed clonal complexes were ST-21 (11.9%), ST-22 (10.3%), and ST-403 (7.1%). ST-21, ST-45, ST-354, ST-403, and ST-443 complexes overlapped between isolates from patients and cattle, whereas ST-45 and ST-574 complexes overlapped between isolates from patients and poultry. All *C. jejuni* were resistant to at least one antibiotic. The highest resistance rate was toward ciprofloxacin (89.7%), followed by tetracycline (74.6%), and nalidixic acid (69.0%).

Conclusion This is the first report of the genotypes and antibiotic resistance of *C. jejuni* in Shenzhen. Overlapping clonal complexes were found between isolates from patients and cattle, and between patients and poultry.

Key words: *Campylobacter jejuni;* Multilocus sequence typing; Antibiotic resistance; Poultry; Cattle; Diarrheal patients

Biomed Environ Sci, 2018; 31(8): 579-585 *doi: 10.3967/bes2018.079* *ISSN: 0895-3988*

www.besjournal.com (full text) *CN: 11-2816/Q*

*This work was supported by Sanming Project of Medicine in Shenzhen [SZSM201803081]; Shenzhen Technology and Innovation Plan, China [JCYJ 20140416095154399]; and Nanshan District Technology and Innovation Plan, Shenzhen, China [2016064].

#Correspondence should be addressed to DUAN Yong Xiang, MD, Professor, Tel: 86-755-26410928, E-mail: szduanyx@163.com

Biographical note of the first author: JU Chang Yan, female, born in 1982, MD, majoring in pathogenic microbiology.

INTRODUCTION

Campylobacter jejuni (*C. jejuni*) is one of the major causes of bacterial gastroenteritis in both developed and developing countries[1-3]. People become infected by consuming contaminated food, particularly poultry meat, raw milk, and water[4-7]. In addition to gastrointestinal illness, *C. jejuni* may also lead to autoimmune conditions known as Guillain-Barré syndrome (GBS) and Miller Fisher syndrome[8]. Zhang et al.[9] reported an outbreak caused by *C. jejuni* in Jilin, China during 2007, in which 32 patients with GBS were recorded, indicating that *Campylobacter* is a threat to human health in China.

C. jejuni has a very wide distribution in animals. Poultry is considered as the major reservoir of *Campylobacter*. The prevalence of *C. jejuni* in chicken meat was reported as 13.7% (31/227) in Tianjin[10] and 17.2% (52/302) in central China[11]. In addition, *Campylobacter* can also inhabit cattle, pigs, ducks, dogs, and other wild and domestic animals[12-15], making it challenging to trace the sources and routes of transmission.

Antibiotic resistance of *C. jejuni* is an increasing concern[16]. Infections by antibiotic resistant strains are usually associated with a longer illness duration, a higher risk of invasive disease, and higher healthcare costs[17-19]. In Shanghai (Eastern China), more than 96% of the *Campylobacter* spp. isolates are resistant to quinolones and tetracyclines[20]. In central China, even higher resistance of *C. jejuni* isolates from retail chicken meat has been reported: 100% resistance to ciprofloxacin and 90% resistance to tetracycline[11].

Shenzhen is the fastest-growing major city in China, with a highly concentrated population and high consumption of meat. Hence, studying the genetic and antibiotic resistance characteristics of *C. jejuni* in Shenzhen is important. However, there is little reported data about *C. jejuni* in Shenzhen.

The aim of this study was to characterize the genetic profile and antibiotic resistance of *C. jejuni* isolated from cattle, poultry, and patients with diarrhea in Shenzhen.

METHODS

The study was approved by the institutional review board of the Nanshan Center for Disease Control and Prevention. Written informed consent was obtained from each adult patient or from the children's parents or guardians.

Sample Collection

During March 1 to November 20, 2016, we enrolled patients who were outpatients presenting with acute diarrhea, which was defined as ≥ 3 passages of watery, loose, mucosal, or bloody-stools during a 24 h period. Stool samples from child patients (≤ 5 years old), adolescent patients (5-17 years old), and adult patients (≥ 18 years old) were collected from four medical facilities, designated as Hospital A, B, Health care C, and Maternal and children's hospital D. A total of 437 patients with diarrhea were enrolled, including 173 child patients, 58 adolescent patients, and 206 adult patients. In total, 437 stool samples were collected.

The poultry meat samples were collected from three retail markets (n = 63), and the cattle meat samples were collected from a slaughterhouse (n = 30) and three retail markets (n = 63). The poultry cloacal swabs (n = 74) were collected from a poultry wholesaler, while the cattle stool samples (n = 103) were collected from a cattle farm (n = 64) and a slaughterhouse (n = 39).

For the stool samples, from both patients and cattle, approximately 0.5 g of stool was collected. Both the stool samples and the cloacal swabs were transferred in Cary-Blair medium at 4 °C within 8 h for bacteria isolation. Approximately 200 g of meat samples were collected in a sterile plastic bag, and transported to laboratory at 4 °C within 4 h for isolation.

Culture, Isolation, and Identification

Two *Campylobacter* isolation kits (ZC-CAMPY-001 and ZC-CAMPY-002, Qingdao Sinova Biotechnology Co. Ltd, Qingdao, China) were used to isolate *Campylobacter* from stool and meat samples, respectively[21]. Briefly, the stool or cloacal swab samples were inoculated into enrichment broth. Each meat sample was placed in a sterile plastic bag containing enrichment media. The enrichment broth was then incubated at 42 °C in a microaerophilic atmosphere (5% O_2, 10% CO_2, and 85% N_2) for 48 h. Approximately 300 μL of the enrichment medium was then spotted onto the surface of a membrane filter from the kit, which was pasted onto Karmali and Columbia agar plates. Suspected colonies were picked after incubation at 42 °C for 48 h in a microaerophilic atmosphere. Finally, Gram staining and biochemical tests were conducted. Species identification was performed using PCR, according to a previously described method[22].

Multilocus Sequence Typing

MLST was performed according to the Pubmlst protocol (https://pubmlst.org/campylobacter/info/primers.shtml)[14]. Briefly, genomic DNA was extracted using a commercial kit (QIAamp DNA mini kit, QIAGEN, German), and seven housekeeping genes (*aspA*, *glnA*, *gltA*, *glyA*, *pgm*, *tkt*, and *uncA*) were amplified using PCR. The amplification reactions were performed in a 20 μL mixture containing 10 μL of 2× PCR master (Quanshijin Biotechnology Ltd. Corp., Beijing, China), 0.5 μL of forward and reverse primer, 1 μL of DNA template, and 7.5 μL of pure water. PCR was performed as 1 cycle of 5 min at 94 °C; 35 cycles of 1 min at 94 °C, 2 min at 50 °C, and 1 min at 72 °C; and a final extension of 5 min at 72 °C. After amplification, 2 μL of the PCR product was subjected to electrophoresis through a 1.5% agarose gel. Then the PCR products were the purified and sequenced. The sequence was subjected to a BLAST search against the PubMLST database, after which the allele numbers were assigned and sequence types (ST) and clonal complexes (CC) were determined. Novel alleles and STs were submitted to the PubMLST *C. jejuni/C. coli* databases.

Antibacterial Susceptibility Testing

Commercial kits (Zhongchuang Biotechnology Ltd. Corp., Qingdao, China) were used to determine the minimum inhibition concentration (MIC) of all *C. jejuni* isolates. The agar dilution method was used[21], and the breakpoints used for each antibiotic were those recommended by National Antimicrobial Resistance Monitoring System (NARMS-2014): Erythromycin (≥ 32 μg/mL), azithromycin (≥ 8 μg/mL), nalidixic acid (≥ 64 μg/mL), ciprofloxacin (≥ 4 μg/mL), gentamycin (≥ 8 μg/mL), streptomycin (≥ 16 μg/mL), chloromycetin (≥ 32 μg/mL), florfenicol (≥ 8 μg/mL), tetracycline (≥ 16 μg/mL), telithromycin (≥ 16 μg/mL), and clindamycin (≥ 8 μg/mL).

Briefly, fresh *C. jejuni* colonies were suspended in an NaCl solution (0.9%) to obtain a suspension with 0.5 McFarland turbidity. One hundred microliters of the suspension were diluted in 900 μL NaCl solution (0.9%) resulting in a concentration range of 10^6-10^7 colony forming units (cfu) per mL. Each well was dispensed with 2 μL of the suspension. The plates were incubated at 37 °C for 48 h in microaerophilic atmosphere. The MIC was defined as the lowest concentration of each antibiotic that could prevent visible growth of *C. jejuni*, and the MIC_{50} was defined as the MIC required to inhibit the growth of 50% of the *C. jejuni* isolates. In addition, multi-drug resistance (MDR) was defined as resistance to three or more antibiotics in this study. *C. jejuni* ATCC33560 was used as the control.

Data Analysis

Statistical analysis was carried out using SPSS 16.0 (SPSS Inc., Chicago, IL, USA) and Microsoft Excel 2016. The prevalence and MDR rate of *C. jejuni* isolated from different sources were compared using the Chi-square test (at a confidence level of 95%). The Simpson's index (D), described previously[23], was used to determine the genetic diversity of *C. jejuni* genotypes. MIC_{50} values were calculated using Microsoft Excel 2016.

RESULTS

A total of 126 *C. jejuni* strains were isolated from samples taken in this study. Multilocus sequence typing and antibacterial susceptibility testing were successfully performed in all isolates.

Prevalence of C. jejuni from Poultry, Cattle, and Patients with Diarrhea

The prevalence of *C. jejuni* from the various sources is shown in Table 1. Statistically, the isolation rate from poultry meat was significantly higher than that from cattle meat ($\chi^2 = 36.222$, $P < 0.001$). However, the isolation rate from poultry cloacal swabs was lower than that from cattle stool ($\chi^2 = 15.950$, $P < 0.001$).

The patients with *C. jejuni* ranged in age from 7 months to 43 years old. Three strains were isolated from 7, 8, and 9 month-old infants. The overall prevalence of *C. jejuni* in the patients with diarrhea was 5.3% (23/437). Separately, the prevalence of *C. jejuni* was 4.0% (7/173) in child patients, 6.9% (4/58)

Table 1. Prevalence of *C. jejuni* in Poultry, Cattle, and Diarrheal Patients in Shenzhen

Source	No. of Samples	No. of Isolates	Prevalence of *C. jejuni* (%)
Poultry meat	63	23	36.5
Cattle meat	93	1	1.1
Cattle feces	103	59	57.3
Poultry cloacal swab	74	20	27.0
Patients' feces	437	23	5.3

in adolescent patients, and 5.8% (12/206) in adult patients (≥ 18 years old). No statistically significant difference was found in the prevalence of *C. jejuni* between the different age groups (χ^2 = 0.955, *P* = 0.620).

Multilocus Sequence Typing

We identified 62 STs among the 126 isolates (Table 2). Among them, 27 STs were not reported previously, and 10 novel alleles were found in this study: GlyA734, 735, 736, 737, and 738; pgm894, 896, 897, and 898; and tkt699. Isolates from patients with diarrhea had the highest proportion of new STs (12/23, 52%), followed by those isolated from poultry sources (22/43, 51.0%), and those from cattle sources (7/60, 11.7%).

Eighty-six isolates belonged to 13 clonal complexes, while 40 isolates could not be assigned to any known clonal complex. The most frequently observed clonal complexes were ST-21 (11.9%), ST-22 (10.3%), and ST-403 (7.1%).

Separately, 27 STs were obtained from 43 poultry isolates, and 18 STs were obtained from 60 cattle isolates. The calculated Simpson's index of the STs from the poultry isolates was 0.977, versus 0.912 from the cattle isolates.

Table 2. ST Type of 126 *C. jejuni* Isolates from Shenzhen

Poultry Source			Cattle Source			Patients Source		
ST	Clone Complex	Number of Isolates	ST	Clone Complex	Number of Isolates	ST	Clone Complex	Number of Isolates
464	464	3	19	21	7	51	443	1
2145	574	1	22	22	13	354	354	1
2895	574	2	45	45	1	403	403	2
4324	NA[a]	1	51	443	2	1811	21	1
6493	NA	2	61	61	6	1919	52	1
6607	NA	3	113	460	1	2131	NA	1
6909	574	2	257	257	6	2132	NA	1
6913	464	1	354	354	3	2328	NA	1
6962	NA	1	403	403	5	4265	52	1
7456	NA	1	583	45	3	8003	403	1
7866	NA	1	2089	NA	2	**8880**	574	2
8089	NA	2	5799	443	1	**8901**	52	1
8847	NA	1	6500	21	1	**8904**	45	1
8877[b]	45	2	7469	464	1	**8905**	354	1
8879	NA	2	7695	21	1	**8906**	52	1
8880	574	1	**8896**[*]	NA	2	**8907**[*]	NA	1
8881[*]	NA	1	**8898**	21	4	**8908**	NA	1
8883[*]	NA	2	**8934**	464	1	**8909**	NA	1
8884	NA	4				**8910**	21	1
8886	NA	1				**8911**[*]	362	1
8887[*]	NA	2				**8935**[*]	403	1
8889[*]	NA	2						
8892	NA	1						
8893[*]	NA	1						
8894[*]	45	1						
8895	NA	1						
8936	NA	1						
Total		43			60			23

Note. [a]NA, not assigned; [b]New STs are given in bold; [*]ST contains the new allele unreported previously.

Moreover, ST-21, ST-45, ST-354, ST-403, and ST-443 overlapped between isolates from patients and cattle, while ST-45 and ST-574 overlapped between isolates from patients and poultry. In addition, ST-45 was the only clonal complex found in all three sources.

Antibacterial Susceptibility Testing

The MICs of the quality control strain (*C. jejuni* ATCC 33560) were within the reference quality control range. Overall, all the isolates were resistant to at least one antibiotic. The highest resistance rate was detected for ciprofloxacin (89.7%), followed by tetracycline (74.6%), and nalidixic acid (69.0%). The resistance rates of *C. jejuni* from different sources are shown in Figure 1.

The MIC_{50}s of nalidixic acid and tetracycline to all *C. jejuni* isolates were ≥ 64 μg/mL, while the MIC_{50}s of erythromycin, azithromycin, gentamycin, telithromycin, and clindamycin to all *C. jejuni isolates* were ≤ 2 μg/mL. For the different sources, *C. jejuni* from poultry had higher or equal MIC_{50}s compared with those from patients or cattle against all 11 antibiotics.

For multidrug resistance (MDR), 88.4% of *C. jejuni* isolated from poultry were resistant to four to nine antibiotics. Among them, one strain was resistant to nine antibiotics, including erythromycin, azithromycin, nalidixic acid, ciprofloxacin, gentamycin, streptomycin, chloromycetin, telithromycin, and clindamycin. This strain was isolated from a chicken cloacal swab from a poultry wholesaler. Similarly, 73.9% of isolates from patients with diarrhea were resistant to four to eight antibiotics. The most prevalent resistance pattern was combined nalidixic acid, ciprofloxacin, florfenicol, and tetracycline resistance (30.4%). In particular, 65.2% of isolates from patients were resistant to florfenicol. In contrast, all *C. jejuni* from cattle were resistant to less than five antibiotics. None of the isolates from cattle were resistant to erythromycin, azithromycin, gentamycin, telithromycin, or clindamycin.

Statistically, the MDR rate among the isolates from poultry (97.6%, 42/43) was significantly higher than that from cattle (60.0%, 36/60) ($\chi^2 = 19.343$, $P < 0.001$). No statistical significance was observed between the MDR rate of isolates from poultry and patients (91.3%, 21/23) ($\chi^2 = 1.401$, $P = 0.236$).

DISCUSSION

C. jejuni is one of the major causes of gastroenteritis worldwide. However, there is limited information about the genetic and antibiotic resistance characteristics of *C. jejuni* in Shenzhen, which makes tracking the origin of transmission challenging. In this study, we conducted multilocus sequence typing and antibiotic susceptibility testing for *C. jejuni* from poultry, cattle, and patients with diarrhea in Shenzhen.

Several studies of *Campylobacter* prevalence in children have been conducted previously. For instance, Wang et al.[24] reported no *Campylobacter*

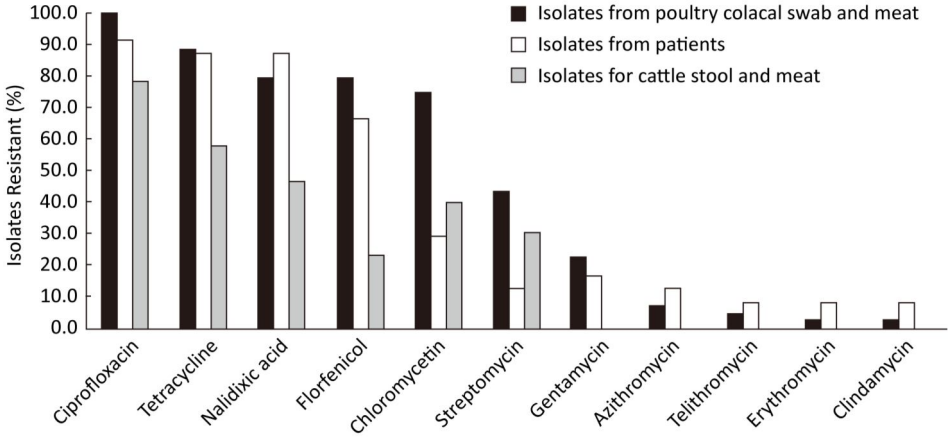

Figure 1. The antibiotic resistance rate of *C. jejuni* isolated from different sources in Shenzhen. The *x*-axis represents the antibiotics. The *y*-axis represents the percentage of resistant isolates. The black area represents the resistance rate of poultry isolates, the white area represents the resistance rate of patient isolates, and the grey area represents the resistance rate of cattle isolates.

infections in patients with diarrhea in Beijing, either in children (under 5 years, 0/1422) or adults (0/1047). Zhu et al.[25] reported that 2.9% of children with diarrhea were infected by *Campylobacter* in Wuhan (Southwest China). Our study revealed a *C. jejuni* prevalence of 4.0% (7/173) in children with diarrhea (≤ 5 years old) and 5.8% (12/206) in adults with diarrhea (≥ 18 years old). The discrepancy in prevalence may be caused by regional differences or the isolation methods that we adopted, which was a standard enhanced filtration based method incorporating a commercial kit.

Poultry are considered as the major reservoir of *Campylobacter* spp. The prevalence of *C. jejuni* in poultry is believed to be higher than that in cattle. However, in the present study, the prevalence of *C. jejuni* in poultry cloacal swabs was only 27.0%, versus 57.3% in cattle feces (Table 1). This unexpected result may have been caused by the sampling method. For poultry, cloacal swabs were collected, whereas feces were collected from cattle. Compared with feces, swabs carry lower sample volume, which may have lead to a lower isolation rate of *C. jejuni* in poultry.

Moreover, in this study, the prevalence of *C. jejuni* in cattle meat (1.1%) was significantly lower than that in poultry meat (36.5%) (Table 1). In addition to the different prevalence of *C. jejuni* in poultry and cattle, fecal contamination during evisceration may have contributed to this discrepancy. Poultry feathers are plucked and then birds are eviscerated. During evisceration, the intestines can rupture, leading to contamination of the skin of the carcass. For cattle, after evisceration, the hide is removed; therefore, contamination of the carcass is less likely. Since the skin on poultry carcasses is retained and the hide of cattle is not, the risk of fecal contamination is higher in poultry than in cattle.

Ma et al.[10] reported that the most prevalent clonal complexes were ST-354 and ST-21 in *C. jejuni* from retail chickens in Tianjin. Zhang et al.[26] also reported that the ST-21 complex was the most common clonal complex of *C. jejuni* among human isolates and chicken isolates in north China. Conversely, in our study, no ST-21 complexes were found in the poultry isolates. In addition, 51.0% of STs from poultry isolates were newly reported. Our results suggested that the *C. jejuni* isolated from poultry in Shenzhen may be independent to other areas, although sampling bias cannot be excluded.

Islam et al.[27] reported that the ST-403 complex was the most prevalent lineage among 49 *C. jejuni* strains recovered from patients with enteritis or GBS. In the present study, we found nine *C. jejuni* isolates that belonged to the ST-403 complex; four of them were isolated from patients and were resistant to five to eight antibiotics, while five of them were isolated from cattle and were resistant to three antibiotics. The strong antibiotic resistance of ST-403 complex isolates from patients requires further research.

In a previous study, the ST-45 complex was identified from raw or undercooked meat, as well as from contact with dogs or cats[28]. In addition, the ST-45 complex has been found in penguins on the Antarctic[29], implying that this complex has a wide host range and is environmentally well adapted. In our study, we identified eight isolates that could be assigned to the ST-45 complex; four of them were from cattle, three were from poultry, and one was from a patient. The ST-45 complex was the only clonal complex that overlapped with all three sources in this study, suggesting that the ST-45 complex is widespread in Shenzhen.

A high prevalence of resistant *C. jejuni* has been reported in China previously[11,20,26], and ciprofloxacin, nalidixic acid, and tetracycline were the most commonly reported resistance pattern. Similarly, our study found the highest resistant rate occurred for ciprofloxacin (89.7%), followed by tetracycline (74.6%), and nalidixic acid (69.0%). However, 65.2% of *C. jejuni* from patients were resistant to florfenicol in this study, which has been barely reported before. Florfencicol is only permitted for veterinary use; therefore, further investigation into the reason for this high resistance to florfenicol is needed.

More research is needed to track the origin of transmission. Nevertheless, we believe this to be the first report on the genetic and antibiotic resistance of *C. jejuni* in Shenzhen. Based on the genetic characteristics of *C. jejuni* isolates identified in this study, our data may facilitate the development of pathogen tracking in Shenzhen.

ACKNOWLEDGMENTS

We thank our colleagues in the four medical facilities for collecting the patients' stool samples.

The United States Environmental Protection Agency through its Office of Research and Development funded and managed the research described here. It has been subjected to Agency review and approved for publication. Mention of

trade names or commercial products does not constitute endorsement or recommendation for use.

AUTHOR CONTRIBUTIONS

ZHANG Mao Jun, Duan YONG Xiang, LU Jing Rang, and JU Chang Yan participated in the design and coordination of the study, analyzed the data, and wrote the manuscript. MA Yan Ping, YU Mu Hua, CHEN Hui, LIU Chu Yun, GU Yi Xin, and FU Yan Yan participated in the sample collection, performed the experiments, and analyzed the data.

CONFLICT OF INTEREST

The authors have no conflicts of interest to disclose.

Received: April 17, 2018;
Accepted: July 24, 2018

REFERENCES

1. Scallan E, Griffin PM, Angulo FJ, et al. Foodborne illness acquired in the United States--unspecified agents. Emerg Infect Dis, 2011; 17, 16-22.
2. Adak GK, Meakins SM, Yip H, et al. Disease risks from foods, England and Wales, 1996-2000. Emerg Infect Dis, 2005; 11, 365-72.
3. Shobo CO, Bester LA, Baijnath S, et al. Antibiotic resistance profiles of Campylobacter species in the South Africa private health care sector. J Infect Dev Ctries, 2016; 10, 1214-21.
4. Schildt M, Savolainen S, Hanninen ML. Long-lasting Campylobacter jejuni contamination of milk associated with gastrointestinal illness in a farming family. Epidemiol Infect, 2006; 134, 401-5.
5. Heuvelink AE, van Heerwaarden C, Zwartkruis-Nahuis A, et al. Two outbreaks of campylobacteriosis associated with the consumption of raw cows' milk. Int J Food Microbiol, 2009; 134, 70-4.
6. Mughini GL, Smid JH, Wagenaar JA, et al. Risk factors for campylobacteriosis of chicken, ruminant, and environmental origin: a combined case-control and source attribution analysis. PLoS One, 2012; 7, e42599.
7. Rosner BM, Schielke A, Didelot X, et al. A combined case-control and molecular source attribution study of human Campylobacter infections in Germany, 2011-2014. Sci Rep, 2017; 7, 5139.
8. Kaakoush NO, Castano-Rodriguez N, Mitchell HM, et al. Global Epidemiology of Campylobacter Infection. Clin Microbiol Rev, 2015; 28, 687-720.
9. Zhang M, Li Q, He L, et al. Association study between an outbreak of Guillain-Barre syndrome in Jilin, China, and preceding Campylobacter jejuni infection. Foodborne Pathog Dis, 2010; 7, 913-9.
10. Ma H, Su Y, Ma L, et al. Prevalence and Characterization of Campylobacter jejuni Isolated from Retail Chicken in Tianjin, China. J Food Prot, 2017; 80, 1032-40.
11. Zhang T, Luo Q, Chen Y, et al. Molecular epidemiology, virulence determinants and antimicrobial resistance of Campylobacter spreading in retail chicken meat in Central China. Gut Pathog, 2016; 8, 48.
12. Sanad YM, Kassem II, Abley M, et al. Genotypic and phenotypic properties of cattle-associated Campylobacter and their implications to public health in the USA. PLoS One, 2011; 6, e25778.
13. Boes J, Nersting L, Nielsen EM, et al. Prevalence and diversity of Campylobacter jejuni in pig herds on farms with and without cattle or poultry. J Food Prot, 2005; 68, 722-7.
14. Wei B, Cha SY, Kang M, et al. Antimicrobial susceptibility profiles and molecular typing of Campylobacter jejuni and Campylobacter coli isolates from ducks in South Korea. Appl Environ Microbiol, 2014; 80, 7604-10.
15. Parsons BN, Cody AJ, Porter CJ, et al. Typing of Campylobacter jejuni isolates from dogs by use of multilocus sequence typing and pulsed-field gel electrophoresis. J Clin Microbiol, 2009; 47, 3466-71.
16. Klein-Jobstl D, Sofka D, Iwersen M, et al. Multilocus Sequence Typing and Antimicrobial Resistance of Campylobacter jejuni Isolated from Dairy Calves in Austria. Front Microbiol, 2016; 7, 72.
17. Nelson JM, Smith KE, Vugia DJ, et al. Prolonged diarrhea due to ciprofloxacin-resistant campylobacter infection. J Infect Dis, 2004; 190, 1150-7.
18. Helms M, Simonsen J, Olsen KE, et al. Adverse health events associated with antimicrobial drug resistance in Campylobacter species: a registry-based cohort study. J Infect Dis, 2005; 191, 1050-5.
19. Quinn T, Bolla JM, Pages JM, et al. Antibiotic-resistant Campylobacter: could efflux pump inhibitors control infection? J Antimicrob Chemother, 2007; 59, 1230-6.
20. Li B, Ma L, Li Y, et al. Antimicrobial Resistance of Campylobacter Species Isolated from Broilers in Live Bird Markets in Shanghai, China. Foodborne Pathog Dis, 2017; 14, 96-102.
21. Li Y, Zhang S, He M, et al. Prevalence and Molecular Characterization of Campylobacter spp. Isolated from Patients with Diarrhea in Shunyi, Beijing. Front Microbiol, 2018; 9, 52.
22. Wang G, Clark CG, Taylor TM, et al. Colony multiplex PCR assay for identification and differentiation of Campylobacter jejuni, C. coli, C. lari, C. upsaliensis, and C. fetus subsp. fetus. J Clin Microbiol, 2002; 40, 4744-7.
23. Ramonaite S, Tamuleviciene E, Alter T, et al. MLST genotypes of Campylobacter jejuni isolated from broiler products, dairy cattle and human campylobacteriosis cases in Lithuania. BMC Infect Dis, 2017; 17, 430.
24. Wang X, Wang J, Sun H, et al. Etiology of Childhood Infectious Diarrhea in a Developed Region of China: Compared to Childhood Diarrhea in a Developing Region and Adult Diarrhea in a Developed Region. PLoS One, 2015; 10, e142136.
25. Zhu XH, Tian L, Cheng ZJ, et al. Viral and Bacterial Etiology of Acute Diarrhea among Children under 5 Years of Age in Wuhan, China. Chin Med J (Engl), 2016; 129, 1939-44.
26. Zhang M, Gu Y, He L, et al. Molecular typing and antimicrobial susceptibility profiles of Campylobacter jejuni isolates from north China. J Med Microbiol, 2010; 59, 1171-7.
27. Wieczorek K, Osek J. Antimicrobial resistance mechanisms among Campylobacter. Biomed Res Int, 2013; 2013, 340605.
28. Karenlampi R, Rautelin H, Schonberg-Norio D, et al. Longitudinal study of Finnish Campylobacter jejuni and C. coli isolates from humans, using multilocus sequence typing, including comparison with epidemiological data and isolates from poultry and cattle. Appl Environ Microbiol, 2007; 73, 148-55.
29. Griekspoor P, Olsen B, Waldenstrom J. Campylobacter jejuni in penguins, Antarctica. Emerg Infect Dis, 2009; 15, 847-8.