ANTIBIOGRAM AND GENOTYPE PROFILES OF *CAMPYLOBACTER COLI* AND *CAMPYLOBACTER JEJUNI* ISOLATES FROM ANIMALS, HUMANS AND LIVESTOCK PRODUCTS IN GYEONGNAM, SOUTH KOREA: ONE HEALTH PERSPECTIVE

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Abstract. *Campylobacter coli* and *C. jejuni* are the two most frequent bacterial causes of food-borne diseases worldwide. Here, in 2021 we isolated two strains of *C. coli* and 72 strains of *C. jejuni* from humans (n = 89), animals (n = 100) and livestock products (n = 100) in Gyeongnam, Republic of Korea. Antibiogram profiles and genetic characteristics, employing pulsed-field gel-electrophoresis (PFGE), of the 74 isolates were determined. Comparative analyses of these properties among *Campylobacter* isolates from three sources were also conducted. The prevalence of quinolone resistance was high (~96%), while that of macrolide resistance was low (~1%). While most isolates of *C. jejuni* were resistant to two or more drugs, one isolate was resistant to four. Using PFGE analysis, 18 clusters of *C. jejuni* and two clusters of *C. coli* isolates were observed, with *C. jejuni* isolates from humans and livestock products in clusters 13 and 18 being 100% similar. Every isolate was given a Pulse Net number, which will be a key source of information for any upcoming epidemiological management program. This study is the first employing the same techniques to characterize *Campylobacter* isolates from animals, people and livestock products collected at the same time period and geographical area. This approach establishes the foundation for implementing a "One Health" approach that links human health, animal welfare and the environment.

Keywords: *Campylobacter coli, Campylobacter jejuni*, antibiogram, food-borne disease, genetic characteristic, One Health approach

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INTRODUCTION

Campylobacter is a gram-negative spirillum found in the intestinal tract of humans, livestock and various wild animals. This microaerophilic, thermophilic bacterium thrives in an environment of 3-10% O_2, 3-5% CO_2 and a temperature of 42°C. Among the more than 20 species of *Campylobacter*, *C. coli* and *C. jejuni* are the most common etiological pathogens of clinical food poisoning, resulting a high health risk of infection with as little as 500-800 bacteria (Zaman, 1992; Salyers and Whitt, 2002). In particular, >50% of poultry carry *C. coli* or *C. jejuni*, with livestock products representing the main source of infection (Kim *et al*, 2010). Secondary contamination from cooking utensils is another significant source of infection; in fact, ingestion of undercooked meat or contamination from chicken intestine contents during slaughter processes can lead to infection even from a single drop of water used to wash infected chickens (Altekruse *et al*, 1999).

The key clinical symptoms of *C. coli* and *C. jejuni* infections include diarrhea, vomiting and fever. In immunocompromised patients, these infections may lead to autoimmune diseases, such as Guillain-Barre and Reiter syndromes (Altekruse *et al*, 1999; Allos, 2001). In Korea, the number of *C. coli*- and *C. jejuni*-related food poisoning outbreaks has steadily increased from 14 (453 patients) in 2018 to 22 (475 patients) in 2021 (https://admin.foodsafetykorea.go.kr/index.do). The increased consumption of livestock products and environmental changes, such as climate warming, are expected to result in an increase in the rates of *C. coli* and *C. jejuni* infections and food poisoning in the future.

Currently, antibiotics are the only specific treatment option for *C. coli* and *C. jejuni* infections. Fluoroquinolones are commonly used to treat *C. coli* and *C. jejuni* infections; however, the frequent use of this class of antibiotics has increased fluoroquinolone resistance, with

>90% of human isolates worldwide exhibiting resistance (Sproston *et al*, 2018). As a result of emerging concerns regarding the treatment of serious infections caused by fluoroquinolone-resistant bacteria, macrolides, including erythromycin and azithromycin, have become the primary treatment options. Although macrolide resistance is low in Korea (0.8%) and the UK (2.2%), it is high in less developed countries, such as China (21.8%), Peru (25.5%) and Thailand (12.5%) (Sproston *et al*, 2018; Schiaffino *et al*, 2019), highlighting the importance of antimicrobial resistance (AMR) surveillance and monitoring.

In light of recent concerns regarding AMR bacteria and zoonoses worldwide, there has been an increased focus on research and data related to the "One Health" approach, in which emphasis is placed on a balance among the health of people, animals and the environment (Atlas and Maloy, 2014). For instance, in New Zealand *Campylobacter* infections in humans is reduced by 74% by control of contamination from poultry carcasses and by implementation of efficient regulatory control measures of *Campylobacter* infection in broiler production (Jeffs *et al*, 2019; Schiaffino *et al*, 2019). This example demonstrates the potential effectiveness of a One Health approach, in which control of *Campylobacter* contamination in the poultry industry reduces the number of campylobacteriosis cases in humans (Gölz *et al*, 2014).

In Korea, despite continuous monitoring of livestock carcasses and feces for traces of *C. coli* and *C. jejuni*, integrated data covering humans, their food sources and the environment are not well-established. Thus, in this study we characterized the antibiogram profiles and genetics of *C. coli* and *C. jejuni* isolates from animals, humans and livestock product from the same spatiotemporal zone. Our primary aim was to provide *Campylobacter* surveillance data across samples from various sources to assist in the establishment of a One Health-based approach to the epidemiological management of *Campylobacter* infection.

MATERIALS AND METHODS

Subjects and sample collection

C. coli and *C. jejuni* isolates were obtained from animals, humans and livestock products from Gyeongnam, Korea. Human rectal smear samples (n = 89) were collected during four outbreaks of *Campylobacter* food

poisoning in Gyeongnam in 2021 (June, July twice and September), namely, three outbreaks in meal service facilities (one in a school and two in corporate settings) and an outbreak in a restaurant. Livestock products and animal samples were collected from February to September 2021, consisting of whole chicken and smoked duck samples (n = 100) from grocery stores in Gyeongnam (kept at 4°C and analyzed on the day of purchase) and chicken and duck carcasses and feces (n = 100) kindly provided by the Gyeongnam Animal Gastric Laboratory (analyzed on the day of collection). Carcasses comprised of slaughtered livestock after removal of the head, skin and internal organs before processing or packaging for distribution. Fecal samples consisted of cecal and intestinal contents of chickens and ducks. Carcass samples were collected in a sterile sample bag (TEMPO SACS; bioMerieux SA, Marcy L'Etoile, France) per animal containing 400 ml of buffered peptone water (BPW; Oxoid, Basingstoke, UK).

Culture and identification of *Campylobacter* isolates

Appropriate culture methods were performed to isolate *Campylobacter* spp. Fecal samples were streaked on modified charcoal cefoperazone deoxycholate agar (mCCDA; Oxoid, Basingstoke, UK) plates. Raw or processed livestock product samples were cultured in a Bolton broth-based enrichment growth medium (Oxoid, Basingstoke, UK). The enrichment medium samples and agar plates were incubated for 48 hours at 42°C under microaerophilic conditions [gas packs for microaerophilic cultures (CampyGen; Thermo Scientific, East Grinstead, UK)]. Subsequently, samples from cultured broths were streaked on mCCDA (Oxoid, Basingstoke, UK) and further cultured as described. Round or irregular-shaped grayish-white and white colonies were collected and cultured on blood agar plates (Hanil Komed, Gyeonggi, Republic of Korea) for 48 hours at 42°C under microaerophilic conditions. An automatic microbe analyzer (Vitek 2 compact; bioMerieux SA, Marcy L'Etoile, France) was used for identification of *C. coli* and *C. jejuni* isolates).

Antibiogram profiling

C. coli and *C. jejuni* isolates were cultured on blood agar plates (Hanil Komed, Gyeonggi, Republic of Korea) at 42°C for 24 hours and colonies suspended in 5 ml of

Cation Adjusted Mueller-Hinton Broth w/TES (Thermo Scientific, East Grinstead, UK). Subsequently, a 100-µl aliquot of the bacterial solution adjusted to 0.5 McFarland unit was mixed with 11 ml of Mueller-Hinton broth supplemented with 5% hemolyzed horse blood (Thermo Scientific, East Grinstead, UK), and 100-µl aliquot of the mixture was applied to an antibiotic plate (SensititreTM CAMPY, Thermo Scientific, East Grinstead, UK), which was then sealed with a transparent plastic wrap and incubated for 24 hours at 42°C under microaerophilic conditions. Changes in turbidity and precipitation were visually evaluated to determine the minimum inhibitory concentration (MIC) of the eight test antibiotics: azithromycin (AZI), ciprofloxacin (CIP), clindamycin (CLI), erythromycin (ERY), florfenicol (FFN), gentamicin (GEN), nalidixic acid (NAL), and tetracycline (TET). The breakpoint for each antibiotic was established according to the 2021 National Antimicrobial Resistance Monitoring System (NARMS) guidelines (US FDA, 2020).

Pulsed-field gel-electrophoresis (PFGE) analysis

Each bacterial isolate was suspended in 2 ml of TE solution (100 mM Tris pH 7.5 and 100 mM EDTA) and calibrated to 20% transparency using a colorimeter (HACH Co, Loveland, CO). Then, 200-µl aliquot of the suspension was mixed with 200 µl of 1.2% SeaKem gold agarose (Lonza, Rockland, ME) to form a plug, which was mixed with 1.5 ml of lysis solution (0.5 M EDTA pH 8.0, 1% (w/v) sodium lauroyl sarcosinate and 40 µl of proteinase K (20 mg/m) and incubated with shaking at 55°C for 1 hour. The plug was then incubated in TE wash solution (10 mM Tris pH 8.0 and 1 mM EDTA) with shaking for 20 minutes at 55°C. This was repeated five times with fresh TE wash solution and the plug was sliced into one mm-thick pieces, incubated with 40 U/µl SmaI (Roche, Indianapolis, IN) at 25°C for 4 hours and subjected to PFGE (CHEF Mapper XA Chiller System; Bio-Rad Laboratories, Hercules, CA) for 18 hours at 120°C under the following conditions: Initial movement, 6.75 seconds; Final movement, 38.35 seconds; 6 V/cm. Gels were stained with SYBR gold (Invitrogen, Eugene, OR) and acquired images were analyzed using a Bionumerics program (Bio-Rad Laboratories Inc, Hercules, CA). Similarity was calculated using 1.5% tolerance, 1.5% optimization dice coefficient and an unweighted pair group mean average (UPGMA) for genetic relationship analysis.

Statistical analysis

The statistical analyses were performed on Excel 2016 software (Microsoft, Redmond, WA). Differences in AMR and multiple drug resistance (MDR) patterns of *Campylobacter* spp among animals, humans and livestock products were analyzed using a Chi-squared test, with a p-value <0.05 considered significant.

Ethical considerations

All procedures involving human participants were conducted according to the ethical standards of the IRB and the 1964 Helsinki Declaration, including its later amendments or comparable ethical standards (Word Medical Association, 2013). Prior written informed consents were obtained from all subjects. Chicken and duck carcass samples were provided with consent from the Gyeongnam Animal Gastric Laboratory, Jinju, Republic of Korea.

RESULTS

***C. coli* and *C. jejuni* isolates collected**

Samples (n = 289) from animals, humans and livestock products collected in Gyeongnam during 2021, *C. coli* (n = 2) and *C. jejuni* (n = 72) isolates were collected and identified. Human rectal smear samples (n = 89) were obtained during four incidences of food poisoning, resulting in the acquisition of only *C. jejuni* isolates (n = 41) (Table 1). The outbreaks mostly occurred in late June, July and early September when temperatures were high. Samples (n = 100) of poultry products (*ie*, whole chicken and smoked duck) collected from grocery stores from April to September 2021 yielded *C. coli* (n = 4) and *C. jejuni* (n = 7) isolates. Samples (n = 100) acquired from the carcasses and feces of chickens and ducks from February to June 2021 yielded only *C. jejuni* isolates (n = 22).

Antibiogram profiles

The isolates showed high rates of resistance to the quinolones, with 95 and 95% resistant to nalidixic acid (NAL) and ciprofloxacin (CIP), respectively (Table 2). Additionally, 40% of the isolates were resistant to tetracycline (TET) but only 1% was resistant to azithromycin (AZI), a macrolide, the latter from a patient with food poisoning. All isolates were still susceptible to clindamycin (CLI), erythromycin (ERY), florfenicol (FFN) and gentamicin (GEN). Of the 74 isolates that showed resistance, 70 were resistant to ≥2 antibiotics, indicating a high rate of multidrug resistance (MDR), 30 to ≥3 antibiotics and one (from a patient with food poisoning) to 4 antibiotics, namely, AZI, CIP, NAL, and TET (Table 3).

Table 1

Detection rates of *Campylobacter coli* and *C. jejuni* by sample types

Sample type	Number of samples	Number of isolates[a] *n* (%)
Humans		
Patient	66	38 (57.6)
Food service employee	12	1 (8.3)
Control group	11	2 (18.2)
Total	89	41 (46.1)
Livestock product		
Chicken	67	7 (10.04)
Duck	33	4 (12.1)[b]
Total	100	11 (11.0)
Animal		
Chicken	70	1 (1.4)
Duck	30	21 (70.0)
Total	100	22 (22.0)

[a]Total number of isolates (*n* = 74); [b]Contains two *C. coli* isolates

Genotypes according to PFGE profiles

PFGE profiles of the *C. coli* and *C. jejuni* strains showed 20 different patterns (clusters), with *C. coli* strains belonging to clusters 19 and 20 and *C. jejuni* to clusters 1-18 (Fig 1). Strains with genetic similarity >80% were classified as belonging to the same cluster. Cluster 5 comprised the greatest number of strains (*n* = 20, 27%), followed by cluster 14 (*n* = 9, 12%) and cluster 1 (*n* = 8, 11%). Strains in each cluster were isolated from the same source, except cluster 13 that contained *C. jejuni* strains from humans (*n* = 5) and livestock products (*n* = 2) and cluster 18 that also contained *C. jejuni* strains from humans (*n* = 1) and livestock products (*n* = 1) (Fig 2). The types of livestock products with the same *C. jejuni*

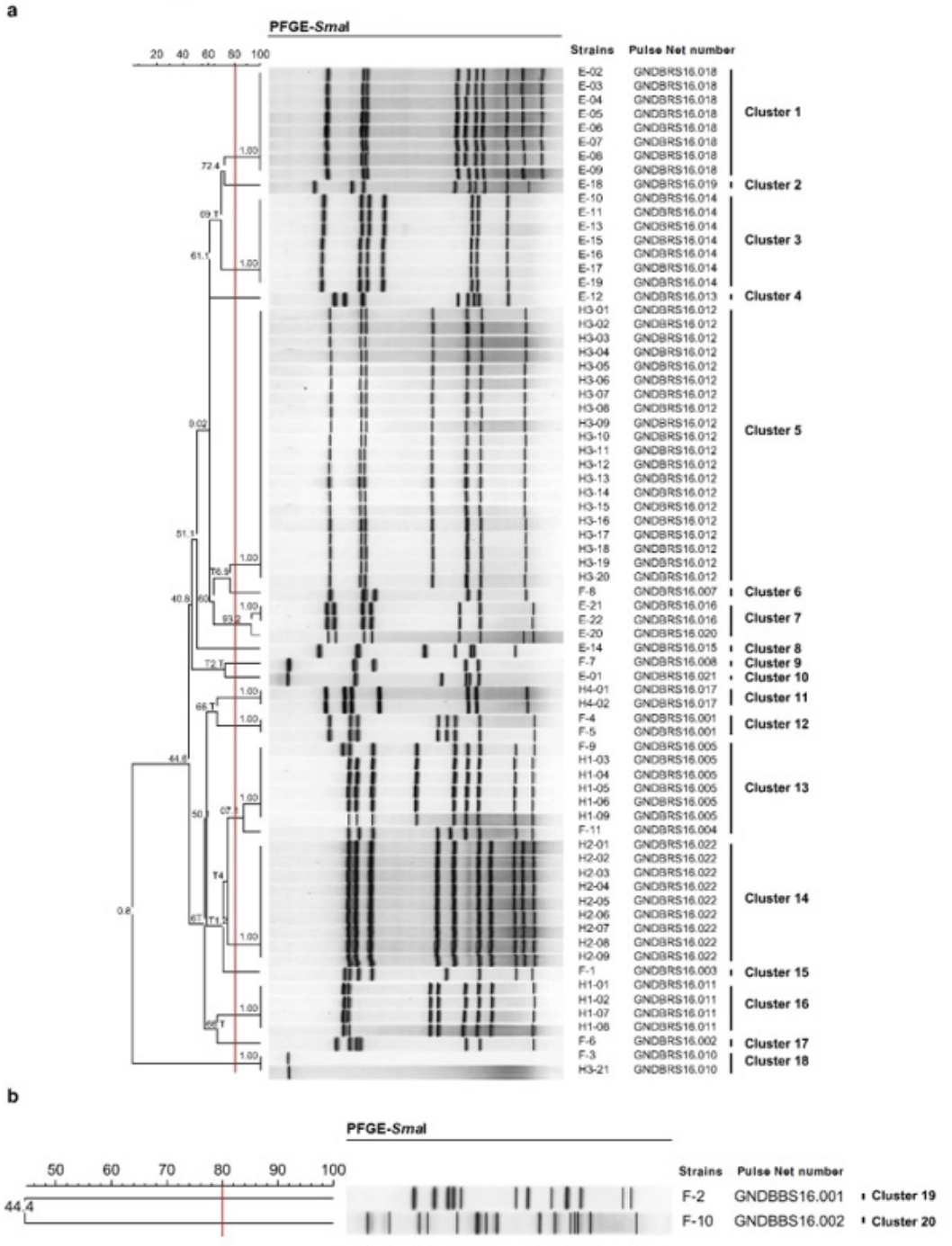

Fig 1 - Dendrograms of PFGE-SmaI clusters of (a) *Campylobacter jejuni* (*n* = 72) and (b) *C. coli* (*n* = 2) isolates

Fig 1 - (cont) Note: Lysate of an isolated bacterial strain embedded in an agarose plug was incubated with 40 U/µl SmaI (Roche, Indianapolis, IN) at 25°C for 4 hours and subjected to PFGE (CHEF Mapper XA Chiller System; Bio-Rad Laboratories, Hercules, CA) for 18 hours at 120°C under the following conditions: Initial movement, 6.75 seconds; Final movement, 38.35 seconds; 6 V/cm. Gels were stained with SYBR gold (Invitrogen, Eugene, OR) and the acquired images were analyzed using a Bionumerics program (Bio-Rad Laboratories Inc, Hercules, CA). The vertical red line demarcates 80% similarity in PFGE-SmaI patterns, a minimum similarity value for assignment of strains to the same cluster.

Every isolate was given a Pulse Net number in the Gyeongnam province, South Korea providing that E refers to *Campylobacter* strain isolated from animal samples; F refers to *Campylobacter* strain isolated from livestock product samples and H refers to *Campylobacter* strain isolated from human samples.

SmaI PFGE: pulsed-field gel-electrophoresis following SmaI digestion

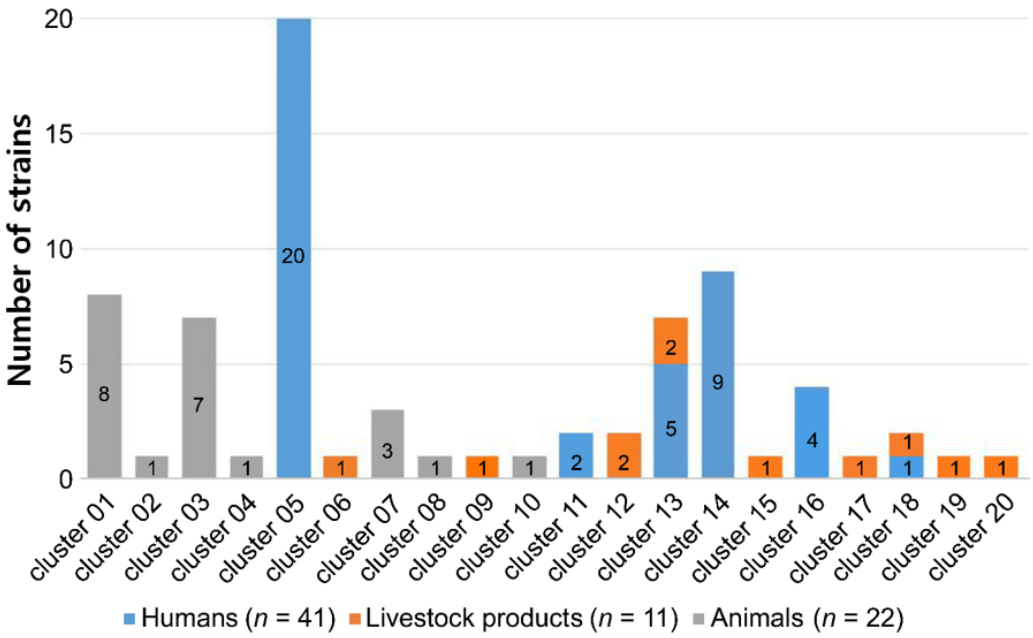

Fig 2 - Distributions among PFGE-SmaI clusters of *Campylobacter coli* (n = 2) and *C. jejuni* (n = 72) strains from animals, humans and livestock products

Clusters refer to the PFGE-SmaI patterns shown in Fig 1.

Table 2

Antimicrobial resistance of *Campylobacter coli* and *C. jejuni* isolates

Antibiotic	MIC* (μg/ml)		Number of resistant isolates, *n* (%)[a]		
	Breakpoint	Range	Humans[b] (N = 41)	Livestock product[b] (N = 11)	Animal[b] (N = 22)
Azithromycin	≥0.5[c]	≤0.015 - 8	1 (2)	0 (0)	0 (0)
Ciprofloxacin	≥1	0.06 - 32	39 (96)	10 (91)	21 (95)
Clindamycin	≥1[c]	≤0.03 - 0.5	0 (0)	0 (0)	0 (0)
Erythromycin	≥8[c]	≤0.03 - 1	0 (0)	0 (0)	0 (0)
Florfenicol	≥8	0.06 - 2	0 (0)	0 (0)	0 (0)
Gentamicin	≥4	≤ 0.12 - 32	0 (0)	0 (0)	0 (0)
Nalidixic acid	≥32	≤4 - ≥64	41 (100)	10 (91)	21 (95)
Tetracycline	≥4	≤0.06 - ≥64	15 (37)	3 (27)	12 (54)

[a]Total >100% as some isolates are resistant to more than one antibiotic; [b]Number >total number of samples as some isolates are resistant to more than one antibiotic; cAll breakpoints presented are for *C. jejuni*. Breakpoint values of *C. coli* for these antibiotics were twice those of *C. jejuni*. For the remaining five antibiotics, the breakpoints were the same for *C. jejuni* and *C. coli*.

*MICs reported in this Table follow CDC (2019).

MIC: minimum inhibitory concentration; μg/ml: microgram per milliliter

genotypes as those from humans were packaged raw meats (*eg*, whole chicken, chicken tenderloin and marinated duck). These results indicate that humans may become infected with *Campylobacter* sp from consuming contaminated livestock products

Among *C. jejuni* strains, resistance to one antibiotic was found in strains belonging to a single cluster, resistance to 2 antibiotics in strains belonging to 9 clusters, resistance to ≥3 antibiotics in strains belonging to 8 clusters, and absence of resistance in strains belonging to 2 clusters (Table 3). In cluster 13, the 5 strains from humans were resistant to 3 antibiotics and the single strain from livestock products resistant to 2 antibiotics, and in cluster 18 each of the strains from humans and livestock products was resistant to the same 3 antibiotics. The 74 strains isolated in this study were assigned Pulse Net numbers for monitoring purposes.

DISCUSSION

Determining the interconnections among animals, humans and environment, known as the One Health concept, was the focus of this study to establish a holistic surveillance of *C. coli* and *C. jejuni* in animal, human and livestock products. To this end, *Campylobacter* strains were isolated from all three sources in the same region (Gyeongnam, Republic of Korea) and at the same time, their antimicrobial susceptibilities to eight antibiotics investigated and PFGE-SmaI profiles generated to obtain a genetic identity. Among the samples (n = 289) from animals, humans and livestock products, *C. coli* (n = 2) and *C. jejuni* (n = 72) strains were isolated, with an overall detection rate of 26%.

Antibiogram profiles revealed a high proportion of the isolated strains resistant to two quinolone antibiotics (97 and 95% to nalidixic acid and ciprofloxacin). The increasing number of reports on *Campylobacter* resistance to quinolones has brought macrolides into the limelight as the primary agents for the treatment of *Campylobacter* infection (Kaakoush *et al*, 2015; Silva *et al*, 2011). The *Campylobacter* strains in our study had low resistance to two macrolides (2% of strains resistant to azithromycin and 0% to erythromycin). In comparison with previous findings (Kim *et al*, 2016; Kim *et al*, 2017; Oh *et al*, 2017; Park *et al*, 2019), our findings showed similar or higher resistance to the two quinolones and similar or lower resistance to the two macrolides. Additionally, despite the differences in the analysis

Table 3

Antibiogram profiles of *Campylobacter coli* (n = 2) and *C. jejuni* (n = 72) isolates in each cluster according to isolates' source

Cluster	Resistance type	Number of resistant isolates		
		Humans (n = 41)	Livestock product (n = 11)	Animal (n = 22)
01	CIP + NAL	0	0	8
02	CIP + NAL	0	0	1
03	CIP + NAL + TET	0	0	7
04	CIP + NAL + TET	0	0	1
05	CIP + NAL	20	0	0
06	CIP + NAL	0	1	0
07	CIP + NAL + TET	0	0	3
08	CIP + NAL + TET	0	0	1
09	N/D	0	1	0
10	N/D	0	0	1
11	NAL	2	0	0
12	CIP + NAL	0	2	0
13	CIP + NAL + TET	5	1	0
	CIP + NAL	0	1	0
14	CIP + NAL + TET	8	0	0
	AZI + CIP + NAL + TET	1	0	0
15	CIP + NAL	0	1	0
16	CIP + NAL	4	0	0
17	CIP + NAL	0	1	0
18	CIP + NAL + TET	1	1	0
19*	CIP + NAL	0	1	0
20*	CIP + NAL + TET	0	1	0

**C. coli* clusters refer to PFGE-SmaI patterns shown in Fig 1.

AZI: azithromycin; CIP: ciprofloxacin; NAL: nalidixic acid; N/D: not detected; TET: tetracycline

methods and interpretation criteria, the AMR rate in our findings was higher than that reported 15 years previously (Park *et al*, 2007).

In the Republic of Korea, the most commonly purchased antibiotics for livestock in 2020 are florfenicol (113,171 kg) followed by erythromycin (9,849 kg) and gentamicin (1,813 kg), with *C. jejuni* susceptible to all three drugs (Korea Food and Drug Safety Evaluation Institute *et al*, 2021). We found that these three types of antibiotics were still suitable to treat *campylobacter*ia infection. Among the isolated MDR strains, one strain resistant to azithromycin, ciprofloxacin, nalidixic acid, and tetracycline was isolated from a patient suffering from food poisoning. Indeed, strains resistant to quinolones and macrolides may pose considerable challenges as no alternative efficacious therapeutic agents are currently available (Hoge *et al*, 1998). Thus, the epidemiology of this particular strain must be carefully monitored. A similar strain with the same MDR pattern was previously isolated by Kim *et al* (2016).

Antibiogram profiles may vary depending on the methods used and interpretation criteria. Typically, breakpoints are established by the Clinical and Laboratory Standards Institute (CLSI, 2023) and the European Committee on Antimicrobial Susceptibility Testing (EUCAST, 2021) as well as various national committees. Standardized antimicrobial susceptibility testing methods and interpretive criteria (breakpoints) are essential for accurate and comparable AMR data on *Campylobacter* spp. However, the criteria to determine their breakpoints are not well-established, limiting direct comparisons. Additionally, data are scattered according to sample types (*eg*, human and livestock samples), hindering integrated data management. Nevertheless, *Campylobacter* antibiograms can significantly affect patients' treatment and public health measures. In particular, resistance to commonly used antimicrobials, such as macrolides and quinolones, limits treatment options and thereby increases treatment failure, prolongs illness and hospitalization and raises risk of mortality. In addition, the spread of resistant strains can complicate epidemiological monitoring and outbreak investigations, impeding infection source identification and effective control measure implementations. Therefore, continued surveillance of *Campylobacter* antibiogram profiles in humans, animals and livestock

products is essential for early detection of emerging resistance and for informed decision-making regarding antimicrobial use in clinical and agricultural settings.

Due to its high resolution, PFGE is considered a suitable method of typing *Campylobacter* spp for epidemiological infection management (Fitzgerald *et al*, 2001). By analyzing the PFGE patterns of different isolates, the genetic relatedness of the isolates/strains can be discerned and used to track their spread and associations with disease. This information can then be applied to investigate outbreaks, identify contamination sources and develop strategies to prevent further disease spread.

PFGE analysis of the 74 isolated *Campylobacter* strains allowed their allocation into 20 distinct clusters. Presence of strains from different sources can infer their associations. For example, if a particular cluster consists of strains obtained from humans and livestock products, it could be inferred that the contaminated livestock products have entered into the consumer food chain. As *Campylobacter* spp can readily cause food poisoning, caution must also be exercised to prevent secondary infections from contaminated cooking utensils. In our study, *Campylobacter*-contaminated livestock products were packaged raw meats, including whole chicken, chicken tenderloin, and marinated ducks. Comparison based on the Korean Pulse Net identification system, *C. jejuni* strains in cluster 18 (one strain each from a food poisoning subject and a livestock product) were identical to those previously isolated from cow feces and patients with diarrhea in other regions of the country (Kim *et al*, 2016; Park *et al*, 2019); the *C. jejuni* strain in cluster 2 (from a livestock product) was identical to those isolated earlier from patients with diarrhea in other regions (Park *et al*, 2019); strains in cluster 13 (five from food poisoning patients and two from livestock products) were the same as those previously detected in chicken (Kim *et al*, 2016); and the strain in cluster 15 (from a livestock product) was identical to those previously isolated from patients with diarrhea in other regions (Kim *et al*, 2016) (Fig 2). These findings suggest that certain *Campylobacter* strains are circulating in animals, humans and livestock products nationwide.

Our findings did not show genetic identities among *Campylobacter* strains isolated from slaughterhouse animals and those from human

sand livestock products (Fig 2). Although *C. jejuni* strains (n = 21) were isolated from animal samples in slaughterhouses, no strains with the same Korean Pulse Net identifications were isolated from the livestock product samples from the same slaughterhouse (data not shown). Moreover, a *C. jejuni* strain isolated from a slaughterhouse was not detected in another slaughterhouse at the same period in Gyeongnam. Given that the slaughterhouses surveyed catered hospitality establishments and restaurants, the products were not considered to be have been distributed in food markets. The representative poultry slaughterhouses in Korea are located primarily in the Jeonbuk and Jeonnam regions. In our study, a total of 100 samples were from commercially available poultry products from various companies over a 6-month period; however, this collection method may have excluded products from small- and medium-size companies with relatively smaller distribution channels, potentially limiting the generalization of the findings. Nevertheless, the results suggested that slaughterhouses surveyed employed satisfactory sanitary and well-managed packaging/processing systems in their distribution chains. Thus, the stages in livestock raising, slaughter, distribution process, cooking, and consumption are connected, so good operating procedures in all stages prior to consumption are important to prevent *Campylobacter* infection and outbreaks.

In conclusion, our study highlights the significance of the analysis of data obtained from *Campylobacter* spp isolated from animals, humans and livestock products in the same area and timeframe, and conducting experiments under the same standard operating procedures. The results indicated that antibiogram profiles were similar between *Campylobacter* strains isolated from the three sources, but differences in the multidrug resistance profiles warrant further investigation. PFGE results proved to be a useful tool to investigate the genetic relatedness of *Campylobacter* isolates/strains from different sources and to identify possible sources of infection. Additionally, to ensure effective management to control appearances of antibiotics resistance, it is necessary to establish ongoing surveillance using standardized methods and data integration systems. These efforts provide the foundation for implementing a One Health approach, where the health of humans, animals and the environment is considered from a holistic viewpoint.

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CONFLICT OF INTEREST DISCLOSURE

The authors declare no conflict of interest.

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