Prevalence and antimicrobial resistance of Campylobacter jejuni and C. coli identified in a slaughterhouse in Argentina

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ABSTRACT

The aim of this study was to evaluate the percentage of Campylobacter (C. jejuni and C. coli) from samples collected at the slaughterhouse to describe the prevalence of resistance to selected antimicrobials, and to characterize the genetic determinants. In total, from 333 samples analyzed, 31% were positive for Campylobacter. More positive samples were detected before the chiller (46%) than after the chiller (16%). C. coli (59%) was more prevalent than C. jejuni (41%). Antimicrobial resistance differences between C. jejuni and C. coli were found (p < 0.001). Multidrug resistance was found in 72% of C. coli isolates and 69% of C. jejuni isolates (p < 0.001). Most C. jejuni isolates (57%) had the three genes of the cmeABC efflux pump. The tet(O) gene and resistance-associated point mutations within both the gyrA and 23S rRNA genes were detected in 100% of C. coli isolates. On the other hand, C. jejuni only had more prevalence of the blaoxa-61 gene than C. coli (p < 0.001), and most of the C. jejuni isolates (70-80%) had the tet(O) and gyrA point mutation. These results could contribute to knowledge about the status of thermotolerant Campylobacter resistant to antimicrobials isolated from food animals in Argentina and to develop an antimicrobial resistance surveillance system.

1. Introduction

The World Health Organization considered that thermotolerant Campylobacter is one of the main causes of enteric infection due to food consumption in developed and developing countries (World Health Organization, 2017; Natsos et al., 2016; Pedersen et al., 2018). In developing countries like Argentina, information on food-borne disease is scant due to the inadequate data provided by the surveillance systems. Additionally, outbreak information is frequently unsubstantial because health authorities lack the capabilities or resources for detection of diarrheal diseases (Zaidi et al., 2008).

C. jejuni and C. coli are the most important species of thermotolerant Campylobacter and they are enteric commensal bacteria of poultry (Kaakoush et al., 2015). Broilers are the main reservoir of Campylobacter spp., and colonization in broiler ceca can reach 10^9 cfu/g of cecal content (Stern et al., 2008; EFSA and ECDC, 2016).

In Argentina, the production of chicken meat has grown substantially during the last years, reaching a total of over 757,9 million chickens processed in 2020 and producing 1,779,000 tonnes of poultry meat, which is approximately 0.13% higher than the figures for 2019. The apparent per capita consumption of chicken meat has increased by 1.2% in the last year, reaching 45.9 kg/inhabitant/year in 2020 (MAGYP, 2020).

Poultry production in Argentina is concentrated within 3800 farms and there are 54 slaughterhouses in the country. During the slaughter process, broiler carcasses may be contaminated with thermotolerant Campylobacter. As a common inhabitant of the gastrointestinal tract of warm-blooded animals, Campylobacter can be expected to contaminate meat during slaughter and evisceration as a result of fecal contamination (Garcia Sanchez et al., 2018; Osimani et al., 2017). The improper handling or consumption of raw or undercooked meat and meat products are the main risk factors associated with campylobacteriosis in...
2. Materials and methods

2.1. Sample collection and Campylobacter isolation

Samples were taken from different areas of the slaughterhouse. The slaughterhouse belongs to a company with 35 chicken farms and 70 retail markets in Argentina. In the slaughterhouse, 600,000 chickens were slaughtered per month. Sampling was performed in nine visits, one per month during 2015 (from April to December). The slaughterhouse was divided in two areas, before and after the chiller. The samples before the chiller were taken from: cecum (n = 27), processing line surfaces (n = 27), workers’ hands (n = 27); and after the chiller: processing line surfaces (n = 27), workers’ hands in the packing area (n = 27), packing area surfaces (n = 27), and carcasses (n = 90). Campylobacter spp. were isolated using selective media Bolton Broth and Modified Charcoal Cefoperazone Deoxycholate (mCCDA) agar plates (ISO 10272-1). The cecum and carcasses were processed as described previously by Zbrun et al. (2017). The knives and surfaces were sampled using sterile cotton swabs. Each cotton was immersed in 5 mL Bolton Broth and incubated for 24 h at 42 °C under microaerobic conditions (5% O2, 10% CO2 and 85% N2). Then, the same procedure described by Zbrun et al. (2017) was used for Campylobacter isolation. The workers’ hands were washed with 200 ml of sterile PBS 1X, and the buffer was collected in a sterile screw flask. Then, the procedure employed was the same as for carcasses (Zbrun et al., 2017).

2.2. Identification of Campylobacter species

Preliminary identification of thermotolerant Campylobacter isolates was based on colony morphology, microscopic appearance (curved Gram-negative bacilli with typical motility), and the following phenotypic characteristics: oxidase and catalase production. All presumptive Campylobacter spp. isolates were identified to the species level (C. jejuni and C. coli) by multiplex PCR, as proposed by Vandamme et al. (1997). DNA was extracted using a Wizard genomic DNA purification kit (Promega®), and PCR products were analyzed on 1.5% agarose gels and stained with GelRed (Biotium®). Positive isolates were sub-cultured on Columbia blood agar and stored in glycerol broth (15% glycerol and 85% serum broth) at −80 °C.

2.3. Antimicrobial susceptibility testing and determination of MICs

The antimicrobial sensitivity of Campylobacter isolates was tested by agar dilution assay as recommended by the Clinical and Laboratory Standards Institute in the standard M100-S23 (CLSI, 2013). C. jejuni and C. coli isolates were tested with eight antimicrobial agents: erythromycin (ERY), ciprofloxacin (CIP), gentamicin (GEN), streptomycin (STR), tetracycline (TET), enrofloxacin (ENR), chloramphenicol (CLO), and ampicillin (AMP) (Table 1). The strains were removed from the freezer and streaked onto Columbia blood agar and then incubated for 48 h at 42 °C under microaerobic conditions. Several colonies were transferred to a tube with 5 ml of Mueller-Hinton broth to reach a standard inoculum adjusted to 0.5 McFarland. Approximately 104 cfu of these suspensions was inoculated onto Mueller-Hinton agar containing a two-fold dilution series of antimicrobials and supplemented with 5% defibrinated sheep blood using a multipoint inoculator (a Steers replicator system) with 1-mm pins. The plates were incubated for 24–48 h at 42 °C under microaerobic conditions. C. jejuni ATCC 35360 was used as a reference strain. The inhibition was evaluated according to the standards of the Clinical and Laboratory Standards Institute (CLSI, 2010). If an isolate was resistant to three or more antimicrobial classes, it was considered to be a multi-resistant profile.

2.4. Detection of antimicrobial resistance determinants

The efflux pump was evaluated by PCR using different protocols for each component of the pump: cmeA (Koolman et al., 2015), cmeB (Lin et al., 2017)
et al., 2002), and cmeC (Fakhr and Logue, 2007). Mutation at position 2075 in domain V of the 23S rRNA gene, associated with high-level erythromycin resistance, was detected by the mismatch amplification mutation assay PCR (MAMA-PCR) (Alonso et al., 2005). Mutations in the quinolone resistance determining region of gyrA, resulting in resistance-associated T86I substitutions, were identified by MAMA-PCR as reported by Zirnstein et al. (2000) and Zirnstein et al. (1999). β-lactamase gene blaOXA-61 was detected as described by Obeng et al. (2012). PCR primers are described in Table 2. PCR products were visualized by electrophoresis in 1.5% agarose gels, stained with GelRed® and viewed under UV light.

2.5. Statistical analysis

The resistant frequencies for each class of antimicrobial agents and multidrug resistance (MDR) in C. jejuni and C. coli isolates, the association between the resistance of each antimicrobial agent and the presence of genes related to the mechanism of resistance were compared with the chi-square test and Fisher Exact Test using Infostat (Universidad Nacional de Córdoba). Differences were considered significant at p < 0.05.

3. Results

3.1. Campylobacter species prevalence in different areas of the slaughterhouse

In total, from 333 samples analyzed, 102 (31%) were positive for Campylobacter and were stored in freezer at −80 °C for subsequent studies. The highest Campylobacter prevalence was detected in cecum (63%), followed by the evisceration knives (26%), and workers’ hands before and after the chiller (26% and 22%). In addition, more positive samples were detected before the chiller (46%) than after the chiller (16%). C. coli (18%) was more prevalent than C. jejuni (13%) in all samples analyzed. Moreover, C. coli was the most prevalent species in cecum and before chilling, but after the chiller its prevalence decreased considerably (Table 3).

### Table 2

| Antimicrobial | Gene       | Primer     | Sequence (5′-3′) | Amplicon length (bp) | Reference |
|---------------|------------|------------|------------------|----------------------|-----------|
| Multiple antimicrobials (Efflux pump) | cmeA | cmeA F | TGGTCATCGCTTTGCTGTA | 957 | Koolman et al. (2015) |
|               | cmeC | cmeC F | AGATGAACTTTGTAAATT | 500 | Fakhr and Logue (2007) |
| Tetracycline   | tet(O) | tet(O) F | GGGGTTTTGGTATGCGG | 559 | Gibreel et al. 2004 |
| Ampicillin     | blaOXA-61 | blaOXA-61 F | TATGAGCGTTATTATCGGTC | 372 | Obeng et al. (2012) |
| Ciprofloxacin  | gyrA C. jejuni | gyrA F | AAATCCGTCTAGCTCTTGTG | 1083 | Wang et al., 2016 |
|               | gyrA C. coli | gyrA F | TATGAGGCTTATTATGCGG | 505 | Zirnstein et al. (2000) |
|                | Mutation Thr-86-Ile C. jejuni | gyrA R | CAACTGTTTCTAGCTCTTGTG | 410 | Wang et al., 2016 |
|                | Mutation Thr-86-Ile C. coli | gyrA R | TATGAGGCTTATTATGCGG | 192 | Zirnstein et al. (2000) |
| Erythromycin   | ARN23S | ARN23S F | GTAACCGCGCCGTCGATCTA | 699 | Jensen and Arestrup (2001) |
|                | Mutation A2075-G ARN23S | ARN23S R | GACCGAAGCTGTACGACG | 184 | Jensen and Arestrup (2001) |

3.2. Antimicrobial resistance and multidrug profiles of Campylobacter isolates

Antimicrobial resistance differences between C. jejuni and C. coli were found (p < 0.001). In general, C. coli isolates were more resistant against the antimicrobials tested than C. jejuni isolates (Fig. 1). The analysis of C. coli antimicrobial resistance shows isolates having higher resistance to ciprofloxacin (100%; 95%CI 94.1%–100.0%), tetracycline (100%; 95%CI 94.1%–100.0%), erythromycin (95%; 95%CI 86.3%–98.2%), enrofloxacin (88%; 95%CI 77.8%–94.2%), and ampicillin (77%; 95%CI 64.5%–85.5%) than C. jejuni. Moreover, several C. coli isolates were classified as “intermediate” when tested on media amended with erythromycin (5%; 95%CI 1.8%–13.7%), enrofloxacin (12%; 95%CI 5.8%–22.2%), or ampicillin (23%; 95%CI 14.5%–35.5%); thus, all C. coli isolates were classified as either “resistant” or “intermediate” with regards to these three antibiotics. C. jejuni isolates showed high resistance.
resistance to ciprofloxacin (81%, 95%CI 66.6%–90.0%), enrofloxacin (76%; 95%CI 61.4%–86.5%) tetracycline (74% 95%CI 58.8%–84.7%), and a lower proportion of isolates were resistant to streptomycin (29%; 95%CI 17.2%–43.7%), ampicillin (26%; 95%CI 15.3%–41.2%), and erythromycin (17%; 95%CI 8.4%–30.7%). Both Campylobacter species were susceptible to gentamicin and chloramphenicol.

Multidrug resistance to three or more classes of antimicrobials was found in 72% (n = 43) of C. coli isolates and 69% (n = 29) of C. jejuni isolates (p < 0.001) (Table 4). The only MDR profile in C. coli was quinolone ciprofloxacin and enrofloxacin, tetracycline, ampicillin and erythromycin. For C. jejuni, quinolone (ciprofloxacin and enrofloxacin), tetracycline and streptomycin was the more prevalent MDR profile (28%).

### 3.3. Prevalence of resistant genes of Campylobacter isolates

The genes from three parts of the efflux pump were evaluated. The majority of C. jejuni isolates (57%) had the three genes of the efflux pump. In contrast, only one C. coli had the three components of the efflux pump. In addition, both species had more prevalence of cmeC than cmeB and cmeA. C. jejuni isolates had more prevalence of cmeA (43%) and cmeB (48%) of the efflux pump (P < 0.001) than C. coli isolates (cmeA 3%, cmeB 28%). Both species had a similar prevalence of cmeC (88.1% C. jejuni and 88.3% C. coli (P = 0.971).

The presence of the tet(O) gene, and resistance-associated point mutations within gyrA and the 23S RNA were detected in 100% of the C. coli isolates. The blaOXA61 gene was more prevalent in C. jejuni than in C. coli (p < 0.001), and most of the C. jejuni isolates (70–80%) possessed both tet(O) and the resistance-associated gyrA point mutation (Fig. 2).

### 3.4. Antimicrobial resistance genes and resistance profile of Campylobacter isolates

The presence of the cmeA (P = 0.573), cmeB (P = 0.824), or cmeC (P = 0.343) genes was not associated with the prevalence of multidrug resistance in C. jejuni isolates. All ciprofloxacin resistant C. jejuni and C. coli had the resistance-associated point mutation in the gyrA gene. However, for enrofloxacin, 20% of susceptible isolates of C. jejuni and all C. coli with intermediate classification harbored the point mutation in the gyrA gene.

### Table 4

| Multi-resistant resistant isolates | Antimicrobial resistance profile | No. of resistant isolates (%) |
|-----------------------------------|---------------------------------|-----------------------------|
| C. coli (n = 60)                   | CIP-TET-AMP-ENR-ERY             | 43 (72%)                    |
| C. jejuni (n = 42)                | CIP-TET-ENR-STR                 | 12 (28%)                    |
|                                   | CIP-TET-AMP-ENR                 | 10 (24%)                    |
|                                   | CIP-TET-AMP-ENR-ERY             | 7 (17%)                     |

In addition, the C. jejuni and C. coli isolates which were phenotypically resistant to tetracycline harbored the tet(O) gene identified by PCR, and all isolates susceptible to tetracycline did not present this gene (Table 5).

The point mutation of the 23S rRNA gene was detected in all C. jejuni and C. coli isolates as resistant and intermediate to erythromycin. Additionally, none of the C. jejuni isolates susceptible to erythromycin presented the mutation (Table 5).

In some C. coli isolates that were resistant (61%) and intermediate (43%) to ampicillin, the blaOXA61 amplicon was detected. In most of the C. jejuni resistant isolates (73%) and in the intermediate resistant isolates, the blaOXA61 amplicon was detected. However, 83% of C. jejuni susceptible isolates harbored this amplicon (Table 5).

### 4. Discussion

In the present study, the presence in the slaughterhouse, microbial resistance and resistance mechanisms of thermotolerant Campylobacter were evaluated. Commercial chickens frequently carry high levels of Campylobacter spp. (primarily C. jejuni and C. coli) in their intestine as part of the normal microbiota (Newell and Wagenaar, 2000; Sahin et al., 2002). While C. jejuni is, in general, the most prevalent species of thermotolerant Campylobacter isolated at farm (Bull et al., 2006; Rossler et al., 2019), sometimes a predominant proportion of Campylobacter isolates from broilers are C. coli (Ma et al., 2014; Damjanova et al., 2011; Zbrun et al., 2013, Rossler et al., 2019).

Interestingly, in this study C. coli (42/90) was observed to be more prevalent than C. jejuni (15/90) in cecum samples. Similar results have been reported previously where C. coli was the predominant Campylobacter species in broiler intestinal tracts, which seems to depend on several factors as the geographical area evaluated (Harihara et al., 2009; Henry et al., 2011; Ma et al., 2014), the age of the chicken and antibiotic selection pressure (Wang et al., 2016). However, in this study, the species proportion changed at the end of the slaughter line, where C. jejuni (10/90) was more prevalent than C. coli (5/90) in broiler carcasses. In this sense, some authors suggest that C. coli is less robust and might be more sensitive to the stress conditions found in poultry abattoirs (Peyrat et al., 2008).

Furthermore, thermotolerant Campylobacter were isolated from samples taken in the processing line surfaces, knives and workers’ hands. Many studies have reported similar results, which can be explained by cross contamination with positive Campylobacter carcasses (Ono and Yamamoto, 1999; Chlebicz and Slizewskas, 2018; Zhang et al., 2018). In addition, biofilm formation may be another cause of Campylobacter presence on line processing surfaces. In this sense, previous research identified that some strains are able to form biofilms and can survive longer and resist inactivation (García-Sánchez et al., 2019; Lamas et al., 2018).

Regardless of the source of Campylobacter spp., a recent meta-
analysis has shown that C. coli isolates presented a higher prevalence of antimicrobial resistance to most antimicrobials than C. jejuni (Signorini et al., 2018). In this study, more than 77% of C. coli isolates were resistant to five (CIP, ERY, TET, ENR and AMP) out of eight antimicrobials evaluated (Fig. 1). Also, 74% of the C. jejuni isolates showed resistance against three (CIP, TET and ENR) out of eight antimicrobials evaluated (Fig. 1). High resistance in thermotolerant Campylobacter was described previously, which may be linked to the use of antimicrobials in food-producing animals in each country (CDDEP, 2015; Lajhar et al., 2015, 255 Unicomb et al., 2006; Cha et al., 2017; Nelson et al., 2007). Antimicrobials used as growth promoters in animals, and the abuse or misuse of those antimicrobials, have many times affected the resistance profile of bacteria isolates (Ventola, 2015). Particularly in Argentina, different government institutions have begun to outline strategies to control the use of antimicrobials. However, nowadays there are no clear regulations for the use of antimicrobials in the different stages of the production of food of animal origin (Lazovski et al., 2017).

Furthermore, results have shown that the MDR rate in C. coli and C. jejuni isolates was high (Table 4). The main difference between the Campylobacter species were erythromycin and ampicillin resistance and might be due to C. coli having better adaptation and survivability under antimicrobial selection pressure (Wang et al., 2016), which allows it to develop resistance to these antimicrobials (Chen et al., 2010).

In different countries such as the United States (Tang et al., 2017; Ricotta et al., 2014), China (Li et al., 2017; Wang et al., 2016), Europa (EFSA, 2019), and Guatemala (Benoit et al., 2014); the most common resistance pattern was ciprofloxacin, nalidixic acid, and tetracycline, in concordance with our results.

An intermediate classification of different antimicrobials in thermotolerant Campylobacter isolates was detected in this study (Fig. 1). C. coli had more prevalence of isolates with an intermediate classification level of resistance; this is a serious public health concern because the “intermediate” category includes isolates which showed reduced susceptibility to antimicrobials in comparison with susceptible isolates (CLSI, 2010). In this sense, most of the C. coli isolates were susceptible to streptomycin. Interestingly, the prevalence of C. jejuni isolates resistant to streptomycin was higher than C. coli isolates. Many studies have found that C. coli isolates were susceptible to streptomycin. Interestingly, the prevalence of C. jejuni isolates resistant to streptomycin was higher than C. coli isolates. Many studies have found that C. coli had higher levels of resistance than C. jejuni to streptomycin (Wieczorek et al., 2013; Aarestrup et al., 1997), but a few studies have detected more prevalence in C. jejuni, as has been found in this study (Nguyen et al., 2016).

Molecular mechanisms of resistance were also evaluated, and PCR analysis was used to detect cmeABC genes. While the cmeABC efflux pump is widely distributed in Campylobacter and it is constitutively expressed (Lin et al., 2002; Payot et al., 2002), only 57% of the C. jejuni isolates tested in this study had the three parts of the cmeABC efflux pump. Similar results were found by O’lah et al. (2006), and it can be explained by: a) the pump being inactive, having a non-functional role

![Fig. 2. Prevalence of genetic determinants to resistance of thermotolerant Campylobacter.](image-url)

### Table 5

| Campylobacter species | Antimicrobial agent | Agar dilution assay | Gene presence |
|-----------------------|---------------------|----------------------|---------------|
|                       | Susceptible isolates | Intermediate isolates | Resistant isolates | Gene | Susceptible isolates | Intermediate isolates | Resistant isolates |
| C. jejuni (n = 42)    | Ciprofloxacin       | 8                    | 0              | 34             | Mut GyrA | 0                  | 0              | 34             |
|                       | Enrofloxacin        | 10                   | 0              | 32             | Mut GyrA | 2                  | 0              | 32             |
|                       | Erythromycin        | 33                   | 2              | 7              | Mut      | 0                  | 2              | 7              |
|                       | Tetracycline        | 11                   | 0              | 31             | 23SrRNA  | tet(O)             | 0              | 0              | 31             |
|                       | Ampicillin          | 29                   | 2              | 11             | blaOXA-61| Mut GyrA           | 24             | 2              | 8              |
| C. coli (n = 60)      | Ciprofloxacin       | 0                    | 0              | 60             | Mut GyrA | 0                  | 0              | 60             |
|                       | Enrofloxacin        | 0                    | 7              | 53             | Mut GyrA | 0                  | 7              | 53             |
|                       | Erythromycin        | 0                    | 3              | 57             | Mut      | 0                  | 3              | 57             |
|                       | Tetracycline        | 0                    | 0              | 60             | tet(O)   | Mut                | 0              | 0              | 60             |
|                       | Ampicillin          | 0                    | 14             | 46             | blaOXA-61| Mut                | 0              | 6              | 28             |
(Olah et al., 2006); or b) the efflux pump genes sequence variation (polymorphism) (Guo et al., 2004).

All isolates of this study which were resistant to ciprofloxacin and enrofloxacin carried a substitution of the amino acid 86 as consequence of a mutation in the gyrA gene, and this result was in agreement with previous reports (El-Adawy et al., 2015; Nguyen et al., 2016; Whitehouse et al., 2018). Interestingly, in two C. jejuni isolates, the gyrA point mutation was detected, but said isolates were not resistant to enrofloxacin. It could be suggested that the Thr-86-Ile substitution may not confer universal resistance to all quinolones as has been previously reported (Dionisi et al., 2004; Corcoran et al., 2005; Bolton et al., 2013).

In Campylobacter, resistance to erythromycin is chromosomally encoded by a point mutation of the 23S rRNA gene. In this study, the mutation was detected by MAMA–PCR in resistant and intermediate isolates. Previously, this point mutation has been associated with high levels of erythromycin resistance (Corcoran et al., 2005; Payot et al., 2004; Taylor and Tracz, 2005).

The results of phenotypic and genetic analyses of resistance to tetracycline were fully concordant. All strains resistant to tetracycline were shown to carry the gene tet(O). A correlation study of susceptibility phenotypes and genotypes using WGS has shown that all tetracycline-resistant isolates (n = 108) carried tet(O), but none of the tetracycline-susceptible isolates had this gene (Zhao et al., 2001).

The mechanisms of resistance to some β-lactams such as ampicillin and some of the expanded-spectrum cephalosporins are variable and not very clearly defined (Lachance et al., 1991; Reina et al., 1994; Tajada et al., 1996). The β-lactamase gene blaOXA-61 has spread widely in C. jejuni and C. coli, and the prevalence of the blaOXA-61 gene in ampicillin-resistant Campylobacter can reach up to 91% (Griggs et al., 2009). The C. coli isolates demonstrated to be resistant or intermediate to ampicillin; however, the blaOXA-61 gene was detected in only 57% of them. In C. jejuni, we detected the gene in 73% of resistant isolates. Other types of β-lactamase were described (Lucain et al., 1985), which could explain these results. Lucain et al. (1985) described four enzymes based on their differing activity against eight β-lactams, relative rates of hydrolysis, molecular weight, immunological specificity, and isoelectric point (pI). However, the roles of beta-lactamases in the mechanism of resistance to ampicillin in campylobacters are not yet clear (Griggs et al., 2009).

However, 83% of C. jejuni susceptible isolates showed the presence of the blaOXA-61 gene. In this sense, Casagrande Proietti et al. (2020) hypothesize that the blaOXA-61 gene was poorly expressed in the ampicillin-sensitive isolates and, therefore, they produced less β-lactamase than resistant isolates.

In conclusion, although the size of the samples analyzed is limited and they come from a single slaughterhouse, this study has revealed that the slaughter process line and the carcasses are often contaminated with thermotolerant Campylobacter, suggesting a possible risk of infection to consumers by improper handling and preparation of poultry meat. Moreover, taking into account the limitations regarding the cut-off points of some of the ATMs used, resistance was detected in most of the antimicrobial agents tested, and many of the Campylobacter isolates showed resistance to three or more antimicrobial groups (MDR). Except for ampicillin, all the resistance molecular mechanisms evaluated were detected and correlated with phenotypic resistance. In Argentina, data on the prevalence of Campylobacter throughout the agry-food chain and the incidence of human campylobacteriosis are uncertain. In addition, only a few studies have evaluated antimicrobial resistance in Campylobacter strains. In 2015, an action plan to optimize the AMR surveillance in Argentina was launched by the National Commission for the Control of Antimicrobial Resistance (CoNaCra), coordinated by the National Directorate of Epidemiology. Thus, this information is essential to establish a public health program to control the disease, and it is fundamental for designing a surveillance program to monitor resistance. Therefore, coordinated actions are recommended to reduce or eliminate the risk of thermotolerant Campylobacter at different stages in the slaughterhouse.

CRediT authorship contribution statement

Mariana E. Schreyer: Investigation, Methodology, Writing – original draft. Carolina R. Olivero: Methodology. Eugenia Rossler: Investigation. Lorena P. Soto: Supervision. Laureano S. Frizzo: Validation, Data curation, Conceptualization. Jorge A. Zimmermann: Investigation. Marcelo L. Signorini: Writing – review & editing, Conceptualization, Formal analysis. Zbrun M. Virginia: Writing – original draft, Writing – review & editing, Conceptualization, Funding acquisition.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Zbrun reports financial support was provided by Agencia Nacional de Promocion Cientifica y Tecnologica. Zbrun reports financial support was provided by National University of the Litoral.

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