

## Antimicrobial resistance profile of *Campylobacter jejuni* from sheep and poultry: Insights from Kashmir, India

Hudza Wali<sup>1</sup>, Ali Khan<sup>2</sup>, Faheem ud din<sup>3</sup>, Sabia Qureshi<sup>3</sup>, Mir Nadeem Hassan<sup>3</sup>, Zahid A Kashoo<sup>3</sup>, Pervaiz Dar<sup>3</sup>, Muddasir S Bandy<sup>4</sup>, Fawaz Bandy<sup>5</sup>, Md. Isfaqul Hussain<sup>3</sup>, Mansoor Nabi<sup>3</sup>, Gulzar Badroo<sup>3</sup>, Shaheen Farooq<sup>3</sup>, Maliha Gulzar<sup>3</sup>, Junaid Mehraj<sup>3</sup>, Mahrukh Hafiz<sup>3</sup>, Kifayat Afzal<sup>3</sup>

<sup>1</sup>University of Kashmir, Department of Clinical Biochemistry, India

<sup>2</sup>University of Nebraska Medical Center, Centre of Public Health, Omaha, Nebraska, USA

<sup>3</sup>Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Faculty of Veterinary Sciences and Animal Husbandry, Division of Veterinary Microbiology & Immunology, Bacteriology Laboratory, Shuhama (Aulesteng), India

<sup>4</sup>Sher-e-Kashmir Institute of Medical Sciences, Department of Clinical Pharmacology, Soura, Srinagar, India

<sup>5</sup>University of Kashmir, Government Medical College, Srinagar, India

Received May 20, 2026

Accepted September 7, 2026

### Abstract

*Campylobacter jejuni* is a leading cause of foodborne gastrointestinal infections in humans globally. This study investigates the antimicrobial resistance profile of *C. jejuni* isolates from sheep and poultry. A total of 50 *C. jejuni* isolates previously isolated from poultry cloacal swabs and sheep rectal swabs/abortion samples were screened for antimicrobial resistance against fluoroquinolones (*gyrA* gene),  $\beta$ -lactams (*blaOXA-61* gene), and tetracyclines (*tet*[O] gene). A total of 20% isolates carried the *gyrA* gene with Thr-86-Ile mutation in the QRDR, 22% of the isolates exhibited  $\beta$ -lactam resistance (*blaOXA-61*), and 14% carried the *tet*(O) gene for tetracycline resistance. The OR625189 and OR625190 sequences corresponding to *gyrA* and mutant *gyrA* gene were deposited in GenBank. No statistically significant differences in resistance gene distribution were observed between poultry and sheep isolates, suggesting shared ecological drivers across host species. Phylogenetic comparisons revealed a high degree of similarity between *C. jejuni* isolates from Kashmir, India and those from Spain and Türkiye, highlighting the global challenge of antimicrobial resistance. These findings reinforce the urgent need for strengthened surveillance, prudent antibiotic use in animal husbandry, and integrated One Health strategies to mitigate the spread of resistant *Campylobacter* strains safeguarding both animal and human health.

Thr-86-Ile mutation, *blaOXA-61*, *tet*(O), AMR

*Campylobacter jejuni* is a leading cause of bacterial gastroenteritis worldwide, poultry and livestock being the major reservoirs of the bacterium (Humphrey et al. 2007). Being zoonotic, *C. jejuni* is transmitted to humans through contaminated food and water, making it a significant public health concern due to its potential for causing severe complication like Guillain Barres syndrome, a rare life-threatening infection in young children and adults (EFSA 2019). The emergence of antimicrobial resistance (AMR) in *C. jejuni* has become a formidable challenge, contributing to increased morbidity and mortality, while significantly complicating the therapeutic management of campylobacteriosis (WHO 2014). There has been an increasing evidence of a substantial rise in antimicrobial resistance among *Campylobacter* spp. against fluoroquinolones (ciprofloxacin),  $\beta$  lactams (ampicillin), and tetracycline's among *Campylobacter* strains, reflecting the selective pressure caused by antimicrobial usage leading to amplification in public health burden of campylobacteriosis (Luber et al. 2003; Moser et al. 2020).

#### Address for correspondence:

Sabia Qureshi  
Bacteriology Laboratory  
Division of Veterinary Microbiology & Immunology  
FVSC&A.H Shuhama (Aulesteng) SKUAST-K  
J&K, India-190006

E-mail: [sabiaqureshi@skuastkashmir.ac.in](mailto:sabiaqureshi@skuastkashmir.ac.in)  
<http://actavet.vfu.cz/>

The development of AMR is exacerbated by the global dynamics of poultry trade and intensive agricultural practices. A marked regional variation in resistance profiles among *C. jejuni* isolates from poultry has been reported globally, emphasizing the need for continuous surveillance and judicious antimicrobial use across both human and veterinary medicine (Anderson et al. 2006; Lopez-Chavarrias et al. 2021). Broiler chickens, one of the major reservoirs for dissemination of resistant *Campylobacter* strains in humans, have reported an alarming high resistance to crucial drugs like fluoroquinolones which remain the drug of choice for treating such infections in humans, thereby limiting therapeutic options (Roasto et al. 2007; Popa et al. 2022).

The emergence of AMR among *C. jejuni* is primarily driven by excessive overuse of antibiotics in both human medicine and animal husbandry, exerting selective pressure favouring persistence of resistant strains (Aarestrup et al. 2001). The increasing resistance to key antimicrobial classes (fluoroquinolones,  $\beta$  lactams, and tetracyclines) reported globally underscores the need for comprehensive surveillance systems and implementation of antibiotic stewardship programmes to ensure prudent antibiotic usage (Wieczorek and Osek 2013).

This study was designed to characterize the antimicrobial resistance profiles of *C. jejuni* isolates recovered from sheep and poultry in Kashmir, India, thereby generating vital insights into local resistance dynamics and contributing to Asian and global understanding of this public health concern. In the context of Kashmir, the interdependence of animal husbandry practices, particularly the region's dependence on agriculture and livestock for economic sustenance, amplifies the risk for zoonotic transmission of resistant strains. Moreover, the cultural and dietary preferences for an increased consumption of poultry and sheep meat further elevate the risk of human exposure to resistant *C. jejuni* (Dar et al. 2013). Additionally, environmental factors also facilitate the spread of resistance genes. Several studies have demonstrated that aquatic environments, particularly water bodies affected by agricultural runoff serve as a reservoir and transmission pathway for resistant bacteria (Sproston et al. 2018). The union territory of Kashmir has extensive river systems interconnected with agricultural lands involved in animal husbandry practices.

## Materials and Methods

### Revival of *C. jejuni* isolates

Lyophilized *C. jejuni* isolates (n = 50) stored at  $-80^{\circ}\text{C}$  in the *Campylobacter* laboratory of the division, were revived for this study. These isolates were previously isolated from poultry cloacal swabs (n = 100), sheep rectal swabs/abortion samples (n = 100). The lyophilized cultures were inoculated in Muller Hinton Broth (Hi Media, Mumbai, India) under microaerophilic conditions at  $42^{\circ}\text{C}$  for 24 h, followed by enrichment in Campylo thioglycollate broth (Hi Media) supplemented with Blaser-Wang supplement (Hi Media), and incubated microaerophilically at  $42^{\circ}\text{C}$  for 48 h. The enriched samples were then streaked on modified cefaperazone charcoal agar (mCCDA, Hi Media) and incubated under similar conditions for 24–48 h. The colonies were identified based on colony morphology, Gram staining, and biochemical tests including catalase, oxidase, and hippurate hydrolysis, as per standard protocol (Harvey 1980).

### DNA extraction and AMR profiling

Bacterial DNA was extracted using the Wizard Genomic DNA Purification Kit (Promega, Madison, USA) as per the manufacturer's instructions. For genus and species confirmation, PCR was performed using specific primers for the *Campylobacter* genus 16SrRNA and *C. jejuni* *mapA* gene (Table 1), as described by Leite et al. (1996) and Denis et al. (1999), respectively. Resistance profiles against quinolones (*gyrA* gene),  $\beta$ -lactamase (*blaOXA-61* gene), and tetracyclines (*tet[O]* gene) were determined using PCR, as per protocol of Wang et al. (2016) for the *gyrA* gene, Obeng et al. (2012) for *blaOXA-61*, and Gibreel et al. (2004) for *tet(O)*. The primers sequences used in study are depicted in Table 1. PCR products were visualized after electrophoresis on a 1.5% agarose gel, stained with ethidium bromide, and viewed under UV light.

### Sequencing and phylogenetic analysis

Representative amplified PCR products were sequenced by outsourcing to Unipath, laboratories, Bangalore India Limited, and the sequences were analyzed using the NCBI BLAST tool. Phylogenetic analysis for studying the genetic relationships and origins of the resistance genes was carried out. Representative PCR products for the

Table 1. Primer sequences for detection of *mapA* gene and antimicrobial resistance profiling of *C. jejuni* isolates.

| Sample | Target gene                      | Primer sequence                                           | Product size (bp) | Reference             |
|--------|----------------------------------|-----------------------------------------------------------|-------------------|-----------------------|
| 1      | 16SrRNA(genus specific)          | F-GGTTAAGTCCCGCAACGAGCCGC<br>R-GGCTGATCTACGATTACTAGCGAT   | 283               | Leite et al. 1996     |
| 2      | <i>MapA</i> ( <i>C. jejuni</i> ) | F-CTATTTTATTTTGAGTGCTTGTTG<br>R-GCTTTATTTGCCATTTGTTTTATTA | 589               | Denis et al. 1999     |
| 3      | <i>gyrA</i> CIP <i>C. jejuni</i> | F-CAACTGGTTCTAGCCTTTTG<br>R-AATTTCATCATAGCCTCACG          | 1083              | Wang et al. 2016      |
| 4      | Thr-86-MAMA <i>gyrA</i>          | F-CAACTGGTTCTAGCCTTTTG<br>R-CAAAGCATCATAAACTGCAA          | 410               | Zirnstein et al. 1999 |
| 5      | <i>blaOXA-61</i>                 | F-AGAGTATAATACAAGCG<br>R-TAGTGAGTTGTCAAGCC                | 372               | Obeng et al. 2012     |
| 6      | <i>Campy tet(O)</i>              | F-GGCGTTTTGTTTATGTGCG<br>R-ATGGACAACCCGACAGAAGC           | 559               | Gibreel et al. 2004   |

*gyrA* gene, the Thr-86-Ile mutation in the *gyrA* gene, *blaOXA-61*, and *tet(O)* were also sequenced. Phylogenetic trees were constructed using the maximum likelihood method to assess the genetic relatedness of the isolates to other *Campylobacter* strains globally.

#### Statistical analysis

Descriptive statistics were used to summarize the prevalence of antimicrobial resistance genes among the isolates. Chi-square tests were performed to assess the association between resistance profiles and the source of isolates (poultry vs sheep). A *P* value of < 0.05 was considered significant.

## Results

In this study, 50 lyophilized cultures of *C. jejuni* were revived. These cultures have been previously isolated poultry cloacal swabs and 25 sheep rectal swabs/aborted contents. Of the 50 *C. jejuni* isolates examined in this study, the majority (35 isolates, 70%) originated from poultry cloacal swabs, while a comparatively smaller proportion (15 isolates, 30%) were recovered from sheep. The *C. jejuni* isolates on revival exhibited typical greyish-white coloured colonies on mCCDA. The gram staining of colonies revealed typical s-shaped, gull-winged, curved or long spiral forms and were positive for catalase and oxidase tests. The development of deep purple colour in hippurate broth indicated the hippuricase activity, characteristic for *C. jejuni*. The 16SrRNA and *mapA* gene corresponded to amplification of 283 bp and 589 bp amplicon in PCR, respectively PCR for *C. jejuni* (Plate VII, Fig. 1).

#### Antimicrobial resistance profiling of *C. jejuni* isolates

The distribution of antibiotic resistance determinants (*gyrA*, *blaOXA-61* and *tet(O)*) in *C. jejuni* isolates from poultry and sheep is illustrated in Fig 1. The presence of *gyrA* (topoisomerase), *blaOXA-61*, and *tet(O)* genes was confirmed by detection of specific amplification products corresponding to 1083 bp, 372 bp, and 559 bp, respectively (Plate VII, Fig. 2a; Fig. 3a,b). The representative amplified PCR products for *gyrA*, *blaOXA-61*, *tet(O)* genes were sequenced by outsourcing to Unipath laboratories, Bangalore, India and the sequences were deposited in Genbank. Out of the 50 *C. jejuni* isolates screened in the present study, *gyrA* gene associated with fluoroquinolone resistance was detected in 20% (10) isolates. Of these, 7 (70%) isolates originated from poultry and 3 (30%) from sheep. All *gyrA* positive isolates carried the Thr-86-Ile point mutation within the quinolone resistance- determining region (QRDR) of the *gyrA* subunit of DNA gyrase (Fig. 2b). Similarly, *blaOXA-61* was identified in 11 (22%) isolates of which 7 (63%) were from poultry and 4 (36.6%) from sheep. A total of 8 (72.7%) isolates exhibited

fluoroquinolone resistance as confirmed by PCR. Notably, 7(14%) isolates demonstrated co-resistance to both fluoroquinolones and  $\beta$ -lactams. The *tet*(O) genes were detected in seven isolates comprising 4 (57%) from poultry and three (42.8%) from sheep. Antimicrobial resistance profile and heat map illustrating the distribution of resistance to these three antibiotic classes across all isolates from poultry and sheep are presented in Figs 4 and 5 (Plate VIII).

#### Sequence analysis of mutation Thr-86-Ile in QRDR of *gyrA* gene

Amplicons corresponding to *gyrA* gene (1083 bp) and the mutant *gyrA* allele (410 bp) associated with fluoroquinolone resistance in *C. jejuni* were sequenced from Unipath lab, Bangalore, India. The resulting DNA sequences have been deposited in GenBank under accession numbers, OR625189 and OR625190.

Sequence alignment using BioEdit and comparative analysis with NCBI BLAST revealed that the isolates in this study clustered with *C. jejuni* strains from Spain exhibiting 100% sequence homology. Phylogenetic reconstruction employing the fast minimum evolution method (maximum sequence difference 0.75) further confirmed that the quinolone resistance-determining region (QRDR) of the *gyrA* gene was identical to strains reported from Spain and Türkiye.

Statistical evaluation using chi-square test did not reveal any significant association between the source of isolates (poultry vs sheep) and the presence of resistance genes (*gyrA*, *blaOXA-61*, *tet*[O]) ( $P > 0.05$ ).

### Discussion

The present study reveals a concerning prevalence of antimicrobial resistance (AMR) genes among *C. jejuni* isolates recovered from both poultry and sheep in the Kashmir region. The detection of the *gyrA* gene in 20% of the isolates, together with Thr-86-Ile mutation, underscores the extent of fluoroquinolone resistance. This finding is consistent with global reports documenting the increase of fluoroquinolone-resistant *C. jejuni* strains (Wieczorek and Osek 2013). The mutation within the QRDR of the *gyrA* gene is widely recognized as principal driver of high-level fluoroquinolone resistance in *C. jejuni*, and its presence in local isolates reflects the global trajectory of rising fluoroquinolone resistance (Zirnstein et al. 1999). The genetic relatedness of Kashmiri isolates to strains from Europe and Asia indicates potential transboundary dissemination of resistant lineages, possibly facilitated by migratory birds and global trade networks (Sproston et al. 2018).

The detection of the *blaOXA-61* gene in 22% of *C. jejuni* isolates raises serious concerns regarding the continued efficacy of  $\beta$ -lactam antibiotics, particularly ampicillin, which remains widely used in veterinary practice. Its occurrence in isolates from both poultry and sheep highlights the risk of resistant strains entering the human food chain. This finding corroborates with international reports that emphasize the growing challenge of  $\beta$ -lactam resistance in *Campylobacter* spp.

Similarly, the identification of the *tet*(O) gene in 14% of isolates, reflects the selective pressure exerted by extensive use of tetracycline in agriculture. The presence of *tet*(O) in both poultry and sheep isolates corroborates the findings from other regions, underscoring the global dissemination of tetracycline-resistant *C. jejuni* strains. Reddy and Zishiri (2017) reported widespread distribution of *tet*(O) and *gyrA* genes in *Campylobacter* isolates from chickens and human clinical cases in South Africa, alongside detection of *blaOXA-61*.

Similarly, investigations in Italy revealed high resistance to ciprofloxacin and tetracycline among *C. jejuni* isolates from humans, poultry, and wild birds, highlighting the pervasive nature of these resistance determinants across diverse ecological niches (Marotta et al. 2019). A study conducted in Ireland reported that approximately 26% of *Campylobacter*

*coli* isolates from broiler chickens exhibited resistance to nalidixic acid and ciprofloxacin, while 29% of *C. jejuni* isolates showed similar resistance patterns (Lynch et al. 2020). Fluoroquinolones, particularly ciprofloxacin, possess broad-spectrum activity and high potency, making them effective agents for treating campylobacteriosis. However, due to the rapid emergence of fluoroquinolone resistance over recent decades, these drugs have been relegated to secondary therapeutic status, with macrolides now preferred as first-line treatment options (Mohan et al. 2025).

More recently Pacifico et al. (2023) identified a low-level tetracycline resistance gene, *tet(O)*<sub>3</sub>, was food isolates of *C. jejuni*. This variant is similar to the *tet(O)* gene in *Streptococcus pneumoniae* but with a truncated promoter sequence underscores the importance of detecting novel resistance genes through whole genome sequencing to strengthen AMR surveillance. These findings reinforce the significance of monitoring AMR trends in *Campylobacter* spp., particularly concerning  $\beta$ -lactam and tetracycline resistance. Understanding the prevalence and mechanisms of resistance genes is critical for devising effective strategies to combat AMR in these pathogens.

The absence of host-specific differences in resistance gene distribution suggests that AMR in *C. jejuni* is a widespread issue across the region's agricultural sector, thus necessitating integrated strategies encompassing both poultry and livestock management. The homogeneity in resistance profiles highlights the likelihood of shared ecological or epidemiological drivers, including common antimicrobial usage practices and overlapping transmission pathways between poultry and small ruminants. This reinforces the need for a comprehensive One Health approach, whereby poultry and sheep populations are jointly monitored to mitigate zoonotic risks of dissemination of fluoroquinolone- and  $\beta$ -lactam-resistant *Campylobacter* strains to humans.

In conclusion, this AMR profile of *C. jejuni* isolates from sheep and poultry in Kashmir highlights a serious public health concern, with resistance determinants spanning fluoroquinolones,  $\beta$ -lactams, and tetracyclines. Importantly, no significant difference was observed in distribution of AMR genes between isolates from different host species sources, highlighting the pervasive nature of resistance across the agricultural sector. The genetic similarities between local isolates and those reported from other regions further emphasize the global challenge posed by AMR in *C. jejuni*. These findings reinforce the need for strengthened antibiotic stewardship, enhanced surveillance, and integrated One Health strategies to curb the dissemination resistant strains and safeguard public and animal health.

#### Conflict of interest

The authors declare that they have no competing interests.

#### Acknowledgements

The study was financed by DBT, GOI, and Grant No: BT/PR40347/ADV/90/286/2020 Dated 22/09/2021.

#### References

- Aarestrup FM, Seyfarth AM, Emborg HD, Pederson K, Hendrikson RS, Bager F 2001: Effect of abolishment of the use of antimicrobial agents for growth promotion on occurrence of antimicrobial resistance in fecal enterococci from food animals in Denmark. *Antimicrob Agents Chemother* **45**: 2054-2059
- Andersen SR, Saadbye P, Shukri NM, Rosenquist H, Neilson NL, Boel J 2006: Antimicrobial resistance among *Campylobacter jejuni* isolated from raw poultry meat at retail level in Denmark. *Int J Food Microbiol* **107**: 250-255
- Dar MA, Ahmad SM, Bhat SA 2013: Prevalence of antimicrobial resistance among *Campylobacter* species isolated from poultry in the Kashmir Himalaya, India. *Vet World* **6**: 703-706
- Denis M, Soumet C, Rivoal K, Ermel G, Blivet D, Salavat G, Colin P 1999: Development of a multiplex PCR assay for simultaneous identification of *Campylobacter jejuni* and *C. coli*. *Lett Appl Microbiol* **29**: 406-410

- EFSA, ECDC 2019: The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2017. *EFSA J* **17**: e05598
- Gibreel A, Tracz DM, Nonaka L, Ngo TM, Connell SR, Taylor DE 2004: Incidence of antibiotic resistance in *Campylobacter jejuni* isolated in Alberta, Canada, from 1999 to 2002, with special reference to *tet(O)*-mediated tetracycline resistance. *Antimicrob Agents Chemother* **48**: 3442-3450
- Harvey S 1980: Hippurate hydrolysis by *Campylobacter fetus*. *J Clin Microbiol* **11**: 435-437
- Humphrey T, O'Brien S, Madsen M 2007: *Campylobacters* as zoonotic pathogens: A food production perspective. *Int J Food Microbiol* **117**: 237-257
- Leite PC, Blom K, Patton CM, Nicholson MA, Steigerwalt AG, Hunter SB, Brenner DJ 1996: Rapid identification of *Campylobacter* species by restriction fragment length polymorphism analysis of a PCR-amplified fragment of the gene coding for 16S rRNA. *J Clin Microbiol* **34**: 62-67
- Lopez Chavarrias V, Ugarte Ruiz M, Bárcena C, Olarra A, Garcia M, Saez JL, Dominguez L, Alvarez J 2021: Monitoring of antimicrobial resistance to aminoglycosides and macrolides in *Campylobacter coli* and *Campylobacter jejuni* from healthy livestock in Spain (2002–2018). *Front Microbiol* **12**: 1-10
- Luber P, Wagner J, Hahn H, Bartelt E 2003: Antimicrobial resistance in *Campylobacter jejuni* and *Campylobacter coli* strains isolated in 1991 and 2001–2002 from poultry and humans in Berlin, Germany. *Antimicrob Agents Chemother* **47**: 3825-3830
- Lynch CT, Lynch H, Egan J, Whyte P, Bolton D, Coffey A, Lucey B 2020: Antimicrobial resistance of *Campylobacter* isolates recovered from broilers in the Republic of Ireland in 2017 and 2018: an update. *Br Poult Sci* **61**: 550-556
- Marotta F, Garofolo G, Di Marcantonio L, Di Serafino G, Neri D, Romantini R, Di Giannatale E 2019: Antimicrobial resistance genotypes and phenotypes of *Campylobacter jejuni* isolated in Italy from humans, birds from wild and urban habitats, and poultry. *PLoS One* **14**: e022380
- Mohan V, Strepis N, Mitsakakis K, Becker K, Chindelevitch L, Shivaperumal N, Swe-Han K, Hays JP 2025: Antimicrobial resistance in *Campylobacter* spp. focussing on *C. jejuni* and *C. coli*: a narrative review. *J Glob Antimicrob Resist* **33**: 100-112
- Moser S, Seth Smith H, Egli A, Kittl S, Overesch G 2020: *Campylobacter jejuni* from canine and bovine cases of campylobacteriosis express high antimicrobial resistance rates against fluoroquinolones and tetracyclines. *J Pathog* **9**: 691
- Obeng AS, Rickard H, Sexton M, Pang Y, Peng H, Barton M 2012: Antimicrobial susceptibilities and resistance genes in *Campylobacter* strains isolated from poultry and pigs in Australia. *J Appl Microbiol* **113**: 294-307
- Pacifico C, Wösten M, Hilbert F 2023: Low-level tetracycline resistance gene *tet(O)*\_3 in *Campylobacter jejuni*. *Antibiotics* **12**: 426
- Popa SA, Morar A, Ban Cucerzan A, Tirziu E, Herman V, Sallam KI, Imre K 2022: Occurrence and antimicrobial resistance profiles of *Campylobacter jejuni* in slaughtered broiler chickens in North-Western Romania. *Antibiotics* **11**: 1713
- Roasto M, Juhkam K, Tamme T, Horman A, Hakkinen L, Reinik M, Kivisto R 2007: High level of antimicrobial resistance in *Campylobacter jejuni* isolated from broiler chickens in Estonia in 2005 and 2006. *J Food Prot* **70**: 1940-1944
- Reddy S, Zishiri O 2017: Detection and prevalence of antimicrobial resistance genes in *Campylobacter* spp. isolated from chickens and humans in South Africa. *Onderstepoort J Vet Res* **84**: a1411
- Sproston EL, Wimalaratna HML, Sheppard SK 2018: Trends in fluoroquinolone resistance in *Campylobacter*. *Microb Genom* **4**: e000198
- Wang Y, Dong Y, Deng F, Liu D, Yao H, Zhang Q, Shen J 2016: Species shift and multidrug resistance of *Campylobacter* from chicken and swine, China, 2008–2014. *J Antimicrob Chemother* **71**: 666-669
- Wieczorek K, Osek J 2013: Antimicrobial resistance mechanisms among *Campylobacter*. *Biomed Res Int* **2013**: 340605
- World Health Organization 2014: Antimicrobial resistance: global report on surveillance. WHO, Geneva, 257 p.
- Zirnstein G, Li Y, Swaminathan B, Angulo F 1999: Ciprofloxacin resistance in *Campylobacter jejuni* isolates: detection of *gyrA* resistance mutations by mismatch amplification mutation assay PCR and DNA sequence analysis. *J Clin Microbiol* **37**: 3276-3280

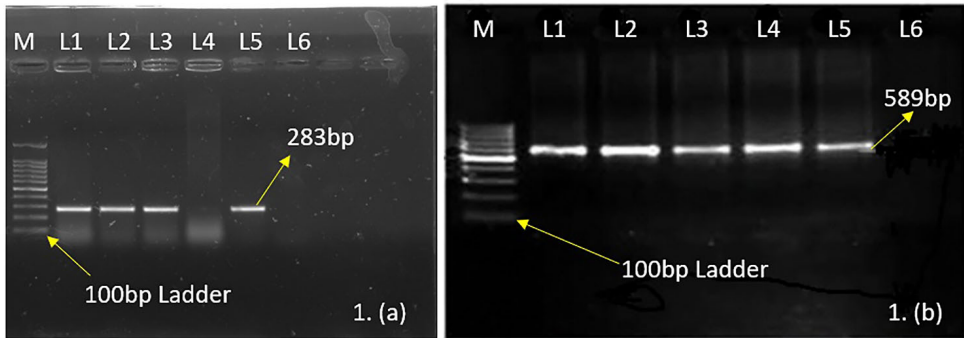


Fig. 1. Agarose gel electrophoresis. (a) 283 bp amplicon of *Campylobacter* genus; Lane M: 100 bp DNA ladder; Lanes 1–4: positive isolates for *Campylobacter* genus; Lane 5: positive control; Lane 6: negative control. (b) 589 bp amplicon of *C. jejuni*; Lane M: 100 bp of DNA ladder; Lane 5: positive control; Lanes 1–4: positive isolates for *C. jejuni*; Lane 6: negative control

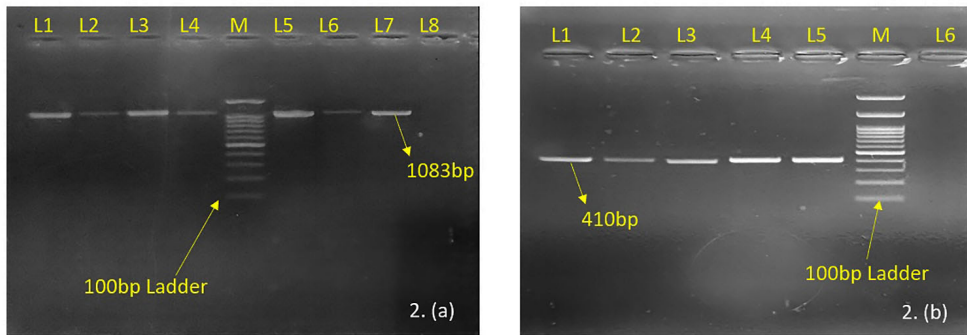


Fig. 2. Agarose gel electrophoresis. (a) 1083 bp amplicon of *gyrA* gene of *C. jejuni*; Lanes 1–6: *gyrA* positive isolates; Lane M: 100 bp DNA ladder; Lane 7: positive control; Lane 8: negative control. (b) 410 bp amplicon for Thr-86-Ile mutation; Lanes 1–4: Thr-86-Ile positive isolates; Lane 5: positive control; Lane M: 100 bp DNA ladder; Lane 6: negative control

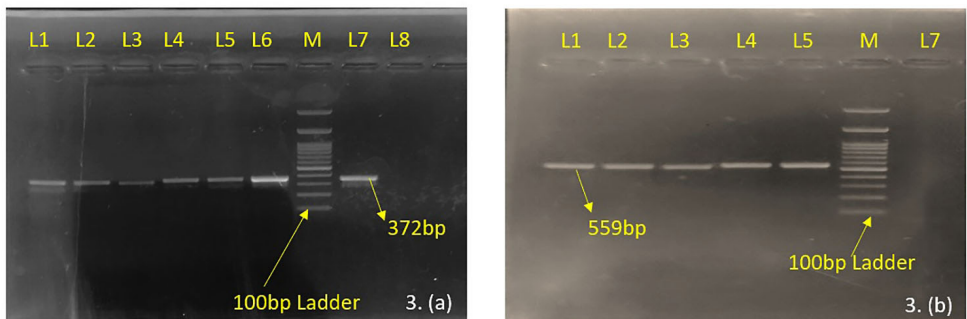


Fig. 3. Agarose gel electrophoresis. (a) 372 bp amplicon of *blaOXA-61* gene of *C. jejuni*; Lanes 1–6: *blaOXA-61* positive isolates; Lane M: 100 bp DNA ladder; Lane 7: positive control; Lane 8: negative control. (b) 559 bp amplicon of *tet(O)* gene of *C. jejuni*; Lanes 1–4: *tet(O)* positive isolates; Lane 5: positive control; Lane M: 100 bp ladder; Lane 6: negative control

Plate VIII

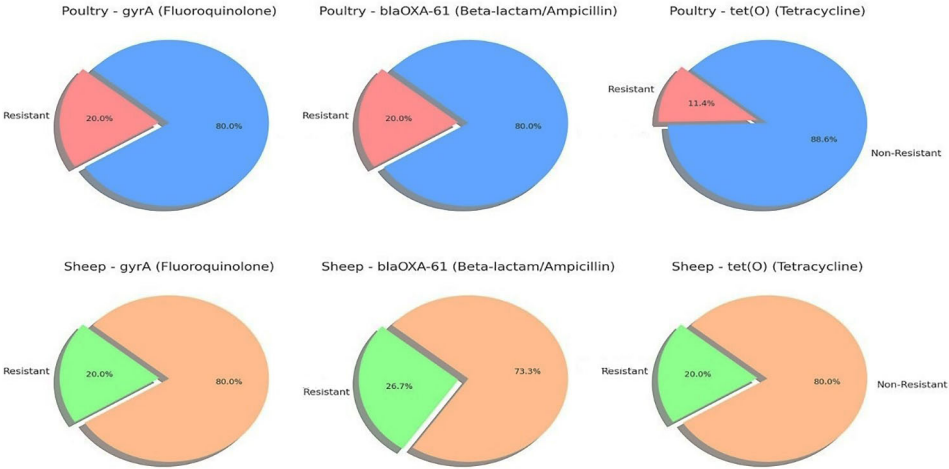


Fig. 4. Antimicrobial resistance profile of *C. jejuni* isolates in poultry (top row) and sheep (bottom row)

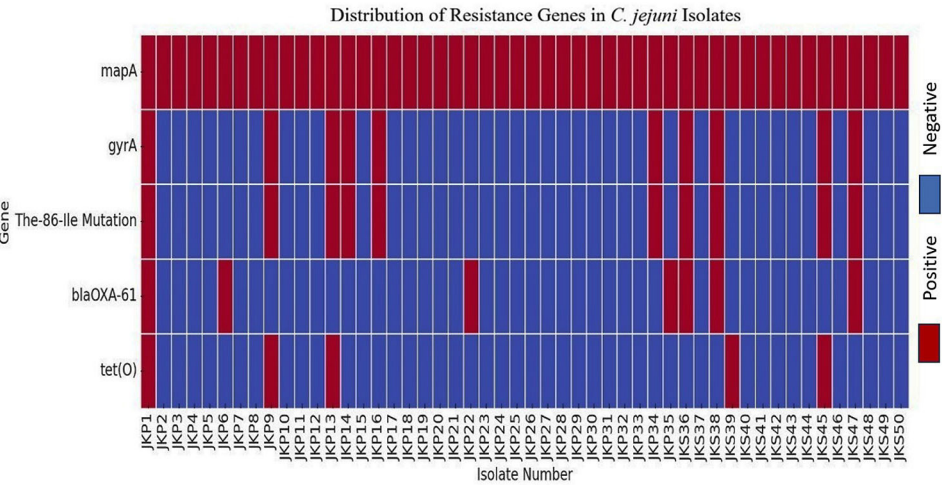


Fig. 5. Heatmap depicting gene presence in *C. jejuni* isolates. Red: gene present in isolate; blue: gene absent in isolate