



**Bibliografi Penyakit Hewan**  
**Perpustakaan BRMP Veteriner**

**Bibliografi Campylobacteriosis:**  
**Tren, Resiko, dan Solusi Kesehatan Publik**



**PERPUSTAKAAN BALAI BESAR PERAKITAN DAN MODERNISASI VETERINER**

**BADAN PERAKITAN DAN MODERNISASI PERTANIAN**

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## Kata Pengantar

Puji syukur kita panjatkan ke hadirat Tuhan Yang Maha Esa, karena atas rahmat dan karunia-Nya bibliografi dengan tema Campylobacteriosis ini dapat tersusun. Bibliografi ini disusun sebagai upaya penyediaan informasi ilmiah yang komprehensif mengenai berbagai aspek terkait bakteri *Campylobacter* dan penyakit campylobacteriosis, baik dari sisi epidemiologi, faktor risiko, deteksi, keragaman genetik, resistensi antimikroba, hingga strategi pengendalian pada sektor pangan dan kesehatan masyarakat.

Kumpulan referensi yang terangkum dalam bibliografi ini memuat hasil-hasil penelitian terkini dari berbagai negara yang meliputi:

- Pola temporal kejadian campylobacteriosis pada manusia yang dikaitkan dengan prevalensi *Campylobacter* di unggas dan produk turunannya.
- Karakterisasi isolat dari hewan (unggas, babi, sapi, bebek) maupun kasus sporadis pada manusia.
- Metode deteksi cepat, teknik PCR spesifik, serta pemanfaatan *big data* dan *machine learning* untuk penelusuran sumber infeksi.
- Analisis risiko terkait konsumsi susu mentah, daging unggas, maupun produk sampingan lainnya.
- Kajian genetik dan molekuler terkait faktor virulensi, keanekaragaman strain, serta gen resistensi antimikroba.
- Evaluasi efektivitas biosekuriti, model pengendalian berbasis risiko, hingga pendekatan *One Health* dalam menurunkan beban penyakit.

Bibliografi ini diharapkan dapat menjadi sumber rujukan yang bermanfaat bagi peneliti, akademisi, mahasiswa, praktisi kesehatan hewan maupun kesehatan masyarakat, serta pihak-pihak yang berkepentingan dalam pengendalian zoonosis berbasis pangan. Dengan adanya bibliografi ini, diharapkan lahir gagasan dan inovasi baru dalam upaya pencegahan, pengendalian, dan penanggulangan penyakit campylobacteriosis di tingkat nasional maupun global.

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Akhir kata, kami menyampaikan terima kasih kepada semua pihak yang telah membantu dalam penyusunan bibliografi ini. Semoga karya sederhana ini dapat memberikan kontribusi positif bagi perkembangan ilmu pengetahuan dan peningkatan kesehatan masyarakat.

Perpustakaan BRMP Veteriner

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1. [The temporal pattern and relationship of Campylobacter prevalence in broiler slaughter batches and human campylobacteriosis cases in Sweden 2009–2019](#), Roland Lindqvist, Wonhee Cha, Rikard Dryselius, Elina Lahti, **International Journal of Food Microbiology**, Volume 378, 2022, 109823, <https://doi.org/10.1016/j.ijfoodmicro.2022.109823>.

**Abstract:**

Thermophilic *Campylobacter* species are the most common cause of bacterial gastroenteritis worldwide, and handling and consumption of broiler meat is considered a major foodborne transmission route. Both the incidence of campylobacteriosis and the prevalence of *Campylobacter* in broilers show seasonality but the impact of this association and broiler prevalence on human incidence is not clear. To explore this relationship we applied two approaches for analyzing time series data using different time resolutions (weekly, bi-weekly or monthly data) of human campylobacteriosis cases and prevalence of *Campylobacter* spp. in broiler slaughter batches in Sweden between 2009 and 2019. The decomposition of time series into seasonal (S), long-term trend (T) and residual components (STL model) showed a close overlap in seasonal patterns in terms of timing and the proportional change of peaks from normalized yearly levels. Starting 2016, when a large outbreak was reported, there was significant overlap in the trend components as well. The trend component of human cases prior to the outbreak corresponded to a linear increase of 6.5 % cases annually. In comparison, the estimated annual increase in broiler consumption was 2.7 %. An additive approach for time-series counts incorporating seasonal and epidemic (cases are a function of previous cases) components found a positive association between human cases and broiler prevalence with an optimal lag of 2 weeks, 1 bi-week, or 0 months. Considering the estimated time between slaughter and consumption, incubation time, and the time between on-set of disease and testing, a 2-week lag may be consistent with transmission via handling and consumption of fresh broiler meat. The best model included broiler prevalence as a factor in the epidemic model component, not in the seasonal component. The outcomes in terms of best model, optimal lags and significance of parameters, using weekly, bi-weekly or monthly data were, in general, in agreement but varied with data resolution when only a subset of the time series, not including any known broiler associated outbreaks, was analyzed. The optimal resolution based on the available data and conditions of the present analysis appeared to be weekly or bi-weekly data. Results suggest that broiler prevalence with a 2 week lag period can explain part of the human cases but has a smaller explanatory impact during the part of the study period not including the large known outbreaks. There is no simple relationship between broiler prevalence and human

cases. Additional factors than broiler prevalence need to be evaluated in order to understand the transmission routes and epidemiology of campylobacteriosis.

**Keywords:** Time series analysis; Seasonality; Fresh broiler meat; Data resolution

2. [Characterization of Campylobacter Isolates Recovered from Clinically Healthy Pigs and from Sporadic Cases of Campylobacteriosis in Humans](#), Evelyne Guévremont, Robert Higgins, Sylvain Quessy, **Journal of Food Protection**, Volume 67, Issue 2, 2004, Pages 228-234, <https://doi.org/10.4315/0362-028X-67.2.228>.

**Abstract:**

Campylobacter spp. were recovered from 660 (77.6%) of 850 swine cecal contents at the abattoir and from 24 (8.6%) of 278 specimens from sporadic cases of human diarrhea during the same period in the same geographical area. Campylobacter coli represented 95.7% of Campylobacter isolates recovered from pigs and 8.3% of those isolated from humans. Genetic profiles were determined by pulsed-field gel electrophoresis (PFGE) using KpnI enzyme to characterize the isolates in combination with phenotypic assays to detect production of cytotoxins, enterotoxins, and hemolysins. Among a subset of isolates (n = 10), up to five colonies from the same animal were characterized by PFGE. In 5 (50%) of 10 of the isolates, more than one genetic profile was observed per pig. Among the 100 isolates from pigs selected for further analysis, 81 different genetic profiles were observed, whereas 20 different genetic profiles were found among the 24 isolates of human origin. Cytotoxicity on Chinese hamster ovary cells was observed in 11 (11%) of 98 isolates from pigs and in 5 (21%) of 24 Campylobacter isolates from humans. No enterotoxin production was detected in Campylobacter isolates in this study, but 17 (71%) of 24 human and 61 (63%) of 97 pig isolates showed hemolytic activity. The study of genotypic and phenotypic profiles of swine and human isolates revealed no epidemiological relationship between isolates. The low genomic relatedness observed between groups of isolates and the weak toxicity level of swine isolates suggest that the hazard of contamination of humans by Campylobacter associated with swine production is low.

3. [Accurate and fast identification of Campylobacter fetus in bulls by real-time PCR targeting a 16S rRNA gene sequence](#), Rafael Delpiazco, Maila Barcellos, Sofía Barros, Laura Betancor, Martín Fraga, Jorge Gil, Gregorio Iraola, Claudia Morsella, Fernando Paolicchi, Ruben Pérez, Franklin Riet-Correa, Margarita Sanguinetti, Alfonso Silva,

**Abstract:**

*Campylobacter fetus* is an important animal pathogen that causes infectious infertility, embryonic mortality and abortions in cattle and sheep flocks. There are two recognized subspecies related with reproductive disorders in livestock: *Campylobacter fetus* subsp. *fetus* (Cff) and *Campylobacter fetus* subsp. *venerealis* (Cfv). Rapid and reliable detection of this pathogenic species in bulls is of utmost importance for disease control in dairy and beef herds as they are asymptomatic carriers. The aim of the present work was to assess the performance a real-time PCR (qPCR) method for the diagnosis of *Campylobacter fetus* in samples from bulls, comparing it with culture and isolation methods. 520 preputial samples were both cultured in Skirrow's medium and analyzed by qPCR. The estimated sensitivity of qPCR was 90.9% (95% CI, 69.4%–100%), and the specificity was 99.4% (95% CI, 98.6% - 100%). The proportion of *C. fetus* positive individuals was 2.1% by isolation and 2.5% by qPCR. Isolates were identified by biochemical tests as Cfv (n = 9) and Cff (n = 2). Our findings support the use of qPCR for fast and accurate detection of *C. fetus* directly from field samples of preputial smegma of bulls. The qPCR method showed to be suitable for massive screenings because it can be performed in pooled samples without losing accuracy and sensitivity.

**Keywords:** *Campylobacter fetus*; Bovine genital campylobacteriosis; qPCR; Molecular diagnosis

4. [Quantitative microbiological risk assessment model for \*Campylobacter\* in raw milk of dairy cows in Germany](#), Anna-Delia Knipper, Tasja Crease, Taras Günther, Matthias Filter, Maarten Nauta, **Microbial Risk Analysis**, Volume 25, 2023, 100274, <https://doi.org/10.1016/j.mran.2023.100274>.

**Abstract:**

The consumer demand for raw milk from dairy cows has increased and local sales via vending machines have been intensified. Therefore, this study aimed to assess the risk associated with the consumption of unboiled raw milk contaminated with *Campylobacter* by estimating the number of campylobacteriosis cases. For this a stochastic quantitative microbial risk assessment (QMRA) model was developed that covered the whole supply chain. Information and data for model parametrization were obtained from research publications. Different probability distributions were used to represent the data whenever possible and probabilistic risk estimation was performed using Monte Carlo simulations. Simulations for outbreaks from single vending machines were performed using the developed QMRA baseline model. Further, different risk

mitigation scenarios along the supply chain were evaluated to support risk managers in controlling Campylobacter. The analysis suggest a role for Campylobacter infections due to fecal contamination of cows' udder. The model can easily be adapted and extended when additional data become available as it is provides in the harmonized exchange Food Safety Knowledge Exchange (FSKX) format.

**Keywords:** QMRA; Modeling; Food safety; Vending machine; Supply chain; Campylobacteriosis

5. [Genetic diversity of Campylobacter jejuni and Campylobacter coli isolated from poultry meat products sold on the retail market in Southern Brazil](#), S.F.R. Würfel, W.P. da Silva, M.G. de Oliveira, N.R. Kleinubing, G.V. Lopes, E.A. Gandra, O.A. Dellagostin, **Poultry Science**, Volume 98, Issue 2, 2019, Pages 932-939, <https://doi.org/10.3382/ps/pey365>.

**Abstract:**

Campylobacter is regarded as the most common bacterial cause of gastroenteritis throughout the world and most cases of human campylobacteriosis can be traced back to the consumption of poultry meat. In Brazil, few studies evaluated the genetic relatedness among Campylobacter isolates. The aim of this research was to evaluate the genetic diversity of Campylobacter spp. isolated from poultry meat products sold on the retail market in Southern Brazil. The presumptive identification of Campylobacter was performed using traditional microbiological analysis, followed by molecular confirmation by PCR. The genetic diversity of isolates was analyzed by pulsed-field gel electrophoresis (PFGE). Campylobacter spp. was isolated from 91.7% (33/36) of the samples, totaling 48 isolates. Campylobacter jejuni was the most prevalent species isolated (90.8%). PFGE data revealed 26 pulsotypes and 18 PFGE patterns composed of only 1 isolate. Campylobacter isolates exhibited high genetic diversity; however, some clones were recurrent in the poultry meat products sold on the retail market. As the south region of Brazil is an important producer and exporter of chicken meat, our results highlight the need to control this pathogen in the food chain in this area of the world to reduce the risks of exposing consumers to campylobacteriosis.

**Keywords:** Campylobacter; food safety; genetic diversity; poultry meat; pulsed-field gel electrophoresis

6. [Prevalence and genetic diversity of Campylobacter spp. in the production chain of broiler chickens in Lebanon and its association with the intestinal protozoan](#)

[Blastocystis sp](#), S Greige, K Rivoal, M Osman, D El Safadi, F Dabboussi, R El Hage, E Viscogliosi, M Hamze, M Chemaly, **Poultry Science**, Volume 98, Issue 11, 2019, Pages 5883-5891, <https://doi.org/10.3382/ps/pez286>.

**Abstract:**

*Campylobacter jejuni* is recognized as the most common foodborne pathogen associated with human gastroenteritis worldwide. Broilers are frequently infected by the bacteria and are considered the main source of exposure to humans. However, despite its public health impact, no recent data are currently available in Lebanon about *Campylobacter* spp. in poultry and human population. Therefore, this study aimed to determine the prevalence and genetic diversity of *Campylobacter* spp. in 227 ceca and on 227 carcasses of broiler chickens collected in Lebanese slaughterhouses. Overall, the prevalence of *Campylobacter* was shown to reach 67.0% in ceca and 17.2% on carcasses of Lebanese poultry. The only 2 *Campylobacter* species identified were *C. jejuni* and *C. coli*, with a slightly higher prevalence of *C. coli* in ceca and of *C. jejuni* on carcasses. A high level of genetic diversity was reported among the 51 *C. jejuni* isolates selected, since 25 distinct profiles were identified according to the comparative genomic fingerprinting typing method based on a subset of 40 genes using the 90% similarity threshold. Predominant clusters observed in Lebanese poultry isolates were also frequently found among French human clinical cases, highlighting that broiler chickens represent a potential reservoir for human campylobacteriosis. In addition, a significantly higher prevalence of *Campylobacter* spp. was found in slaughterhouse workers than in a cohort of hospitalized patients with no contact with poultry, confirming that contaminated broiler chickens in slaughterhouse appeared to be a non-negligible source of *Campylobacter* spp. transmission. Interestingly, a significant association between *Campylobacter* spp. and *Blastocystis* sp. has been observed. This correlation suggested that the presence of *Campylobacter* spp. would be favored when *Blastocystis* sp. is present and, similarly, the absence of one would favor the absence of the other. This is the first large-scale investigation focusing on the impact of *Campylobacter* spp. in broiler chickens in Lebanon and confirmed the need to implement prevention and control measures in the poultry production to reduce the burden of campylobacteriosis in the human population.

**Keywords:** *Campylobacter*; *Blastocystis*; zoonosis; genetic diversity; poultry

7. [Antimicrobial resistance genes and plasmids in \*Campylobacter jejuni\* from broiler production chain in Southern Brazil](#), Natalie Rauber Kleinubing, Tassiana Ramires, Simone de Fátima Rauber Würfel, Louise Haubert, Letícia Klein Scheik, Frederico Schmitt Kremer, Graciela Volz Lopes, Wladimir Padilha da Silva, **LWT - Food Science and Technology**, Volume 144, 2021, 111202, <https://doi.org/10.1016/j.lwt.2021.111202>.

### **Abstract:**

*Campylobacter jejuni* is the main cause of foodborne gastroenteritis in humans throughout the world. Besides impairing the treatment of campylobacteriosis, the presence of resistant *C. jejuni* isolates in the food production chain raises a concern to human health. The aims of this study were to perform the phenotypic and genotypic characterization of antimicrobial resistance in *C. jejuni* isolates from broiler production chain in Southern Brazil, as well as to verify the presence of plasmids among the isolates. In this study, 82.2% of *C. jejuni* isolates presented resistance to at least one antimicrobial tested, and 46.4% were multidrug resistant. The *cmeB* and *cmeG* genes, which encode to multidrug efflux pumps, were reported in 91.3% of the resistant isolates. The *tet(O)* gene was found in 81.2% of the tetracycline-resistant isolates. All the isolates with phenotypic resistance to kanamycin were positive for the presence of the *aphA-3* gene. Regarding the  $\beta$ -lactams, the *bla<sub>oxa-61</sub>* gene was present in 66.7% of the ampicillin-resistant isolates. Thus, the high rates of antimicrobial resistance and the presence of plasmids harboring antimicrobial resistance genes found in *C. jejuni* isolates highlights the importance of a prudent and judicious use of antimicrobial agents in animal production in Brazil.

**Keywords:** *Campylobacter* spp.; Efflux pumps; Multidrug resistance

8. [Sharing Milk but Not Messages: Campylobacteriosis Associated with Consumption of Raw Milk from a Cow-Share Program in Alaska, 2011](#), L.J. Castrodale, R.F. Gerlach, C.M. Xavier, B.J. Smith, M.P. Cooper, J.B. McLaughlin, **Journal of Food Protection**, Volume 76, Issue 5, 2013, Pages 744-747, <https://doi.org/10.4315/0362-028X.JFP-12-329>.

### **Abstract:**

Alaska public and environmental health authorities investigated a cluster of campylobacteriosis cases among people who had consumed raw, unpasteurized milk obtained from a cow-share program in Alaska. Although raw milk is not permitted by law to be offered commercially, consumers can enter into cow-share agreements whereby they contribute funds for the upkeep of cows and in turn receive a share of the milk for their personal use. Laboratory testing of stool specimens collected from ill persons and from cows on the farm revealed an indistinguishable strain of *Campylobacter*. In this outbreak, numerous confirmed and suspected cases were not among cow shareholders; therefore, these individuals had not been advised of the potential health hazards associated with consumption of raw milk nor were they informed of the outbreak developments.

9. [Outbreak of campylobacteriosis following pre-cooked sausage consumption](#), Christopher Graham, Rosemary Whyte, Brent Gilpin, Angela Cornelius, J. Andrew Hudson, Dianne Morrison, Helen Graham, Carolyn Nicol, **Australian and New Zealand Journal of Public Health**, Volume 29, Issue 6, 2005, Pages 507-510, <https://doi.org/10.1111/j.1467-842X.2005.tb00239.x>.

**Abstract:**

A small outbreak of campylobacteriosis involving three cases was investigated in terms of Campylobacter types present in the suspect food (precooked sausages) and clinical samples from the cases. Method: Foods and faecal samples from people involved in the incident, which occurred in Christchurch, New Zealand, were tested for the presence of Campylobacter and identification of the species made. Isolates were typed by Penner serotyping and macrorestriction analysis using pulsed-field gel electrophoresis (PFGE). Investigations were conducted as to whether the contamination was on the surface or the interior of the sausages. Results: All isolates from food and faecal samples were identified as *C. jejuni* and were indistinguishable from one another by the typing methods employed. Only the surfaces of the sausages were contaminated. Three other isolates of an indistinguishable subtype were isolated from campylobacteriosis cases in Christchurch occurring over approximately the same period. Conclusions and Implications: Given the rarity of the subtype isolated from the three family members and the three other cases, it is possible that the outbreak was larger than the initial investigation revealed. It is likely that the sausages were contaminated after they had been cooked by the retailer and were not reheated prior to consumption. This report illustrates the role of cross-contamination in an outbreak with an unusual food vehicle for campylobacteriosis. Physical separation of cooked and raw product is necessary to prevent recurrences of outbreaks similar to the one described here.

10. [Core-shell nanoparticles from fucoidan neoglycans: Synthesis, characterization with capability of glycomimetic ligands for Campylobacter jejuni](#), Giovanna Sandoval Larios, José Ángel Huerta Ocampo, Jose Andrei Sarabia Sainz, Alfonso García Galaz, Ana María Guzmán-Partida, Tomás Jesús Madera Santana, Gabriela Ramos-Clamont Montfort, **Carbohydrate Polymer Technologies and Applications**, Volume 6, 2023, 100384, <https://doi.org/10.1016/j.carpta.2023.100384>.

**Abstract:**

Campylobacteriosis produced by *Campylobacter jejuni* is the main cause of bacterial gastroenteritis worldwide and the binding of this pathogen to fucosylated glycoconjugates expressed on host cells is a determining factor for the infection. The aim of this work was to

synthesize and characterize core-shell nanoparticles from fucoidan neoglycans as potential glycomimetic ligands for *Campylobacter jejuni*. Fucoidan oligosaccharides (OFuc) were obtained by mild hydrolysis of fucoidan. OFuc were separated by ultrafiltration, characterized by dynamic light scattering (DLS), infrared spectroscopy (FTIR), Fluorophore-assisted carbohydrate electrophoresis and lectin recognition. The OFuc1 were then conjugated with bovine serum albumin (BSA) by controlled glycation. The formation of fucosylated BSA (BSA-OFuc1) was confirmed by FTIR, increased surface charge, polyacrylamide gel electrophoresis, mass spectrometry and *Ulex europaeus* I lectin recognition. Afterwards core-shell BSA/BSA-OFuc1 nanoparticles were obtained by crosslinking. These nanoparticles presented hemispherical form with size and charge distribution of  $312.1 \pm 3.2$  nm and  $-34.4 \pm 0.3$  mV respectively and were selectively recognized by *C. jejuni* by an ELISA-like lectin assay (ELLA). These results reveal the potential of core-shell nanoparticles from fucoidan neoglycans as glycomimetic ligands for *Campylobacter jejuni* and open further opportunities to explore potential applications in the pharmaceutical industry.

**Keywords:** Maillard fucosylation; Biorecognition; Fucoidan neoglycans; *Campylobacter jejuni*; Core-shell nanoparticles; Glycomimetic ligands

**11. [Economics of Reducing Campylobacter at Different Levels within the Belgian Poultry](#)**

**[Meat Chain](#)**, Xavier Gellynck, Winy Messens, Dirk Halet, Koen Grijspeerdt, Emma Hartnett, Jacques Viaene, **Journal of Food Protection**, Volume 71, Issue 3, 2008, Pages 479-485, <https://doi.org/10.4315/0362-028X-71.3.479>.

**Abstract:**

*Campylobacter* infections pose a serious public health problem in Belgium. Poultry meat is most likely responsible for 40% of human campylobacteriosis cases in Belgium. On a yearly basis, consumption of poultry meat causes at least 22,000 campylobacteriosis cases, with a cost of illness of €10.9 million. Several intervention measures have been proposed in literature, aiming to reduce the contamination of poultry meat and thus lead to significant reductions of human campylobacteriosis cases. This study aimed to evaluate the cost-benefit ratio, i.e., the ratio of reduced costs of illness on intervention costs of various intervention measures. These measures were selected by representatives from the poultry meat sector and experts in the field of poultry science. The selection comprised measures at the farm level (phage therapy), at the processing plant (spraying of carcasses with lactic acid or electrolyzed oxidizing water, crust freezing, or irradiation), and at the consumer level (improving kitchen hygiene and application of home freezing). Among these measures, the decontamination of carcasses with electrolyzed oxidizing water applied in the processing plant was the most efficient (17.66), followed by the use of lactic

acid (4.06). In addition, phage therapy generated a positive cost-benefit ratio (2.54). Irradiation indicated the highest efficacy, but its cost-benefit ratio was rather low (0.31). There seems to be less gain by trying to improve food handling in the kitchen. The cost to reach consumers is large, while only a very limited fraction of the consumers is willing to change its behavior. The outcome of this study poses valuable information for future risk-management decisions in Belgium.

12. [Genomic Insights into the Increased Occurrence of Campylobacteriosis Caused by Antimicrobial-Resistant \*Campylobacter coli\*](#), Penghang Zhang, Xiaoai Zhang, Yuzhu Liu, Qingpo Cui, Xiaoxia Qin, Yanlin Niu, Chao Wang, TongYu Wang, Qian Chen, Shuangyang Ding, Xiaochen Ma, Zhangqi Shen, Vaughn S. Cooper, **mBio**, Volume 13, Issue 6, 2022, <https://doi.org/10.1128/mbio.02835-22>.

**Abstract:**

*Campylobacter* is the leading bacterial cause of diarrheal illnesses worldwide. *Campylobacter jejuni* and *C. coli* are the most common species accounting for campylobacteriosis. Although the proportion of campylobacteriosis caused by *C. coli* is increasing rapidly in China, the underlying mechanisms of this emergence remain unclear. In this study, we analyzed the whole-genome sequences and associated environments of 1,195 *C. coli* isolates with human, poultry, or porcine origins from 1980 to 2021. *C. coli* isolates of human origin were closely related to those from poultry, suggesting that poultry was the main source of *C. coli* infection in humans. Analysis of antimicrobial resistance determinants indicated that the prevalence of multidrug-resistant *C. coli* has increased dramatically since the 2010s, coinciding with the shift in abundance from *C. jejuni* to *C. coli* in Chinese poultry. Compared with *C. jejuni*, drug-resistant *C. coli* strains were better adapted and showed increased proliferation in the poultry production environment, where multiple antimicrobial agents were frequently used. This study provides an empirical basis for the molecular mechanisms that have enabled *C. coli* to become the dominant *Campylobacter* species in poultry; we also emphasize the importance of poultry products as sources of campylobacteriosis caused by *C. coli* in human patients.

**IMPORTANCE** The proportion of campylobacteriosis caused by *C. coli* is increasing rapidly in China. Coincidentally, the dominant species of *Campylobacter* occurring in poultry products has shifted from *C. jejuni* to *C. coli*. Here, we analyzed the whole-genome sequences of 1,195 *C. coli* isolates from different origins. The phylogenetic relationship among *C. coli* isolates suggests that poultry was the main source of *C. coli* infection in humans. Further analysis indicated that antimicrobial resistance in *C. coli* strains has increased dramatically since the 2010s, which could facilitate their adaptation in the poultry production environment, where multiple antimicrobial agents are frequently used. Thus, our findings suggest that the judicious use of antimicrobial

agents could mitigate the emergence of multidrug-resistant *C. coli* strains and enhance clinical outcomes by restoring drug sensitivity in *Campylobacter*.

**Keywords:** *Campylobacter coli*; whole-genome sequencing; core genome multilocus sequence typing; antimicrobial resistance

13. [Development of a “big data” groundwater microbial contamination index and spatial comparisons with enteric infection rates in southern Ontario](#), Ioan Petculescu, Paul Hynds, R. Stephen Brown, Martin Boudou, Kevin McDermott, Anna Majury, **Science of The Total Environment**, Volume 947, 2024, 174408, <https://doi.org/10.1016/j.scitotenv.2024.174408>.

**Abstract:**

Big data have become increasingly important for policymakers and scientists but have yet to be employed for the development of spatially specific groundwater contamination indices or protecting human and environmental health. The current study sought to develop a series of indices via analyses of three variables: Non-*E. coli* coliform (NEC) concentration, *E. coli* concentration, and the calculated NEC:*E. coli* concentration ratio. A large microbial water quality dataset comprising 1,104,094 samples collected from 292,638 Ontarian wells between 2010 and 2021 was used. Getis-Ord  $G_i^*$  ( $G_i^*$ ), Local Moran's  $I$  (LMI), and space-time scanning were employed for index development based on identified cluster recurrence.  $G_i^*$  and LMI identify hot and cold spots, i.e., spatially proximal subregions with similarly high or low contamination magnitudes. Indices were statistically compared with mapped well density and age-adjusted enteric infection rates (i.e., campylobacteriosis, cryptosporidiosis, giardiasis, verotoxigenic *E. coli* (VTEC) enteritis) at a subregional ( $N = 298$ ) resolution for evaluation and final index selection. Findings suggest that index development via  $G_i^*$  represented the most efficacious approach. Developed  $G_i^*$  indices exhibited no correlation with well density, implying that indices are not biased by rural population density.  $G_i^*$  indices exhibited positive correlations with mapped infection rates, and were particularly associated with higher bacterial (*Campylobacter*, VTEC) infection rates among younger sub-populations ( $p < 0.05$ ). Conversely, no association was found between developed indices and giardiasis rates, an infection not typically associated with private groundwater contamination. Findings suggest that a notable proportion of bacterial infections are associated with groundwater and that the developed  $G_i^*$  index represents an appropriate spatiotemporal reflection of long-term groundwater quality. Bacterial infection correlations with the NEC:*E. coli* ratio index ( $p < 0.001$ ) were markedly different compared to correlations with the *E. coli* index, implying that the ratio may supplement *E. coli* monitoring as a groundwater assessment metric capable of elucidating contamination mechanisms. This study may serve as a

methodological blueprint for the development of big data-based groundwater contamination indices across the globe.

**Keywords:** Groundwater; Private water wells; Total coliforms; Waterborne illness; E. coli; Spatial autocorrelation

**14. [Exudate From Retail Chicken Liver Packaging Allows for Survival of Naturally Occurring Campylobacter, Coliforms, and Aerobic Microorganisms Under Drying Conditions](#),**

Elizabeth A. McMillan, Mark E. Berrang, Eric S. Adams, Richard J. Meinersmann, **Journal of Food Protection**, Volume 86, Issue 8, 2023, 100123, <https://doi.org/10.1016/j.jfp.2023.100123>.

**Abstract:**

Campylobacter spp. are a leading cause of human foodborne illness associated with chicken meat products in the United States. Chicken livers, including exudate from packaging, commonly carry Campylobacter and could be a source of illness if mishandled. Survivability of naturally occurring Campylobacter, total aerobic bacteria, and coliforms was determined under drying conditions in two consumer simulated environments: moist sponge and solid surface. Fresh chicken liver exudate was dispensed onto sponges and glass slides and allowed to dry under ambient conditions for 7 days. Bacterial concentration was measured at 0, 6, 24, 48, 72, and 168 h. Total aerobic population did not decrease by more than one log over 7 days and did not correlate to water activity or time in either simulation. Coliform concentrations increased in sponge simulations but decreased in solid surface simulations. Further, coliform concentrations were significantly higher in sponge simulations than in solid surface. Campylobacter was naturally present in exudate and survived at least to 6 h in every trial. Campylobacter was recoverable at 24 h in some sponge trials. However, Campylobacter concentration was strongly correlated to water activity. Fresh chicken liver exudate could present a risk of campylobacteriosis to consumers if mishandled even after drying.

**Keywords:** Campylobacter; Chicken liver; Drying

**15. [Clinical manifestations and risk factors of campylobacter gastroenteritis in children in](#)**

**Taiwan**, Yen-Ting Guo, Chao A. Hsiung, Fang-Tzy Wu, Hsin Chi, Yhu-Chering Huang, Ching-Chuan Liu, Yi-Chuan Huang, Hsiao-Chuan Lin, Shu-Man Shih, Ching-Yi Huang, Luan-Yin Chang, Yu-Huai Ho, Chun-Yi Lu, Li-Min Huang, **Biomedical Journal**, Volume 46, Issue 6, 2023, 100590, <https://doi.org/10.1016/j.bj.2023.03.003>.

## Abstract:

### Background

Campylobacteriosis is a common cause of bacterial gastroenteritis worldwide. This study aimed to investigate the potential risk factors, clinical and laboratory manifestations of children with campylobacteriosis under five years old in Taiwan.

### Methods

This retrospective case–control study was conducted in ten major hospitals in Taiwan from 2014 to 2017. Laboratory tests and stool specimen were collected and analyzed together with questionnaire survey. Multivariate stepwise logistic regression model was used for identification of risk factors.

### Results

A total of 64 campylobacteriosis cases were included with a median age of 25 months. We observed a less prolonged vomiting ( $p = 0.047$ ), more bloody ( $p < 0.001$ ) and mucoid ( $p = 0.005$ ) stools, and lower AST levels ( $p = 0.020$ ) in patients with campylobacteriosis. Lower parental educational attainment ( $p < 0.001$ ), direct contact with acute gastroenteritis patients ( $p < 0.001$ ), as well as diarrhea in the mutually cared children ( $p = 0.007$ ) were linked to campylobacteriosis. Consumption of municipal water ( $p < 0.001$ ), milk (OR 0.34, 95% CI 0.118–0.979), and soft beverages (OR 0.41, 95% CI 0.192–0.888) were identified as protective factors, while consuming takeout food ( $p = 0.032$ ) and seafood ( $p = 0.019$ ) increased risk of campylobacteriosis.

### Conclusions

Shorter vomiting duration, bloody and mucoid stool, and less elevated AST levels are manifestations suggestive of campylobacteriosis. Risk factors of campylobacteriosis were low parental educational attainment, direct contact with acute gastroenteritis patients, diarrhea in mutually cared children, takeout food and seafood intake. Potential protective factors include municipal water, milk, and soft beverage intake.

**Keywords:** Acute gastroenteritis; Campylobacter; Children

16. [Quantitative Risk Assessment of Verocytotoxin-Producing Escherichia coli O157 and Campylobacter jejuni Related to Consumption of Raw Milk in a Province in Northern Italy](#), F. Giacometti, A. Serraino, P. Bonilauri, F. Ostanello, P. Daminelli, G. Finazzi, M.N.

Losio, G. Marchetti, G. Liuzzo, R.G. Zanoni, R. Rosmini, **Journal of Food Protection**, Volume 75, Issue 11, 2012, Pages 2031-2038, <https://doi.org/10.4315/0362-028X.JFP-12-163>.

**Abstract:**

A quantitative risk assessment was developed to describe the risk of campylobacteriosis and hemolytic uremic syndrome (HUS) linked to consumption of raw milk sold in vending machines in Northern Italy. Exposure assessment considered the microbiological status of dairy farms, expected milk contamination, storage conditions from bulk tank to home storage, microbial growth during storage, destruction experiments, consumption frequency of raw milk, age of consumers, serving size, and consumption preference. The differential risk between milk handled under regulation conditions (4°C throughout all phases) and the worst field handling conditions was considered. The probability of *Campylobacter jejuni* infection was modeled with a single-hit dose-response beta-Poisson model, whereas for HUS an exponential dose-response model was chosen and two probabilities were used to model the higher susceptibility of children younger than 5 years old. For every 10,000 to 20,000 consumers each year, the models predicted for the best and worst storage conditions, respectively, 2.12 and 1.14 campylobacteriosis cases and 0.02 and 0.09 HUS cases in the 0- to 5-year age group and 0.1 and 0.5 HUS cases in the >5-year age group. The expected pediatric HUS cases do not differ considerably from those reported in Italy by the Minister of Health. The model developed may be a useful tool for extending the assessment of the risk of campylobacteriosis and HUS due to raw milk consumption at the national level in Italy. Considering the epidemiological implications of this study, the risk of illness linked to raw milk consumption should not be ignored and could be reduced by the use of simple measures. Boiling milk before consumption and strict control of temperatures by farmers during raw milk distribution have significant effects on campylobacteriosis and HUS and are essential measures for risk management.

17. [Acute illness from \*Campylobacter jejuni\* may require high doses while infection occurs at low doses](#), Peter F.M. Teunis, Axel Bonačić Marinović, David R. Tribble, Chad K. Porter, Arno Swart, **Epidemics**, Volume 24, 2018, Pages 1-20, <https://doi.org/10.1016/j.epidem.2018.02.001>.

**Abstract:**

Data from a set of different studies on the infectivity and pathogenicity of *Campylobacter jejuni* were analyzed with a multilevel model, allowing for effects of host species (nonhuman primates and humans) and different strains of the pathogen. All challenge studies involved high doses of the pathogen, resulting in all exposed subjects to become infected. In only one study a dose

response effect (increasing trend with dose) for infection was observed. High susceptibility to infection with *C. jejuni* was found in a joint analysis of outbreaks and challenge studies. For that reason four outbreaks, associated with raw milk consumption, were also included in the present study. The high doses used for inoculation did not cause all infected subjects to develop acute enteric symptoms. The observed outcomes are consistent with a dose response effect for acute symptoms among infected subjects: a conditional illness dose response relation. Nonhuman primates and human volunteers did not appear to have different susceptibilities for developing enteric symptoms, but exposure in outbreaks (raw milk) did lead to a higher probability of symptomatic campylobacteriosis.

**Keywords:** Campylobacter jejuni; Hierarchical dose response; Natural experiments; Challenge studies; Infectivity

18. [Assessment of probiotic \*Bacillus velezensis\* supplementation to reduce \*Campylobacter jejuni\* colonization in chickens](https://doi.org/10.1016/j.psj.2024.103897), Yifang Cui, Jiajia Zhu, Pengxiang Li, Fangfang Guo, Bing Yang, Xia Su, Hongzhan Zhou, Kui Zhu, Fuzhou Xu, **Poultry Science**, Volume 103, Issue 8, 2024, 103897, <https://doi.org/10.1016/j.psj.2024.103897>.

**Abstract:**

*Campylobacter jejuni* continues to be a major public health issue worldwide. Poultry are recognized as the main reservoir for this foodborne pathogen. Implementing measures to decrease *C. jejuni* colonization on farms has been regarded as the most effective strategy to control the incidence of campylobacteriosis. The probiotics supplementation has been regarded as an attractive approach against *C. jejuni* in chickens. Here the inhibitory effects of one probiotic *B. velezensis* isolate CAU277 against *C. jejuni* was evaluated in vitro and in vivo. The in vitro antimicrobial activity showed that the supernatant of *B. velezensis* exhibited the most pronounced inhibitory effects on *Campylobacter* strains compared to other bacterial species. When co-cultured with *B. velezensis*, the growth of *C. jejuni* reduced significantly from 7.46 log<sub>10</sub> CFU/mL (24 h) to 1.02 log<sub>10</sub> CFU/mL (48 h). Further, the antimicrobial activity of *B. velezensis* against *C. jejuni* remained stable under a broad range of temperature, pH, and protease treatments. The in vivo experiments demonstrated that oral administration of *B. velezensis* significantly reduced the colonization of *C. jejuni* by 2.0 log<sub>10</sub> CFU/g of feces in chicken cecum at 15 d postinoculation. In addition, the supplementary of *B. velezensis* significantly increased microbial species richness and diversity in chicken ileum, especially enhanced the bacterial population of Alistipes and Christensenellaceae, and decreased the existence of Lachnoclostridium. Our study presents that *B. velezensis* possesses antimicrobial activities

against *C. jejuni* and promotes microbiota diversity in chicken intestines. These findings indicate a potential to develop an effective probiotic additive to control *C. jejuni* infection in chicken.

**Keywords:** probiotic; *Bacillus velezensis*; antimicrobial activity; *Campylobacter jejuni*; chicken

19. [Phase variation modulates the multi-phenotypes displayed by clinical \*Campylobacter jejuni\* strains](#), Irene Ortega-Sanz, Carolina Bocigas, Beatriz Melero, Jordi Rovira, **Food Microbiology**, Volume 117, 2024, 104397, <https://doi.org/10.1016/j.fm.2023.104397>.

**Abstract:**

The high incidence and prevalence of *Campylobacter* spp. in the food supply chain entail the importance to understand their mechanisms developed to withstand harsh environmental conditions encountered. Different stress conditions and phenotypic approaches were evaluated to study the behaviour of five clinical *C. jejuni* isolates with different genotypes, including the tolerance to oxygen and the oxidants hydrogen peroxide and cumene hydroperoxide, the motility and the ability to form biofilm on polystyrene and stainless steel at different temperatures and atmospheres. Whole Genome Sequencing was performed to analyse the occurrence of 216 genes involved in these mechanisms plus phase variation. The isolates showed high tolerance to oxygen and peroxide stress with different swimming motility performances and biofilm formation abilities. Aerotolerance was related with a reduced sensitive to peroxide stress and a loss of motility that promotes biofilm formation depending on the material surface. Comparative genomics did not reveal any clear gene pattern, although phase variation occurring during host infection was observed to be crucial for the modulation of the different survival mechanisms adopted by the bacteria. These findings reveal that the bacteria can combine diverse and complex strategies in an efficient manner to survive and persist in the environment.

**Keywords:** *Campylobacteriosis*; Aerotolerance; Oxidative stress; Motility; Biofilm formation; Genomics

20. [Meta-analyses of the global multilocus genotypes of the human pathogen \*Campylobacter jejuni\*](#), Monir Poorrashidi, Megan Hitchcock, Jianping Xu, **Genome**, Volume 67, Issue 6, 2024, Pages 189-203, <https://doi.org/10.1139/gen-2023-0041>.

**Abstract:**

*Campylobacter* infections are a leading cause of bacterial diarrheal illness worldwide, with increasing reports of outbreaks in both developing and developed countries. Most studies investigating strain genotypes and epidemiology of *Campylobacter jejuni* examined on a local scale. Using the archived multilocus sequence typing data at seven loci, and associated strain

metadata from the PubMLST database, here we investigated the spatial and temporal genetic structure of the global population of *C. jejuni*. Our analyses revealed evidence for clonal dispersals of multiple sequence types (STs) among countries and continents. However, despite the observed clonal dispersal and that most genetic variations were found within individual geographic subpopulations, both the non-clone-corrected and clone-corrected samples showed evidence of significant genetic differentiation among national and continental subpopulations, with non-clone-corrected samples showing greater differentiation than clone-corrected samples. Phylogenetic incompatibility analyses provided evidence for recombination within each continental subpopulation. However, linkage disequilibrium analyses rejected the hypothesis of random recombination across the samples. Temporally, multiple STs were found to persist across four decades and the five globally most common STs showed relatively stable frequencies over the last two decades. We discussed the implications of our results to food security, disease transmission, and public health management.

**Keywords:** campylobacteriosis; gene flow; geographic differentiation; recombination; clonal persistence; clonal expansion

21. [Comparative history of Campylobacter contamination on chicken meat and campylobacteriosis cases in the United States: 1994–2018](#), Michael S. Williams, Eric D. Ebel, Epiphany Nyirabahizi, *International Journal of Food Microbiology*, Volume 342, 2021, 109075, <https://doi.org/10.1016/j.ijfoodmicro.2021.109075>.

**Abstract:**

In many countries campylobacteriosis ranks as one of the most frequently reported foodborne illnesses and poultry is the commodity that is most often associated with these illnesses. Nevertheless, efforts to reduce the occurrence of pathogen contamination on poultry are often more focused on Salmonella. While some control measures are pathogen specific, such as pre-harvest vaccination for Salmonella, improvements in sanitary dressing and interventions applied during the slaughter process can be effective against all forms of microbial contamination. To investigate the potential effectiveness of these non-specific pathogen reduction strategies in the United States, it is helpful to assess if, and by how much, Campylobacter contamination of chicken meat has changed across time. This study assesses change considering data collected in both slaughter and retail establishments and comparing observed trends in contamination with trends in human surveillance data. The results support the assertion that substantial reductions in Campylobacter contamination of chicken meat in the late 1990s and early 2000s contributed to a reduction in the human case rate of campylobacteriosis. Further reductions in chicken meat contamination between 2013 and 2018 are more difficult to associate with trends in human

illnesses, with one contributing factor being the inclusion of culture independent diagnostic test results in the official case counts during that time. Other contributing factors are discussed.

**Keywords:** Foodborne pathogens; Surveillance; Poultry; Interventions

22. [Campylobacteriosis: the role of poultry meat](#), C.P.A. Skarp, M.-L. Hänninen, H.I.K. Rautelin, **Clinical Microbiology and Infection**, Volume 22, Issue 2, 2016, Pages 103-109, <https://doi.org/10.1016/j.cmi.2015.11.019>.

**Abstract:**

The incidence of human infections caused by *Campylobacter jejuni* and *Campylobacter coli*, the main bacterial agents of gastrointestinal disease, has been increasing worldwide. Here, we review the role of poultry as a source and reservoir for *Campylobacter*. Contamination and subsequent colonization of broiler flocks at the farm level often lead to transmission of *Campylobacter* along the poultry production chain and contamination of poultry meat at retail. Yet *Campylobacter* prevalence in poultry, as well as the contamination level of poultry products, vary greatly between different countries so there are differences in the intervention strategies that need to be applied. Temporal patterns in poultry do not always coincide with those found in human infections. Studies in rural and urban areas have revealed differences in *Campylobacter* infections attributed to poultry, as poultry seems to be the predominant reservoir in urban, but not necessarily in rural, settings. Furthermore, foreign travel is considered a major risk factor in acquiring the disease, especially for individuals living in the northern European countries. Intervention strategies aimed at reducing *Campylobacter* colonization in poultry and focused at the farm level have been successful in reducing the number of *Campylobacter* cases in several countries. Increasing farm biosecurity and education of consumers are likely to limit the risk of infection. Overall, poultry is an important reservoir and source of human campylobacteriosis, although the contribution of other sources, reservoirs and transmission warrants more research.

**Keywords:** Antimicrobial resistance; *Campylobacter*; *Campylobacter coli*; *Campylobacter jejuni*; infection; intervention measures; molecular epidemiology; poultry; transmission

23. [Human campylobacteriosis: A public health concern of global importance](#), Aboi Igwaran, Anthony Ifeanyi Okoh, **Heliyon**, Volume 5, Issue 11, 2019, e02814, <https://doi.org/10.1016/j.heliyon.2019.e02814>.

**Abstract:**

Campylobacter species are among the leading cause of bacterial foodborne and waterborne infections. In addition, Campylobacter is one of the major causative agent of bacterial gastrointestinal infections and the rise in the incidence of Campylobacter infections have been reported worldwide. Also, the emergence of some Campylobacter species as one of the main causative agent of diarrhea and the propensity of these bacteria species to resist the actions of antimicrobial agents; position them as a serious threat to the public health. This paper reviews Campylobacter pathogenicity, infections, isolation and diagnosis, their reservoirs, transmission pathways, epidemiology of Campylobacter outbreaks, prevention and treatment option, antibiotics resistance and control of antibiotics use.

**Keywords:** Campylobacter; Gastrointestinal; Pathogenesis; Infection; Toxins; Resistance; Microbiology

24. [Virulence factors of foodborne pathogen Campylobacter jejuni](https://doi.org/10.1016/j.micpath.2021.105265), Graciela Volz Lopes, Tassiana Ramires, Natalie Rauber Kleinubing, Letícia Klein Scheik, Ângela Maria Fiorentini, Wladimir Padilha da Silva, **Microbial Pathogenesis**, Volume 161, Part A, 2021, 105265, <https://doi.org/10.1016/j.micpath.2021.105265>.

**Abstract:**

Campylobacter jejuni is a highly frequent cause of gastrointestinal foodborne disease in humans throughout the world. Disease outcomes vary from mild to severe diarrhea, and in rare cases the Guillain-Barré syndrome or reactive arthritis can develop as a post-infection complication. Transmission to humans usually occurs via the consumption of a range of foods, especially those associated with the consumption of raw or undercooked poultry meat, unpasteurized milk, and water-based environmental sources. When associated to food or water ingestion, the C. jejuni enters the human host intestine via the oral route and colonizes the distal ileum and colon. When it adheres and colonizes the intestinal cell surfaces, the C. jejuni is expected to express several putative virulence factors, which cause damage to the intestine either directly, by cell invasion and/or production of toxin(s), or indirectly, by triggering inflammatory responses. This review article highlights various C. jejuni characteristics — such as motility and chemotaxis — that contribute to the biological fitness of the pathogen, as well as factors involved in human host cell adhesion and invasion, and their potential role in the development of the disease. We have analyzed and critically discussed nearly 180 scientific articles covering the latest improvements in the field.

**Keywords:** Thermophilic campylobacter; campylobacteriosis; Diarrhea; Motility; Adhesion; Invasion

25. [A comparison of European surveillance programs for Campylobacter in broilers](#), Abbey Olsen, Silvia Bonardi, Lisa Barco, Marianne Sandberg, Nina Langkabel, Mati Roasto, Michał Majewski, Brigitte Brugger, Arja H. Kautto, Bojan Blagojevic, Joao B. Cota, Gunvor Elise Nagel-Alne, Adeline Huneau, Riikka Laukkanen-Ninios, Sophie Lebouquin-Leneveu, Ole Alvseike, Maria Fredriksson-Ahomaa, Madalena Vieira-Pinto, Eija Kaukonen, **Food Control**, Volume 155, 2024, 110059, <https://doi.org/10.1016/j.foodcont.2023.110059>.

**Abstract:**

Campylobacter is an important foodborne pathogen as it is associated with significant disease burden across Europe. Among various sources, Campylobacter infections in humans are often related to the consumption of undercooked poultry meat or improper handling of poultry meat. Many European countries have implemented measures to reduce human exposure to Campylobacter from broiler meat. In this paper, surveillance programs implemented in some European countries is summarized. Our findings reveal that many European countries test neck skin samples for Campylobacter as per the Process Hygiene Criterion (PHC) set by the European Regulation. Variations to the legal plan are seen in some countries, as in Norway and Iceland, where weekly sampling is performed during infection peak periods only, or in Iceland, where the Campylobacter limit is set at 500 CFU/g instead of 1000 CFU/g. Furthermore, northern European countries have implemented national Campylobacter surveillance plans. Denmark tests cloaca and leg skin samples at the slaughterhouses and meat samples at the retail, while Finland, Norway, and Sweden test caeca at slaughterhouses. In contrast, Iceland tests feces on farms. Iceland and Norway test flocks close to the slaughter date and when a farm tests positive, competent authority implement measures such as logistic slaughter, heat treatment or freeze the meat from these flocks. In Iceland, frozen meat is further processed prior to being put on the market. While the incidence of campylobacteriosis has declined in all European countries except France since the introduction of PHC in 2018, it is uncertain whether this decrease is due to prevalence reduction or underreporting during the COVID-19 pandemic. Future investigations with more comprehensive data, devoid of potential confounding factors, are necessary to validate this potential trend. However, it is evident that the implementation of national action plans can be successful in reducing the incidence of human campylobacteriosis, as demonstrated by Iceland.

**Keywords:** Campylobacter; Surveillance; Monitoring; Broilers; Poultry; Europe

26. [Prevalence and risk factors for thermotolerant species of Campylobacter in poultry meat at retail in Europe](#), Andrea Osimani, Lucia Aquilanti, Marina Pasquini, Francesca

Clementi, **Poultry Science**, Volume 96, Issue 9, 2017, Pages 3382-3391,  
<https://doi.org/10.3382/ps/pex143>.

**Abstract:**

The thermotolerant species *Campylobacter jejuni*, *Campylobacter coli*, *Campylobacter lari* and *Campylobacter upsaliensis* are the causative agents of the human illness called campylobacteriosis. This infection represents a threat for the health of consumers in Europe. It is well known that poultry meat is an important food vehicle of *Campylobacter* infection. As emerged from the reported scientific literature published between 2006 and 2016, poultry meat sold at retail level in Europe represents an important source of the pathogen. The contamination level of poultry meat sold at retail can vary depending on pre- and post-harvest factors. Among the pre-harvest measures, strict biosecurity practices must be guaranteed; moreover, among post-harvest control measures scalding, chilling and removal of faecal residues can reduce the contamination level of *Campylobacter*. An additional issue is represented by increasing proportion of *Campylobacter* isolates resistant to tetracyclines, ciprofloxacin, and nalidixic acid, thus feeding a serious concern on the effectiveness of antibiotic treatment for human campylobacteriosis in a near future.

**Keywords:** campylobacteriosis; retail; antibiotic resistance; chicken rearing; meat safety

27. [A model using an inter-sectorial data integration process indicates that reducing \*Campylobacter\* cross-contamination at slaughter mitigates the risk of human campylobacteriosis effectively](#), Alessandro Foddai, Maarten Nauta, Johanne Ellis-lversen, **Microbial Risk Analysis**, Volume 23, 2023, 100248,  
<https://doi.org/10.1016/j.mran.2023.100248>.

**Abstract:**

The risk of human campylobacteriosis due to Danish broiler flocks cross-contaminated (CC) at slaughter with *Campylobacter* spp. was assessed. National surveillance data (2018) on flock *Campylobacter* status (called animal level component (AL)) and on contamination of chilled carcasses ready for consumption (food safety component (FS)), were compared. The AL component consisted of PCR testing results on pools of cloacal swabs collected from 3,012 conventional flocks, while the FS component presented culture testing of leg skins from 999 (of the 3,012) randomly sampled flocks. Datasets were integrated on flocks tested in both components, by combinations of farm-ID, house-unit and sampling date. The CC flocks were those entering the slaughterhouse as AL-negative, but resulting FS-positive. All remaining carcass positive flocks were instead classified as Non-CC flocks. The apparent prevalence (AP) of carcass

positive flocks and the colony forming units per gram (cfu/g), measured by the FS component, were fed into a published simulation model, to assess under three simulation scenarios: the mean monthly risk per serving during 2018, relative (RR) to that of 2013 (reference year in the current Danish Action Plan). In the baseline scenario, the original AL status and the FS cfu/g were maintained. In the alternative scenarios I and II, the FS cfu/g were set = 0 (i.e. negative) for the Non-CC and for the CC flocks, respectively. Thus, scenario I and the differences between the other two scenarios, provided the contribution of the CC flocks to the AP and to the RR. The (overall) annual median log<sub>10</sub> cfu/g was ≈ 2.8 (min. = 1.0; max. = 4.0) for the Non-CC flocks and 1.4 (1.0; 3.9) for the CC flocks. The median monthly difference in AP, between the baseline scenario and scenario II was 7% (min = 2% in January; max = 19% in August), while the difference in risk was 0.04% (0.001%; 0.11%), which was similar to the mean monthly risk under scenario I. If cross-contamination had not occurred (scenario II), the annual AP would have reduced from 24.3% to 16.1% and the RR would have reduced from 0.92 to 0.77. Therefore, ≈16% of the public health risk posed by Danish conventional broiler meat, appeared attributable to CC flocks. Reducing cross-contamination could mitigate the risk of human campylobacteriosis notably. This study illustrates how inter-sectorial surveillance data integration, can be used to optimize National Action Plans against *Campylobacter* spp. and other similar foodborne pathogens.

**Keywords:** *Campylobacter* spp.; Surveillance; Data integration; Risk mitigation; Cross-contamination; Campylobacteriosis

28. [A meta-analysis of case-control studies examining sporadic campylobacteriosis in Australia and New Zealand from 1990 to 2016](#), Liana Varrone, Kathryn Glass, Russell J. Stafford, Martyn D. Kirk, Linda Selvey, **Australian and New Zealand Journal of Public Health**, Volume 44, Issue 4, 2020, Pages 313-319, <https://doi.org/10.1111/1753-6405.12998>.

#### **Abstract:**

##### **Objective**

We conducted a meta-analysis of case-control studies to identify locally relevant risk factors for sporadic campylobacteriosis in Australia and New Zealand.

##### **Methods**

We searched Medline, Web of Science, ProQuest and Google Scholar using PRISMA guidelines. Reference lists and grey literature were hand-searched. Meta-analyses were conducted in the R package 'metafor' using published odds ratios and 95% confidence intervals.

## Results

We identified 325 articles, from which we included 10 that described case-control studies. Four risk factors were statistically significant in the meta-analysis: eating undercooked poultry (OR=4.28, 95%CI 3.09–5.93); eating poultry cooked outside the home (OR=2.13, 95%CI 1.66–2.72); having pet chickens (OR=3.29, 95%CI 2.12–5.10); and overseas travel (OR=5.55, 95%CI 3.20–9.63). Among children, having pet dogs showed elevated but not significant risk (OR=1.57, 95%CI 0.99–2.49).

## Conclusions

We identified consumption of chicken meat and contact with domestic chickens as important risk factors for campylobacteriosis in Australia and New Zealand.

## Implications for public health

While consumption of chicken meat is a well-known risk factor for campylobacteriosis, zoonotic transmission is often overlooked. This research indicates a greater need for public health awareness surrounding zoonotic campylobacteriosis, especially for young children.

**Keywords:** campylobacteriosis; Australia; New Zealand; meta-analysis

29. [Survey of New Zealand Poultry Consumers' Handling of Raw Poultry and Food Safety Awareness To Provide Insight into Risk Factors for Campylobacteriosis](#), Ali Al-Sakkaf, Elizabeth Redmond, Charles Brennan, Ravi Gooneratne, **Journal of Food Protection**, Volume 84, Issue 9, 2021, Pages 1640-1647, <https://doi.org/10.4315/JFP-21-034>.

### Abstract:

New Zealand (NZ) has a high rate of reported campylobacteriosis cases. Cross-contamination in home kitchens during poultry handling is considered the main factor in campylobacteriosis transmission. The main aim of this study was to measure NZ consumers' food safety awareness and self-reported food safety practices associated with handling raw poultry. This study will contribute to the existing knowledge to explain the reasons behind the increase of campylobacteriosis incidents. Findings can help inform future consumer education campaigns to help reduce the incidence of campylobacteriosis in NZ. A cross-sectional survey composed of 31 multiple-choice questions was designed, piloted, and used to collect information about the last time consumers purchased and prepared raw poultry at home. A street-intercept survey in public places, such as supermarkets in the Canterbury region, was used to recruit respondents for this study. A descriptive and inferential data analysis was performed, including a one-way analysis of

variance test used to compare the mean scored responses of the respondents among different sociodemographics. Overall, 301 valid responses were obtained. Scores representing reported safe food practices ranged between 2 and 19 (maximum 21), with a mean score of 9.83 (standard deviation of 3.50 with a standard error of 0.20). There was some variation in correctly answered questions by respondents for food hygiene (25%), cross-contamination prevention (55%), temperature control and storage practices (49%), and food safety (52%). Approximately 30% of the respondents reported symptoms of a foodborne disease experienced once to four times during the past 12 months. The study identified low adherence to current recommended food safety practices, including safe food storage and temperature control. The findings can be used to inform a communication campaign regarding food safety needs to be designed urgently in NZ to reduce the rate of campylobacteriosis.

**Keywords:** Campylobacteriosis; Consumer handling; Cross-contamination; Questionnaire; Raw chicken and poultry; Survey

**30. [Sources and transmission routes of campylobacteriosis: A combined analysis of genome and exposure data](#)**, Lapo Mughini-Gras, Roan Pijnacker, Claudia Coipan,

Annemieke C. Mulder, Adriana Fernandes Veludo, Sharona de Rijk, Angela H.A.M. van Hoek, Ralph Buij, Gerard Muskens, Miriam Koene, Kees Veldman, Birgitta Duim, Linda van der Graaf-van Bloois, Coen van der Weijden, Sjoerd Kuiling, Anjo Verbruggen, Joke van der Giessen, Marieke Opsteegh, Menno van der Voort, Greetje A.A. Castelij, Franciska M. Schets, Hetty Blaak, Jaap A. Wagenaar, Aldert L. Zomer, Eelco Franz,

**Journal of Infection**, Volume 82, Issue 2, 2021, Pages 216-226,  
<https://doi.org/10.1016/j.jinf.2020.09.039>.

**Abstract:**

**Objectives**

To determine the contributions of several animal and environmental sources of human campylobacteriosis and identify source-specific risk factors.

**Methods**

1417 *Campylobacter jejuni/coli* isolates from the Netherlands in 2017–2019 were whole-genome sequenced, including isolates from human cases (n = 280), chickens/turkeys (n = 238), laying hens (n = 56), cattle (n = 158), veal calves (n = 49), sheep/goats (n = 111), pigs (n = 110), dogs/cats (n = 100), wild birds (n = 62), and surface water (n = 253). Questionnaire-based

exposure data was collected. Source attribution was performed using core-genome multilocus sequence typing. Risk factors were determined on the attribution estimates.

## Results

Cases were mostly attributed to chickens/turkeys (48.2%), dogs/cats (18.0%), cattle (12.1%), and surface water (8.5%). Of the associations identified, never consuming chicken, as well as frequent chicken consumption, and rarely washing hands after touching raw meat, were risk factors for chicken/turkey-attributable infections. Consuming unpasteurized milk or barbecued beef increased the risk for cattle-attributable infections. Risk factors for infections attributable to environmental sources were open water swimming, contact with dog faeces, and consuming non-chicken/turkey avian meat like game birds.

## Conclusions

Poultry and cattle are the main livestock sources of campylobacteriosis, while pets and surface water are important non-livestock sources. Foodborne transmission is only partially consistent with the attributions, as frequency and alternative pathways of exposure are significant.

**Keywords:** Source attribution; Core-genome MLST; Campylobacter; Zoonosis; Risk factors

31. [Source attributed case-control study of campylobacteriosis in New Zealand](#), R.J. Lake, D.M. Campbell, S.C. Hathaway, E. Ashmore, P.J. Cressey, B.J. Horn, S. Pirikahu, J.M. Sherwood, M.G. Baker, P. Shoemack, J. Benschop, J.C. Marshall, A.C. Midwinter, D.A. Wilkinson, N.P. French, *International Journal of Infectious Diseases*, Volume 103, 2021, Pages 268-277, <https://doi.org/10.1016/j.ijid.2020.11.167>.

## Abstract:

### Background

Following an initial reduction in human campylobacteriosis in New Zealand after the implementation of poultry food chain-focused interventions during 2006–2008, further decline has been relatively small. We report a year-long study of notified campylobacteriosis cases, incorporating a case control study combined with a source attribution study. The purpose was to generate up-to-date evidence on the relative contributions of different sources of campylobacteriosis in New Zealand.

## Methods

The study approach included: • A case-control study of notified cases (aged six months or more) sampled in a major urban centre (Auckland, every second case) and a mixed urban/rural area (Manawatū/Whanganui, every case), between 12 March 2018 and 11 March 2019. • Source attribution of human campylobacteriosis cases sampled from these two regions over the study period by modelling of multilocus sequence typing data of *Campylobacter jejuni* and *C. coli* isolates from faecal samples of notified human cases and relevant sources (poultry, cattle, sheep).

## Results

Most cases (84%) were infected with strains attributed to a poultry source, while 14% were attributed to a cattle source. Approximately 90% of urban campylobacteriosis cases were attributed to poultry sources, compared to almost 75% of rural cases. Poultry consumption per se was not identified as a significant risk factor. However specific risk factors related to poultry meat preparation and consumption did result in statistically significantly elevated odds ratios.

## Conclusions

The overall findings combining source attribution and analysis of specific risk factors indicate that poultry meat remains a dominant pathway for exposure and infection.

**Keywords:** Campylobacteriosis; Case control; Source attributed; New Zealand; Poultry

32. [Re-examining the causes of campylobacteriosis](https://doi.org/10.1016/S1201-9712(02)90181-5), Louis Anthony Cox, *International Journal of Infectious Diseases*, Volume 6, Supplement 3, 2002, Pages S26-S36, [https://doi.org/10.1016/S1201-9712\(02\)90181-5](https://doi.org/10.1016/S1201-9712(02)90181-5).

### Abstract:

The development of fluoroquinolone (FQ)-resistant strains of *Campylobacter* (CP) in chickens is favored by enrofloxacin, which is used to combat respiratory disease in chicken broilers. Thus, it seems plausible that eating chicken treated with FQs could increase the risk of FQ-resistant CP illness. We call this hypothesis 'Causal Model 1'. It is the dominant paradigm driving current regulatory efforts in the USA to ban FQ use in chickens. Although plausible, Causal Model 1 does not explain why several recent data sets indicate that eating chicken (and even touching raw chicken) at home can reduce the risk of CP illness. An alternative, Causal Model 2, instead attributes the risk of sporadic domestic CP cases primarily to commercial cooking of hamburgers, chicken, and other meats. This paper re-examines case-control data collected by the Centers for

Disease Control (CDC), and re-analyzes previously published case-control data to assess the evidence for Causal Models 1 and 2. We apply causal graph, classification tree, conditional independence and Bayesian Model Averaging (BMA) methods of data analysis to identify potential causal relationships of interest in the case-control data. Available case-control data are generally consistent with Causal Model 2, but not Causal Model 1, because they indicate that chicken (and other meats) are protective against campylobacteriosis risk when prepared at home, and are only risky when consumed in commercial establishments such as restaurants. This suggests that poor hygiene in some restaurants may be a predominant cause of campylobacteriosis in humans, while chicken-borne CP plays at most a minor (statistically undetectable) role in human health risk. Both domestic and international data support this model. If true, Causal Model 2 implies that current regulatory efforts in the USA to protect human health by focusing on chicken-borne CP may be ineffective, conferring no detectable human health benefit. Instead, improving restaurant hygiene for a small minority of high-risk restaurants (as well, perhaps, as reducing over-use of FQs in human medicine) are the interventions most likely to create significant human health benefits, based on currently available data.

**33. [Continuous Source Outbreak of Campylobacteriosis Traced to Chicken](#), Andrew D.**

Pearson, Melody H. Greenwood, Jackie Donaldson, Timothy D. Healing, Dennis M. Jones, Manouchehr Shahamat, R. Kevin A. Feltham, Rita R. Colwell, **Journal of Food Protection**, Volume 63, Issue 3, 2000, Pages 309-314, <https://doi.org/10.4315/0362-028X-63.3.309>.

**Abstract:**

Poultry is a source of human campylobacteriosis, but a large continuous source outbreak, heretofore, has not been attributed to both a single source of poultry and single serotype of Campylobacter. Here we report an outbreak of *C. jejuni* affecting 6 catering college trainees and 13 patrons of a restaurant in southern England. An epidemiological investigation successfully tracked the outbreak source to the farm of origin. Frequency of occurrence of campylobacters and outbreak serotype distribution were determined in index cases, the local population, and local chicken suppliers. The source farm was investigated and the effect of interventions assessed. A single outbreak serotype of *C. jejuni* was isolated from trainee chefs, patrons, and chicken supplied to the college by Wholesaler A. The Campylobacter isolation rate for Wholesaler A was 89% (98% outbreak serotype), compared to 40% for non-Wholesaler A (10% outbreak serotype). The isolation rate for 14 months averaged 85% (99% outbreak serotype) in chickens grown on two farms (X and Y) supplying Wholesaler A, contributing ~40% to all local cases. In the research reported here, a specific strain and hygiene practice were found to be important for understanding transmission of Campylobacter from poultry to humans in this outbreak.

34. [Genomic resistant determinants of multidrug-resistant \*Campylobacter\* spp. isolates in Peru](#), Francesca Schiaffino, Craig T. Parker, Maribel Paredes Olortegui, Ben Pascoe, Katia Manzanares Villanueva, Paul F. Garcia Bardales, Evangelos Mourkas, Steven Huynh, Pablo Peñataro Yori, Lucero Romaina Cachique, Hannah K. Gray, Guillermo Salvatierra, Hermann Silva Delgado, Samuel K. Sheppard, Kerry K. Cooper, Margaret N. Kosek, *Journal of Global Antimicrobial Resistance*, Volume 36, 2024, Pages 309-318, <https://doi.org/10.1016/j.jgar.2024.01.009>.

#### **Abstract:**

#### **Objectives**

Antimicrobial resistant (AMR) *Campylobacter* is a global health threat; however, there is limited information on genomic determinants of resistance in low- and middle-income countries. We evaluated genomic determinants of AMR using a collection of whole genome sequenced *Campylobacter jejuni* and *C. coli* isolates from Iquitos, Peru.

#### **Methods**

*Campylobacter* isolates from two paediatric cohort studies enriched with isolates that demonstrated resistance to ciprofloxacin and azithromycin were sequenced and mined for AMR determinants.

#### **Results**

The *gyrA* mutation leading to the Thr86Ile amino acid change was the only *gyrA* mutation associated with fluoroquinolone resistance identified. The A2075G mutation in 23S rRNA was present, but three other 23S rRNA mutations previously associated with macrolide resistance were not identified. A resistant-enhancing variant of the *cmeABC* efflux pump genotype (RE-*cmeABC*) was identified in 36.1% (35/97) of *C. jejuni* genomes and 17.9% (12/67) of *C. coli* genomes. Mutations identified in the CmeR-binding site, an inverted repeat sequence in the *cmeABC* promoter region that increases expression of the operon, were identified in 24/97 *C. jejuni* and 14/67 *C. coli* genomes. The presence of these variants, in addition to RE-*cmeABC*, was noted in 18 of the 24 *C. jejuni* and 9 of the 14 *C. coli* genomes.

#### **Conclusions**

Both RE-*cmeABC* and mutations in the CmeR-binding site were strongly associated with the MDR phenotype in *C. jejuni* and *C. coli*. This is the first report of RE-*cmeABC* in Peru and suggests it is a major driver of resistance to the principal therapies used to treat human campylobacteriosis in this setting.

**Keywords:** Campylobacteriosis; Antibiotic resistance; Gastroenteritis; Iquitos; Whole genome sequencing

35. [Campylobacter fetus subspecies specific PCR assays inferred from comparative genomic analysis for accurate subspecies identification](#), Linda van der Graaf - van Bloois, Aldert L. Zomer, Birgitta Duim, Jaap A. Wagenaar, **Journal of Microbiological Methods**, Volume 226, 2024, 107049, <https://doi.org/10.1016/j.mimet.2024.107049>.

**Abstract:**

Bovine Genital Campylobacteriosis (BGC) is caused by *Campylobacter fetus* subsp. *venerealis* and is a notifiable disease to the WOA (World Organisation for Animal Health). For an effective BGC control program, the reliable differentiation of *Campylobacter fetus* subsp. *venerealis* (Cfv) from the closely related *Campylobacter fetus* subsp. *fetus* (Cff) is required. However, the available molecular *C. fetus* subspecies identification assays lack sensitivity and specificity to differentiate *C. fetus* isolates based on their phenotypic or genotypic differences. Furthermore, the current biochemical subspecies identification is not fully congruent with the genomic differentiation of *C. fetus* strains. In this study, the genome sequences of 41 *C. fetus* strains with well identified subspecies, were analyzed with the large-scale BLAST score ratio (LS-BSR) pipeline to identify Cff and Cfv specific sequences. With this analysis, the *asd* gene encoding an aspartate-semialdehyde dehydrogenase was identified, which contained a 6-bp Cff-specific sequence, and this 6-bp sequence was absent in the *asd* gene of Cfv strains. This sequence was used for the development of PCR assays to differentiate Cff and Cfv strains. The *C. fetus* subspecies identification of the developed *asd* PCR assays was in full congruence with the genomic classification of strains and are recommended for molecular identification of *C. fetus* subspecies in BGC control programs. The *asd* PCR can be assessed on sequenced genomes using a web interface containing the Cfvcatch tool, which includes placement of the tested genome in a phylogenetic tree with reference *C. fetus* genomes to distinguish the two subspecies and to detect antimicrobial resistance genes.

**Keywords:** *Campylobacter fetus*; *Campylobacter fetus* subspecies *venerealis*; Subspecies identification; Bovine Genital Campylobacteriosis

36. [Machine learning to attribute the source of Campylobacter infections in the United States: A retrospective analysis of national surveillance data](#), Ben Pascoe, Georgina Fletcher, Johan Pensar, Sion C. Bayliss, Evangelos Mourkas, Jessica K. Calland, Matthew D. Hitchings, Lavin A. Joseph, Charlotte G. Lane, Tiffany Greenlee, Nicolas Arning, Daniel

J. Wilson, Keith A. Jolley, Jukka Corander, Martin C.J. Maiden, Craig T. Parker, Kerry K. Cooper, Erica B. Rose, Kelli Hiett, Beau B. Bruce, Samuel K. Sheppard, **Journal of Infection**, Volume 89, Issue 5, 2024, 106265, <https://doi.org/10.1016/j.jinf.2024.106265>.

### **Abstract:**

#### **Objectives**

Integrating pathogen genomic surveillance with bioinformatics can enhance public health responses by identifying risk and guiding interventions. This study focusses on the two predominant *Campylobacter* species, which are commonly found in the gut of birds and mammals and often infect humans via contaminated food. Rising incidence and antimicrobial resistance (AMR) are a global concern, and there is an urgent need to quantify the main routes to human infection.

#### **Methods**

During routine US national surveillance (2009–2019), 8856 *Campylobacter* genomes from human infections and 16,703 from possible sources were sequenced. Using machine learning and probabilistic models, we target genetic variation associated with host adaptation to attribute the source of human infections and estimate the importance of different disease reservoirs.

#### **Results**

Poultry was identified as the primary source of human infections, responsible for an estimated 68% of cases, followed by cattle (28%), and only a small contribution from wild birds (3%) and pork sources (1%). There was also evidence of an increase in multidrug resistance, particularly among isolates attributed to chickens.

#### **Conclusions**

National surveillance and source attribution can guide policy, and our study suggests that interventions targeting poultry will yield the greatest reductions in campylobacteriosis and spread of AMR in the US.

#### **Data availability**

All sequence reads were uploaded and shared on NCBI's Sequence Read Archive (SRA) associated with BioProjects; PRJNA239251 (CDC / PulseNet surveillance), PRJNA287430 (FSIS surveillance), PRJNA292668 & PRJNA292664 (NARMS) and PRJNA258022 (FDA surveillance). Publicly available genomes, including reference genomes and isolates sampled worldwide from wild birds are associated with BioProject accessions: PRJNA176480, PRJNA177352, PRJNA342755,

PRJNA345429, PRJNA312235, PRJNA415188, PRJNA524300, PRJNA528879, PRJNA529798, PRJNA575343, PRJNA524315 and PRJNA689604. Contiguous assemblies of all genome sequences compared are available at Mendeley data (assembled *C. coli* genomes doi: 10.17632/gxswjvxyh3.1; assembled *C. jejuni* genomes doi: 10.17632/6ngsz3dtbd.1) and individual project and accession numbers can be found in Supplementary tables S1 and S2, which also includes pubMLST identifiers for assembled genomes. Figshare (10.6084/m9.figshare.20279928). Interactive phylogenies are hosted on microreact separately for *C. jejuni* (<https://microreact.org/project/pascoe-us-cjejuni>) and *C. coli* (<https://microreact.org/project/pascoe-us-ccoli>).

**Keywords:** Campylobacteriosis; Gastroenteritis; Source attribution; Machine learning; Chicken consumption

**37. [The prevalence, counts, and MLST genotypes of Campylobacter in poultry meat and genomic comparison with clinical isolates](#)**, Triin Tedersoo, Mati Roasto, Mihkel

Mäesaar, Veljo Kisand, Marina Ivanova, Kadrin Meremäe, **Poultry Science**, Volume 101, Issue 4, 2022, 101703, <https://doi.org/10.1016/j.psj.2022.101703>.

**Abstract:**

Since 2005 campylobacteriosis has been the most commonly reported gastrointestinal infection in humans in the European Union with more than 200,000 cases annually. Also Campylobacter is one of the most frequent cause of food-borne outbreaks with 319 outbreaks reported to EFSA, involving 1,254 cases of disease and 125 hospitalizations in EU in 2019. Importantly poultry meat is one of the most common source for the sporadic Campylobacter infections and for strong-evidence campylobacteriosis food-borne outbreaks in EU. In present study, 429 fresh broiler chicken meat samples of Estonian, Latvian, and Lithuanian origin were collected from Estonian retail level and analyzed on a monthly basis between September 2018 and October 2019. Campylobacter spp. were isolated in 141 (32.9%) of 429 broiler chicken meat samples. Altogether 3 (1.8%), 49 (36.8%), and 89 (66.9%) of Estonian, Latvian, and Lithuanian origin broiler chicken meat samples were positive for Campylobacter spp. Among Campylobacter-positive samples, 62 (14.5%) contained Campylobacter spp. below 100 CFU/g and in 28 (6.5%) samples the count of Campylobacter spp. exceeded 1,000 CFU/g. A high prevalence of Campylobacter spp. in fresh broiler chicken meat of Lithuanian and Latvian origin in Estonian retail was observed. Additionally, 22 different multilocus sequence types were identified among 55 genotyped isolates of broiler chicken meat and human origin, of which 45 were Campylobacter jejuni (*C. jejuni*) and 10 were Campylobacter coli (*C. coli*). The most prevalent multilocus sequence types among *C. jejuni* was ST2229 and among *C. coli* ST832, ST872. *C. jejuni* genotypes found in both

broiler chicken meat and human origin samples were ST122, ST464, ST7355, and ST9882, which indicates that imported fresh broiler chicken meat is likely the cause of human campylobacteriosis in Estonia.

**Keywords:** Campylobacter spp.; prevalence; counts; MLST sequence types; fresh broiler chicken meat

38. [Antimicrobial resistance and genetic relatedness among Campylobacter coli and Campylobacter jejuni from humans and retail chicken meat in Taiwan](#), Hsiao-Lun Wei, Ying-Shu Liao, Bo-Han Chen, Ru-Hsiou Teng, You-Wun Wang, Jui-Hsien Chang, Chien-Shun Chiou, **Journal of Global Antimicrobial Resistance**, Volume 38, 2024, Pages 27-34, <https://doi.org/10.1016/j.jgar.2024.05.013>.

#### **Abstract:**

##### **Objectives**

Campylobacter is a significant zoonotic pathogen primarily transmitted through poultry. Our study aimed to assess antimicrobial resistance and genetic relationships among Campylobacter isolates from retail chicken meat and humans in Taiwan.

##### **Methods**

Campylobacter isolates were analysed using whole-genome sequencing to investigate their antimicrobial resistance, genetic determinants of resistance, and genotypes.

##### **Results**

Campylobacter coli and Campylobacter jejuni accounted for 44.9% and 55.1% of chicken meat isolates, and 11.4% and 88.6% of human isolates, respectively. C. coli displayed significantly higher resistance levels. Furthermore, isolates from chicken meat exhibited higher levels of resistance to most tested antimicrobials compared to isolates from humans. Multidrug resistance was observed in 96.3% of C. coli and 43.3% of C. jejuni isolates from chicken meat and 80.6% of C. coli and 15.8% of C. jejuni isolates from humans. Macrolide resistance was observed in 85.5% of C. coli isolates, primarily attributed to the erm(B) rather than the A2075G mutation in 23S rRNA. Among the 511 genomes, we identified 133 conventional MLST sequence types, indicating significant diversity among Campylobacter strains. Notably, hierarchical Core-genome multilocus sequence typing clustering, including HC0, HC5, and HC10, revealed a significant proportion of closely related isolates from chicken meat and humans.

## Conclusions

Our research highlights significant associations in antimicrobial resistance and genetic relatedness between *Campylobacter* isolates from chicken meat and humans in Taiwan. The genetic analysis data suggest that campylobacteriosis outbreaks may occur more frequently in Taiwan than previously assumed. Our study emphasizes the need for strategies to control multidrug-resistant strains and enhance outbreak prevention.

**Keywords:** *Campylobacter*; Antimicrobial resistance (AMR); Whole-genome sequencing (WGS); Antimicrobial resistance gene (ARG); Core-genome multilocus sequence typing (cgMLST); Molecular epidemiology

39. [Detection and Molecular Typing of \*Campylobacter\* Isolates from Human and Animal Faeces in Coastal Belt of Odisha, India](#), Nirmal Kumar Mohakud, Saumya Darshana Patra, Subrat Kumar, Priyadarshi Soumyaranjan Sahu, Namrata Misra, Arpit Kumar Shrivastava, **Indian Journal of Medical Microbiology**, Volume 37, Issue 3, 2019, Pages 345-350, [https://doi.org/10.4103/ijmm.IJMM\\_19\\_394](https://doi.org/10.4103/ijmm.IJMM_19_394).

### Abstract:

**Introduction:** *Campylobacter*-mediated diarrhoea is one of the major causes of gastroenteritis globally. A majority of the *Campylobacter* spp. that cause disease in humans have been isolated from animals. Faecal contamination of food and water is the identified frequent cause of human campylobacteriosis. **Methodology:** In the present study, faecal samples from patients with symptoms of acute diarrhoea (n = 310) and domestic animals including cows (n = 60), sheep (n = 45) and goats (n = 45) were collected from the same localities in the peri-urban Bhubaneswar city. Genomic DNA isolation followed by polymerase chain reaction and sequencing was employed to analyse *Campylobacter* spp.-positive samples. **Results:** Of the 460 faecal samples, 16.77% of human samples and 25.33% of animal samples were found to be positive for *Campylobacter* spp. Among animals, the isolation rate was highest in sheep followed by cows and goats with 9.33%, 8.66% and 7.33%, respectively. The highest number of *Campylobacter*-positive cases was diagnosed in infants of 2–5 years age. Concurrent infection of other pathogens in addition to *Campylobacter* spp. was frequently detected in the samples. **Conclusion:** The present study showed the incidence of *Campylobacter* infections in human and different animal species in and around Bhubaneswar, Odisha. The analysis suggested that domestic animals can be the potential sources for human campylobacteriosis in the region.

**Keywords:** *Campylobacter* spp.; diarrhoea; Odisha; phylogenetic analysis

40. [PorA specific primers for the identification of Campylobacter species in food and clinical samples](#), Marco Fontanot, Lucilla Iacumin, Francesca Cecchini, Giuseppe Comi, Marisa Manzano, **LWT - Food Science and Technology**, Volume 58, Issue 1, 2014, Pages 86-92, <https://doi.org/10.1016/j.lwt.2014.03.006>.

**Abstract:**

Campylobacteriosis is a public health problem with considerable socio-economic impact. As the European Food Safety Authority has emphasized the importance of a surveillance programme for campylobacteriosis, the aim of the present study was the optimization of a specific and sensitive PCR protocol able to detect Campylobacter species responsible for gastrointestinal infections. Raw poultry meat samples were analysed for the presence of Campylobacter sp., by plating onto mCCD (Modified Charcoal-Cefoperazone-Deoxycholate) Agar and Campylobacter Selective Preston Agar and using four sets of species-specific primers for Campylobacter jejuni, Campylobacter coli, Campylobacter upsaliensis and Campylobacter lari designed to bridge the porA gene. The resulting primers demonstrated a sensitivity of 0.01 ng/μl for the C. coli-specific, C. lari-specific, and C. upsaliensis-specific primer sets and 0.5 ng/μl for the C. jejuni-specific primer sets using DNA from pure cultures. Non-specific amplification of non-target DNA was not observed indicating excellent specificity. The primers were useful for the analyses of poultry meat samples both for direct plating onto mCCDA, and for DNA extracted directly from the cells grown for 48 h in Preston enrichment broth. The sets of primers were also useful when used for species identification of human isolates.

**Keywords:** Campylobacter; porA; PCR; Campylobacteriosis; Food contamination

41. [How to choose geographical units in ecological studies: Proposal and application to campylobacteriosis](#), Julie Arsenault, Pascal Michel, Olaf Berke, André Ravel, Pierre Gosselin, **Spatial and Spatio-temporal Epidemiology**, Volume 7, 2013, Pages 11-24, <https://doi.org/10.1016/j.sste.2013.04.004>.

**Abstract:**

In spatial epidemiology, the choice of an appropriate geographical unit of analysis is a key decision that will influence most aspects of the study. In this study, we proposed and applied a set of measurable criteria applicable for orienting the choice of geographical unit. Nine criteria were selected, covering many aspects such as biological relevance, communicability of results, ease of data access, distribution of exposure variables, cases and population, and shape of unit.

These criteria were then applied to compare various geographical units derived from administrative, health services, and natural frameworks that could be used for the study of the spatial distribution of campylobacteriosis in the province of Quebec, Canada. In this study, municipality was the geographical unit that performed the best according to our assessment and given the specific objectives and time period of the study. Future research areas for optimizing the choice of geographical unit are discussed.

**Keywords:** Campylobacteriosis; Ecological study; Geographical unit; Modifiable areal unit problem (MAUP)

42. [Prevalence and Comparison of Genetic Profiles of Campylobacter Strains Isolated from Poultry and Sporadic Cases of Campylobacteriosis in Humans](#), Éric Nadeau, Serge Messier, Sylvain Quessey, **Journal of Food Protection**, Volume 65, Issue 1, 2002, Pages 73-78, <https://doi.org/10.4315/0362-028X-65.1.73>.

**Abstract:**

Between July 1998 and June 1999, 93 lots of broiler chickens distributed on 57 farms were sampled in two abattoirs of the province of Québec (Canada). A total of 2,325 samples of cecal material were analyzed to determine the prevalence of campylobacters. Biotyping and pulsed-field gel electrophoresis (PFGE) were done on 20% of the Campylobacter isolates to study the distribution within poultry production. Macrorestriction profiles were compared with profiles of 24 Campylobacter strains isolated from sporadic cases of human diarrheic patients in order to evaluate genetic relationships. Approximately 40% of the broiler chickens in 60% of the lots and 67% of the farms were colonized. Biotypes I and II of Campylobacter jejuni were the most prevalent biotypes in poultry and human isolates. The PFGE dendograms revealed a high genetic diversity among poultry isolates, with 49 different genotypes from the 56 positive lots. More than 75% of these lots were colonized by a unique genotype. All positive lots raised simultaneously on the same farm had common genotype(s). Different genotypes were isolated from lots raised at different grow-out periods on a farm. In some cases, identical genotypes were found at different grow-out periods on a farm and also from different farms. Macrorestriction profiles showed that approximately 20% of human Campylobacter isolates were genetically related to genotypes found in poultry. This genetic relationship and the high prevalence of C. jejuni biotypes I and II in poultry indicated that Campylobacter in broiler production of the province of Québec could be a potential source of hazard for public health.

43. [The worldwide trend of Campylobacter spp., infection from duck-related isolates and associated phenotypic and genotypic antibiotic resistance, since 1985: identifying opportunities and challenges for prevention and control](https://doi.org/10.1016/j.psj.2021.101213), Saeid Jafari, Mahdi Ebrahimi, Taradon Luangtongkum, **Poultry Science**, Volume 100, Issue 8, 2021, 101213, <https://doi.org/10.1016/j.psj.2021.101213>.

**Abstract:**

Campylobacter, a leading cause of foodborne diseases, is well recognized worldwide. Poultry and poultry products are considered as major sites for Campylobacter infection in humans. The extensive uses of antibiotics mostly as growth promoters and for therapeutic purposes have led to the emergence of antibiotic-resistant strains of foodborne pathogens including Campylobacter. A key tenet of this paper is the need for reviewing the previous studies conducted around the globe on the prevalence and antimicrobial resistance of Campylobacter spp. isolates in duck to better understand the sources and trends of infection. Based on published data, the prevalence of Campylobacter spp. in duck and duck-related samples ranged from 0% to 100% and was largely influenced by the isolation method. Among Campylobacter spp., *C. jejuni* was the predominant cause of campylobacteriosis, followed by *C. coli*. Campylobacter spp. from ducks were mostly resistant to fluoroquinolones and tetracycline and a lesser extent to gentamicin, chloramphenicol, and erythromycin. Some studies showed that ducks may pose a risk for acquiring campylobacteriosis because they had genotypes quite similar to human isolates detected previously. A continued monitoring approach is needed, at national and international levels, with enhanced surveillance and reporting of trends, as well as harmonization of surveillance systems toward a one-health approach to monitoring antimicrobial resistance in animal production particularly if increased resistance rates are being demonstrated.

**Keywords:** antibiotic resistance; Campylobacter; duck; genotyping; prevalence

44. [A procedure for surveillance data-driven risk assessment to inform Campylobacter risk-based control](https://doi.org/10.1016/j.mran.2024.100322), Alessandro Foddai, Marianne Sandberg, Maarten Nauta, **Microbial Risk Analysis**, Volumes 27–28, 2024, 100322, <https://doi.org/10.1016/j.mran.2024.100322>.

**Abstract:**

In this study is presented a procedure for surveillance data-driven risk assessment, which can be used to inform inter-sectorial Campylobacter risk-based control, e.g. within National Action Plans and One Health (OH) systems. Campylobacter surveillance data (2019 to 2022) and a published quantitative microbial risk assessment (QMRA) model were used, to show the procedure.

Moreover, an interface tool was developed in Excel for showing descriptive statistics on measured apparent flock prevalence (AP) and concentrations (colony forming units per gram, cfu/g) on the meat, together with their related QMRA outputs. Currently (mid-2024), Danish fresh broiler meat is produced by four slaughterhouse companies (A, B, C and D), where approximately 30 % of the annually slaughtered broiler flocks are randomly culture tested, on one leg skin (LS) sample per flock sampled from chilled carcasses. Data variables were: date of sampling, farm-ID, within farm house-ID, flock-ID, slaughterhouse name, sample-ID, and Campylobacter concentrations. Flocks were classified as carcass positive with a concentration  $\geq 10$  cfu/g. The data was fed into the QMRA model to assess: a) the average risk of human campylobacteriosis per serving (during a month or year), and b) the monthly/annual risk of 2022 relative (RR) to the baseline (average) risk from the previous three years. The descriptive statistics and the risk assessment (RA) were carried out at national level and for each slaughterhouse. In 2022, the national RR was 1.03, implying that the average annual risk increased by approximately 3 % compared to the baseline. Nevertheless, for slaughterhouses A, B and D, the annual risk decreased by  $\approx 22$  %, 21 % and 43 %, respectively; whereas for slaughterhouse C it increased by 48 %. Monthly risk estimates showed seasonal variations, according to the visualized changes of AP and meat contaminations. The national monthly RR was  $>1$  in July and from September to December. During those months: slaughterhouse C had always  $RR > 1$ , slaughterhouse A had a relative increase of risk in July, slaughterhouse B in July and November, and slaughterhouse D in October and December. The procedure and the tools used in this study, allow identifying the impact of seasonality and food-chain stages (i.e. slaughterhouses and their broilers sourcing farms) on the risk per serving, so that Campylobacter risk-based control could be implemented accordingly, from farm to fork, across consecutive surveillance periods. The same principles could be applied in other countries, food chains, and/or for other foodborne pathogens, when similar data and QMRA models are available.

**Keywords:** Surveillance data; Risk communication; Food chain; Broiler meat; Risk management

45. [Campylobacter species and genotype distribution in Finnish beef liver – Retail liver juice ideal for isolation and quantification](#), Jenna Luoto, Riikka Keto-Timonen, Rauni Kivistö, *International Journal of Food Microbiology*, Volume 411, 2024, 110524, <https://doi.org/10.1016/j.ijfoodmicro.2023.110524>.

**Abstract:**

Campylobacteriosis, primarily caused by Campylobacter jejuni and C. coli, is the main bacterial zoonosis worldwide. While poultry is recognized as the main reservoir, bovines are considered another important reservoir for Campylobacter spp. found in human infections. In contrast to

chicken, retail beef is seldom contaminated by *Campylobacter* species. However, beef liver is recognized to be frequently contaminated and has been linked to human infections via epidemiological investigations. Our aims were to evaluate the prevalence of *Campylobacter* spp. inside and on the surface of beef liver pieces at retail in Finland and to analyse the population in more detail using whole genome sequencing (WGS) to assess the public health relevance. A total of 90 retail beef livers were studied using both enrichment of the external peptone-saline rinse of the liver piece and direct culture from the inside after surface sterilization. Furthermore, 46 of the livers were also studied using direct culture of retail beef liver juice collected from the bottom of the consumer package to estimate the concentration of *Campylobacter* species. Overall, 44 (49 %) of the samples were positive for *Campylobacter* species, *C. jejuni*, *C. fetus* and *C. lari* being identified in 42 %, 8.9 % and 1.1 % of the samples, respectively. Direct culture of retail liver juice was a sensitive and convenient method for *Campylobacter* spp. detection, resulting in 48 % prevalence and a mean concentration of 49 cfu/ml (maximum 335 cfu/ml). Two samples (2.2 %), containing large hepatic ducts, were positive for *C. jejuni* internally, representing multilocus sequence typing (MLST) sequence type ST-19 and ST-21. WGS, core genome phylogeny and core genome MLST revealed that in most cases only one clearly distinct clone of clinically relevant *C. jejuni* or *C. fetus* was isolated from a single lot of samples. However, in some cases several distinct clones were identified simultaneously even from a single liver piece. In epidemiological investigations, it is thus highly advisable to genotype multiple isolates to capture the whole diversity of *Campylobacter* spp. from suspected food sources. Good kitchen hygiene, avoidance of cross-contamination and thorough cooking are important for limiting the transmission of campylobacteriosis.

**Keywords:** Multilocus sequence typing; Core genome; MLST; *C. jejuni*; *C. fetus*; *C. lari*

46. [The impacts of biosecurity measures on \*Campylobacter\* contamination in broiler houses and slaughterhouses in the Netherlands: A simulation modelling approach](#),

Andrijana Horvat, Pieter A. Luning, Catherine DiGennaro, Edien Rommens, Els van Daalen, Miriam Koene, Mohammad S. Jalali, **Food Control**, Volume 141, 2022, 109151, <https://doi.org/10.1016/j.foodcont.2022.109151>.

**Abstract:**

Intestinal campylobacteriosis, caused by *Campylobacter* ingestion, is the most reported zoonosis in the EU; it is societally costly and can lead to more severe sequelae. To reduce *Campylobacter* infections, biosecurity measures at both farms and slaughterhouses are warranted. However, the potential improvements achieved by these interventions have not been quantified. We used a systems science approach to develop a simulation model, synthesizing information from

interviews with stakeholders in the Dutch broiler production industry and the current literature. The model includes both farms and slaughterhouses in a “system of systems,” helping to clarify the complexity of interrelated components of these systems and analyse the impact of various interventions. Insects, transportation crates, farm personnel, and catchers were identified as potential *Campylobacter* sources and modelled as elements of feedback loops. Insect control, farm hygiene, visitor control, thinning, and transportation control interventions were analysed. The model was shown to accurately describe the seasonality of *Campylobacter*, which supports its validity. Model simulation revealed that insect control interventions had the strongest impacts, followed by combined farm hygiene and visitor control, and combined thinning and transportation control. Insect control interventions alone reduced the peak percentage of contaminated chickens from 51% to 26% and the peak percentage of highly contaminated (>1000 CFU/g) neck samples of chicken carcasses from 13% to 8%. Implementing all interventions concurrently reduced the peak percentages of contaminated chickens to 5% and highly contaminated chicken neck samples to 2%. These results suggest that multiple biosecurity measures must be implemented to reduce *Campylobacter* contamination.

**Keywords:** *Campylobacter*; Broiler chicken; Simulation modelling; Systems science; System dynamics; Interventions

47. [Avian campylobacteriosis, prevalence, sources, hazards, antibiotic resistance, poultry meat contamination, and control measures: a comprehensive review](https://doi.org/10.1016/j.psj.2023.102786), Mohamed T. El-Saadony, Ahmed M. Saad, Tao Yang, Heba M. Salem, Sameh A. Korma, Ahmed Ezzat Ahmed, Walid F.A. Mosa, Taia A. Abd El-Mageed, Samy Selim, Soad K. Al Jaouni, Rashed A. Zaghoul, Mohamed E. Abd El-Hack, Khaled A. El-Tarabily, Salam A. Ibrahim, **Poultry Science**, Volume 102, Issue 9, 2023, 102786, <https://doi.org/10.1016/j.psj.2023.102786>.

**Abstract:**

Avian campylobacteriosis is a zoonotic infection that poses human health hazards. *Campylobacter* is usually colonized in the avian gut revealing mild signs in the infected birds, but retail chicken carcasses have high contamination levels of *Campylobacter* spp. Consequently, the contaminated avian products constitute the main source of human infection with campylobacteriosis and result in severe clinical symptoms such as diarrhea, abdominal pain, spasm, and deaths in sensitive cases. Thus, the current review aims to shed light on the prevalence of *Campylobacter* in broiler chickens, *Campylobacter* colonization, bird immunity against *Campylobacter*, sources of poultry infection, antibiotic resistance, poultry meat contamination, human health hazard, and the use of standard antimicrobial technology during the chicken processing of possible control strategies to overcome such problems.

**Keywords:** broiler processing; Campylobacter; control strategies; foodborne infection; natural compounds

48. [Risk-based control of Campylobacter spp. in broiler farms and slaughtered flocks to mitigate risk of human campylobacteriosis – A One Health approach](#), Alessandro Foddai, Maarten Nauta, Johanne Ellis-Iversen, *Microbial Risk Analysis*, Volume 21, 2022, 100190, <https://doi.org/10.1016/j.mran.2021.100190>.

**Abstract:**

Effects of risk-based control of Campylobacter spp. in Danish broiler farms and flocks were simulated, to assess potential reductions of human risk of campylobacteriosis, associated to the consumption of poultry meat produced in Denmark. Two national data streams were used and represented: Flock status by testing cloacal swabs (CS, 2018–2019) and carcass status by testing leg skin samples (LS, 2019). In the CS surveillance component all flocks slaughtered at the two major Danish slaughterhouses were tested with a polymerase chain reaction (PCR), while in LS one third randomly selected flocks were tested by culture (results in colony forming units per gram, cfu/g). Each farm was identified by its Central Husbandry Register (CHR) number. Two risk farm classification strategies (I-II) were based on CS data from 2018. Farms were classified as: always negative (Neg-CHRs), low risk (LowR-CHRs) and high risk (HighR-CHRs) farms. In strategy I, HighR-CHRs had more than five positive flocks, while in strategy II; they had more than 27.8% of the slaughtered flocks positive. Those two cut-offs were the annual 3rd quartiles across positive farms. Thereafter, a risk assessment model was used to estimate the annual relative risk (RR) of human campylobacteriosis in 2019, compared to that of 2013. Three hypothetical levels of cfu/g reductions (A, B and C) were simulated on the LS positive flocks (> 10 cfu/g) slaughtered by HighR-CHRs and were pairwise combined with the two classification strategies, yielding six risk-mitigation scenarios (A I-II; B I-II; C I-II). In scenarios A I-II, zero cfu/g were simulated, while in scenarios B and C, the original cfu/g were divided by three and by two. For each scenario, RRs were compared to the RR of the original cfu/g (scenario O). In 2018, if all flocks from HighR-CHRs had been negative, the annual CS flock prevalence would have reduced from 19.7% to 7.6% (strategy I) or 9.6% (strategy II). Whereas in 2019, it would have reduced from 17.1% to 7.8% or 11.6%. In both years, HighR-CHRs delivered a high percentage of the total annual positive flocks (61.4–54.4% under strategy I and 51.2–32.6% with strategy II). In 2019, if HighR-CHRs had delivered only LS negative flocks, the RR would have reduced from 0.94 (scenario “O”) to 0.51 (A-I). Other scenarios showed smaller RR reductions. Targeting high risk farms/flocks for intensive control could improve One Health-ness of national action plans against Campylobacter spp.

**Keywords:** Campylobacter spp.; Campylobacteriosis; One Health; Risk-based control; Broilers

49. [The role of whey on the performance and campylobacteriosis in broiler chicks](#), V. Tsiouris, E. Economou, T. Lazou, I. Georgopoulou, E. Sossidou, **Poultry Science**, Volume 98, Issue 1, 2019, Pages 236-243, <https://doi.org/10.3382/ps/pey388>.

**Abstract:**

The objective of the present study was to investigate the effect of the whey on broiler chicks' performance, welfare, and caecal *Campylobacter* counts under experimental and field conditions. In the experimental study, 120-d-old broiler chicks were randomly allocated to four treatment groups, as described below: group A, which served as negative control; group B, fed with a diet supplemented with 1% whey; group C, challenged with *Campylobacter jejuni*; and group D, supplemented with 1% whey and challenged with *C. jejuni*, respectively. Performance indexes and caecal *C. jejuni* counts were calculated. In addition to the performance indexes, the hock burn and the foot pad dermatitis lesions score were measured to assess the welfare status of broiler chicks. In order to evaluate the use of whey under field conditions, a second study was performed in a broiler farm with two identical houses. The evaluation of the experimental data revealed that the use of whey did not affect significantly the performance ( $P \leq 0.05$ ) and the caecal *C. jejuni* counts ( $P \leq 0.05$ ). There were neither footpad dermatitis lesions nor hock burn lesions in any of the experimental groups. In the field study, the use of whey had no effect on the performance indexes ( $P \leq 0.05$ ). It can be concluded that the addition of whey has no negative effect on poultry and may provide an alternative natural feed additive for the broiler feed industry.

**Keywords:** *Campylobacter*; whey; broiler; performance; welfare

50. [Mechanistic concepts involved in biofilm associated processes of \*Campylobacter jejuni\*: persistence and inhibition in poultry environments](#), Iulia A. Bundurus, Igori Balta, Ioan Pet, Lavinia Stef, Cosmin Alin Popescu, David McCleery, Joanne Lemon, Todd Callaway, Alastair Douglas, Nicolae Corcionivoschi, **Poultry Science**, Volume 103, Issue 12, 2024, 104328, <https://doi.org/10.1016/j.psj.2024.104328>.

**Abstract:**

*Campylobacter* species, predominantly *Campylobacter jejuni*, remains a significant zoonotic pathogen worldwide, with the poultry sector being the primary vector for human transmission. In recent years, there has been a notable rise in the incidence of human campylobacteriosis, necessitating a deeper understanding of the pathogen's survival mechanisms and transmission dynamics. Biofilm presence significantly contributes to *C. jejuni* persistence in poultry and subsequent food product contamination, and this review describes the intricate processes

involved in biofilm formation. The ability of *Campylobacter* to form biofilms on various surfaces, including stainless steel, plastic, and glass, is a critical survival strategy. *Campylobacter* biofilms, with their remarkable resilience, protect the pathogen from environmental stresses such as desiccation, pH extremes, biocides and sanitizing agents. This review explores the molecular and genetic mechanisms of *C. jejuni* biofilm formation, highlighting regulatory genes involved in motility, chemotaxis, and stress responses. Flagellar proteins, particularly *flaA*, *flaB*, *flaG*, and adhesins like *cadF* and *flpA*, are identified as the main molecular components in biofilm development. The role of mixed-species biofilms, where *C. jejuni* integrates into existing biofilms of other bacteria to enhance pathogen resilience, is also discussed. This review also considers alternative interventions to control *C. jejuni* in poultry production, in the context of increasing antibiotic resistance. It explores the effectiveness of prebiotics, probiotics, synbiotics, bacteriocins, bacteriophages, vaccines, and organic acids, with a focus on their mechanisms of action in reducing bacterial colonization and biofilm formation. Studies show that mixtures of organic acids and compounds like Carvacrol and Eugenol significantly downregulate genes linked with motility and adhesion, thereby disrupting biofilm integrity. It discusses the impact of environmental factors, such as temperature and oxygen levels on biofilm formation, providing insights into how industrial conditions can be manipulated to reduce contamination. This paper stresses the need for a multifaceted approach to control *Campylobacter* in poultry, integrating molecular and genetic insights with practical interventions. By advancing our understanding of biofilm dynamics and gene regulation, we aim to inform the development of more effective strategies to enhance food safety and protect public health.

**Keywords:** *Campylobacter* biofilm; poultry environment; mechanistic concept; biofilm inhibition; *Campylobacter* persistence