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A selection of *Campylobacter* research publications 2024/2025

Sevinc Ferrari 2025.09.30

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EURL Campylobacter

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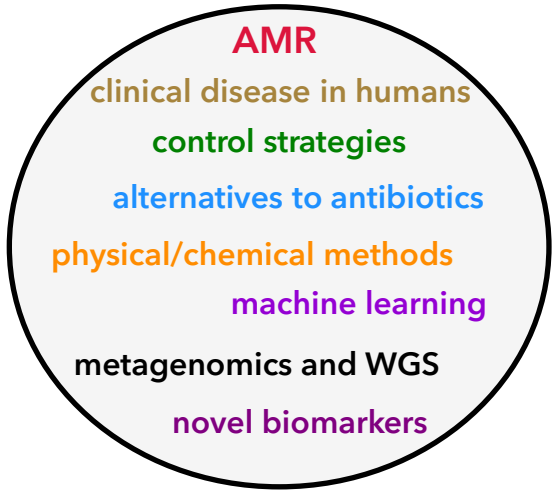
Publication search

Search word *Campylobacter*, from September 2024- August 2025

700 hits ⟶ 26 publications selected



Selection criteria: relevance to our projects and/or had an author from our NRLs

Articles mainly focusing on AMR and clinical disease in humans were excluded.

Topic areas

- Methodology related/Diagnostic methods
- Prevension approaches/Biosecurity
- Characterization/Genomics
- Epidemiology/Source attribution
- New species
- Reviews/overviews

Methodology related/Diagnostic methods

- **Evaluation of methods for detection of Campylobacter in raw milk: A multi-country study.** Ástvaldsson Á, Andersson G, Svensson L, Bruckner K, Denis M, Ferrari S, Golden O, Heise J, Lavander M, Repérant E, Riedel HM Stingl K, Skarin H. Int J Food Microbiol. 2025 Jan

Photo: iStock

- **Effect of incubation temperature, time, and freezing on diversity of Campylobacter spp. recovered from naturally contaminated retail beef livers.** Rauni Kivistö, Jenna Tuononen Int J Food Microbiol. 2025 April

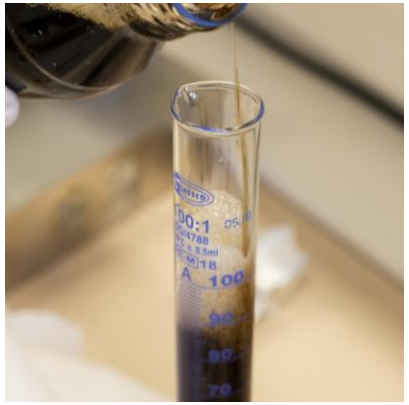


Photo: Linda Svensson, SVA

- **Quantitative comparison of thermotolerant *Campylobacter* spp. Growth in Preston broth with and without growth supplement** Sarah Brueggemann-Schwarze, Sandra Preuss, Juan Cruz Goegana, Christiane Buhler, Janine Heise, Kerstin Stingle. Int J Food Microbiol. 2025 July

- **A machine learning approach for rapid early detection of *Campylobacter* spp. using absorbance spectra collected from enrichment cultures.** Zhang et al. PLoS One. 2024 Sep 6

- **Detection and characterization of *Campylobacter* in air samples from poultry houses using shot-gun metagenomics - a pilot study.** Haverkamp THA, Spilsberg B, Johannessen GS, Torp M, Sekse C. BMC Microbiol. 2024 Oct

Effect of incubation temperature, time, and freezing on diversity of *Campylobacter spp*. recovered from naturally contaminated retail beef livers. Rauni Kivistö, Jenna Tuononen Int J Food Microbiol. 2025 April

20 retail beef livers analysed

- Direct culture on mCCDA - 37 °C and 41.5 °C for 24, 48, 72 h
- Identification and characterization - real-time colony PCR and WGS
- Effect of freezing at −20 °C for 6 months (direct culture and enrichment)
- cgMLST and AMR on selected isolates.

Results

- 85% positive for *Campylobacter* spp. *C. jejuni* in all positive samples; *C. fetus* in 30%
- Lower temperature (37 °C) and longer incubation (72 h) improved recovery, especially of *C. fetus*.
- Freezing reduced counts by 0.6–1.4 log, viable *Campylobacter* in 20% of samples.
- *C. jejuni* showed greater genomic diversity than *C. fetus*.
- Some *C. jejuni* carried AMR genes, but multidrug resistance was rare.

Prevension approaches /Biosecurity

- **Application of hot water and cold air to reduce bacterial contamination on broiler carcasses** Beterams A, Kirse A, Kreienbrock L, Stingl K, Bandick N, Reich F. Front Microbiol. 2024 Sep

- **Occurrence of *Campylobacter*, Listeria monocytogenes, and extended-spectrum beta-lactamase Escherichia coli in slaughterhouses before and after cleaning and disinfection** Madeleine Moazzami, Emma Bergenkvist, Sofia Boqvist, Sara Frosth, Solveig Langsrud, Trond Møretrø, Ivar Vågsholm, Ingrid Hansson. Food Microbiol. 2025 Jan

- **Effect of feeding biochar, oat hulls, yeast fermentate, and organic acids on reduction of *Campylobacter* in free-range broilers from hatching to slaughter.** NaoTakeuchi-Storm, Cristina Calvo-Fernandez, Annette Nygaard Jensen, Giulia Ravenni, Marianne Sandberg, Ulrik Birk Henriksen, Brian Lassen. Poultry Science. 2025 Feb

Photo: Kon/Shutterstock

Application of hot water and cold air to reduce bacterial contamination on broiler carcasses Beterams A, Kirse A, Kreienbrock L, Stingl K, Bandick N, Reich F. Front Microbiol. 2024 Sep

Two physical treatments as an additional step post-evisceration were evaluated:

- **Hot water immersion: 70, 75, 80 °C for 20–30 s (carcasses inoculated with *Campylobacter* jejuni and *Salmonella*). Quantification using culturing and viable qPCR (v-qPCR)**
- **Cold air (SafeChill™): −80 °C and −90 °C for 20, 30, 40 s (naturally contaminated carcasses with Campylobacter).**

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Results

- **Hot water: reduced *Campylobacter* and *Salmonella* by ~1 $\log_{10}$ CFU/ml at 70–80 °C.**
- **With v-qPCR 0.5–0.8 $\log_{10}$ IPIU/ml reduction (survival of viable but non-culturable (VBNC) cells)**
- **Cold air: reduced *Campylobacter* by 0.4–0.5 $\log_{10}$ CFU/ml at −90 °C; effect linked to initial contamination level.**

Conclusions

Hot water immersion more effective than cold air. v-qPCR showed underestimation of viable pathogens.

Both methods could be integrated into slaughterhouses processes, but real-world validation is needed.

Characterization/Genomics

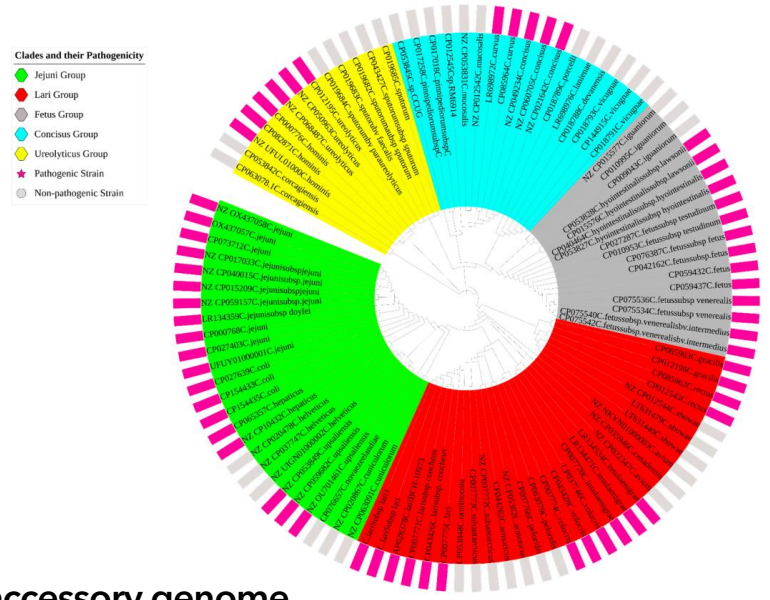
- **Identification of Novel Gene-Specific Markers for Differentiating Various Pathogenic *Campylobacter* Species Using a Pangenome Analysis Approach** Kuufire E. et al. Pathogens. 2025 May

- **Characterization of aquatic clade 2 and 3 *Campylobacter coli* isolates from Slovenia reveals admixture with other *Campylobacter* species** Lorenzen S. et al. BMC Microbiol. 2025 May

- **Longitudinal and cross-sectional sampling and whole genome sequencing of *Campylobacter* in a chicken abattoir reveal highly dynamic population structure** Tong S. et al., Appl Environ Microbiol. 2025 May

- **Enhanced laboratory surveillance study of *Campylobacter* species in England.** Swift C, Crewdson A, Chan YW, Painset A, Douglas A, Gokool S, Jenkins C, Godbole G.J Med Microbiol. 2025 Jun

Identification of Novel Gene-Specific Markers for Differentiating Various Pathogenic *Campylobacter* Species Using a Pangenome Analysis Approach Kuufire E. et al. Pathogens. 2025 May 14



Methods

- Dataset: 105 high-quality genomes of 33 *Campylobacter* species and 9 subspecies
- Pangenome analysis using the Roary ILP Bacterial Core Annotation Pipeline (RIBAP)
- Focus on species- and subspecies-specific genetic markers
- In silico validation against large genomic datasets to test specificity and coverage

Results

- Large genomic diversity, small core genome dominated by ribosomal genes, highly variable accessory genome.
- 54 unique genetic markers with ≥90% specificity and coverage, more than 50% being hypothetical proteins.
- Functions: DNA synthesis, repair, metabolism, and transport; some may influence virulence.

Conclusion

Novel gene-specific markers identified for differentiating *Campylobacter* species, valuable for rapid diagnostics, outbreak tracing, and food safety monitoring.

Characterization of aquatic clade 2 and 3 *Campylobacter coli* isolates from Slovenia reveals admixture with other *Campylobacter* species Lorenzen S. et al. BMC Microbiol. 2025 May

C. coli: clade 1 - clinical and agricultural sources

clades 2 and 3 - aquatic environments.

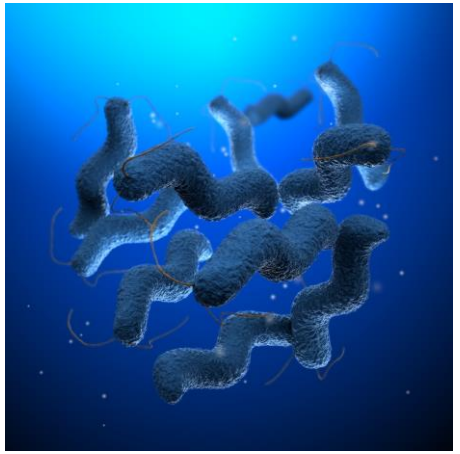


Photo: Shutterstock

Methods

- 48 water samples from 19 water bodies were analyzed
- Phylogenetic analyses using cgMLST and k-mer analysis
- Phenotypic tests: growth, biofilm formation, motility, autoagglutination, antibiotic resistance, water survival, and metabolic profiling

Results

- 11 *C. coli* isolates from clades 2 and 3 (admixture with C. jejuni and C. lari)
- A potentially new *Campylobacter* species
- Clade 3 isolates showed higher motility and water survival than clade 2 isolates.
- Antibiotic resistance was generally low
- Colony morphology differed: clade 2 colonies irregular and flat, clade 3 circular and opaque

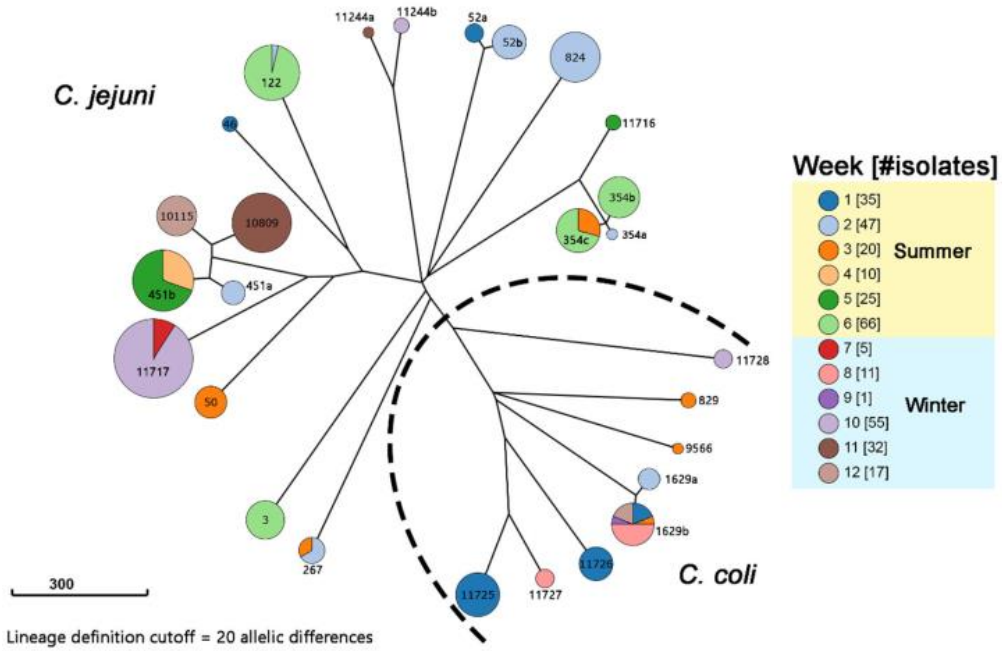
Longitudinal and cross-sectional sampling and whole genome sequencing of *Campylobacter* in a chicken abattoir reveal highly dynamic population structure Tong S. et al., Appl Environ Microbiol. 2025 May

Method

- Sampling – 12 weeks in total (two rounds: summer and winter, 2020)
- 456 samples: chicken guts, meat rinses, transport crates, machinery swabs
- WGS, cgMLST, plasmid typing, AMR gene typing

Results

- 324 isolates identified (268 C. jejuni and 56 C. coli), 27 distinct lineages
- 448 plasmids characterized, including resistance-associated plasmids
- High prevalence of AMR
- Subpopulations within lineages



- Abattoir environment (machines, crates, surfaces) showed high contamination, acting as cross-contamination hubs.
- Meat and environmental samples often shared lineages not found in gut samples → batch-to-batch dissemination.
- Seasonality: higher prevalence and diversity in summer vs. winter.
- Strong genomic overlap between abattoir isolates and regional/community strains, indicating public health risk

Epidemiology/Source Attribution

- **Implementation of a national monitoring programme of *Campylobacter* in Irish broilers to measure progress of on-farm and primary processing control measures** Golden O, Gutierrez M, O'Flaherty J, Unger K, Doyle B, Keogh T, McLernon J, Pearce R, O'Brien T, Byrne W. Zoonoses Public Health. 2024 Sep

- **Age-related presence and genetic diversity of *Campylobacter* spp. in young and adult yellow-legged gulls (Larus michahellis) in Croatia.** Ječmenica B, Duvnjak S, Humski A, Taylor LT, Kralj J, Krstulović F, Amšel Zelenika T, Mašović V, Jurinović L. Environ Microbiol Rep. 2024 Oct

- **Identification of Bacterial Pathogens in Organic Food of Animal Origin in Poland.** Sosnowski M, Wieczorek K, Osek J. Foods. 2024 Nov

- **Prevalence and antimicrobial resistant *Campylobacter* spp. in broiler chicken carcasses and hygiene practises in informal urban markets in a low-income setting.** Okello P, Bjöersdorff OG, Hansson I, Boqvist S, Erume J.PLoS One. 2025 Jan

- **Source attribution of human *Campylobacter* infection: a multi-country model in the European Union** Thystrup C, Brinch ML, Henri C, Mughini-Gras L, Franz E, Wieczorek K, Gutierrez M, Prendergast DM, Duffy G, Burgess CM, Bolton D, Alvarez J, Lopez-Chavarrias V, Rosendal T, Clemente L, Amaro A, Zomer AL, Grimstrup Joensen K, Nielsen EM, Scavia G, Skarżyńska M, Pinto M, Oleastro M, Cha W, Thépault A, Rivoal K, Denis M, Chemaly M, Hald T. Front Microbiol. 2025 Feb

- **Campylobacter in Raw Chicken Meat at Retail Level: Quantitative and Qualitative Assessment, Genomic Profiling, and Comparison With Isolates From Human Infections.** Lucien Kelbert, Karen Barmettler, Jule Anna Horlbog, Marc J A Stevens, Nicole Cernela, Magdalena Nüesch-Inderbinen, Roger Stephan. J Food Prot. 2025 May

Source attribution of human *Campylobacter* infection: a multi-country model in the European Union Thystrup C et al. Front Microbiol. 2025 Feb

A machine-learning model was constructed to predict the sources of human campylobacteriosis cases across multiple countries.

- **Available WGS data from >6,000 isolates from humans, animals, food and environment analyzed (from seven EU countries).**
- **A machine learning model (random forest and logit boost algorithms) using k-mer frequency patterns was constructed to attribute human infections to potential sources.**

- **Most cases linked to broilers and cattle, mainly domestic sources.**
- **The number of samples and the diversity of sources from where they are collected greatly influenced the accuracy of predictions.**
- **Overrepresented sources, like broilers, tended to be over-attributed, while underrepresented sources were underestimated.**
- **To improve future models standardized sampling strategies with a more balanced distribution of samples across sources is needed.**

New species

- ***Campylobacter californiensis* sp. nov., isolated from cattle and feral swine** Miller WG. et al. Int J Syst Evol Microbiol. 2024 Oct
- ***Campylobacter molothri* sp. nov. isolated from wild birds** Miller WG et.a. Int J Syst Evol Microbiol. 2025 Feb
- ***Campylobacter canis* sp. nov. isolated from the oral cavity of dogs** Camacho-Suntaxi T. et al. Int J Syst Evol Microbiol. 2025 Aug
- **A potentially new *Campylobacter* species** Lorenzen et al. 2025

Photo: Kon/Shutterstock

Reviews/Overviews

- **Aerotolerancy of *Campylobacter* spp.: A Comprehensive Review** Delaporte E. et al. Pathogens. 2024 Sep 28

- **Culture-Based Standard Methods for the Isolation of *Campylobacter* spp. in Food and Water** Neyaz LA et al. Pol J Microbiol. 2024 Dec

- **Mechanistic concepts involved in biofilm associated processes of *Campylobacter jejuni:* persistence and inhibition in poultry environments** Bundurus IA. et al. Poult Sci. 2024 Dec

- **Method of controlling Microbial contamination of food.** Urban-Chmiel R, Osek J, Wieczorek K. Pathogens. 2025 May

- **Source attribution studies of foodborne pathogens, 2010-2023: a review and collection of estimates.** Davydova A. et al. Food Microbiology 2025 May

Key trends 2024/2025

- Advanced detection and typing methods
- Intervention studies in food production
- Source attribution models
- Discovery of new *Campylobacter* species

Thank you!

Questions?

Photo: Linda Svensson, SVA

- sevinc.ferrari@sva.se
- www.sva.se