

## **Epidemiology of Campylobacter across the United Kingdom and 30 European Economic Area countries.**

Akosua Serwaa Boaitey-Biko[1, 2], Bruno Silvester Lopes[2]

1. Leeds Teaching Hospitals NHS Trust

2. Teesside University

**Background:** Campylobacter is the leading cause of > 160 million gastroenteritis, with > 37,000 deaths worldwide. In the UK, it causes 630,000 cases, accounts for approximately 120,000 general practitioner (GP) consultations, and costs the economy £1 billion annually.

**Aims:** This study examines Campylobacter incidence and disease burden in the UK (England, Wales, and Scotland) and 30 European Economic Area countries during 2018-2022. It analyses the epidemiology, virulence mechanisms, and antibiotic resistance in major pathogenic strains from various host reservoirs across Scotland.

**Methods:** The incidence of Campylobacter in the UK was analysed, and compared with the incidence in 30 EEA countries (2018–2022). Whole genome analysis of 3,428 isolates from Scotland, antimicrobial resistance to fluoroquinolones, tetracycline, macrolides, and beta-lactams, and 113 key virulence genes were studied.

**Results:** Scotland reported a higher average incidence of campylobacteriosis (108.9/100,000) than England and Wales (99.9/100,000). Czechia had the highest average incidence (177/100,000) in this period, exceeding the EU average (146/100,000), reflecting both high disease burden and robust national surveillance. Poland, Cyprus, Greece, Bulgaria, and Romania recorded the lowest incidence (3–4.1/100,000), likely due to underreporting, and lack of harmonised reporting across the EU. Fourteen major strains were identified in Scotland, including *C. jejuni* ST50, ST21, and *C. coli* ST827. Poultry (22.6%, n=774) was the primary reservoir. ST5136 was the predominant multi-drug-resistant clone exclusively associated with poultry. Compared to *C. jejuni*, *C. coli* ST827 lacked 27 virulence genes involved in toxin production and immune evasion, indicating lower virulence potential. There was 91.7% beta-lactam resistance across all *C. jejuni* and *C. coli* strains, and -57 promoter mutation was detected in a third of *C. jejuni* isolates which is linked with the hyper-production of beta-lactamase.

**Conclusion:** Strengthening data frameworks is essential to enhance public health strategies and ease burden across the NHS. Whole genome analysis provides insights into new emerging trends of antibiotic resistant and virulent strains of Campylobacter.

References:

1. European Food Safety Authority and European Centre for Disease Prevention and Control (EFSA and ECDC, 2019). 'The European Union One Health 2018 Zoonoses Report', EFSA Journal, 17(12). Available at: <https://doi.org/10.2903/j.efsa.2019.5926>.
2. Goddard, M.R., O'Brien, S., Williams, N., Guitian, J., Grant, A., Cody, A., Colles, F., Buffet, J.-C., Adlen, E., Stephens, A., Godfray, C.J. and Maiden, M.C.J. (2022) 'A Restatement Of The Natural Science Evidence Base Regarding The Source, Spread And Control Of Campylobacter Species Causing Human Disease', Proceedings of the Royal Society Biological Sciences, 289(1977) p. 20220400. Available at: <https://doi.org/10.1098/rspb.2022.0400>.
3. Haldenby, S., Bronowski, C., Nelson, C., Kenny, J., Martinez-Rodriguez, C., Chaudhuri, R., Williams, N.J., Forbes, K., Strachan, N.J., Pulman, J., Winstanley, I.N., Corless, C.E., Humphrey, T.J., Bolton, F.J., O'Brien, S.J., Hall, N., Hertz-Fowler, C. and Winstanley, C. (2020) 'Increasing Prevalence Of A Fluoroquinolone Resistance Mutation Amongst Campylobacter jejuni Isolates From Four Human Infectious Intestinal Disease Studies In The United Kingdom', PLOS ONE. Edited by B. Lin, 15(1), p. e0227535. Available at: <https://doi.org/10.1371/journal.pone.0227535>.
4. Hendrickson, S.M., Thomas, A., Raué, H.P., Prongay, K., Haertel, A.J., Rhoades, N.S., Slifka, J.F., Gao, L., Quintel, B.K., Amanna, I.J. and Messaoudi, I., (2023) 'Campylobacter Vaccination Reduces Diarrheal Disease and Infant Growth Stunting Among Rhesus Macaques', Nature communications, 14(1), p.3806. Available at: <https://doi.org/10.1038/s41467-023-39433-1>.
5. Lopes, B.S., Strachan, N.J.C., Meenakshi Ramjee, Thomson, A., MacRae, M., Shaw, S. and Forbes, K.J. (2019) 'Nationwide Stepwise Emergence and Evolution of Multidrug-Resistant Campylobacter jejuni Sequence Type 5136, United Kingdom', Emerging infectious diseases, 25(7), pp. 1320–1329. Available at: <https://doi.org/10.3201/eid2507.181572>.