



Erratum

Erratum to Antimicrobial resistance in *Campylobacter* spp. focussing on *C. jejuni* and *C. coli* – A Narrative Review' Journal of Global Antimicrobial Resistance Volume 43 (2025) Pages 372–389☆



Vathsala Mohan^{a,b,*}, Nikolaos Strepis^c, Konstantinos Mitsakakis^{d,e}, Karsten Becker^f, Leonid Chindelevitch^g, Nirajmohan Shivaperumal^a, Khine Swe Swe-Han^h, John P. Hays^c

^a School of Biomedical and Health Sciences, University of Western Australia, Perth, Western Australia, Australia

^b Commonwealth Science and Industrial Research Organisation, Perth, Western Australia, Australia

^c Department of Medical Microbiology & Infectious Diseases, Erasmus University Medical Centre Rotterdam (Erasmus MC), Rotterdam, the Netherlands

^d Laboratory for MEMS Applications, IMTEK—Department of Microsystems Engineering, University of Freiburg, Freiburg, Germany

^e Hahn-Schickard, Freiburg, Germany

^f Friedrich Loeffler-Institute of Medical Microbiology, University Medicine Greifswald, Greifswald, Germany

^g MRC Centre for Global Infectious Disease Analysis, Imperial College London, London, England, UK

^h Department of Medical Microbiology, National Health Laboratory Services, School of Laboratory Medicine and Medical Sciences, Nelson R Mandela School of Medicine, University of KwaZulu-Natal, Durban, South Africa

The publisher regrets Incorrect Fig. 4.

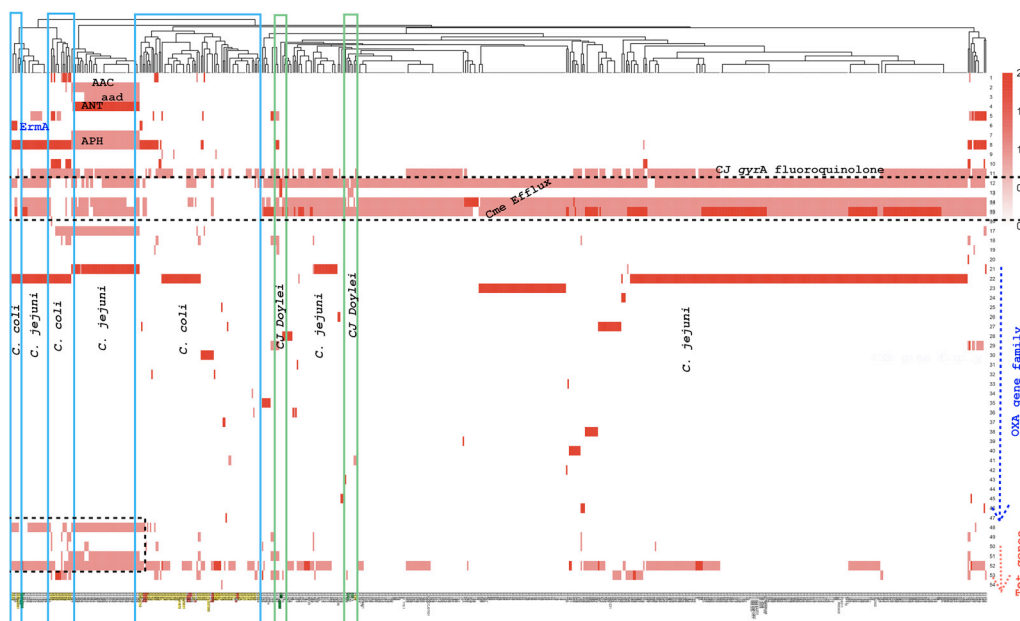


Fig. 4. Presence of AMR genes as predicted by WGS in the public genomes of *Campylobacter coli* and *Campylobacter jejuni* isolates. The heatmap and the Maximum Likelihood phylogenetic tree were performed using R Studio version 14.2. The presence of the AMR genes prediction was carried out with an identity score of >95 to <99% (light red) and 100% identity (dark red) hit with the reference sequence of the CARD database. There were 53 AMR genes that were identified based on the WGS prediction. Blue rectangles represent *C. coli* genomes and green rectangles represent *C. jejuni* subsp. *doylei* genomes. The figure shows the numbers 1–54 that are the AMR genes on the Y-axis and genomes on the X-axis, highlighting the blaOXA family genes, ermA, aminoglycoside genetic determinant, fluoroquinolone determinants and cme efflux genes. The details of the resistance determining gene list can be found in the Supplemental Table S2. Figure generated by authors for this publication [1].

Note to JM: Errors in article heads, particularly titles, author names, affiliations must not be repeated. In such cases, use the correct title, authors, affiliation(s), etc.

DOL of original article: [10.1016/j.jgar.2025.05.008](https://doi.org/10.1016/j.jgar.2025.05.008)

* Corresponding author details:

E-mail address: 00111008@uwa.edu.au (V. Mohan).

<https://doi.org/10.1016/j.jgar.2025.08.007>

2213-7165/© 2025 The Authors. Published by Elsevier Ltd on behalf of International Society for Antimicrobial Chemotherapy. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

The publisher would like to apologise for any inconvenience caused.

Reference

- [1] Mohan V, Strepis N, Mitsakakis K, Becker K, Chindelevitch L, Shivaperumal N, Swe-Han KS, Hays JP. Antimicrobial resistance in *Campylobacter* spp. focussing on *C. jejuni* and *C. coli* - A narrative review. *J Glob Antimicrob Resist* 2025;43:372–89. doi:[10.1016/j.jgar.2025.05.008](https://doi.org/10.1016/j.jgar.2025.05.008).