# Article information:

Genomic Insights into the Increased Occurrence of Campylobacteriosis Caused by Antimicrobial-Resistant Campylobacter coli - PMC
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9765411/>

# Article summary:

1. Whole-genome sequencing of 1,195 Campylobacter coli isolates from 1980 to 2021 revealed that C. coli is the dominant species in poultry and the main source of infection in humans.

2. 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.

3. This study provides an empirical basis for the molecular mechanisms that have enabled C. coli to become the dominant Campylobacter species in poultry and emphasizes the importance of poultry products as sources of campylobacteriosis caused by C. coli in human patients

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article is generally reliable and trustworthy, as it is based on a comprehensive analysis of whole-genome sequences from 1,195 Campylobacter coli isolates collected from 1980 to 2021, including 141 newly isolated and sequenced isolates from humans, poultry, swine, dairy cattle, natural environment, and other animals. The data was combined from both GenBank and the authors' lab for phylogenetic analysis using multilocus sequence typing (MLST) and core genome multilocus sequence typing (cgMLST). The results showed a close genetic relationship between human-derived isolates and those from poultry and their associated environments, indicating that poultry was likely the main source of C. coli infection in humans. Furthermore, antimicrobial resistance determinants were analyzed to determine whether phenotypic resistance could be predicted using WGS; this analysis showed a high correlation rate between AMR phenotype and genotype (92.60%), with a sensitivity of 93.03%, specificity of 91.19%, positive predictive value (PPV) of 97.25%, and negative predictive value (NPV) of 79.62%.

The article does not appear to be biased or one-sided; it presents both sides equally by providing evidence for its claims as well as exploring counterarguments where appropriate (e.g., discussing possible risks associated with antimicrobial use). There are no promotional content or partiality present either; instead, all claims are supported by evidence provided throughout the article or referenced studies/sources cited at the end of it. The only potential issue is that some points may be missing or unexplored; for example, there is no discussion about how long-term use or over

# Topics for further research:

* Campylobacter coli transmission
* Antimicrobial resistance determinants
* Long-term antimicrobial use risks
* Campylobacter coli epidemiology
* Whole-genome sequencing analysis
* Core genome multilocus sequence typing

# Report location:

<https://www.fullpicture.app/item/a37fe30d6863c6aadc3ec8e6808b1022>