



# *Campylobacter* isolated from LMIC poultry production networks show regional links to antimicrobial resistance and novel *C. coli* clusters

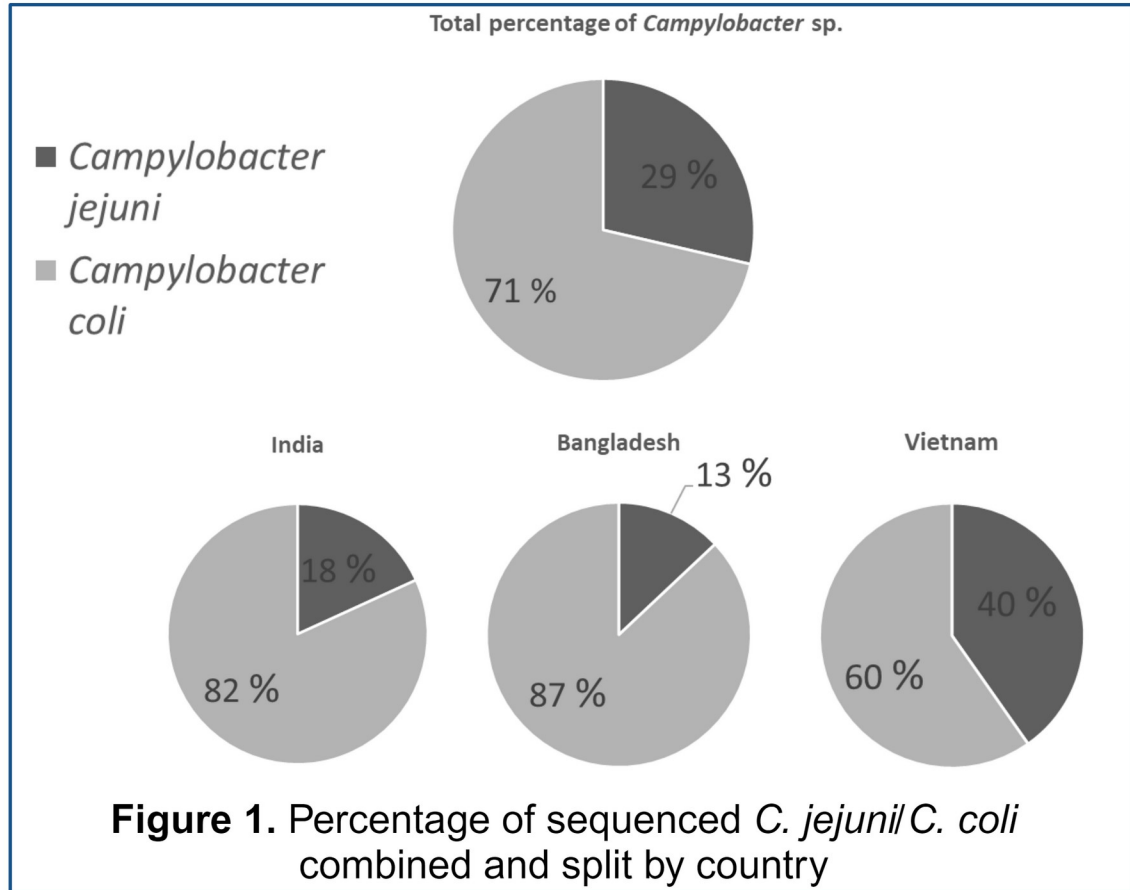
Name: Burhan Lehri, Richard Stabler

## Introduction

Diarrhoeal disease ranks as the second largest cause of global mortality due to infectious agents<sup>(1)</sup>. Alarming, it is responsible for approximately 9% of all deaths in children under five years old<sup>(2)</sup>. Currently, there is a growing demand for low-cost poultry products, especially in rapidly developing countries. This demand is driving the intensification of poultry farming practices, which in turn is increasing the incidence of food-related bacterial gastroenteritis. The most common causative agent of this gastroenteritis is *Campylobacter* spp.<sup>(1, 3)</sup>; a pathogen that is increasingly showing more resistance to first line antibiotics. Given its importance, monitoring antimicrobial resistance (AMR) profiles in *Campylobacter* spp. becomes imperative. To address this, the study employs whole genome sequencing (WGS) to identify antimicrobial resistance gene (ARG) profiles of isolated *Campylobacter* spp. from three rapidly developing countries in South and Southeast Asia.

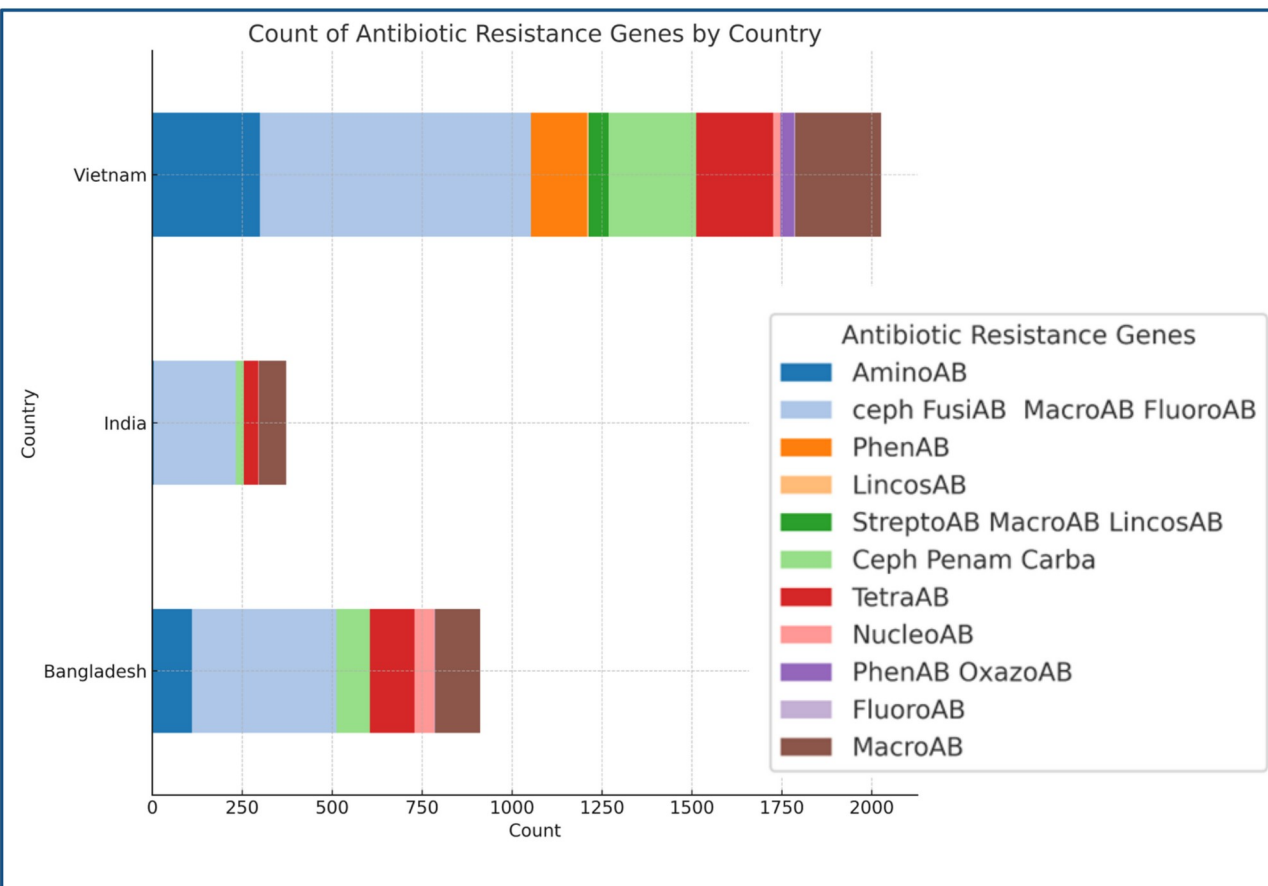
## Method

- Illumina MiSeq sequencer was used to sequencing *campylobacter* sp.
- ARGs were identified using CARD database, version 2023.
- Core genome Multilocus Sequence Typing (cgMLST) was determined using ChewBBACA, which integrated all complete *Campylobacter coli* and *jejuni* genome sequences available within the RefSeq database.

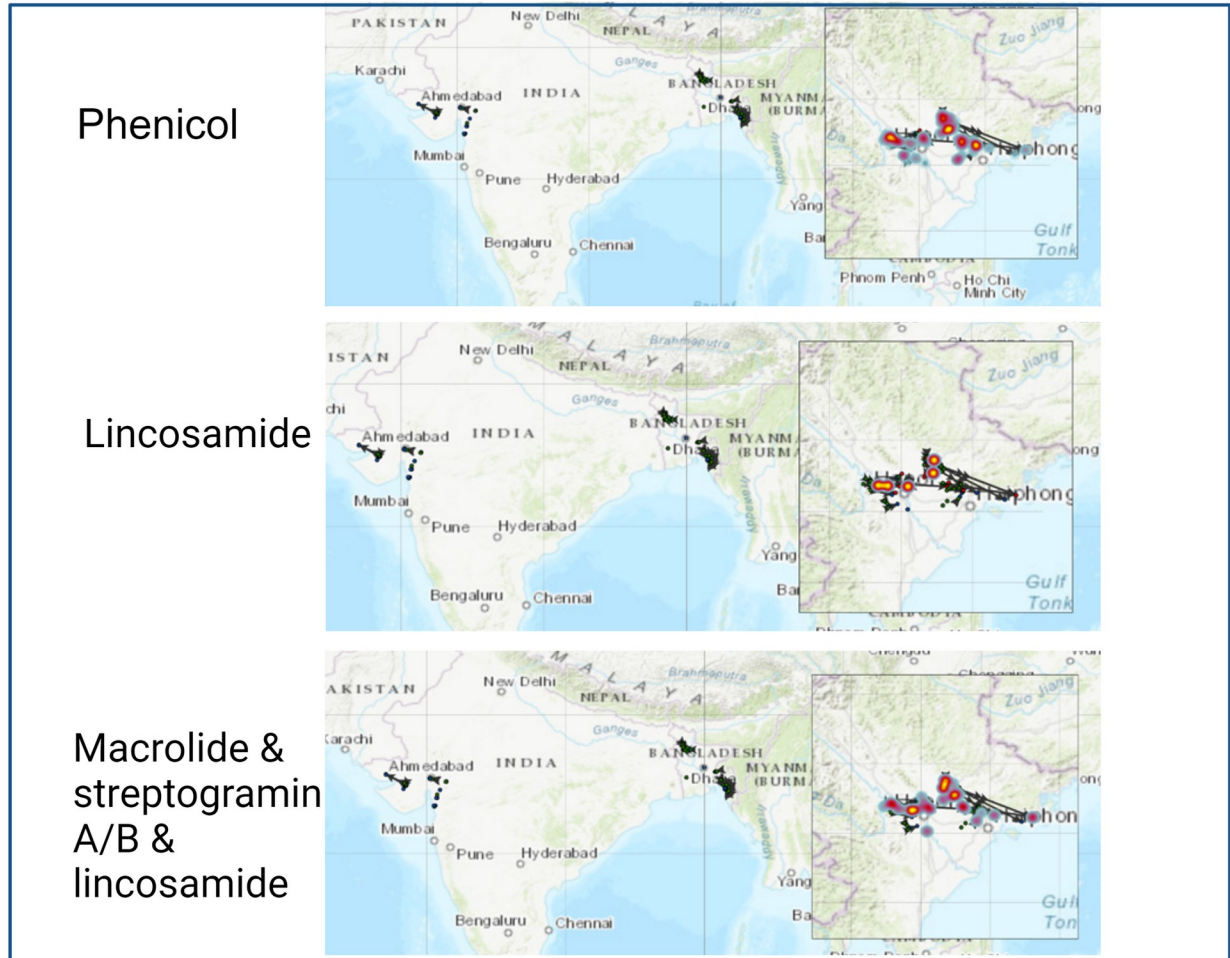


## Result

- The total number of samples sequenced were 454. Of the 454 samples; 131, 77 and 246 were from India, Bangladesh, and Vietnam respectively.
- More *C. coli* than *C. jejuni* were identified for within sites of interest (Figure. 1).



**Figure 2.** Frequency of ARGs that infer resistance to drug classes, split by country

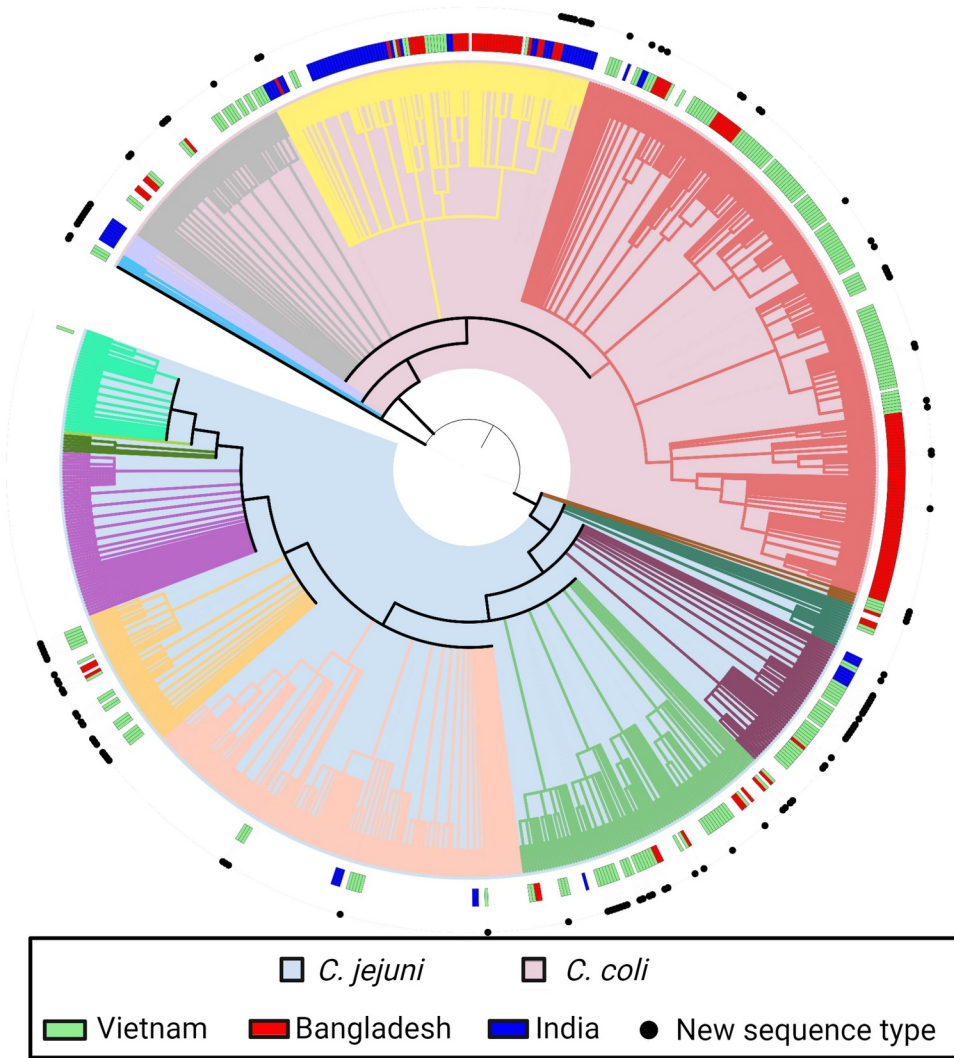


**Figure 3.** Spread of mentioned ARGs across sampling sites

**Result**

- Vietnam had a greater variety of resistance related genes, with ARGs to Phenicol, Lincosamide, and ARGs that could cause resistance to a combination of Macrolide, Streptogramin A/B, and Lincosamide (Figure 2), these ARGs were spread across Vietnam (Figure 3).
- A significantly higher proportion of genes associated with nucleoside resistance was found in Bangladesh (Figure 2).
- Concerning Macrolide and Fluoroquinolone resistance, the data indicates a resistance rate of approximately 50-40% in Bangladesh and Vietnam, with comparatively lower rates observed in India (Figure 2).
- The data suggest limited variety of ARGs found in India (Figure 2).





**Figure 4.** ChewBBACA output showing coregenome based clustering of *C. coli* & *C.jejuni*

## Result

Multiple newly identified strains were discovered, as represented by the dots in Figure 4. An analysis of the core genome of the *Campylobacter* isolates and their clades, denoted by the colored branches in Figure 4, revealed that *C. coli* strains tend to cluster geographically. The red *C. coli* clade predominantly comprises isolates from Bangladesh and Vietnam, in contrast to those from other countries. Additionally, these geographical clusters can be further subdivided into subclades where strains group more narrowly based on their specific locations. For example, some subclades have greater concentration of Indian/Vietnamese/Bangladesh isolates. The yellow *C. coli* clade contains a higher number of isolates from India and Bangladesh, as opposed to the red clade

## Conclusion

Based on ARG patterns observed in *Campylobacter* spp., we identified that Vietnam and Bangladesh exhibit a greater diversity of ARGs compared to India. Vietnam harbors ARGs associated with resistance to phenicol, macrolide, streptogramin A/B, and lincosamide, which are not present in India and Bangladesh. Meanwhile, Bangladesh shows a higher proportion of nucleoside resistance than both Vietnam and India, suggesting a more intensive use of antibiotics in Vietnam and Bangladesh relative to India. Furthermore, we have observed that *C. coli* strains tend to cluster according to their geographical origins, which indicates local adaptation and evolutionary divergence likely driven by unique environmental pressures.

## References

1. Bochen Cao by, Stevens GA, Ho J, Ma Fat D, Cao Gretchen Stevens BA, Ma D, et al. Global Health Estimates Technical Paper. 2020 [cited 2022 Aug 2]; Available from: [http://www.who.int/gho/mortality\\_burden\\_disease/en/index.html](http://www.who.int/gho/mortality_burden_disease/en/index.html)
2. Diarrhoea - UNICEF DATA [Internet]. [cited 2022 Aug 2]. Available from: <https://data.unicef.org/topic/child-health/diarrhoeal-disease/>
3. Igwaran A, Okoh AI. Human campylobacteriosis: A public health concern of global importance. *Heliyon*. 2019 Nov 1;5(11):e02814.