

# A One Health Assessment of Antimicrobial Resistance Genes in *Escherichia coli* from Laguna de Bay, Its Tributary Rivers, and Surrounding Backyard Farms in the Philippines

Patrick Philip A. Salvador, Kherson P. Gandola, Aryana Lee G. Bertuso, Aira Charlien R. de Guzman, Laurice Beatrice Raphaele O. dela Peña, Lance Matthew F. Farinas, and Windell L. Rivera

## AFFILIATIONS

Pathogen-Host-Environment Interactions Research Laboratory, Institute of Biology, College of Science, University of the Philippines Diliman, Quezon City 1101, Philippines

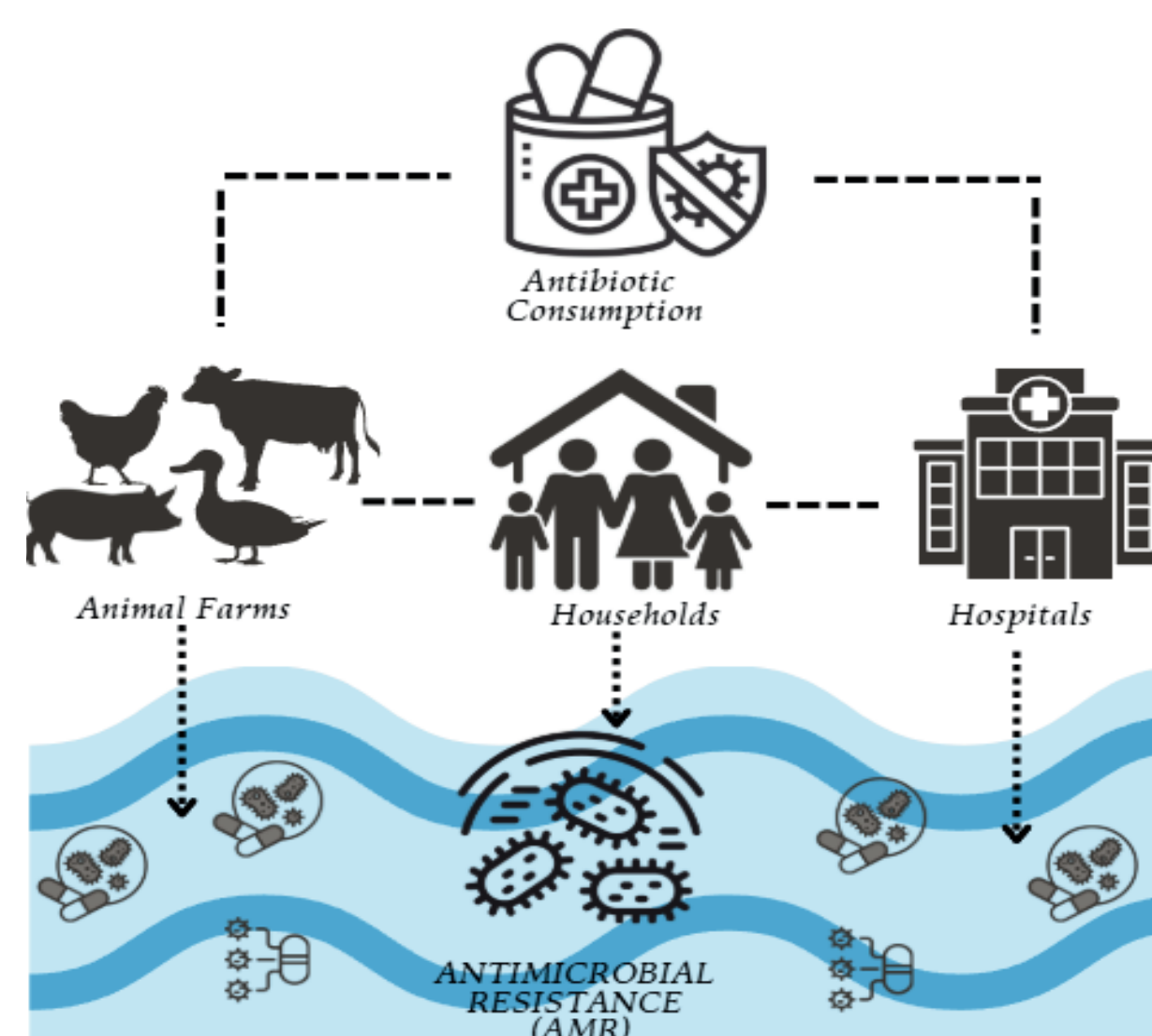
## ABSTRACT

Laguna Lake, a major multi-use freshwater system in the Philippines, is increasingly threatened by antimicrobial resistance (AMR) linked to environmental and agricultural sources. This study analyzed 2,728 *Escherichia coli* isolates from lake waters, tributary rivers, and nearby backyard farms, revealing that *tetA* and *blaTEM* were the most prevalent antimicrobial resistance genes (ARGs) across both environmental and animal hosts. This study confirms widespread ARG occurrence in the Laguna Lake ecosystem and provides baseline data for monitoring and mitigating AMR spread in environmental and agricultural settings.

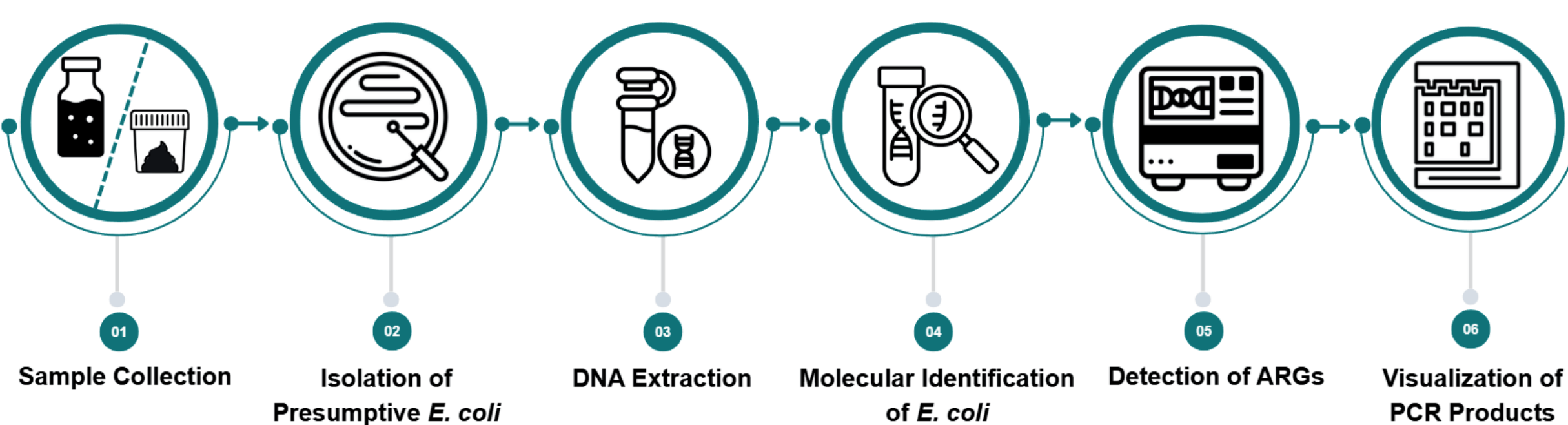
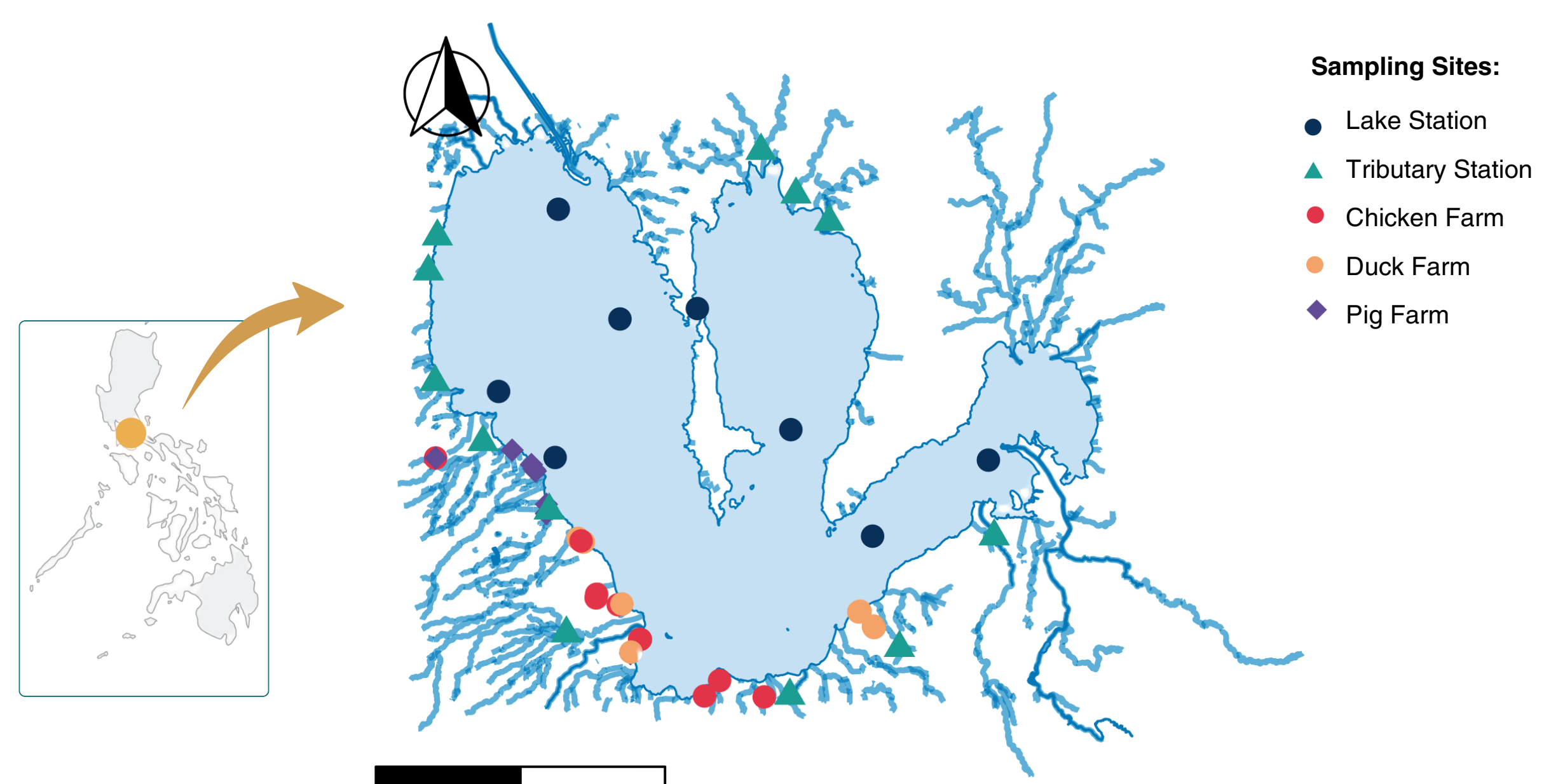
## INTRODUCTION

Laguna Lake, the largest lake in the Philippines, supports diverse economic, ecological, and recreational activities. Increasing anthropogenic pressures, including improper antibiotic use and backyard farming, contribute to the emergence and dissemination of antimicrobial-resistant bacteria (ARB) in this ecosystem. *Escherichia coli* is widely used to assess fecal contamination and the presence of ARGs in both environmental and animal sources. Despite growing concerns about AMR in the Philippines, the prevalence of ARGs across Laguna Lake and its

surrounding farms remains understudied. Therefore, this study aimed to characterize the ARG profiles and distribution among *E. coli* isolates from Laguna Lake, its tributaries, and adjacent backyard farms.



## MATERIALS & METHODS



## RESULTS

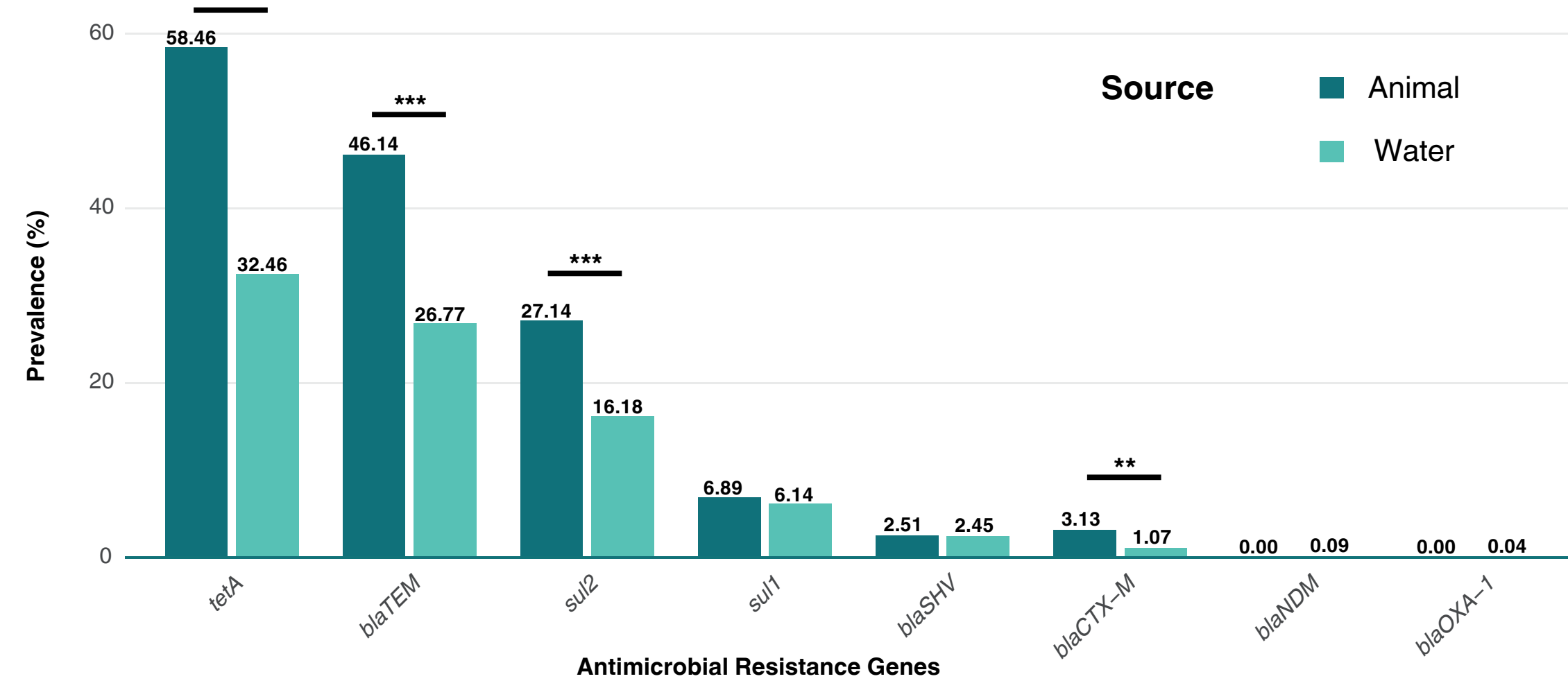


Fig. 1. Comparative Prevalence of ARGs in *E. coli* from Animal Hosts and Water Samples. \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$

*tetA*, *blaTEM*, and *sul2* were the three most prevalent ARGs across both sources, with significantly higher frequencies observed in animal hosts than in water ( $p < 0.001$ ).

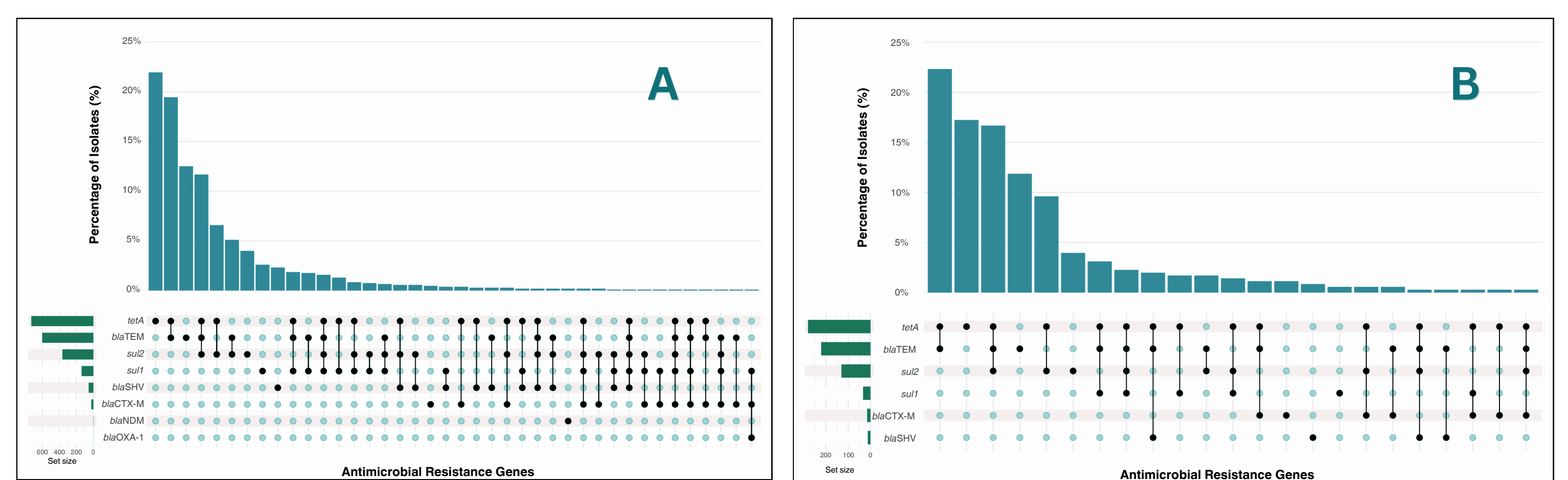


Fig. 2. Co-occurrence and Distribution of ARG Profiles in *E. coli* from (A) Water and (B) Animal Sources

- The ***tetA*-*blaTEM*** combination was most frequent in both sources (~22% in animal, ~19% in water), while a multidrug resistance core of *tetA*, *blaTEM*, and *sul2* was also observed (~16% in animal, ~12% in water).
- Environmental water exhibited greater genetic diversity, harboring high-risk carbapenemase genes (*blaNDM* and *blaOXA-1*) that were absent from animal isolates.

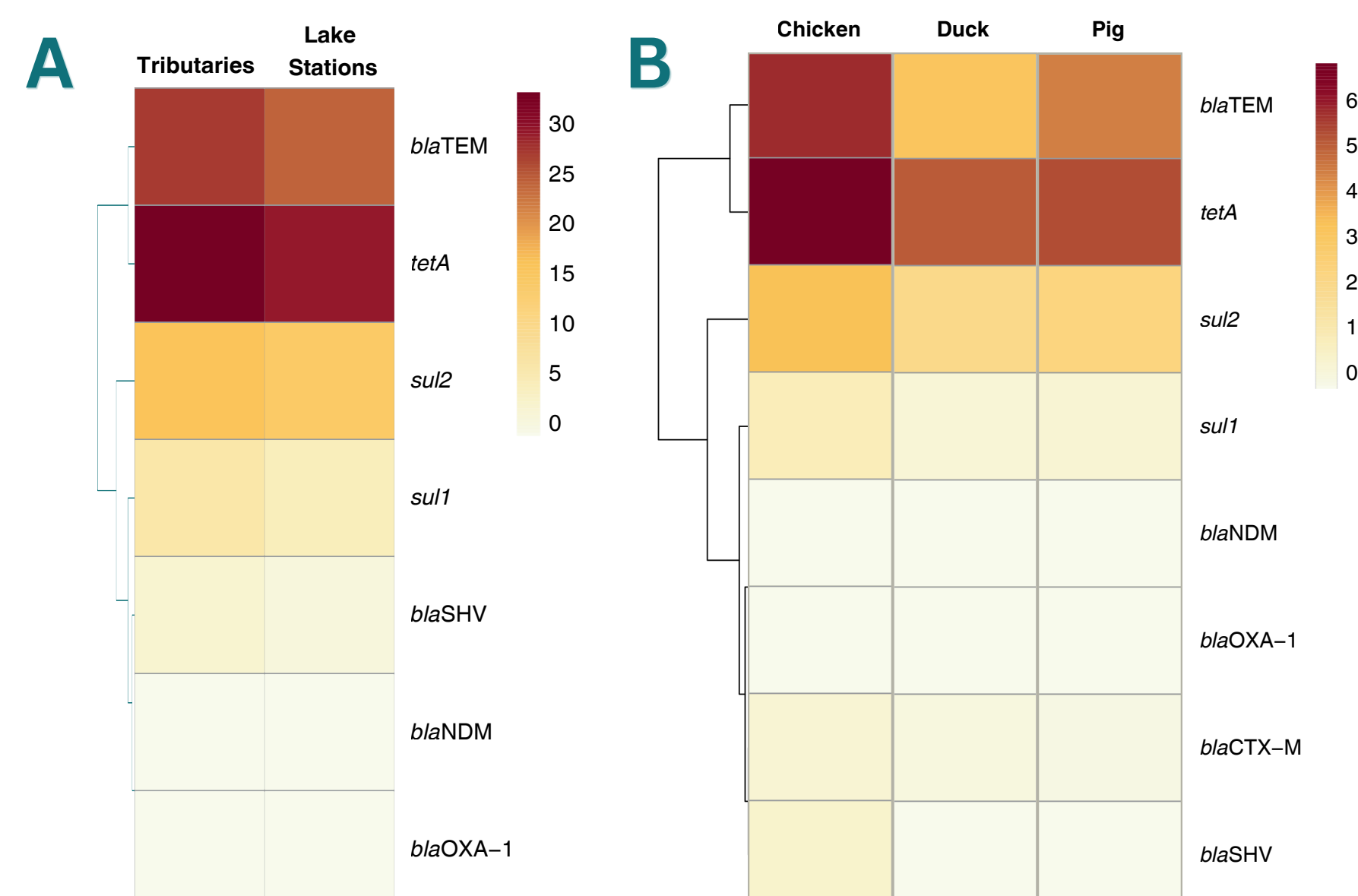


Fig. 3. Heatmap of ARG Prevalence Across Specific (A) Water Sampling Sites and (B) Animal Hosts

- Tributary rivers showed higher ARG prevalence than lake stations, suggesting that they are the primary pathways for AMR entering the lake.
- Among animal hosts, chickens harbored the highest ARG density, particularly *tetA* and *blaTEM*, indicating severe selective pressure within poultry production.

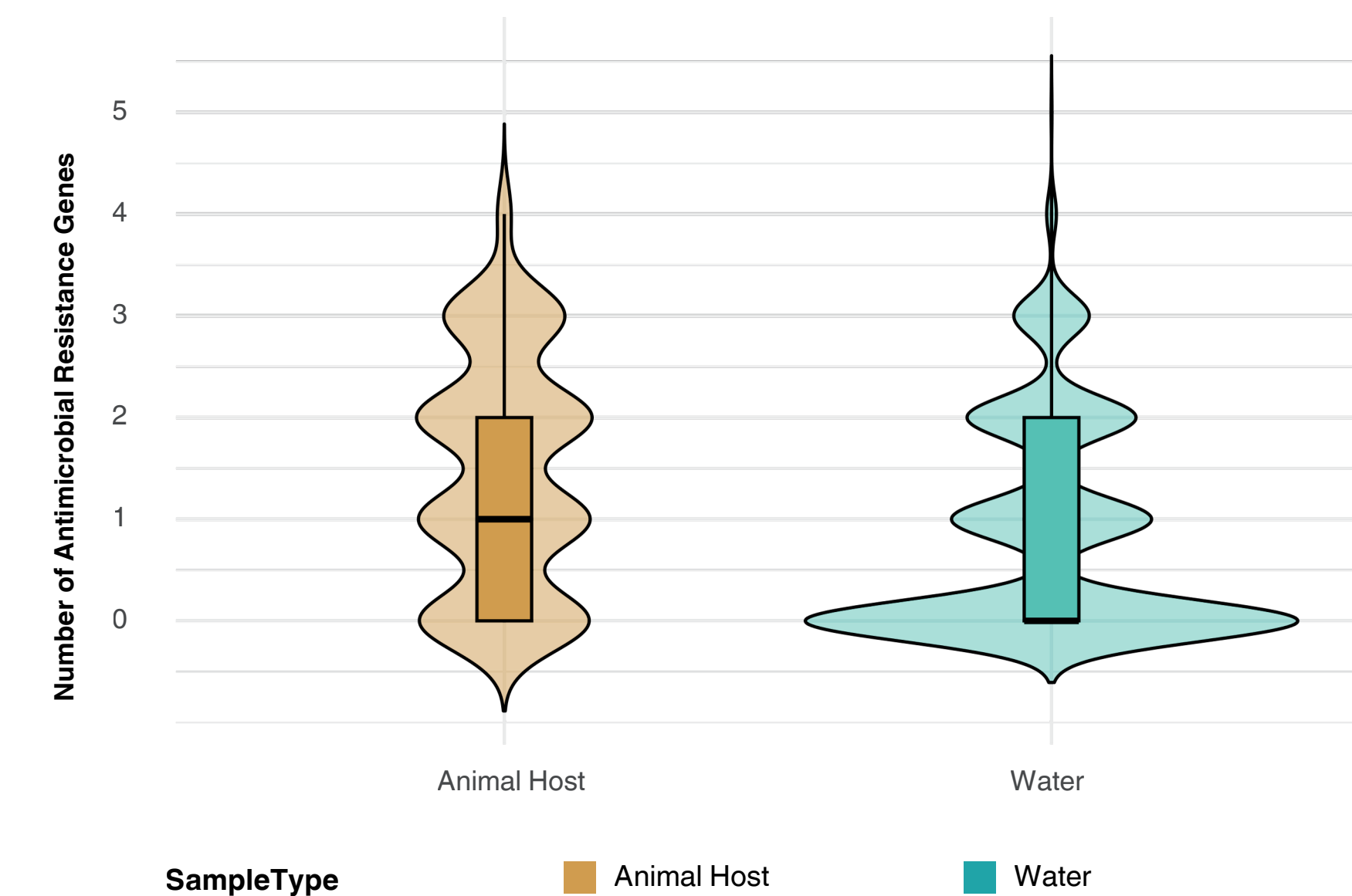


Fig. 4. Distribution of ARG Counts in *E. coli* Isolates from Animal Hosts and Water Samples

- Animal-derived *E. coli* carried a higher resistance-gene burden (median = 1) than water isolates (median = 0), which were largely negative for the screened ARGs.
- Backyard farms served as concentrated reservoirs of multi-resistance (1-3 genes), whereas aquatic environments were dominated by susceptible strains.

## CONCLUSION

The study confirms that *Escherichia coli* harboring various antimicrobial resistance genes (ARGs) are prevalent throughout Laguna Lake, its tributaries, and surrounding backyard farms. These findings establish essential baseline information for monitoring environmental contamination and designing targeted interventions to reduce the dissemination of antimicrobial resistance in the Philippines.

## REFERENCES



## ACKNOWLEDGEMENTS

### AFFILIATED INSTITUTIONS



### PARTNER & FUNDING ORGANIZATIONS



✉ pasalvador@up.edu.ph  
✉ arphilake.pheirl@gmail.com  
✉ pheirl.science.upd@up.edu.ph