

Insights into comprehensive antimicrobial resistance pattern of poultry



caeca in Gujarat, India

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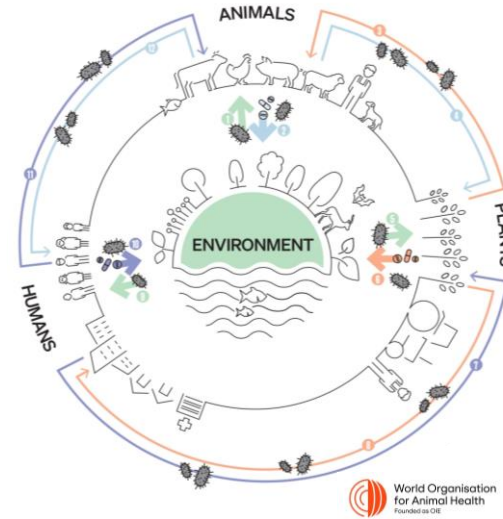
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Introduction

- Antimicrobial resistance (AMR) is a serious global public health threat in 21st century.
- Poultry gut act as important reservoirs of AMR genes with the potential for transmission to humans via the food chain.



Objective

Create a comprehensive profile of AMR genes in chicken caeca of Gujarat

Materials and methods

Chicken caecal contents from 106 broiler and 44 deshi (indigenous) birds were collected, extracted metagenomic DNA was used for amplicon sequencing followed by analysis to check the presence of AMR genes.

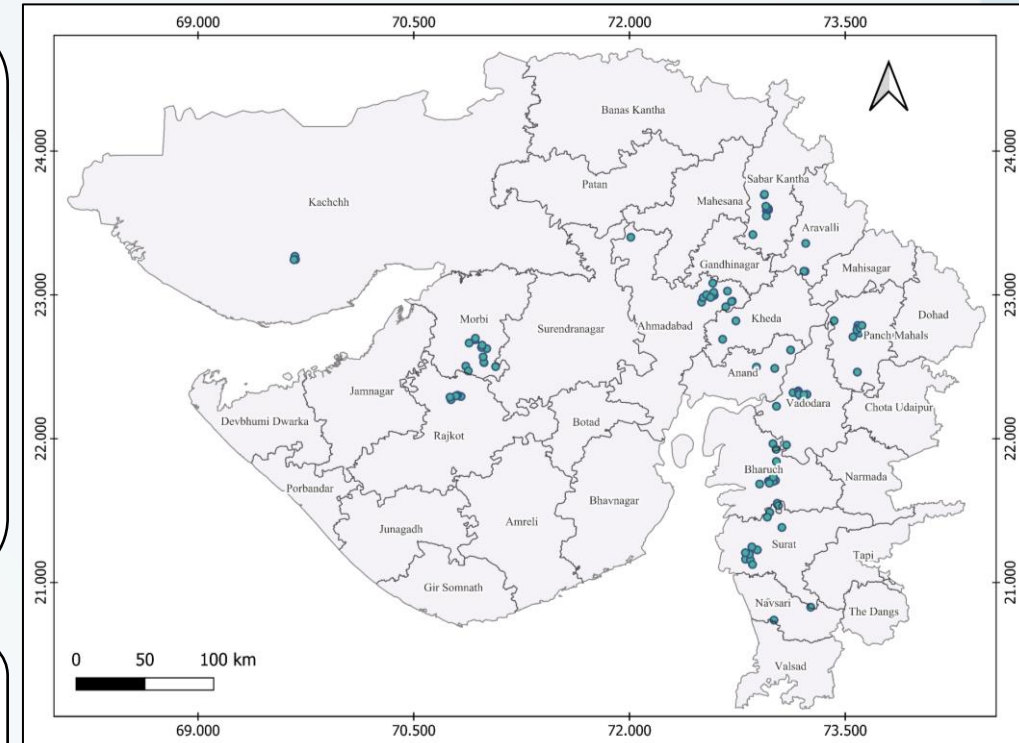


Figure 1: Study area map of Gujarat state with circles indicating the sampling coordinates

Results

Core ARGs

A total 103 gene resistant to 18 different antimicrobial classes were detected

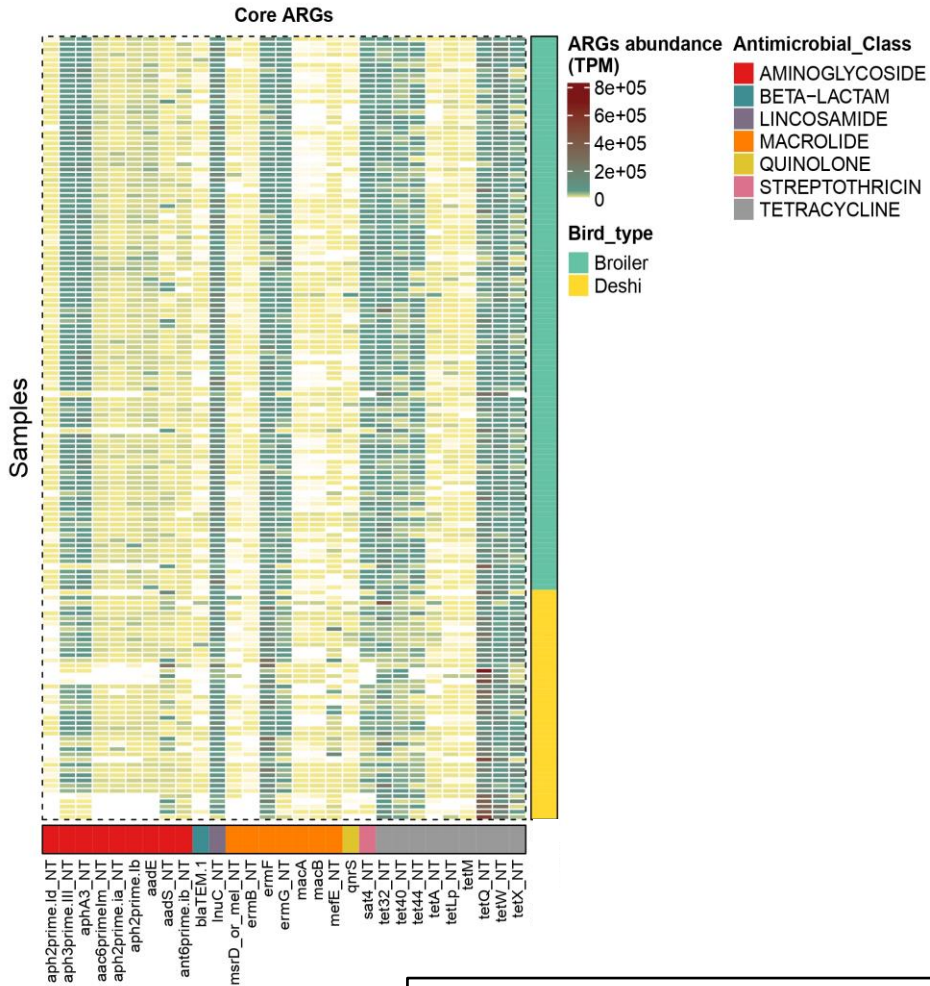


Figure 2: Heatmap of core ARGs

Correlations

- Usually, AMR genes conferring resistance to same class of antimicrobials were positively correlated.
- Some macrolide resistance genes were positively correlated with aminoglycoside resistance genes, while tetracycline resistance genes showed a negative correlation.

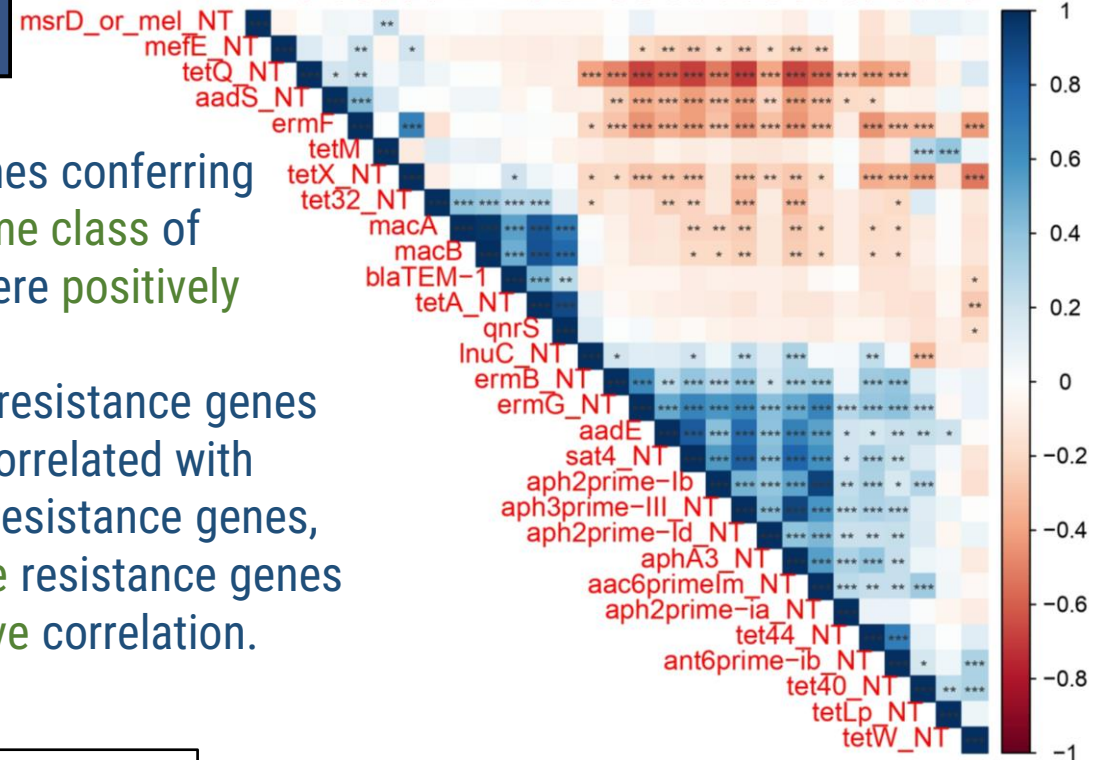


Figure 3: Correlogram of core ARGs

Diversity between samples

- Broiler: more similar to each other
- Deshi (Indigenous) : more different from each other
- A total 26 significantly different AMR genes were found between broiler and indigenous chicken

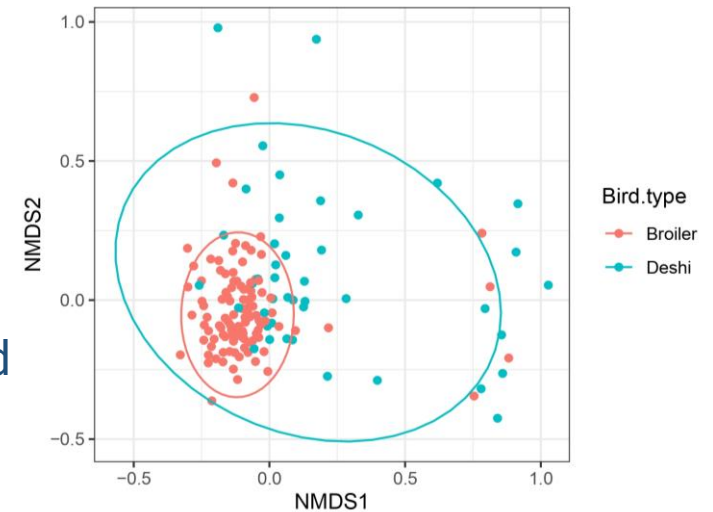


Figure 4: NMDS plot with Bray-Curtis matrix

Hierarchical cluster analysis

- In hierarchical clustering, samples from broiler tend to remain in one single cluster than deshi chicken.
- Cluster 1: majority of broiler and some deshi birds
- Cluster 2: deshi birds

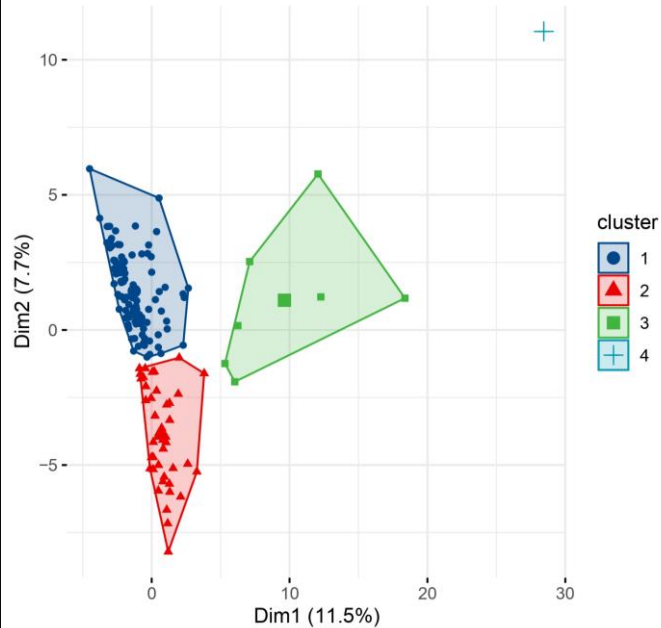


Figure 5: HCA clustering of samples

Figure 6: ARGs against critically important antibacterial

A: *qnrS* (quinolones)

B: *mefE* (macrolides)

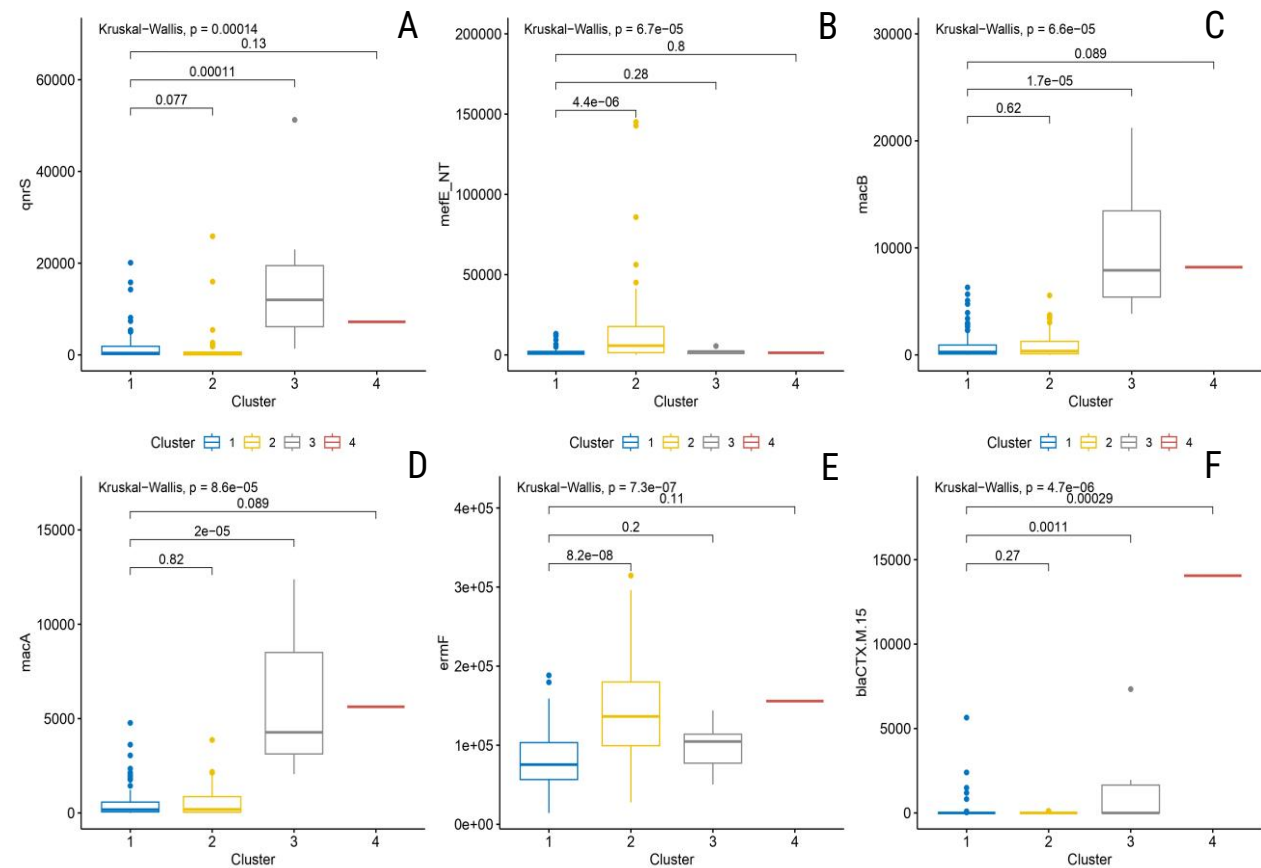
C: *macB* (macrolides)

D: *macA* (macrolides)

E: *ermF* (macrolides)

F: *blaCTX.M.15*

(cephalosporins)



Conclusions

- Tetracycline antibiotic resistance is quite common in gut commensals.
- Cluster 3 samples have comparatively higher amount of resistance genes against critically important antimicrobial agents used for human, may pose a potential risk to human health.
- Monitoring resistance patterns is crucial in developing effective strategies to combat its prevalence in developing countries worldwide.