Concurrent study of poultry enterotypes and resistomes may enable the detection of acquired antimicrobial resistance

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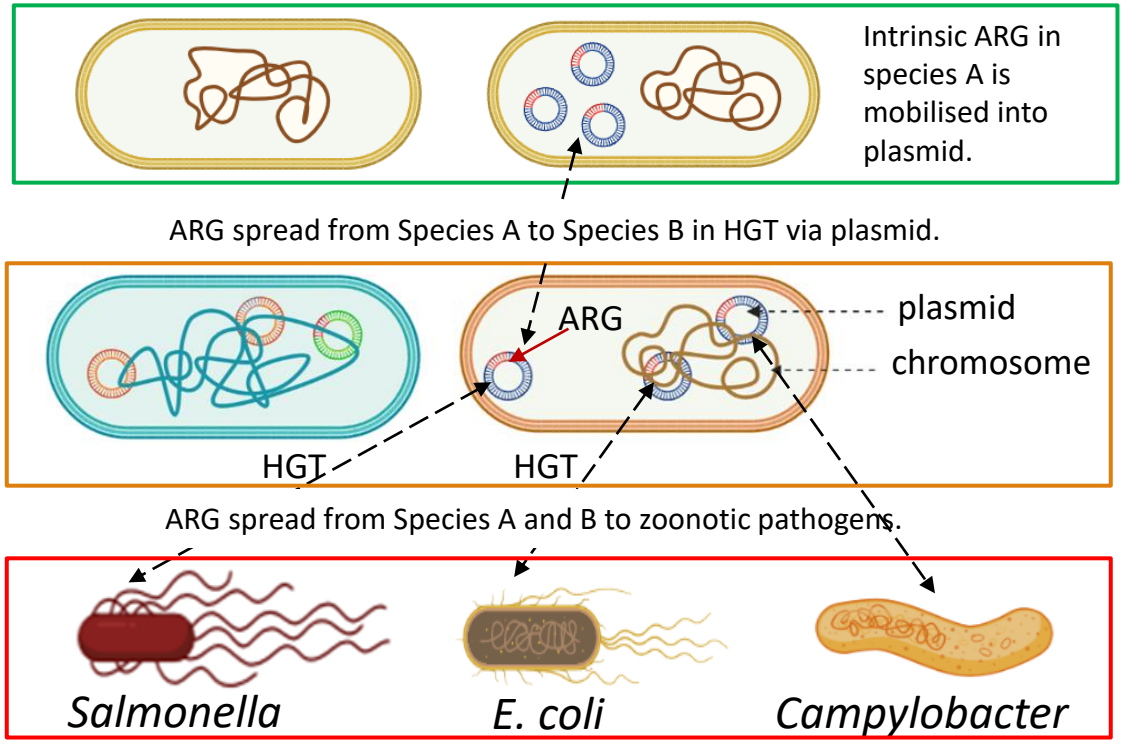
Key Question: Can we detect acquired AMR signal from innate AMR background?

- Identifying poultry farming practices that decrease the abundance of zoonotic pathogens and antimicrobial resistance genes (ARGs) is needed to reduce the threat of acquired resistance in food-borne pathogens.
- However, surveillance of antimicrobial resistance (AMR) is notoriously difficult because:
  - i) ARGs can be spread between species via horizontal gene transfer (HGT)
  - ii) the vast majority of ARGs in any resistome represent the normal innate resistance of a microbial population.
- This makes the detection of an acquired AMR signal very difficult against the innate AMR background.



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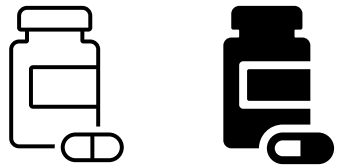
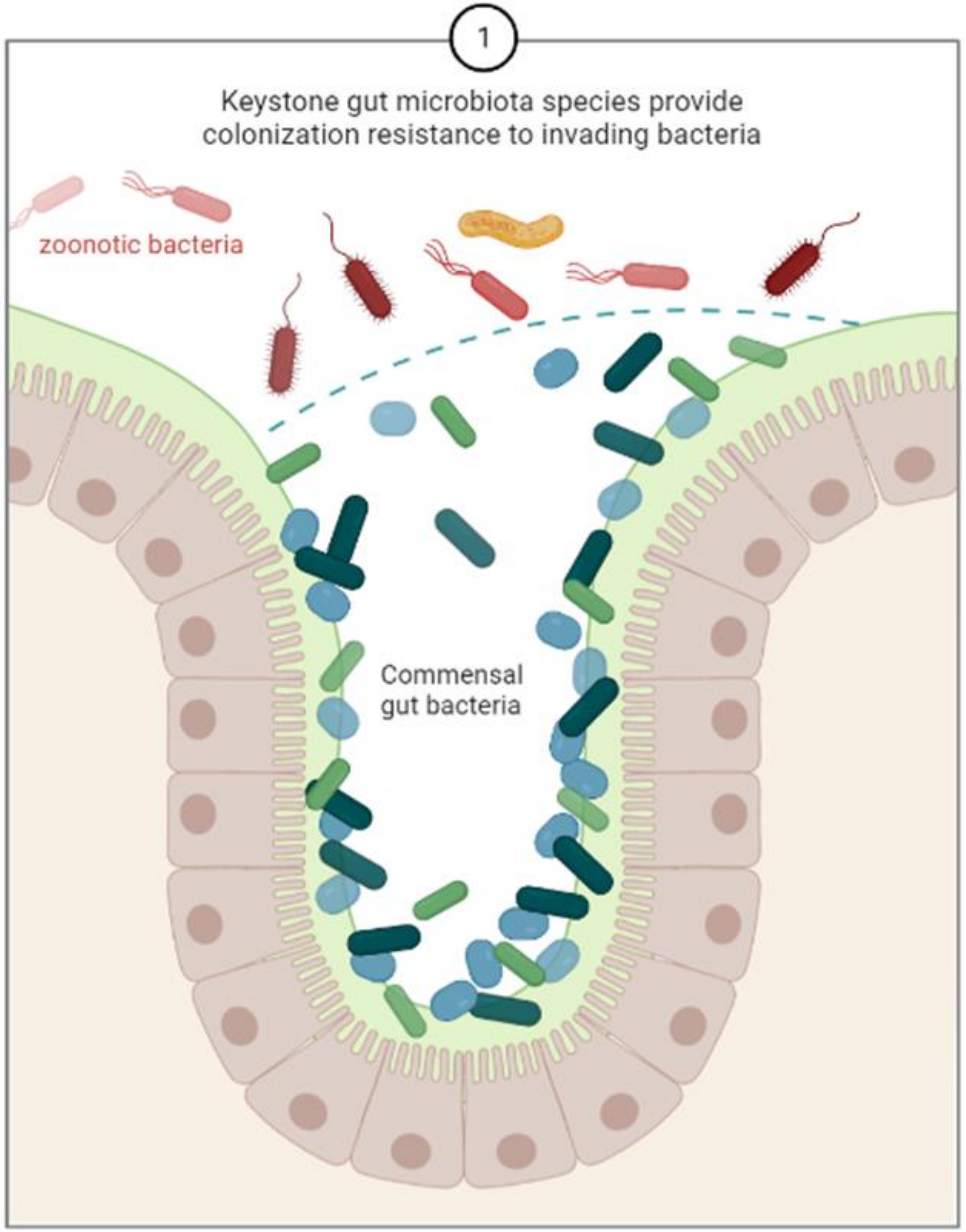
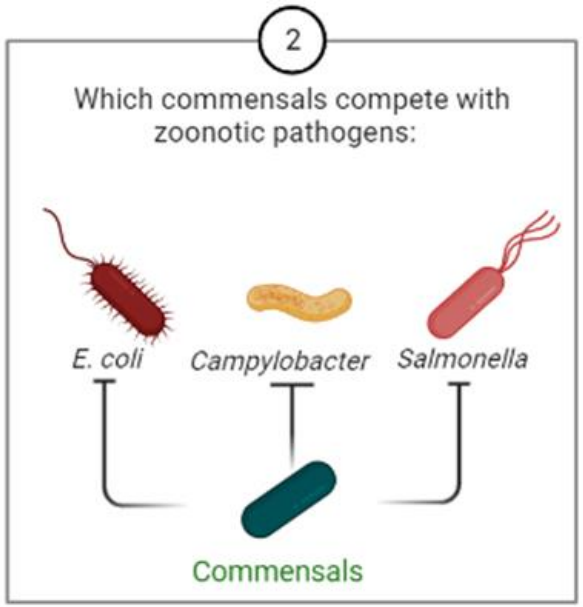
Methods

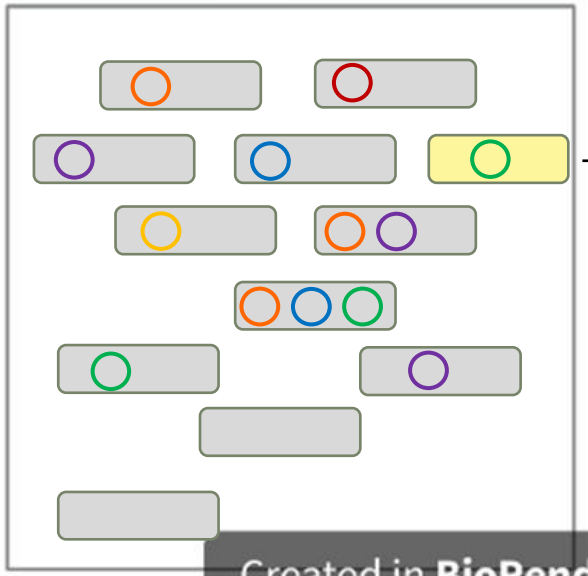


Amplification of 478 AMR genes (covered by 815 amplicons) + 19 custom amplicons for Colistin and Quinolone resistance.





16S rRNA (Enterotypes)



AMR AmpliSeq (Resistomes)

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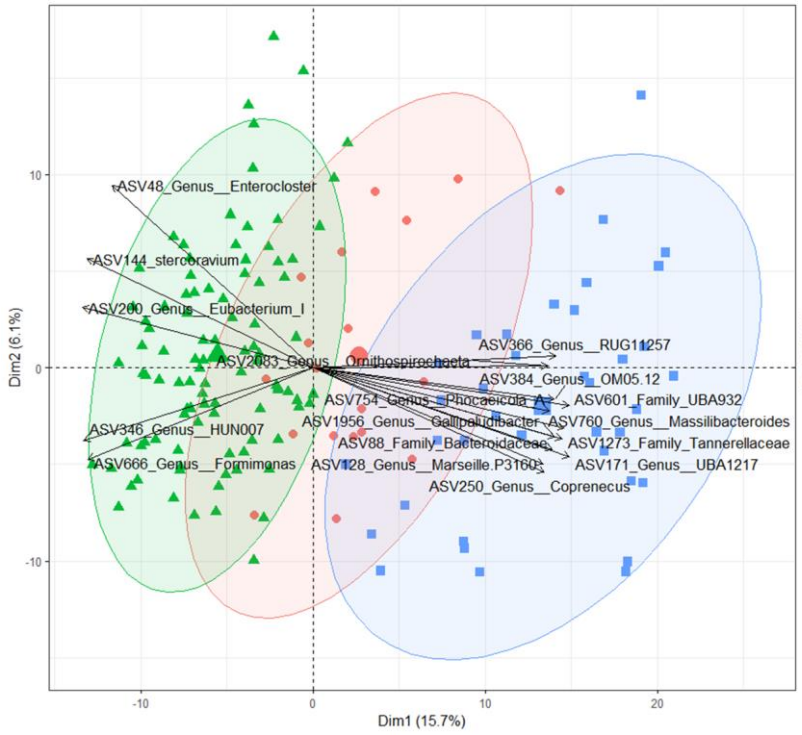
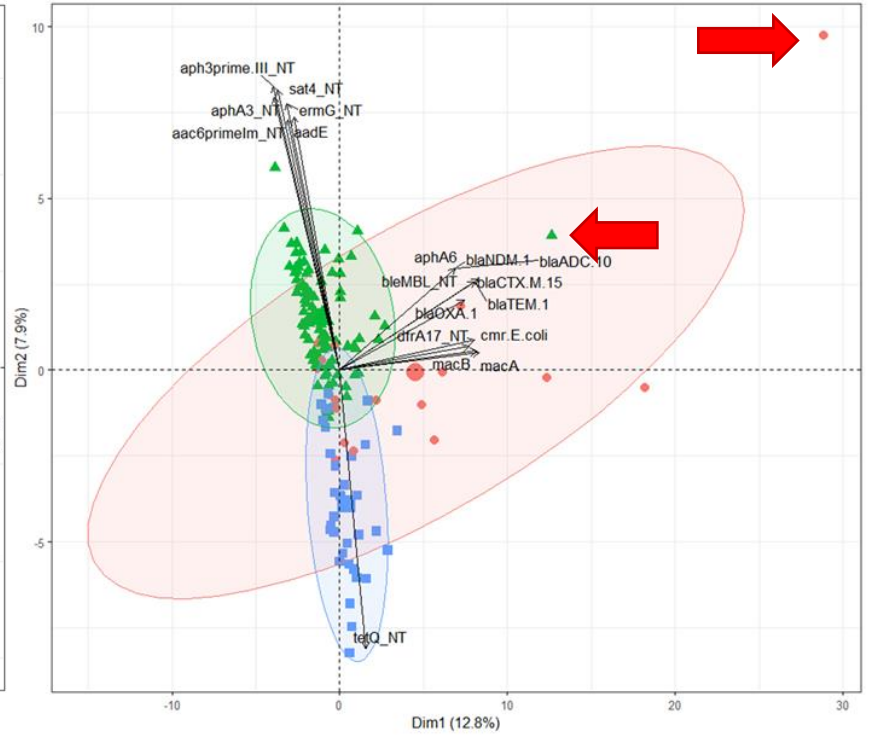
Results

Enterotypes



Resistomes

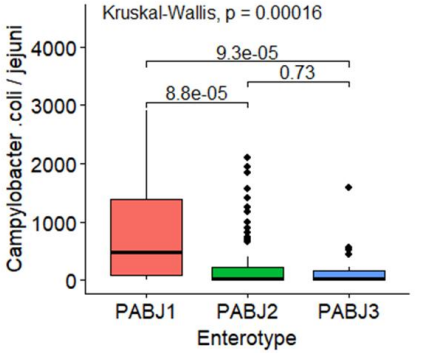


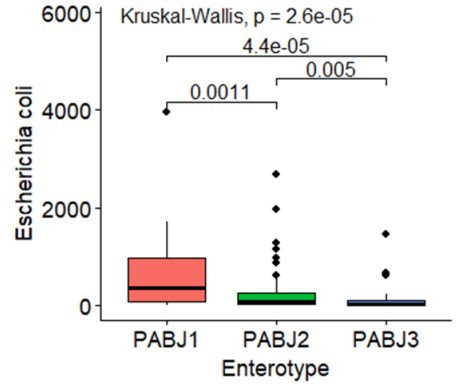
Could these outliers represent acquired resistance?

Cluster 1

Cluster 2

Cluster 3





Enterotypes have different abundance of zoonotic pathogens.

Strong correlation between enterotype and resistome suggesting resistome mostly determined by innate resistance of population. Outliers are present.

Discussion and Future Work

We will test the " detection of acquired resistance" hypothesis using data from shotgun sequencing, antimicrobial residue data, whole genome sequencing data as well as geographical, farm biosecurity and link-tracing metadata. The integration of datasets may suggest a surveillance method to detect acquired resistance, as well as ways to model future risk.