



Establishment Chronicles: Exploring the Microbiome and Antimicrobial Resistance Gene Landscape in Aging Broilers through High-Throughput Sequencing



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Introduction

- Chicken production is a viable and sustainable way to produce high-quality protein for safe consumption, but increased human demand for dietary protein is driving the expansion of chicken production can amplifying the risk posed by many zoonotic pathogens.
- Understanding and possibly altering the composition of poultry microbiota could prove useful to enhance health and productivity while reducing zoonotic risk.
- A notable concern of AMR (antimicrobial resistance) to the poultry industry pose a serious threat to public health, as it can render standard treatments ineffective, leading to increased morbidity, mortality, and healthcare costs.
- The detection of ARGs (antimicrobial resistance genes) carriage in poultry microbiota is important to assess the emergence and spread of AMR and to develop effective strategies for mitigation and reduction.

Objectives

The current study was undertaken to delineate the taxonomic composition of the microbial consortium inhabiting the caecal contents of broiler chickens (exotic Cobb-400) and simultaneous profiling the antimicrobial resistance (AMR) genes successively from birth to market age.

Methodology

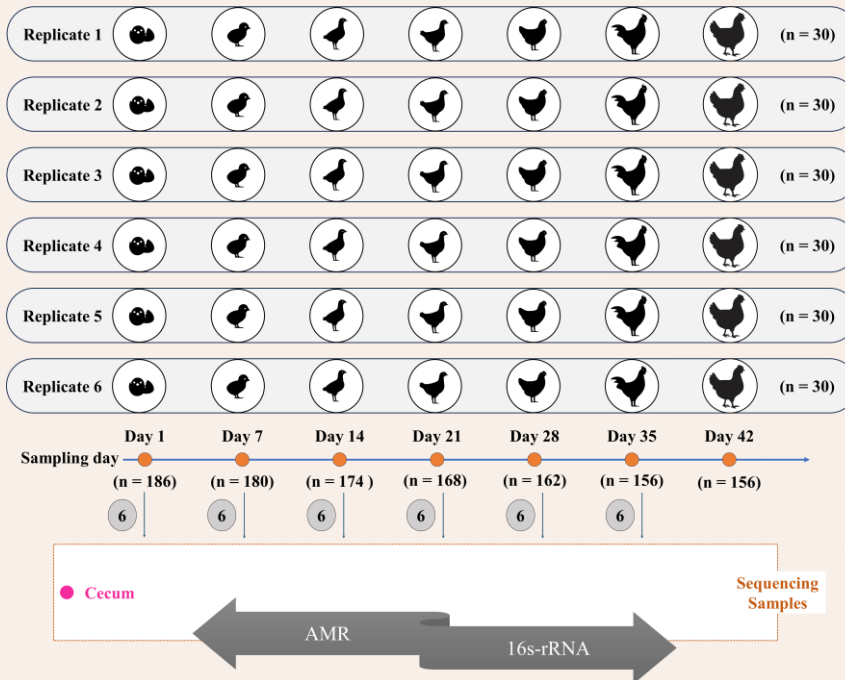


Figure A: Graphical representation of study design and sample collection

Results

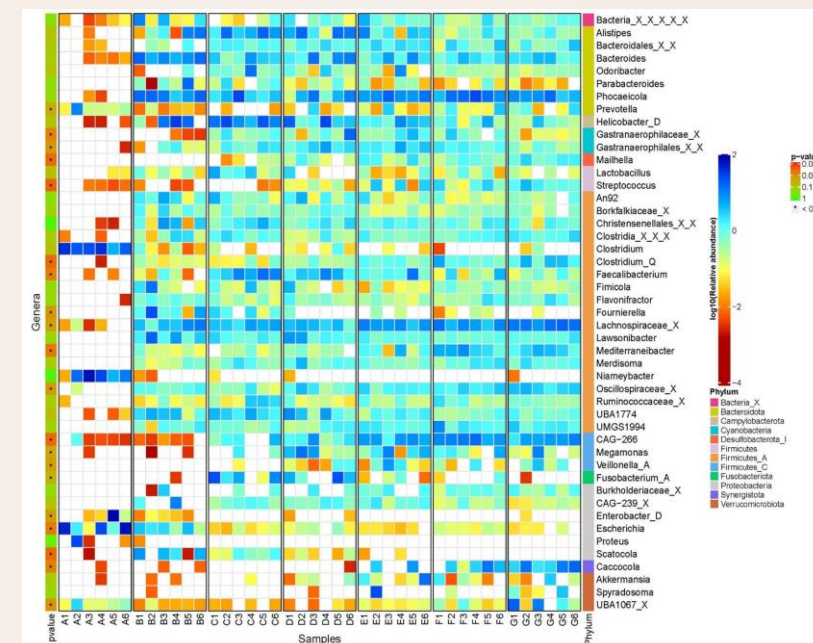


Figure B: Heatmap of identified ASVs at genus level across all sample collection.

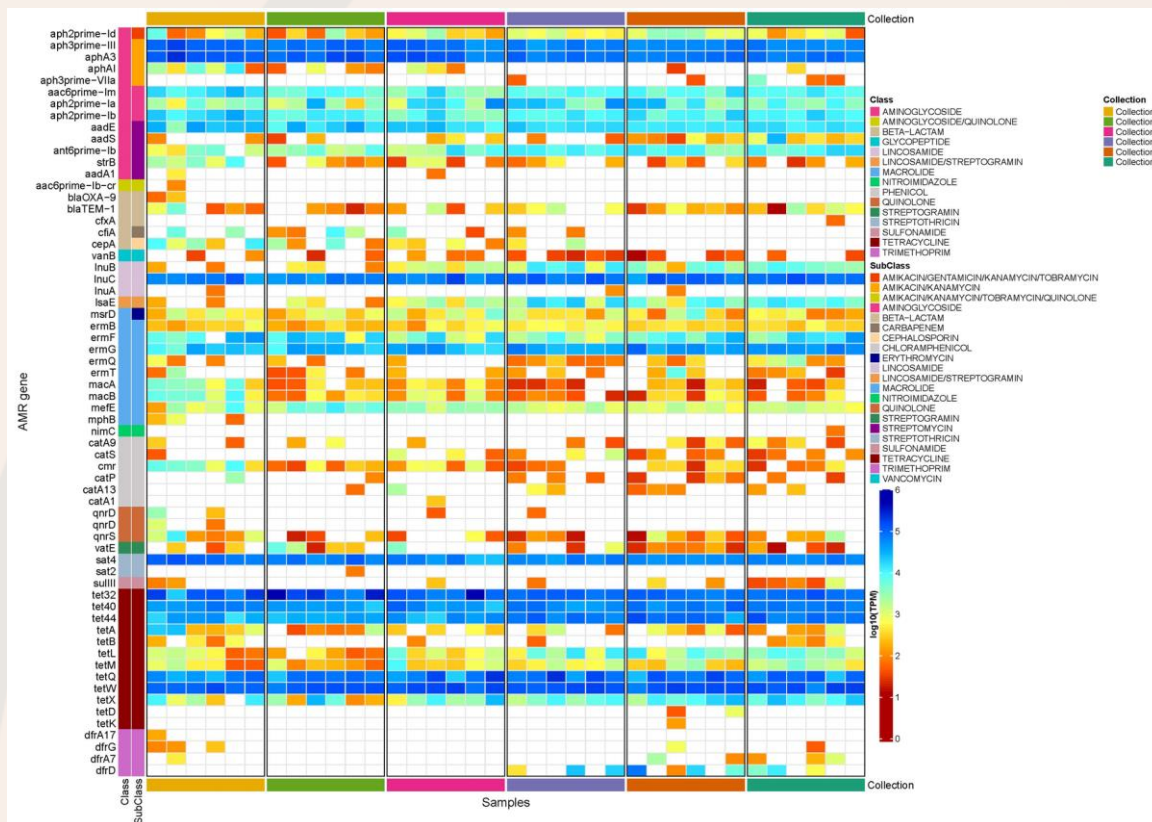


Figure C: Heatmap of AMR class detection across in all collection points.

Results (continued)

- Least diversity was observed in the Collection 1 with significantly increasing diversity with increase in age (Figure B). *Firmicutes_A* and *Bacteroidota* phyla were the most abundant phyla in Collections 2 to 7.
- Clostridium*, *Escherichia* and *Niameybacter* were the most abundant genera in Collection 1 while *Alistipes*, *Phocaeicola*, *Bacteroides*, *Phascolarctobacterium* and some unknown organisms from *Lachnospiraceae* and *Helicobacteraceae* family were the most abundant. Total 71 genera differed significantly among Collections 2 to 7 (Figure B).
- Out of total 493 genes/targets, 172 were detected from all samples including 82 with reads >5. Most of these reads were assigned to targets giving resistance to aminoglycoside, tetracycline and macrolides. At a finer level *ermG*, *tet32*, *tetW*, *aphA3*, *tetQ*, *InuC*, *aph3prime-III*, *sat4*, *tet44* and *tet40* genes were detected with very high abundance (Figure C).

Conclusions

Gaining insights into the mechanisms governing microbiota colonization as well as unravelling the genetic intricacies of resistance mechanisms present in the chicken gut, we not only enhance our understanding of microbial colonization but also gain crucial insights into the dynamics of antibiotic resistance.