Exploring Probiotics and Upper Respiratory Tract Microbiome Interactions for Healthy Chickens without Antibiotics

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Outline



| Background | Objectives | Methods | Results | Conclusion and Next Steps |
|---|--|--|---|---|
| Probiotics and Poultry Health Chicken URT and Microbiome Infectious Coryza: URT Infection model | Impact of infection (Avibacterium paragalinarum) on the Upper Respiratory Tract Microbiome of Chickens | • Experimental Design • Key Measures | Impact of infection on URT microbiome Strain-specific Impacts Temporal pattern in microbiome change | URT microbiome changes following infection. Probiotics can be used to mitigate AP infections |

What are probiotics?



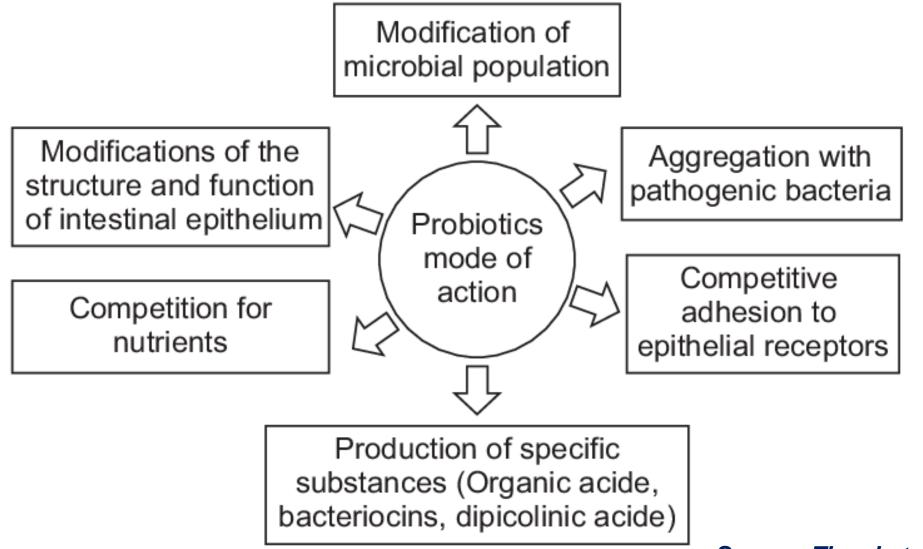


 Live, non-pathogenic microbes that confer health benefits when administered in appropriate amounts.

Include various species of *Lactobacillus*,
 Bifidobacterium, *Bacillus*, and *Enterococcus*,
 etc. (Stavropoulou and Bezirtzoglou, 2020).

 Primarily used for mitigating gut diseases in poultry, with growing research on respiratory health benefits.

Probiotics: How they work?

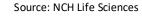


Source: Tiwari et al., 2012

Probiotics: Effects on Poultry Health



- Lower the incidence of various enteric diseases.
 Enhance immune response
 - Improves nutrient absorption, stress resilience, and overall productivity (Ayana & Kamutambuko, 2024).
 - However, studies on using probiotics to modulate the Upper Respiratory Tract microbiome for disease mitigation are limited.



Chicken Upper Respiratory Tract (URT) & Microbiome



Comprises the external nares, nasal cavity,

oropharynx, larynx and trachea.

- Harbors rich microbial community (Oladokon and Sharif, 2024).
- Altered microbiome in the URT can lead to
 secondary infections or exacerbation of primary
 diseases in poultry (Kursa et al., 2022).

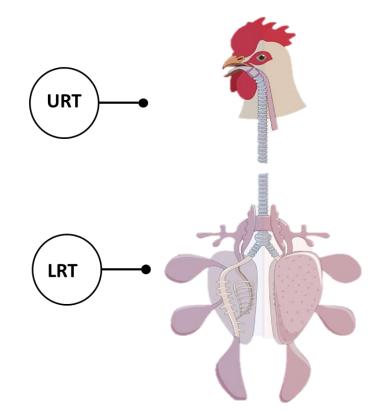


Figure: Anatomy of the respiratory tract of chickens [source: Mach et al., 2021]

Infectious Coryza (IC), an URT infection model



- Etiology: Avibacterium
 - paragallinarum (AP)
- Transmitted through aerosols
 containing AP and primarily affects
 the URT.
- Symptoms: Swollen head, nasal
 discharge, lachrymation, reduced
 feed and water consumption



Figure 2. Clinical signs of Infectious Coryza in Chickens [source: Huo et al., 2023]

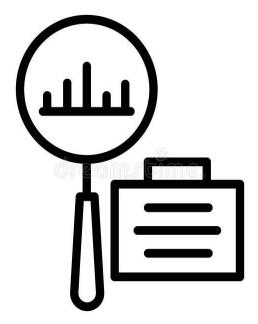
Knowledge Gaps



- $\,\circ\,\,$ Limited studies on the effect of probiotics/infection on URT
 - microbiome in chickens.

 \circ Impact of AP infection on URT microbiome is unknown.

Unclear if different strains of AP influence the microbiome differently



Objectives



Impact of infection (Avibacterium paragalinarum) on the Upper Respiratory Tract Microbiome of Chickens



Evaluate the impact of AP infection on URT microbiome



Evaluate the impact of different strains of AP on URT microbiome



Determine temporal changes in URT microbiome during infection



Methods: Experimental Design

- $\,\circ\,$ Five groups of 28-day-old SPF chickens
 - Four groups infected with different *Avibacterium paragallinarum* (AP) strains.
 - One uninfected control group
- Intra-nasal instillation with 10^7 CFU of AP for challenge infection.

Choanal swabs collected on days 2, 4, 7, and
9 post-challenge

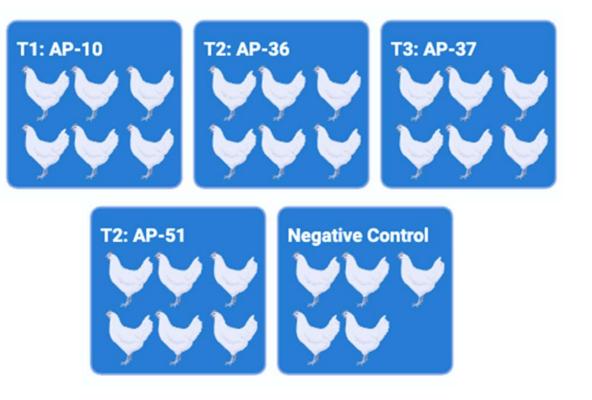
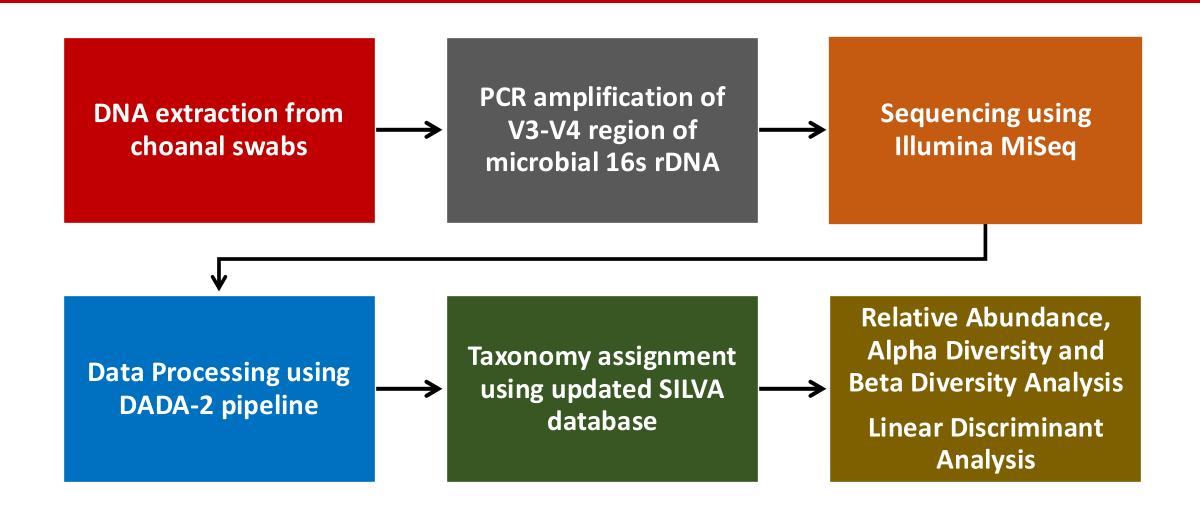


Figure : Experimental groups designed for the challenge trial in 28-days old specific pathogen free (SPF) chickens

Methods: Experimental Design





Microbial Composition Measures

Relative Abundance

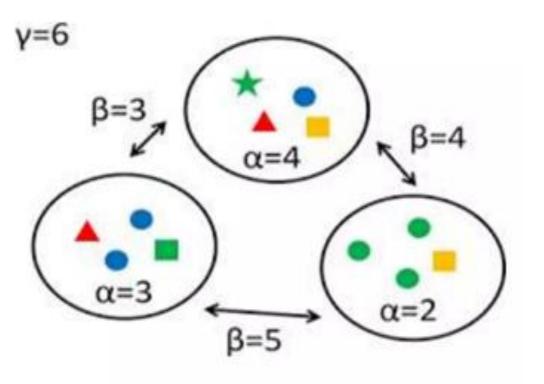
• Measures the proportion of each bacterial species within a community.

Alpha Diversity

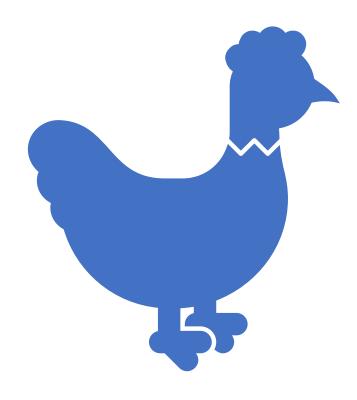
 Measures how many different types of bacteria are present in a single chicken's or a group respiratory tract.

Beta Diversity

• Measures how similar or different the bacterial communities are between different chickens or groups of chickens.







Results

1. Impact of AP Infection in the URT Microbiome of Chickens

Firmicutes, followed by Proteobacteria, Actinobacteria and Bacteroidota were the dominant phyla in the chicken URT



Figure: Relative abundance of different phyla in the URT microbiome

AP was highly abundant in 2 groups(AP-10 and AP-36) while negligible in other 2 groups

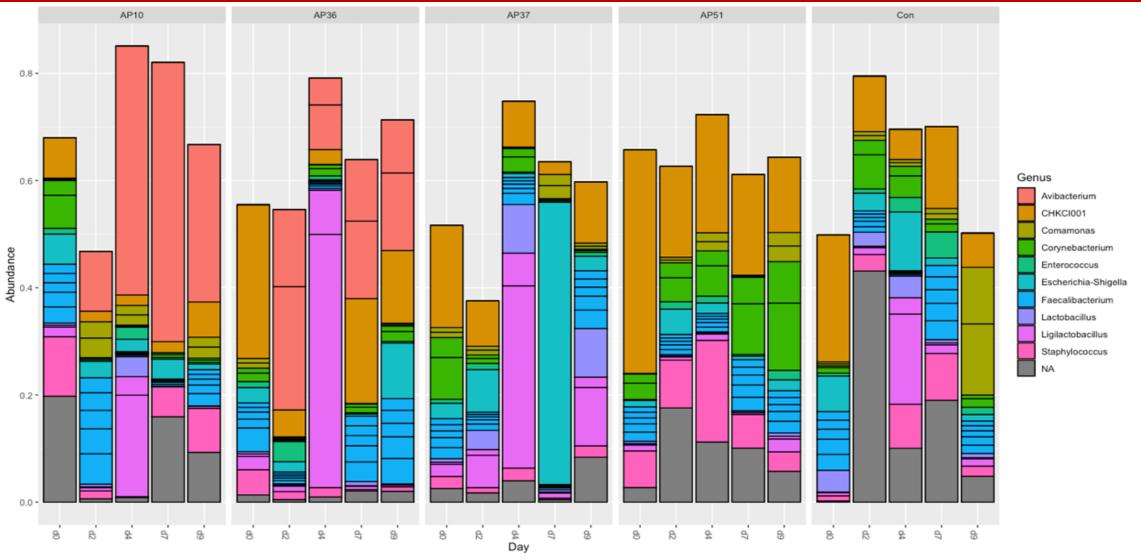


Figure : Relative abundance of the top-20 genera in the URT microbiome

AP and two genera of *Lactobacillaceae* were highly enriched in infected chickens.

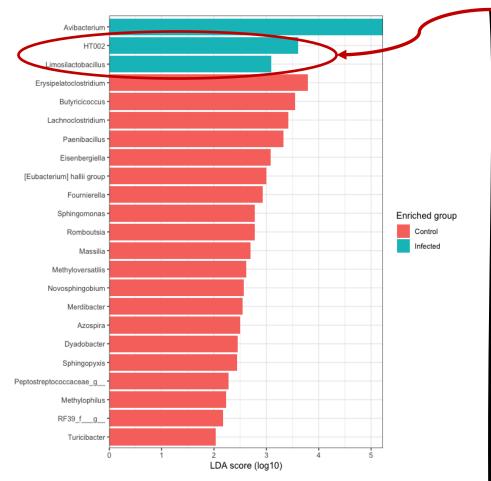


Figure: LEfSE plot shows the genera differentially abundant in the infected and non-infected groups with LDA score >2

HT002 and *Limosilactobacillus*: Genera within 0 *Lactobacillaceae*, associated with the oral and gut microbiomes, respectively. Although the mechanism is not clear, 0 Lactobacillaceae was also found to be enriched during acute H9N2 avian influenza infection (Davis et al., 2023).

 $_{\odot}~$ Further study needed. (if cause or result of infection)

dant

Reduced microbial diversity and altered community composition due to AP infection in chicken URT

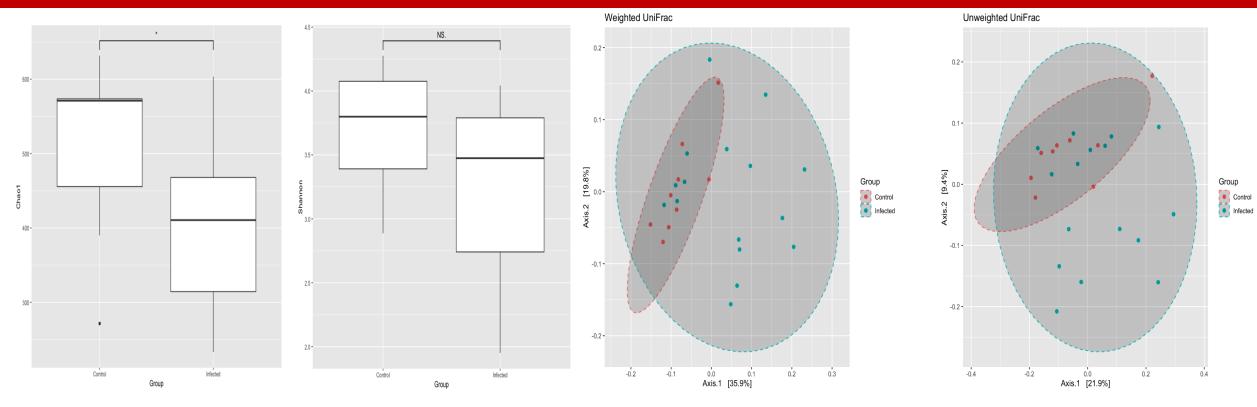
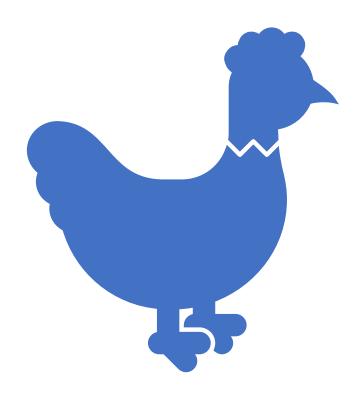


Figure : α -diversity of the microbiota in the Infected and Uninfected chickens by Chao1 and Shannon Index was significantly different by chao1 index (p= p=0.03145)

Figure : θ -diversity between the infected and uninfected control groups by Weighted and Unweighted UniFrac- distances was significantly different (p= 0.014 and p=0.028 respectively)



Results

2. Impact of Different Strains in the URT Microbiome of Chickens

Infection by different AP strains resulted in distinct microbiome profiles.

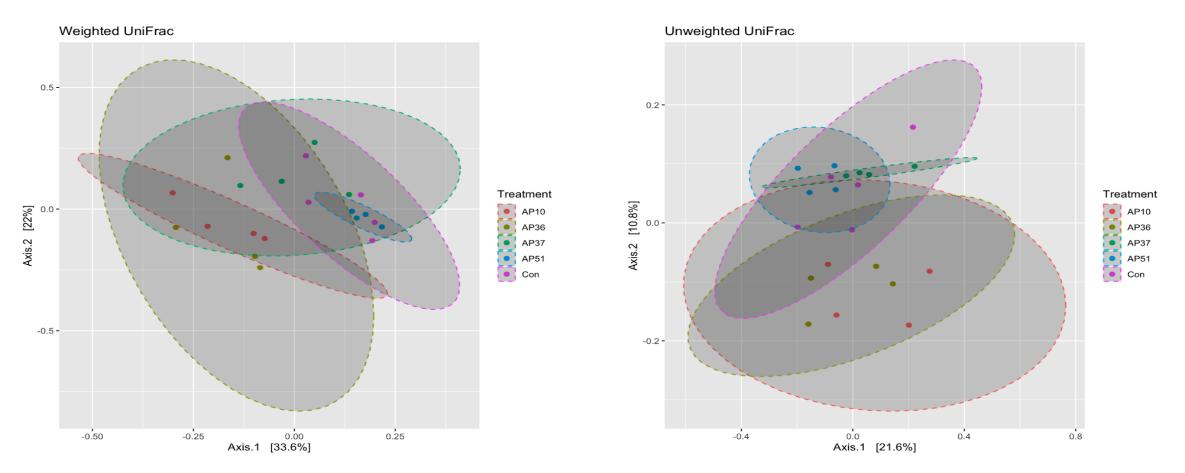
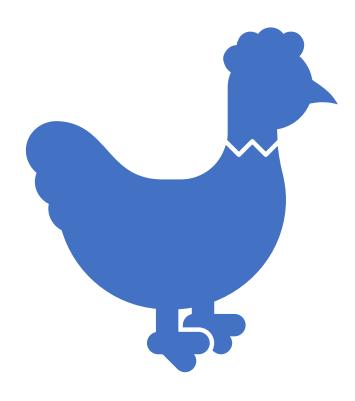


Figure : 6-diversity of the URT microbiome after infection by different strains of AP by Weighted and Unweighted UniFrac- distances was significantly different (p=0.001)



Results

3. Temporal Changes in the URT Microbiome during the course of Infection

AP infection reduced alpha diversity during early days followed by gradual return to normal level

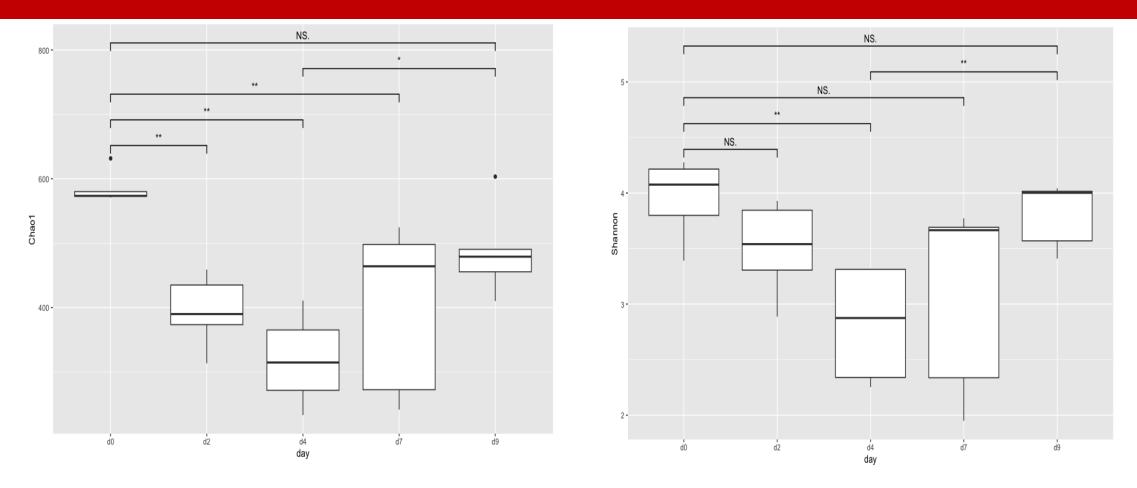


Figure : α -diversity of the URT microbiome during IC infection by Chao1 and Shannon Index was significantly different between the different days

Conclusion and Next Steps

- The URT of the chicken has a highly diverse and complex microbiome
- AP infection reduces richness and alters community composition.
- The alteration of URT microbiome found to be strainspecific and has temporal pattern.
- Two genera of Lactobacillaceae enriched in the infected chickens and further work needed to understand their role.



Next Steps

Evaluate Naturally Attenuated AP Strains as Live Vaccine Candidates Evaluate the use of 3 identified probiotic candidates to mitigate AP infection in poultry



Long Term Impact

1. Probiotics could be a promising antibiotic alternative to mitigate for

URT infections

2. Reduction in antibiotic use reduction of AMR Enhanced poultry health

and productivity

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