

# Understanding the Respiratory Microbiome of Poultry

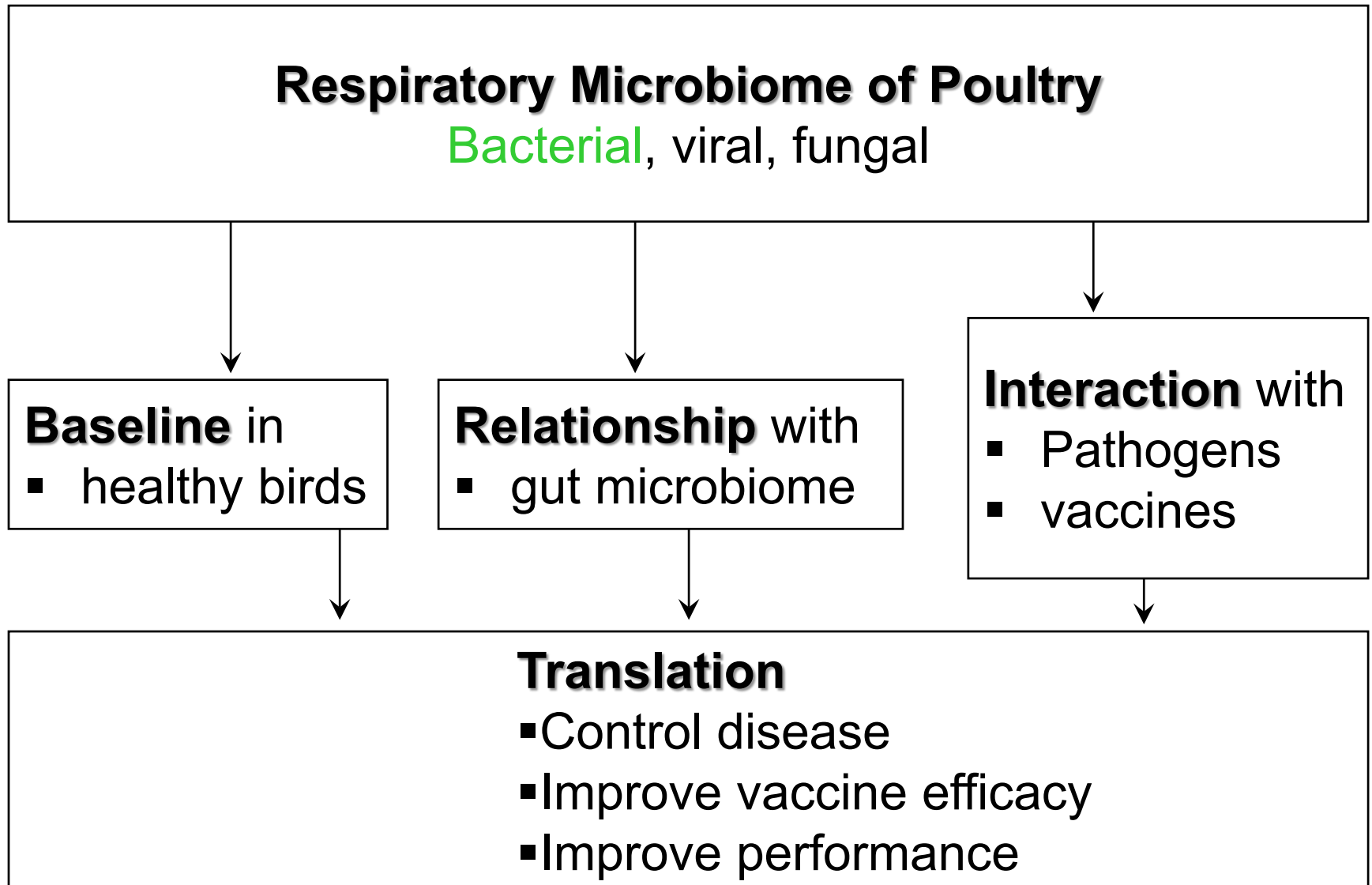
John Ngunjiri



**THE OHIO STATE UNIVERSITY**

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# Project goals



# Progress

## ❖ Baseline microbiome

### ☐ Turkeys

- ✓ Completed → sampling
- ✓ Ongoing → Sequencing and data analysis

### ☐ Chicken layers

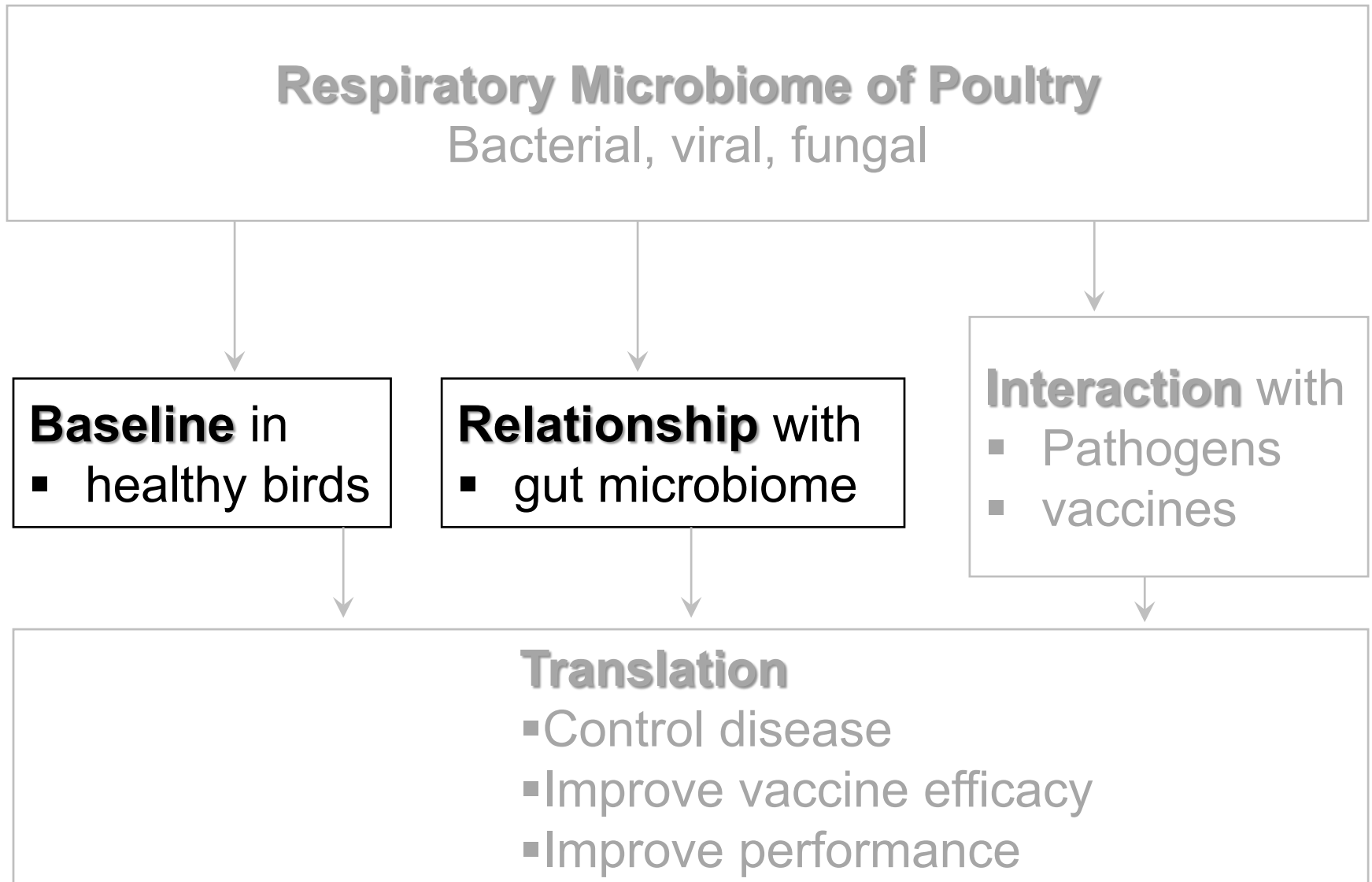
- ✓ Completed → commercial flock sampling, 16S sequencing, data analysis
- ✓ Ongoing → SPF flock sampling

## ❖ Virus-microbiome interactions

### ☐ LPAIV and IBDV in chickens

### ☐ LPAIV and reovirus in turkeys

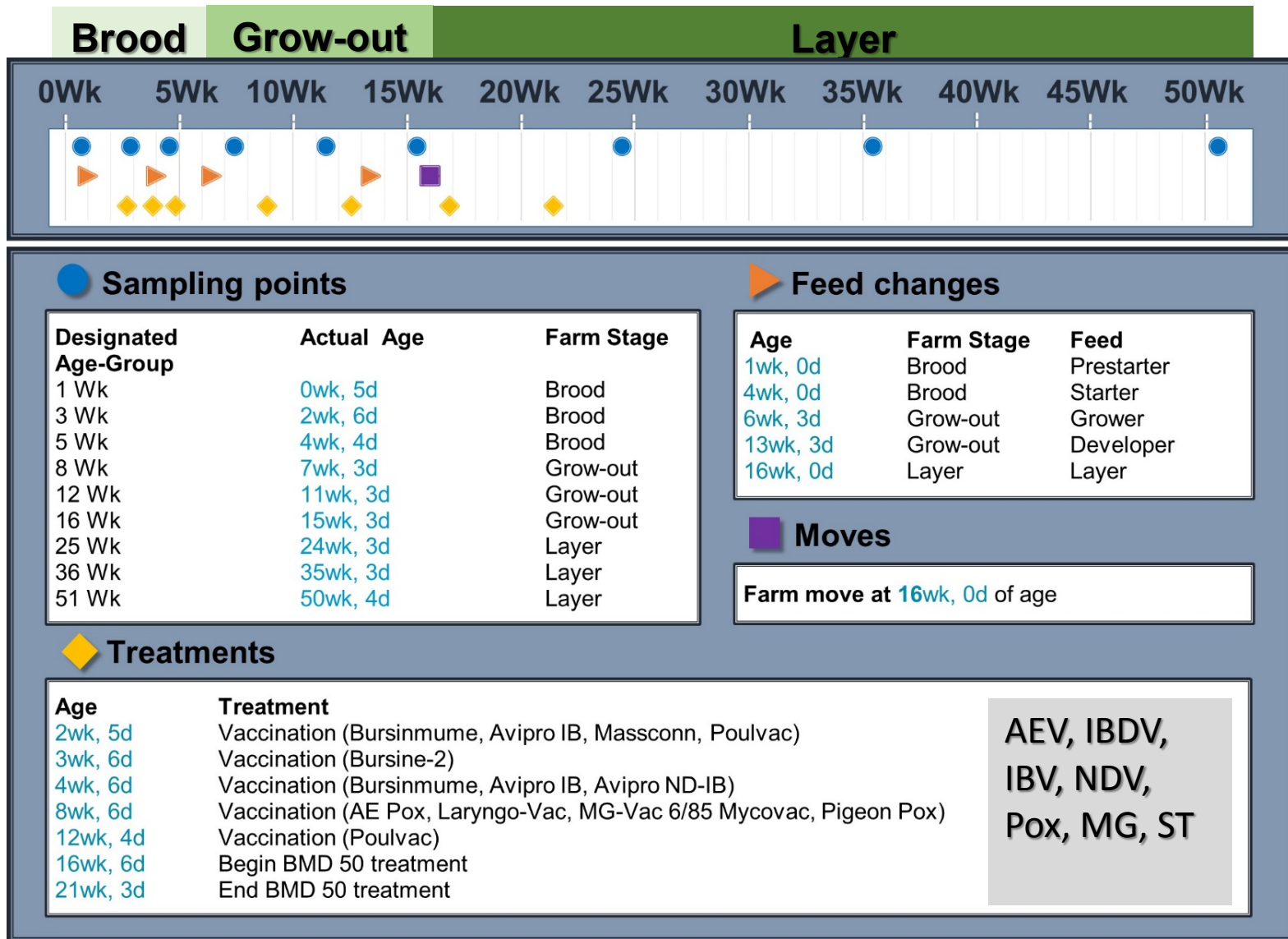
# Project goals



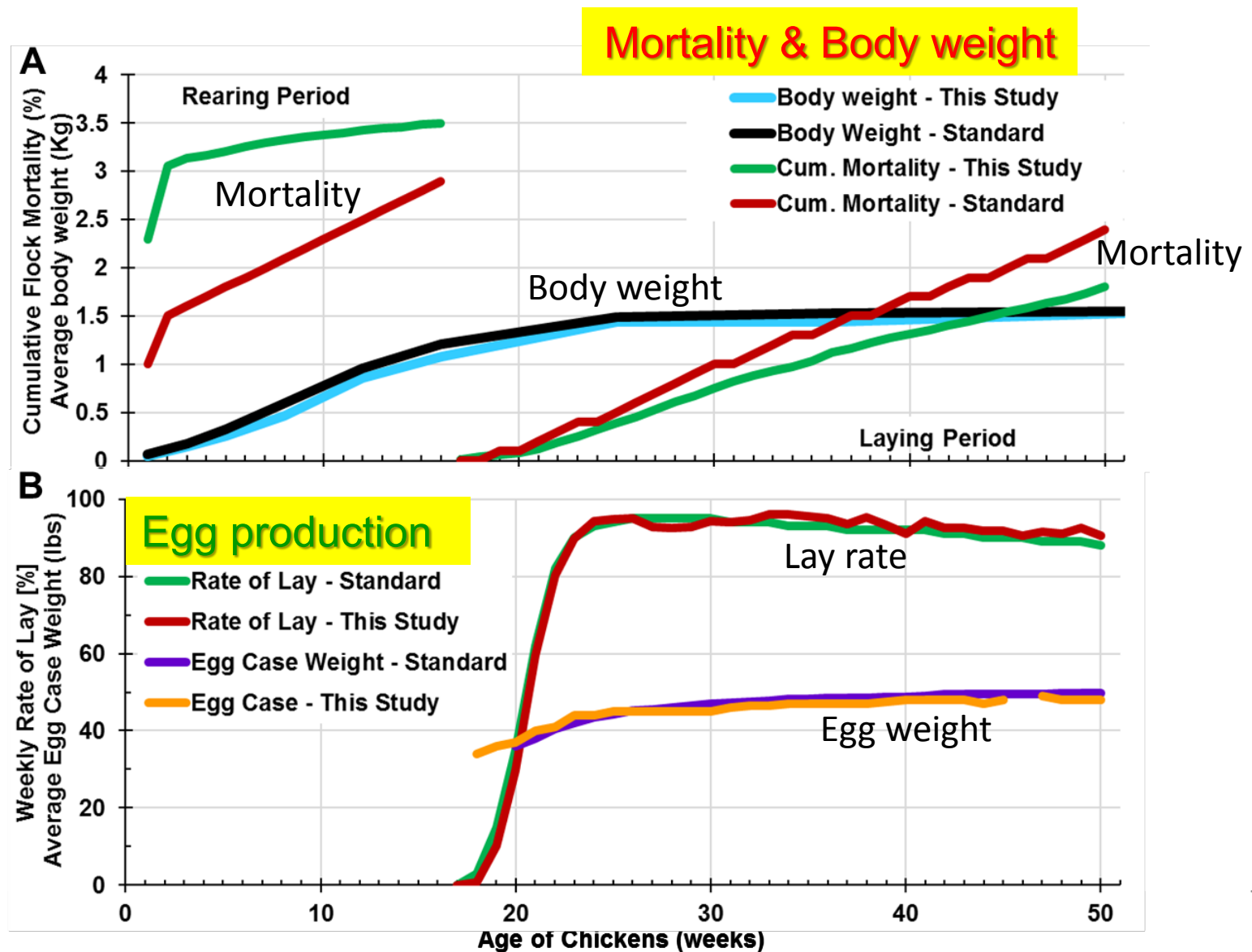
# Commercial chicken layer flock

- ❖ Hy-Line W-36 layers
- ❖ More than 80,000 chickens
- ❖ Sampled a total of 201 birds at different stages of farm sequence

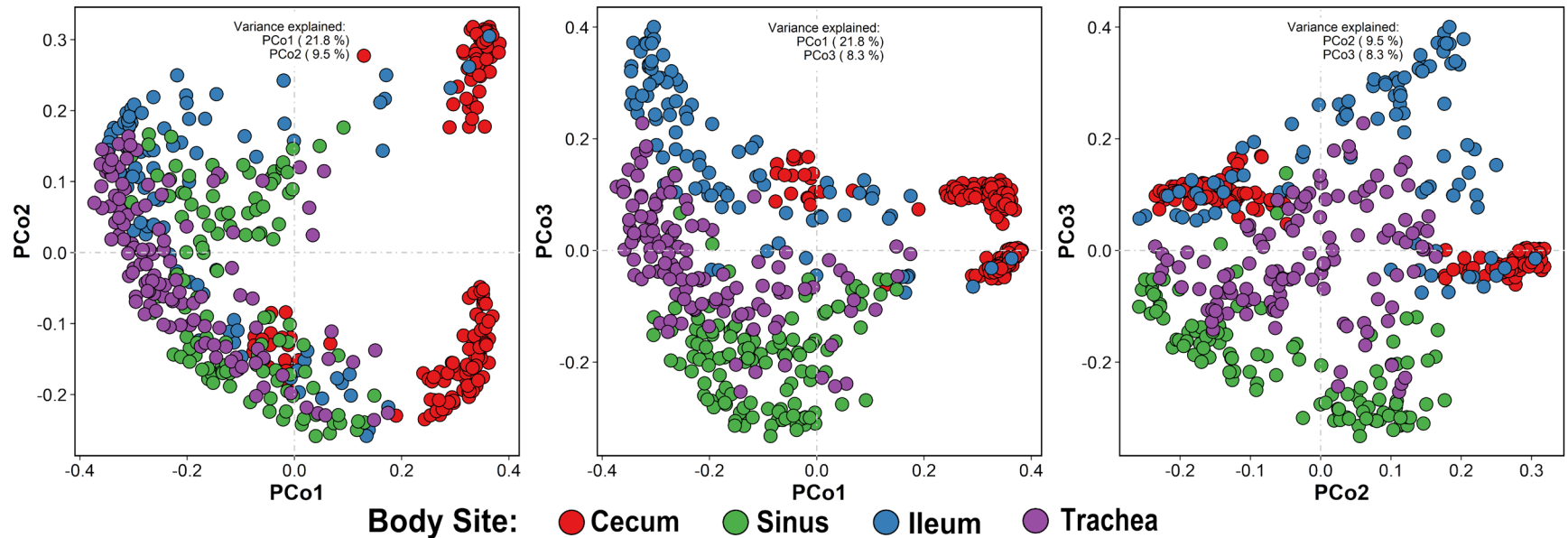
# Sampling timeline and flock management



# Flock performance



# Sample distribution in microbial community space



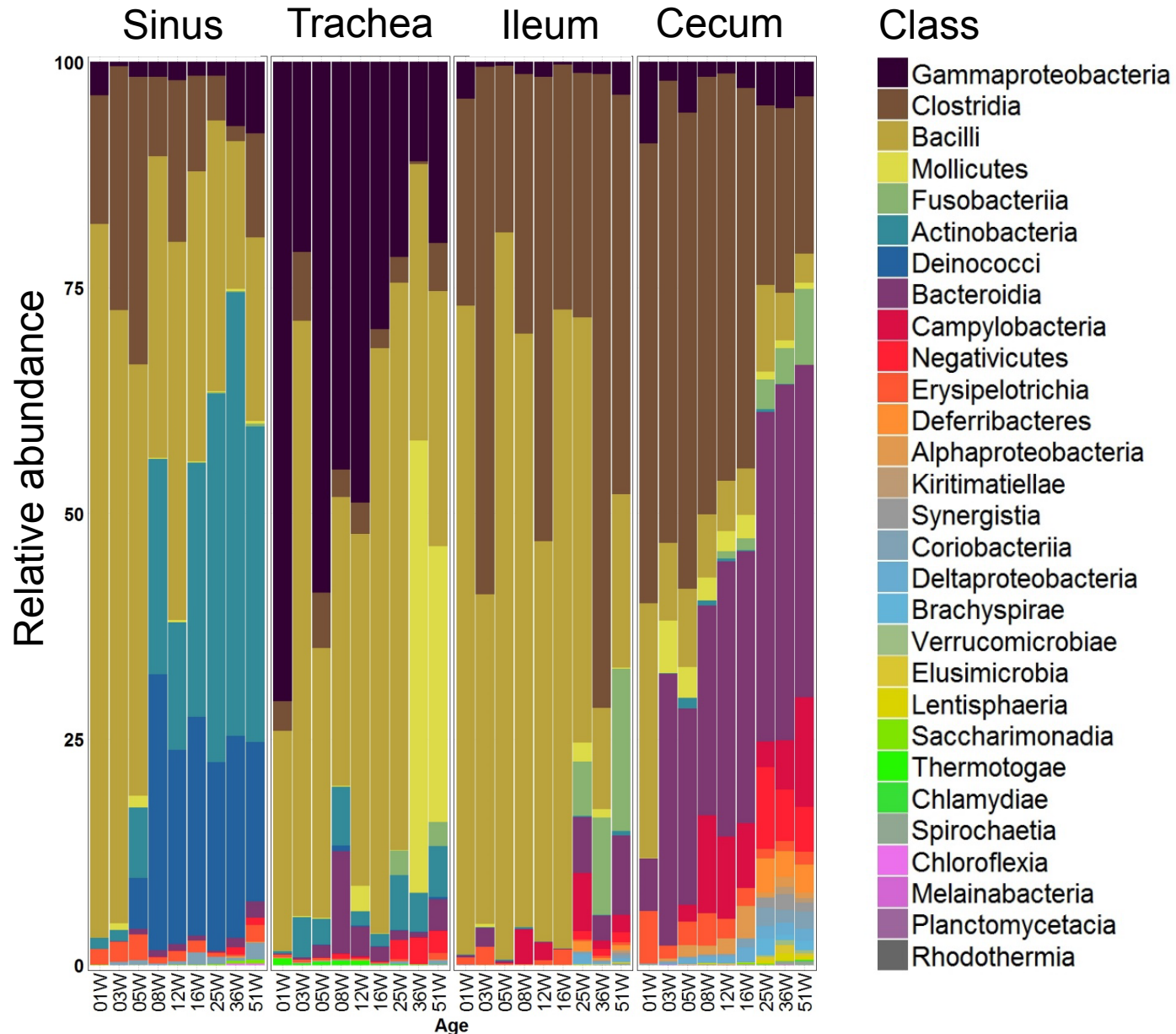
## Comparisons using ANOSIM

	Sinus	Trachea	Ileum
Trachea	0.522		
Ileum	0.669	0.400	
Cecum	0.877	0.863	0.730

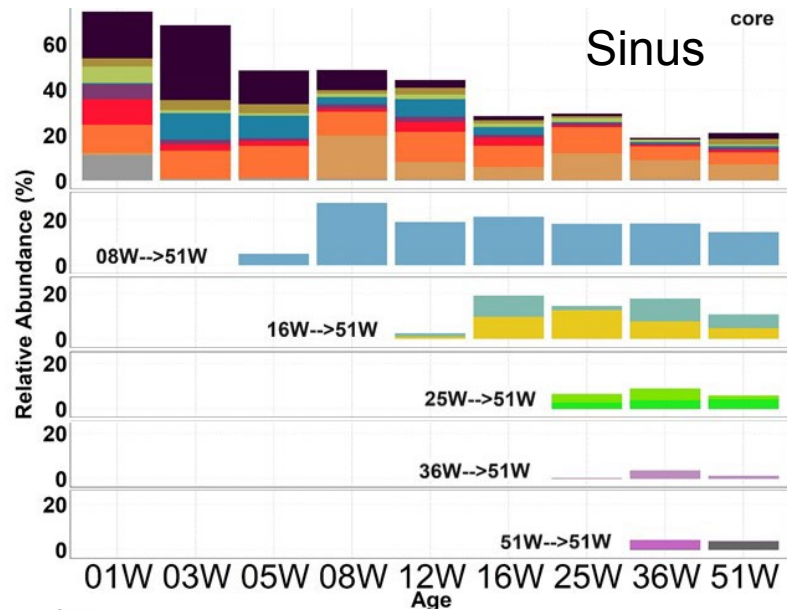
□ Ileal microbiota is compositionally closer to respiratory microbiota than to cecum.



# Taxonomic links between body sites

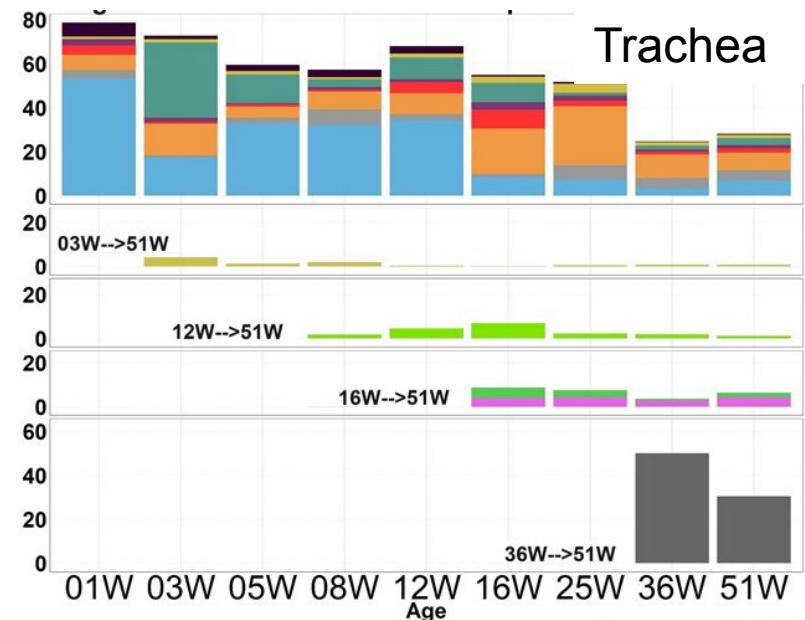


# Core respiratory OTUs



otu

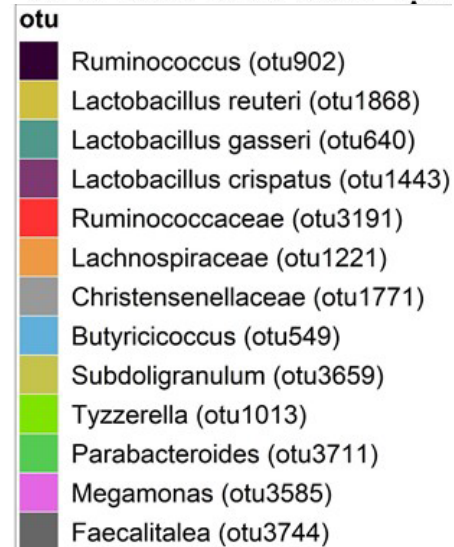
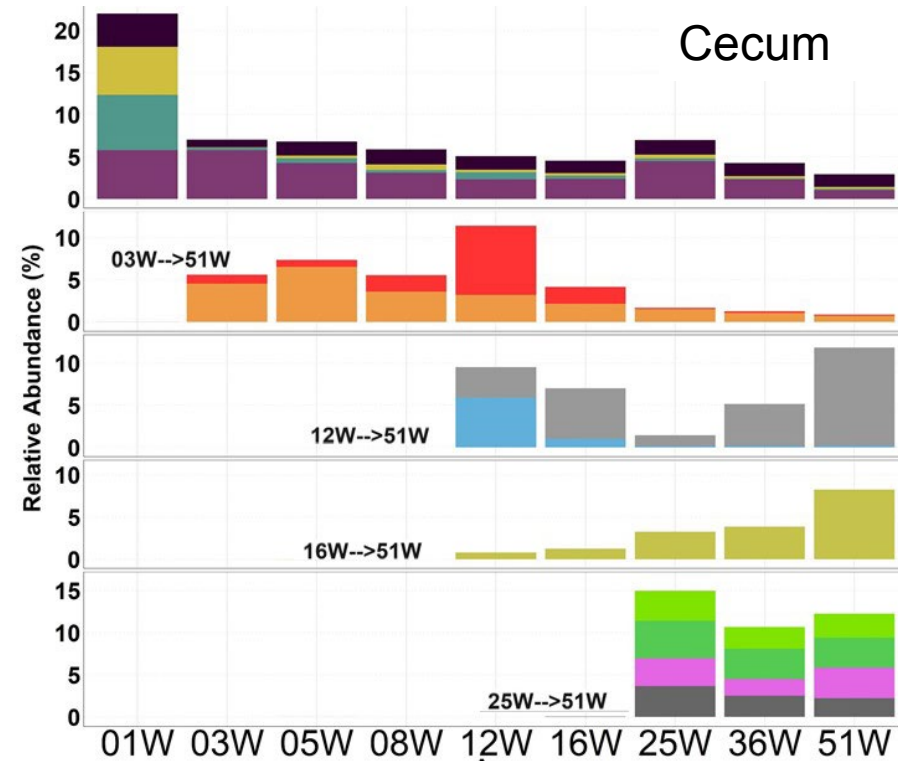
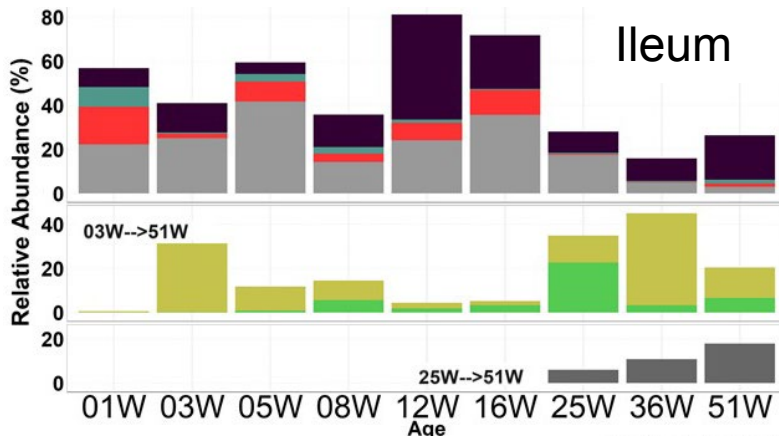
- Staphylococcus (otu2329)
- Ruminococcus (otu902)
- Lactobacillus vaginalis (otu1563)
- Lactobacillus salivarius (otu1028)
- Lactobacillus reuteri (otu1868)
- Lactobacillus gasseri (otu640)
- Lactobacillus crispatus (otu1443)
- Kocuria (otu3182)
- Enterococcus (otu58)
- Deinococcus (otu2860)
- Olsenella (otu1133)
- Microbacteriaceae (otu12784)
- Kocuria (otu8504)
- Faecalitalea (otu3744)
- Thermomicrobiales (otu3807)
- Deinococcus (otu4917)
- Bacteroides caecigallinarum (otu1741)



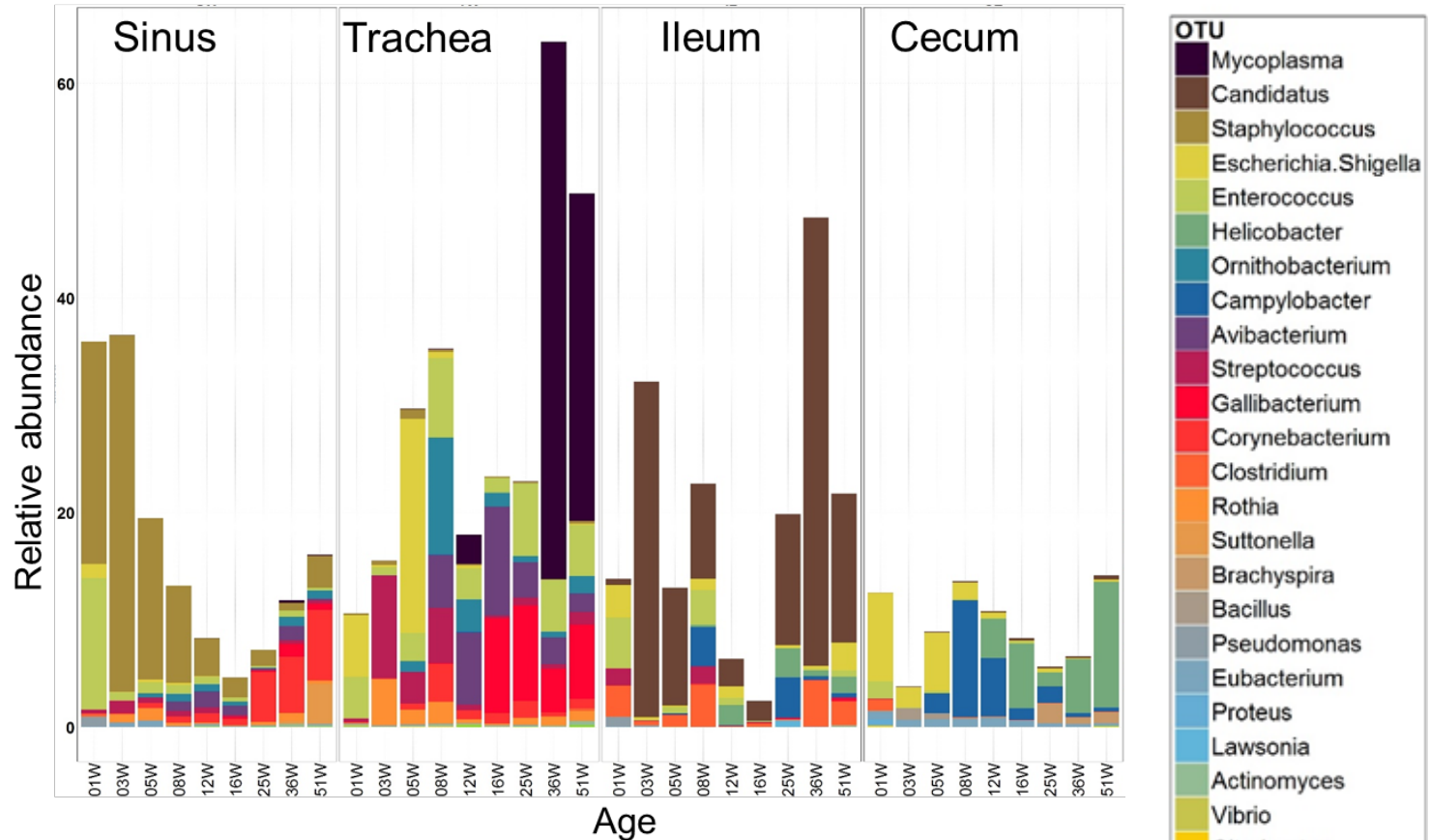
otu

- Paraburkholderia tropica (otu2002)
- Lactobacillus vaginalis (otu1563)
- Lactobacillus salivarius (otu1028)
- Lactobacillus reuteri (otu1868)
- Lactobacillus gasseri (otu640)
- Lactobacillus crispatus (otu1443)
- Enterococcus (otu58)
- Burkholderiaceae (otu1219)
- Rothia (otu3177)
- Avibacterium (otu2402)
- Gallibacterium (otu81)
- Gallibacterium (otu3129)
- Mycoplasma (otu798)

# Core gut OTUs



# Sub-clinical levels of potential pathogens

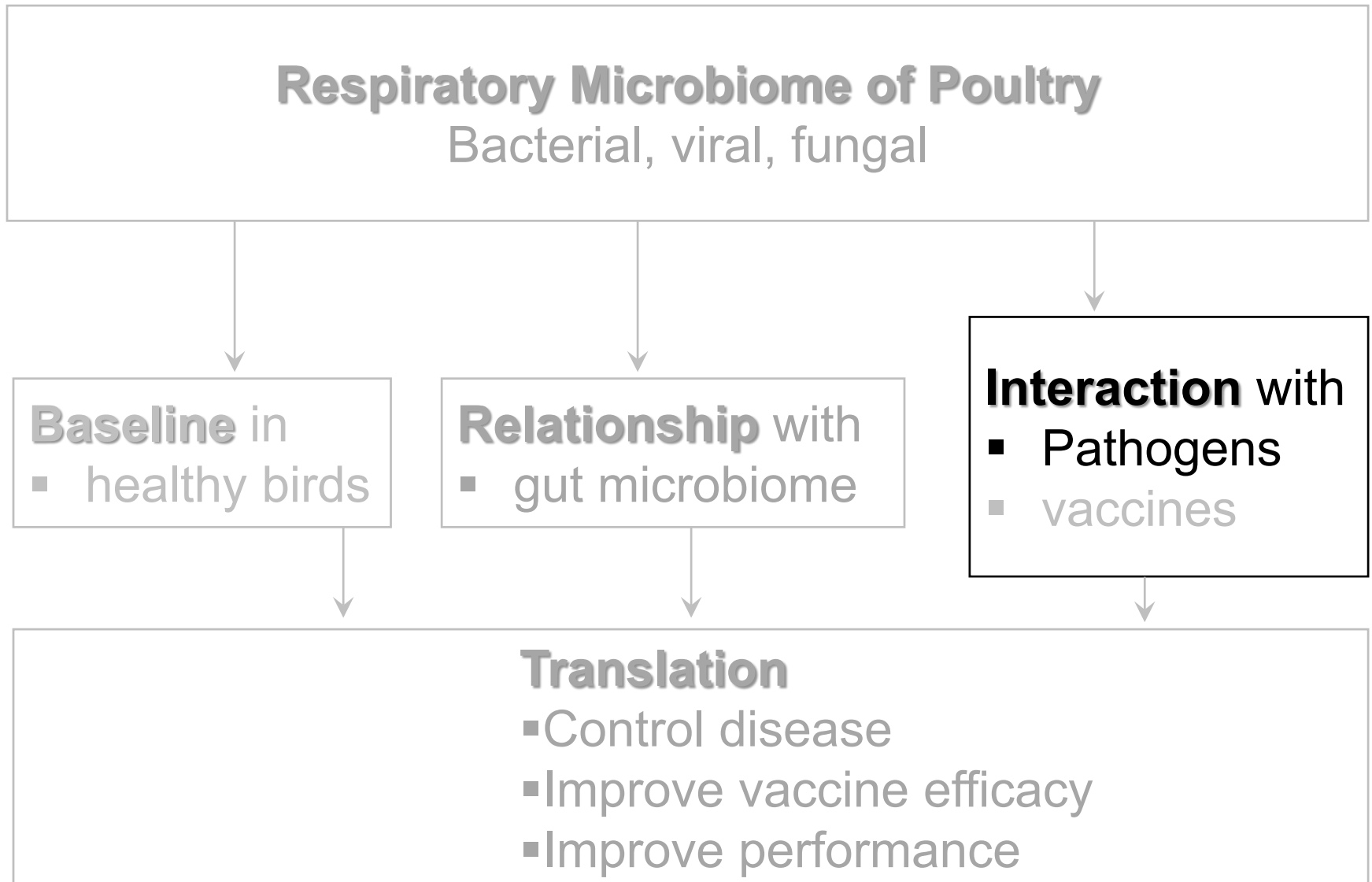


- ❑ Most of these genera shared between ileum and respiratory sites
- ❑ Confirmed subclinical levels of:
  - ✓ Mycoplasma synoviae, ORT, APEC, Clostridium perfringens

# SUMMARY: commercial chicken layers

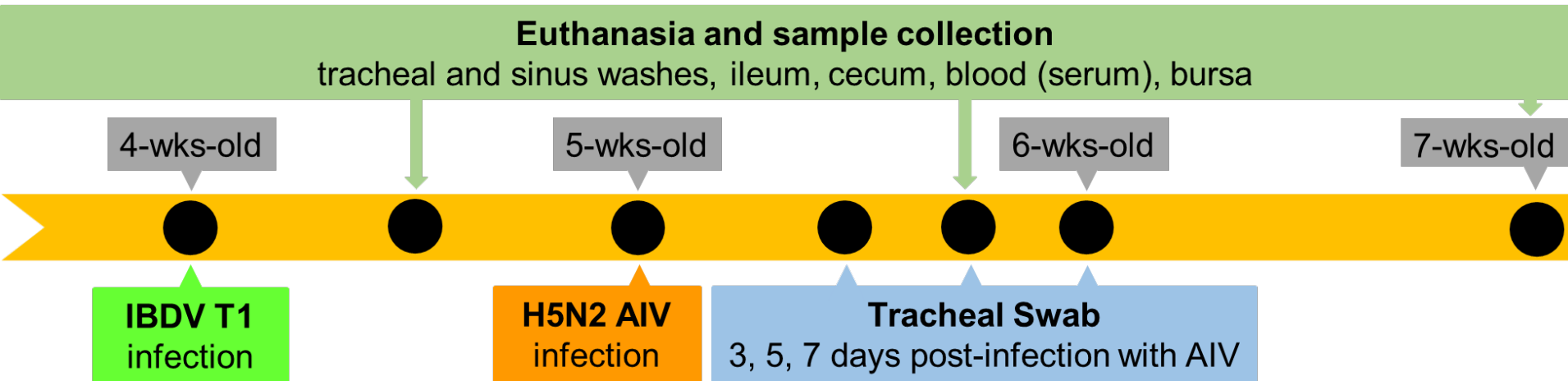
- ❖ Cecal microbiota was drastically altered in the layer stage
- ❖ Ileal microbiota are related to the respiratory microbiota, possibly due to aerosolization of fecal bacteria
- ❖ Confirmed pathogens emerged and persisted at subclinical levels, in an optimally performing flock
- ❖ Inter-system enrichment and spread of pathogens
  - ❑ Gut → respiratory, and vice versa

# Project goals



# Impact of virus infection on microbiome

- In collaboration with Dr. Daral Jackwood

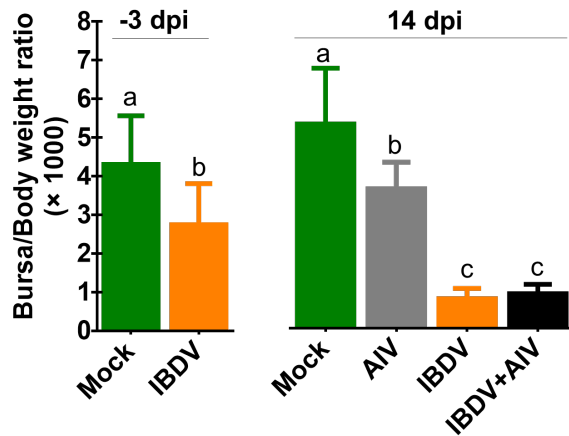


AIV = poultry-adapted CKPA virus



# Bursa atrophy, immunosuppression, AIV shedding

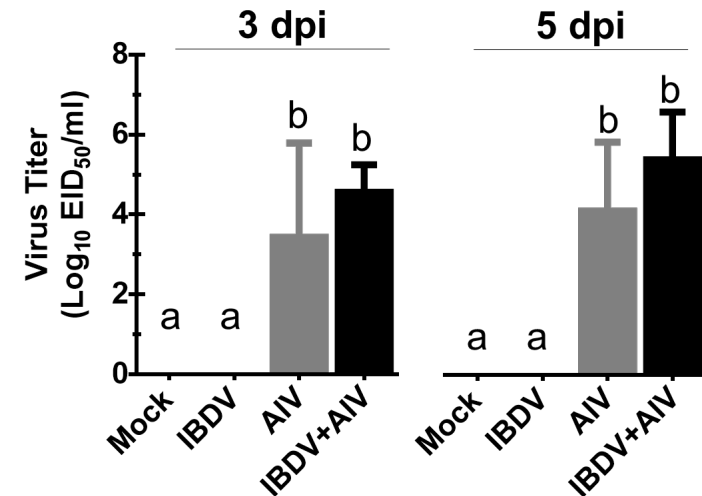
Bursal atrophy



Suppression of AIV  
HI antibody response

	Log2 HI Antibody titer (Mean ± SD)
Mock	0 <sup>a</sup>
IBDV	0 <sup>a</sup>
AIV	7.1±1.07 <sup>b</sup>
IBDV+AIV	5.9±0.9 <sup>c</sup>

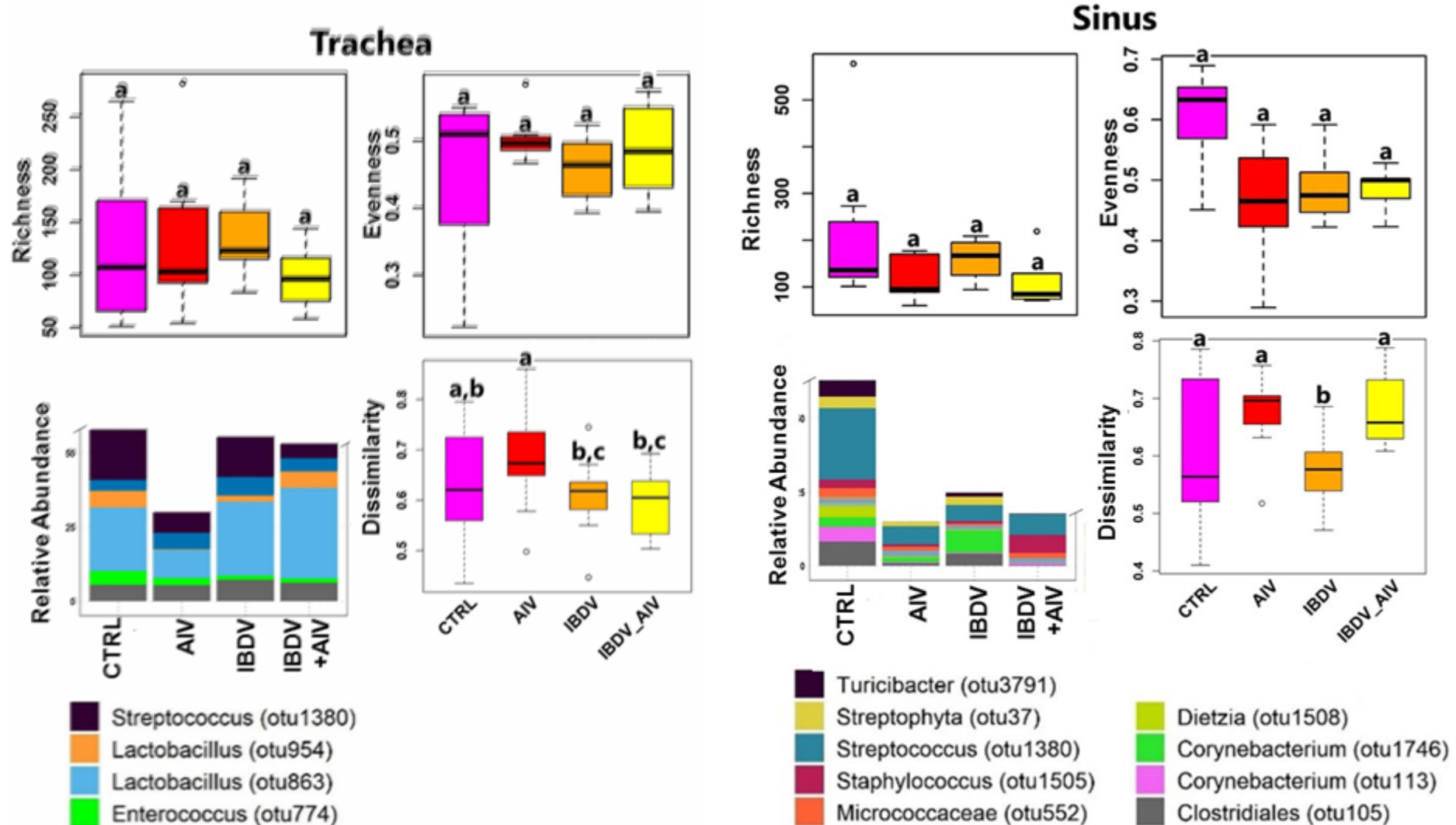
Enhancement of AIV  
replication in trachea



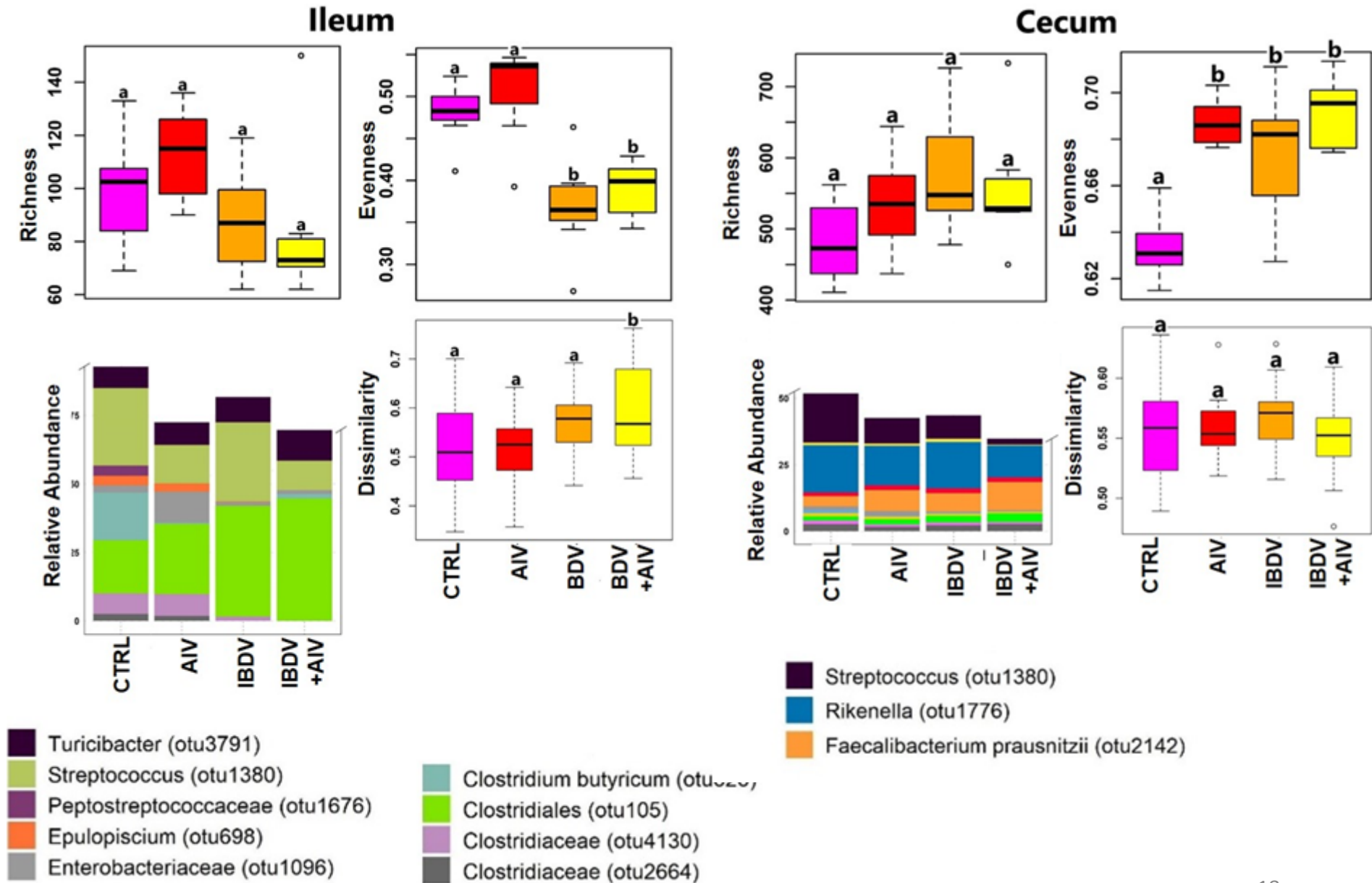
- ❑ Bursa atrophy was observed in IBDV and AIV groups
- ❑ Significant reduction of AIV antibodies in IBDV-infected chickens
- ❑ Enhanced AIV replication in trachea of IBDV-infected chickens



# Impact of virus on respiratory system



# Impact of virus on gut



# SUMMARY: virus infection in SPF chicken

- ❖ Remarkable general suppression of sinus core by virus
- ❖ Systemic differences in virus impacts on bacterial diversity
  - ❑ Respiratory → Community dissimilarity (between birds)
  - ❑ Gut → Species evenness (individual birds)
- ❖ Differential effects of IBDV and AIV
  - ❑ Tend to be body site-specific

# FUTURE DIRECTIONS

- ❖ Controlled microbiome experiments
  - ❑ Inter-system enrichment and spread of pathogens
    - role of live vaccines and viral infections
  - ❑ Long term impacts of virus-induced disruption of bacterial diversity
    - susceptibility to disease
    - performance.
- ❖ Target respiratory and ileal microbiome to reduce impact of respiratory pathogens
- ❖ Incorporate components of viral and fungal microbiome and the host

# Acknowledgement



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