

The effect of feed and farm on microbiome composition and how this affects bird performance

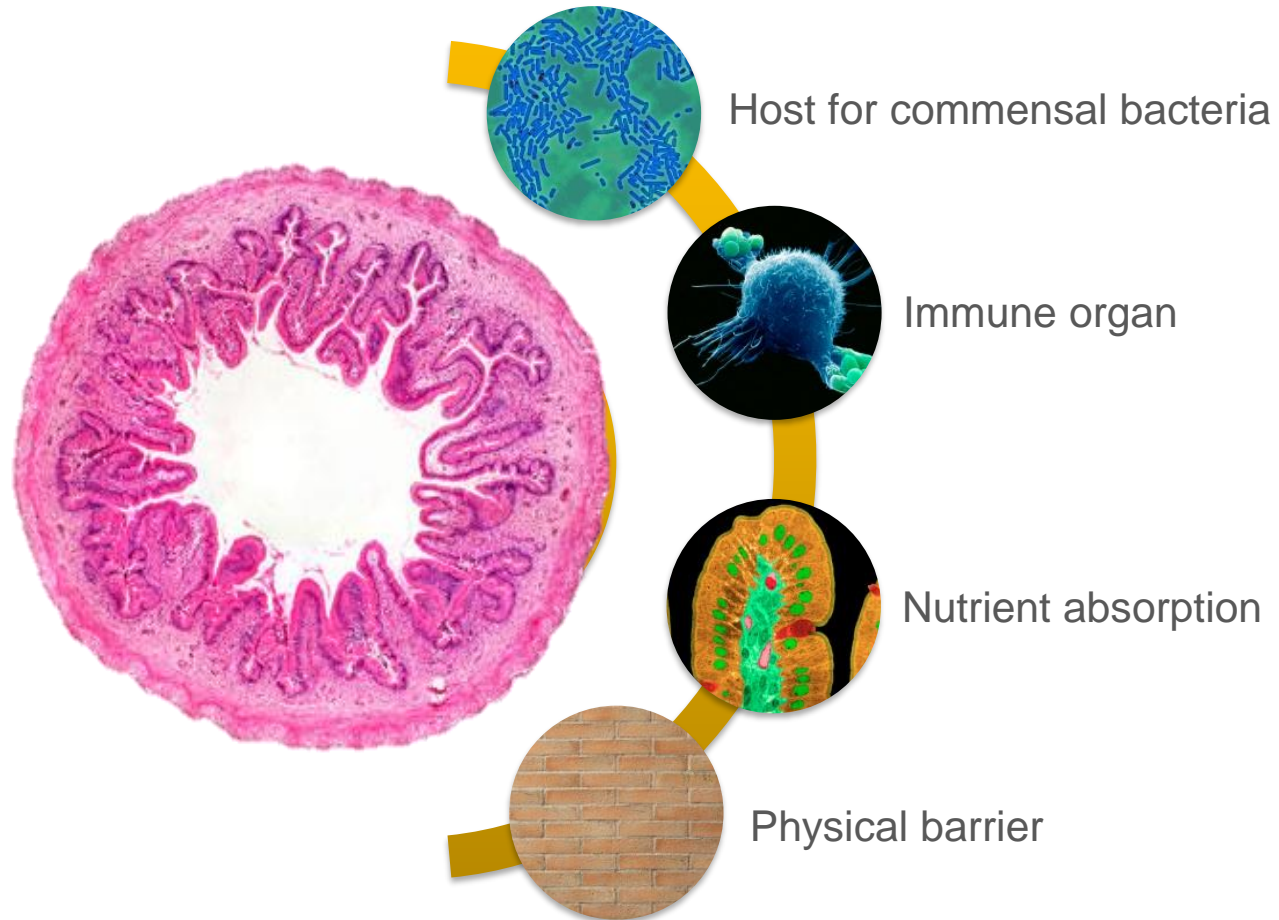
Dr. Henk Enting
Cargill Animal Nutrition



Introduction

- Initial focus on improvement of gut health by nutrition when AGP were banned
- After the pressure to reduce antibiotics in drinking water the focus shifted to improvement of farm management
- The focus on gut health and farm management has not resulted in 100% reduction in the use of antibiotics
- There is still quite a large gap between genotype and phenotype: more knowledge is needed about the effect of microbiome on bird performance and interactions between microbiome and immune responses

Initial focus of AGP reduction: main gut functions



Host for commensal microflora

- Well-balanced, low numbers of potentially pathogenic strains
- Prevention of bacterial overgrowth

Immune organ / function

- Appropriate responses
- Inflammatory reaction and control

Nutrient absorption

- Epithelial cell growth and differentiation
- Maximize absorption → reduce substrate for bacteria

Physical barrier

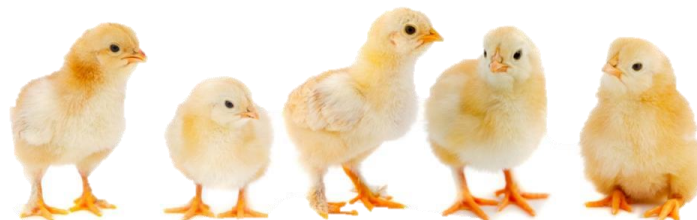
- Prevent adhesion of pathogenic bacteria
- Prevent translocation of bacteria

Current status

- The focus on the main gut functions and farm management has resulted in a strong reduction in the use of antibiotics in feed and drinking water in a number of countries
- However, a total ban on the use of antibiotics is difficult to achieve
- More in depth knowledge is required about gut function and immune responses to close the gap between genotype and phenotype

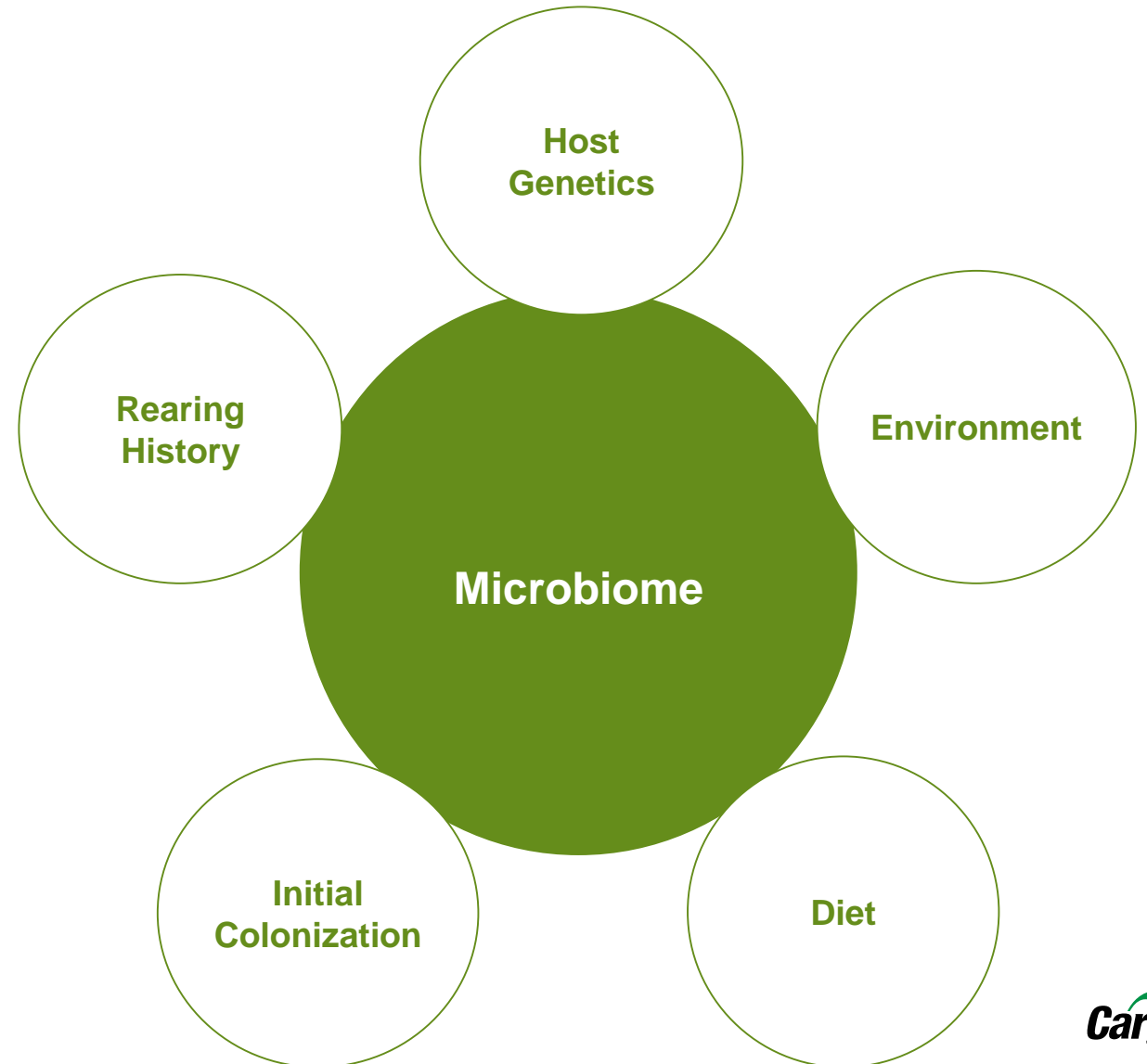
First question:

What is the effect of the microbiome on broiler and breeder performance?



There are critical challenges to gaining insights into microbiome

- A large degree of internal variability limits our ability to interpret the data
- The microbiome is a product of factors that are often difficult to precisely control
- The core technologies are continuously being improved which further limits interpretability across historical experiments and datasets



Monitoring microbiota in poultry: current work

- An 16S derived microflora array was developed and trialed
 - The microbiota markers with best correlation of bird performance were selected
 - Due to several years of trial data – it was approached as a big data problem
 - Based on 12,000+ samples – we see a link between performance & microbiota composition
- **performance of broiler chickens can be predicted with close to 90 % accuracy based on the microbiota composition**

Monitoring microbiota in poultry: main trial findings

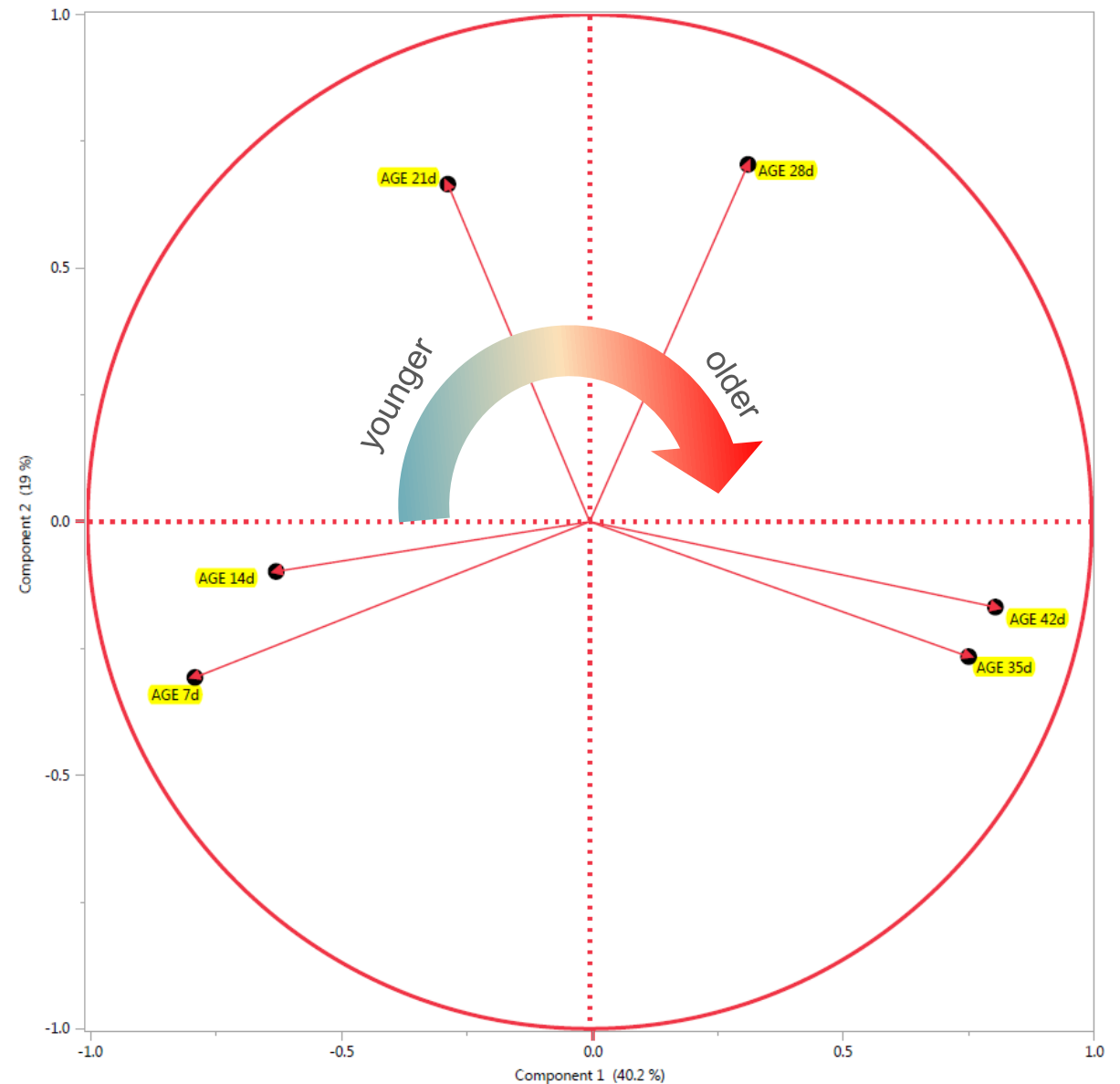
- A faster speed of maturation of the microbiota has a positive effect on performance
- There are clear effects of raw materials, nutrients and feed additives on microbiota composition
- There are clear differences in microbiota composition between good and less good performing flocks → moving the microbiota of less good performance flocks towards the one of good performing flocks can improve performance

In summary...

Increasing the speed of maturation of the microbiota may help to reduce antibiotics use

Effect of age on microbiota

- Gut microbial profile has a maturation pattern following birds' age
- A faster speed of maturation coincides with a better bird performance
- In house hatched birds show a faster speed of maturation and in house hatching may help to reduce the use of antibiotics

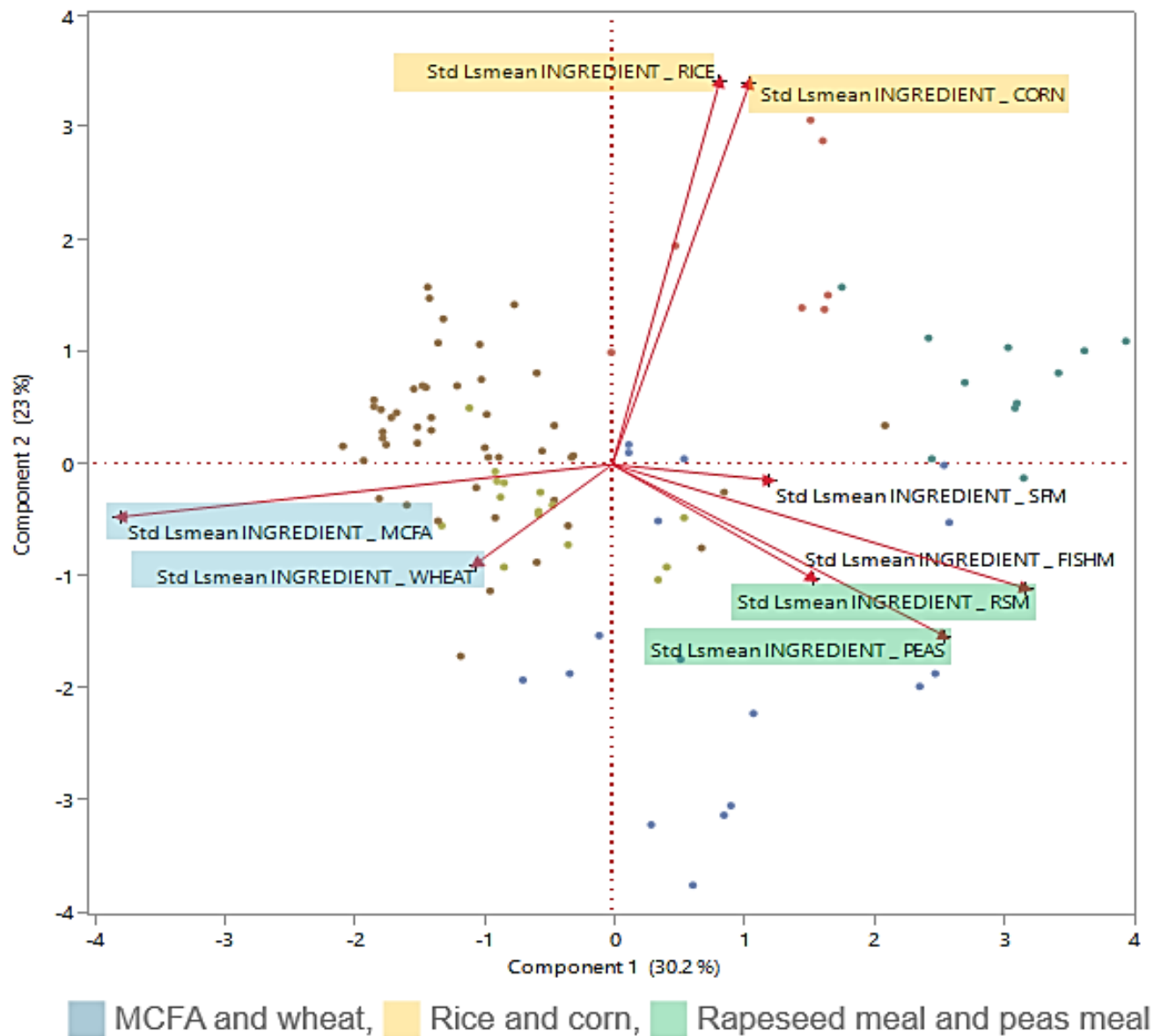


In summary...

**There are clear effects of raw materials, nutrients
and feed additives on microbiota composition**

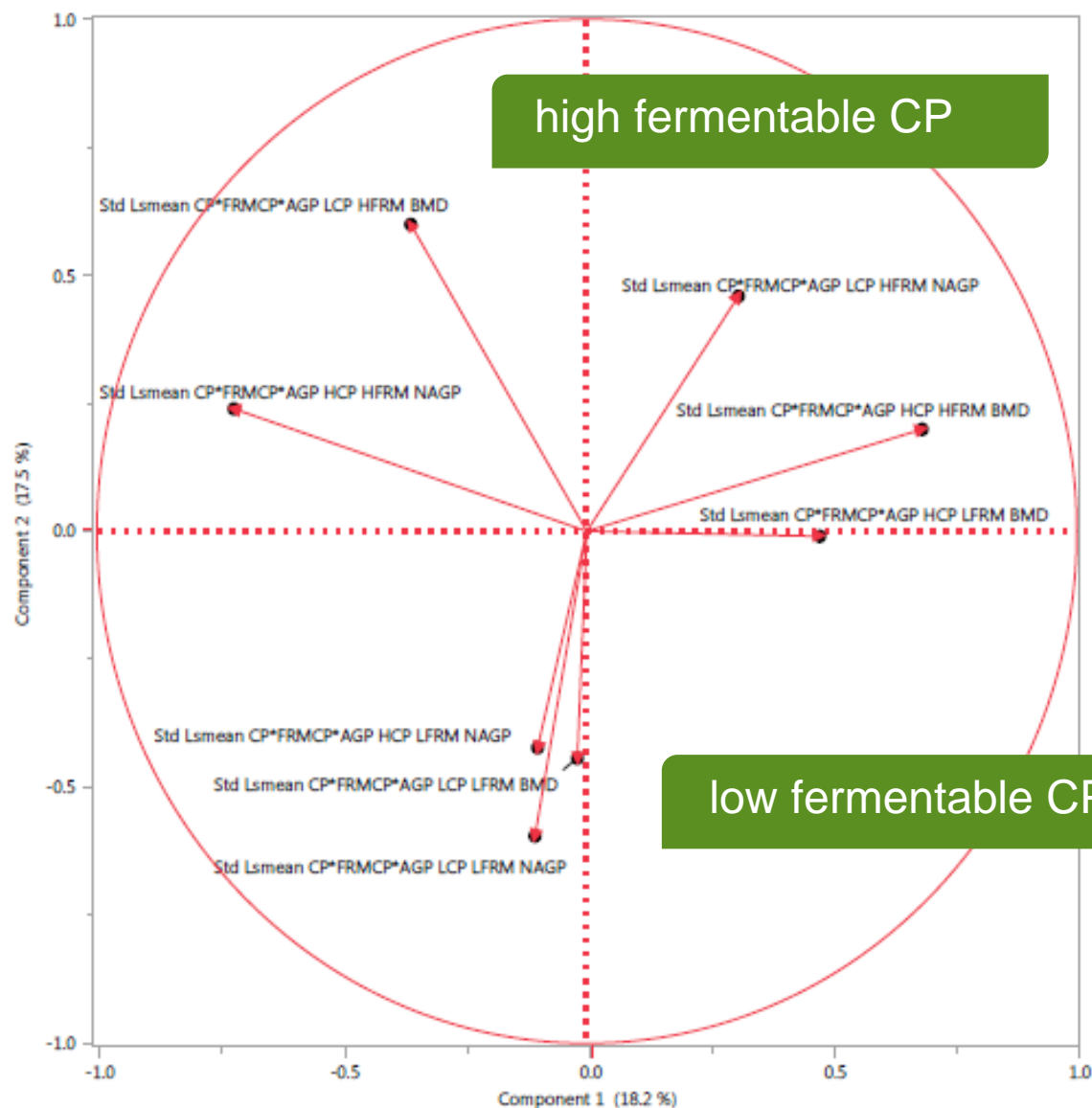
Effect of raw materials on microbiota

- Feed raw materials can shift composition of microbiota
- Corn and rice result in a different profile than for example wheat and MCFA, and protein rich raw materials have another microbiota profile



Effect of nutrients on microbiota

- Low fermentable crude protein (CP) was associated with Bifidobacterium, Clostridium botulinum and Dorea romicigenerans
- High fermentable CP was associated with E. coli, Salmonella, Campylobacter



Effect of raw materials on microbiota

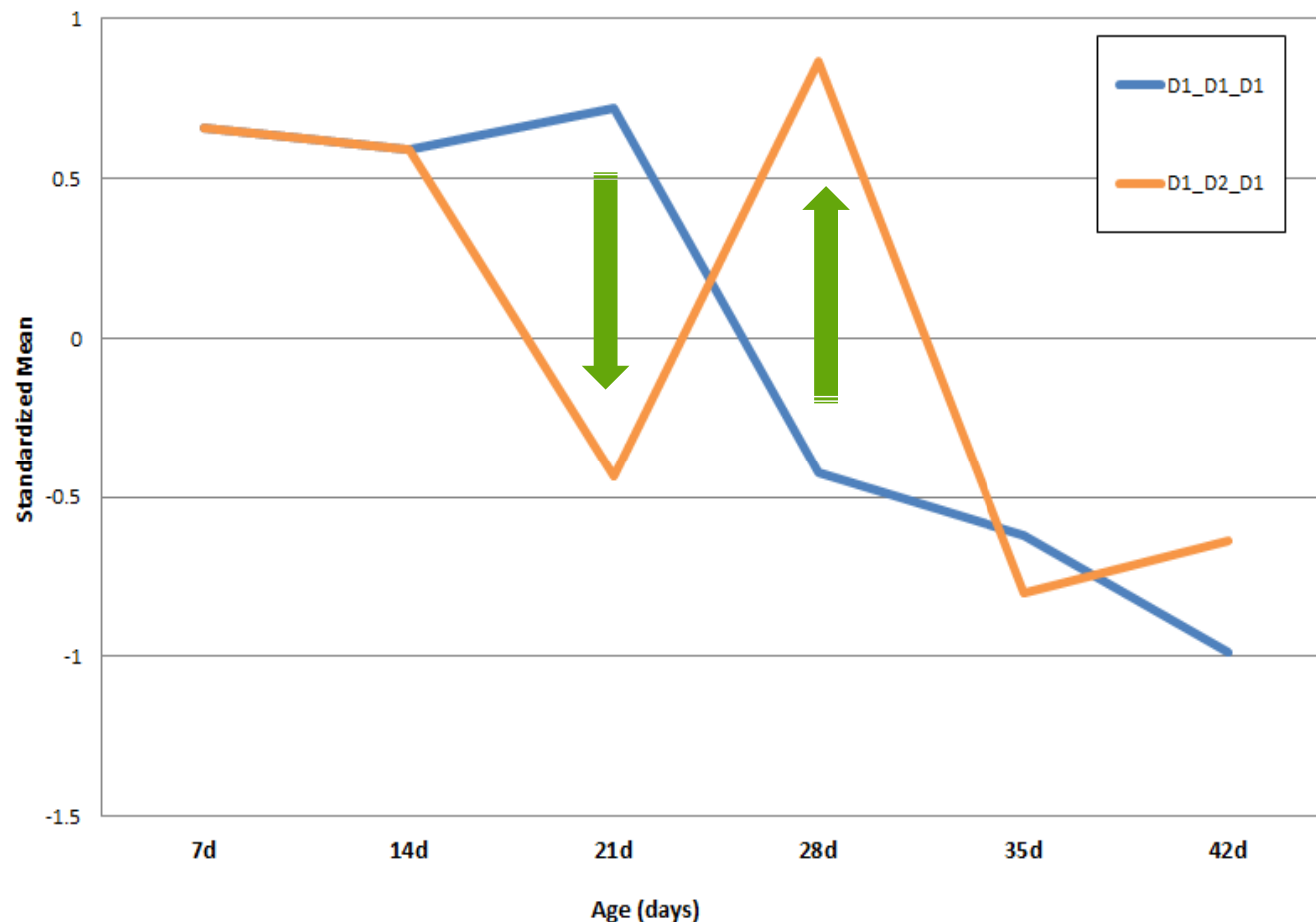
- A change from corn to wheat based feed can cause large changes in microflora increasing the risk of performance loss and wet litter

→ apply gradual changes

D1_D1_D1: all corn

D1_D2_D1: corn-wheat-corn

Bacteria Response to Diet Changes -1



Conclusion...

Differences in microbiota between *good and bad* performing flocks may help to better adjust our nutritional strategies

Example 1

PILOT GOOD VS BAD

Microbial results – cluster analysis

- Cluster analysis and heat map of broiler intestinal bacteria significantly different between “Good” and “Bad” farms at 21, 28 and 35 days of age.

Brenneria

Lachnospiraceae Incertae Sedis 8

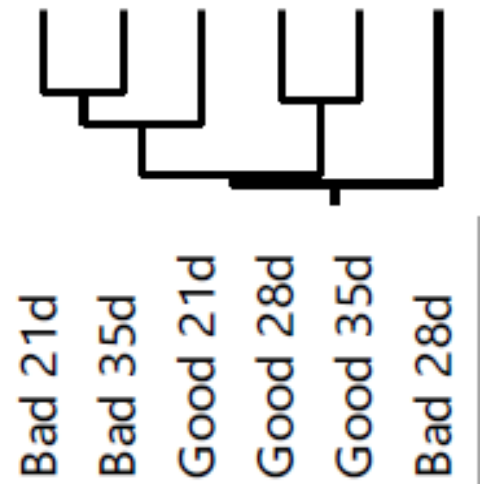
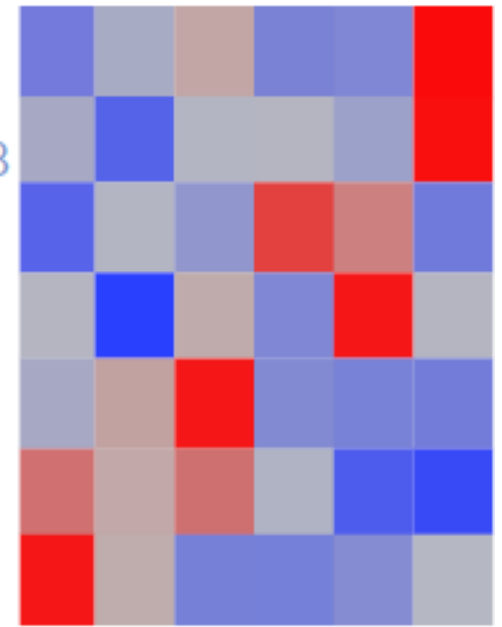
Clostridium bartlettii 2

Holdemania

Lactobacillus crispatus 1

Lactobacillus crispatus 3

Campylobacter



Example 2

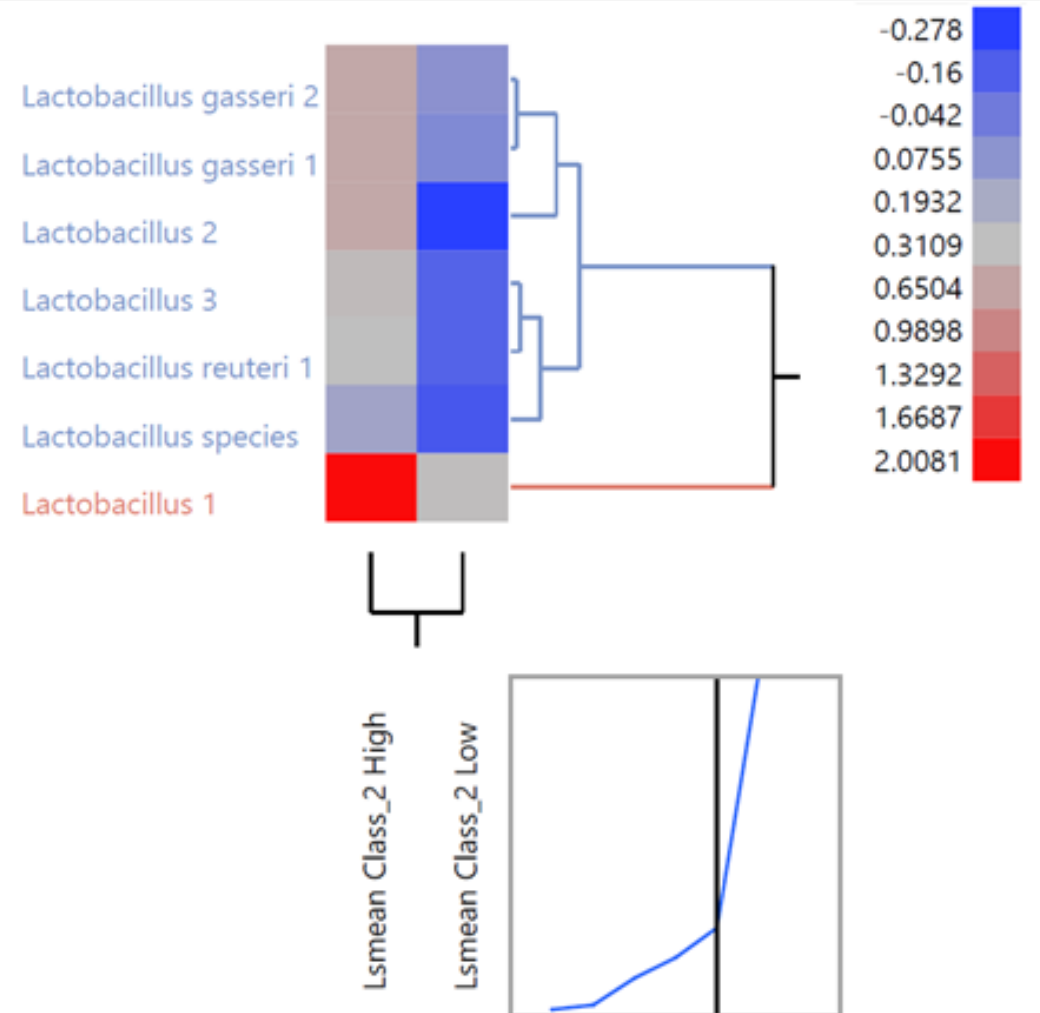
LOW and HIGH incidence of pododermatitis

- All significantly different bacteria between farms with “Low” and “High” incidence of pododermatitis were Lactobacillus
- General Lactobacillus and some specific species showed higher abundance in HIGH Podo farms

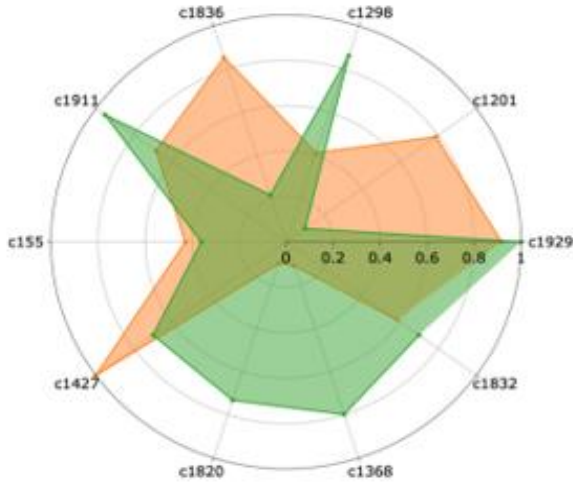
Hierarchical Clustering of LSMeans

Method = Fast Ward

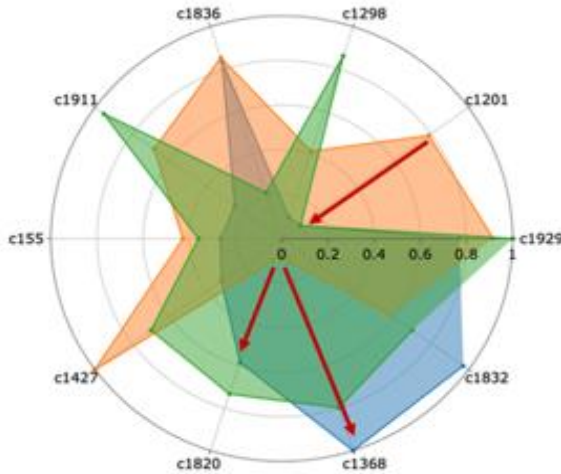
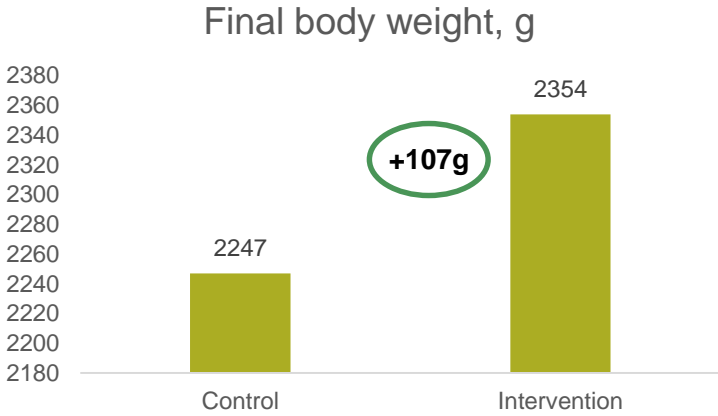
Dendrogram



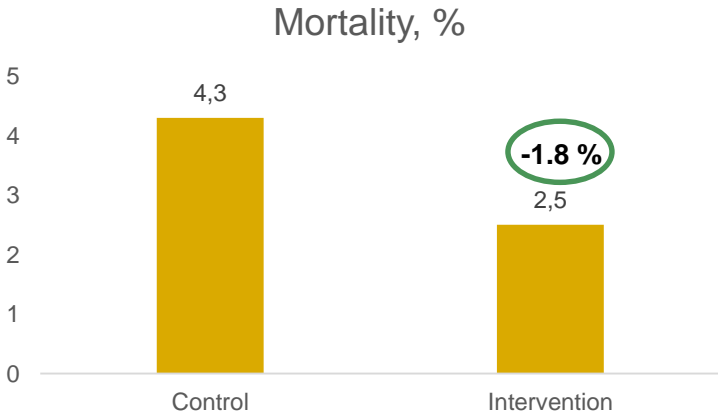
Example 3: intervention study



The excess of *Lactobacillus* and lack of *Bacteroides* were characteristic for control group (orange)

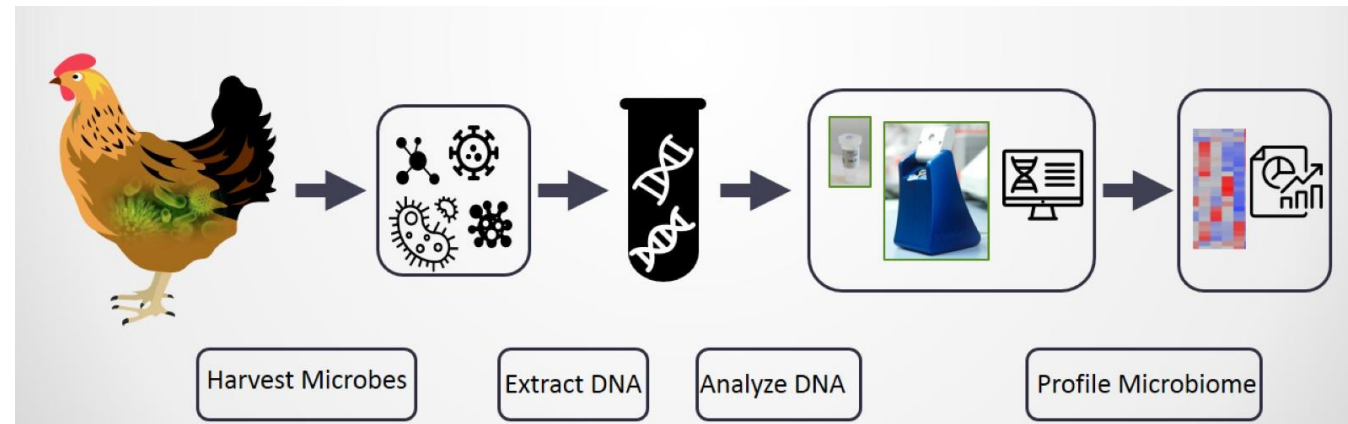


Intervention reduced the overgrowth of *Lactobacillus* and increased the level of *Bacteroides* to the level representative for good performing farms in the database



Understanding the role of microbiota

- Monitoring of microbiota in the field can help to find differences between farms in relation to performance and to better adjust nutritional strategies to the farm conditions
- Kers et al. (2018) indicated that microbiota studies have to deal with many hidden host and environmental variables: study designs can have a large impact on the results and interpretation of these → large datasets may be required to find patterns and effective intervention strategies

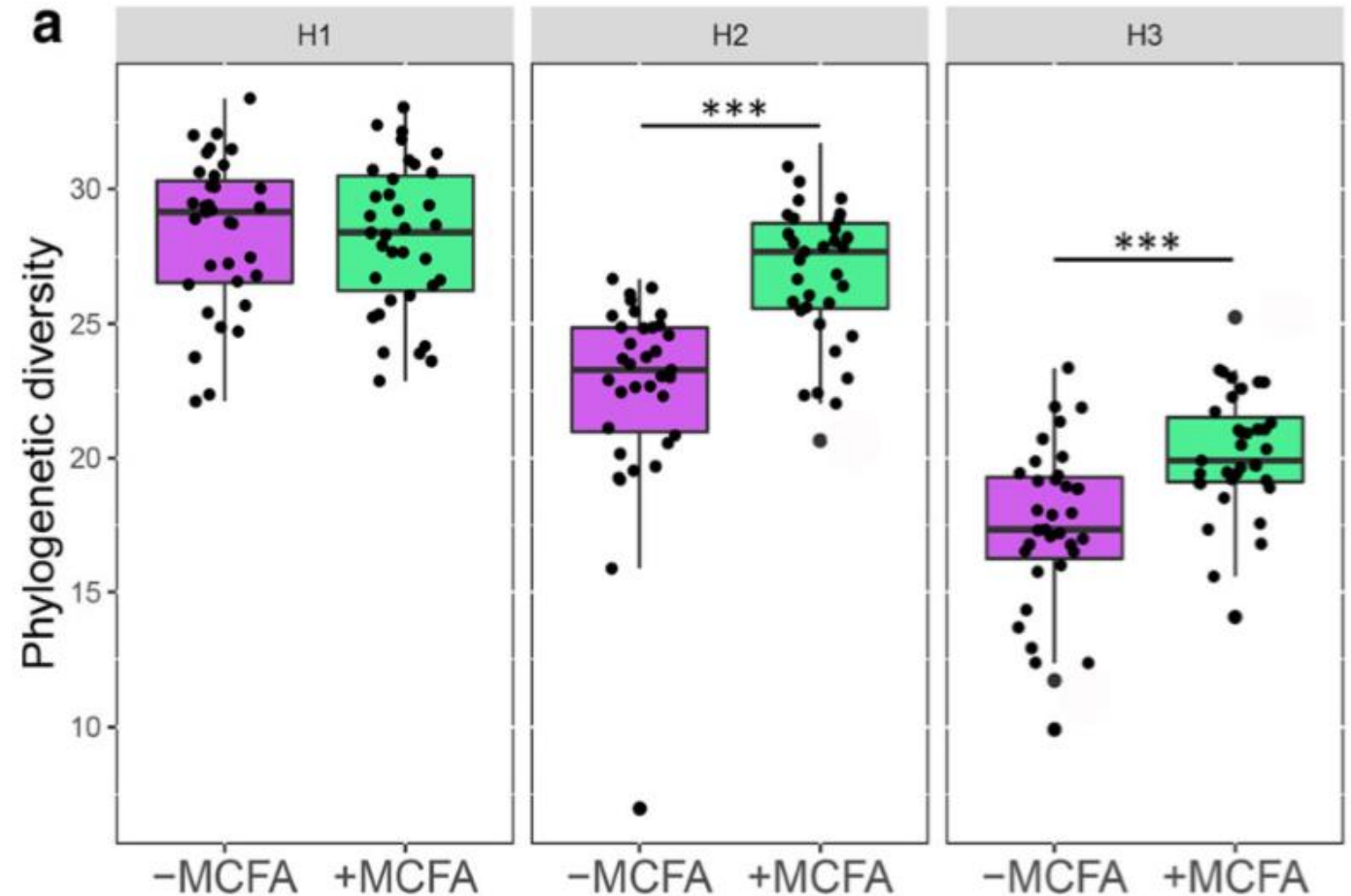


Effect housing conditions on microbiota changes with a dietary intervention (MCFA)

Phylogenetic diversity in caeca in different housing types:

- H1 - feed research facility
- H2 - extensively cleaned stable with floor pens
- H3 - isolators

(Kers et al., 2019)

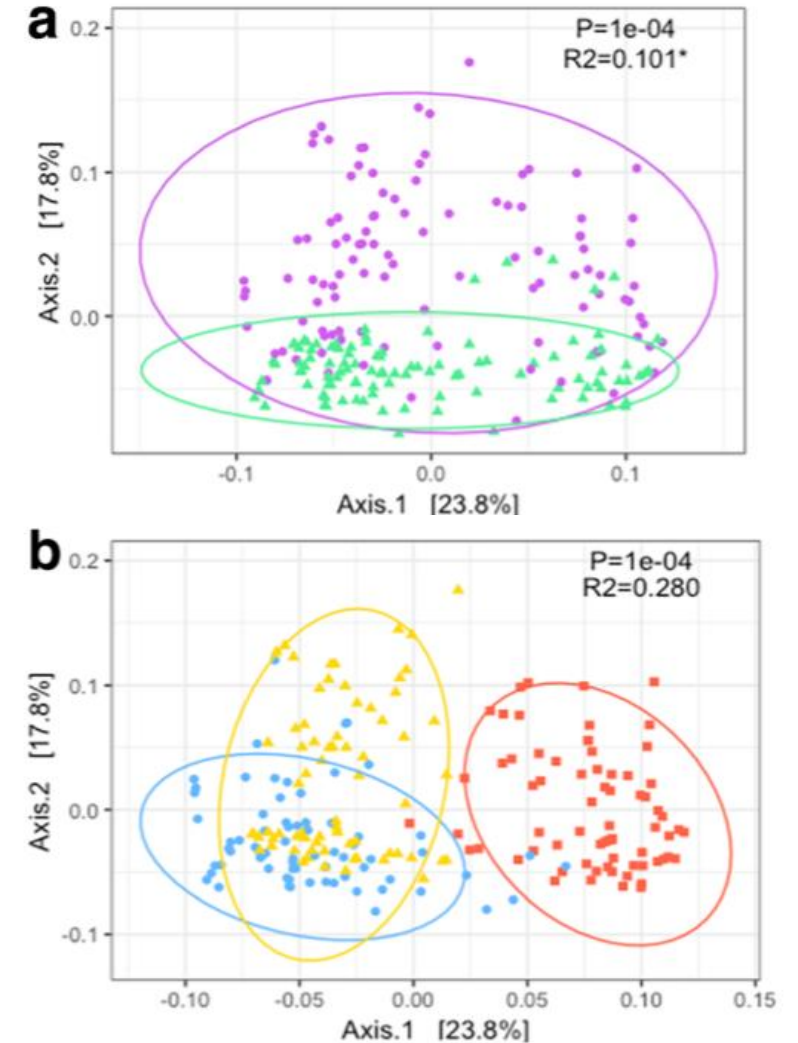


Effect housing conditions on microbiota changes with a dietary intervention (MCFA) *continued...*

Weighed UniFrac based PCoA analysis across the six experiment groups:

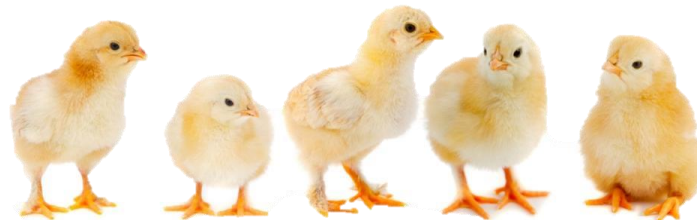
- a - diet effect across housing units
- b - housing condition effect

(Kers et al., 2019)



Conclusions microbiota work

- Knowledge about how raw materials, nutrients and feed additives change microbiota can help to adjust nutritional strategies to improve performance and to reduce the use of antibiotics
- Effects of nutritional interventions can be strongly dependent on the housing conditions / environment: interpretation of trial results should be done in combination with housing effects
- Large sets of microbiota data are required to find patterns and relationships with growth, feed conversion ratio, mortality and antibiotic use





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