



EFFECT OF GUT MICROBIOTA ON PRODUCTION TRAITS, INTERACTION WITH GENETICS

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Between feed and meat

► Digestion = building a microbiota

Maternal transmission

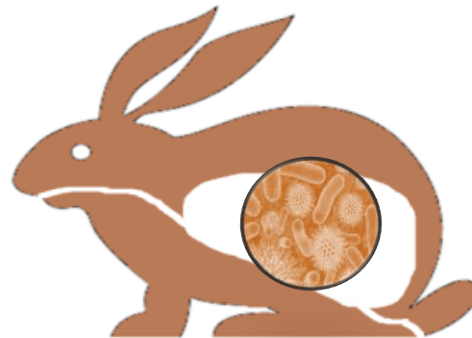
Contact with (others') feces

Genetics

Age

Sex

Physiological status



MANAGEMENT

use of anti-microbials

feed

water

animal density

temperature and humidity

...

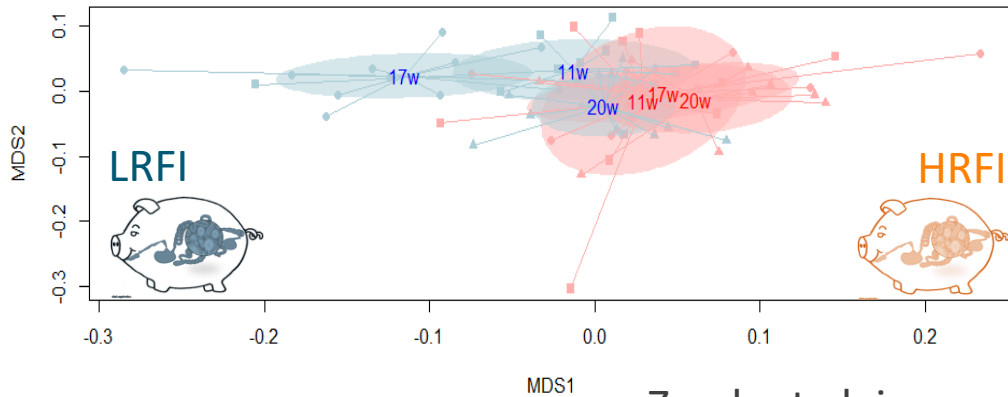
→ What should be accounted for to improve performances thanks to microbiota?

→ How to disentangle and test the effects of these factors?

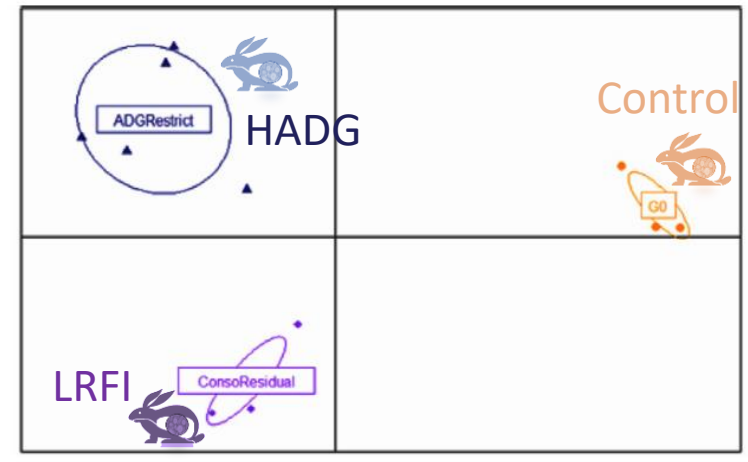


Genetic determinism of microbiota composition

Based on selected lines



Zemb et al, in prep



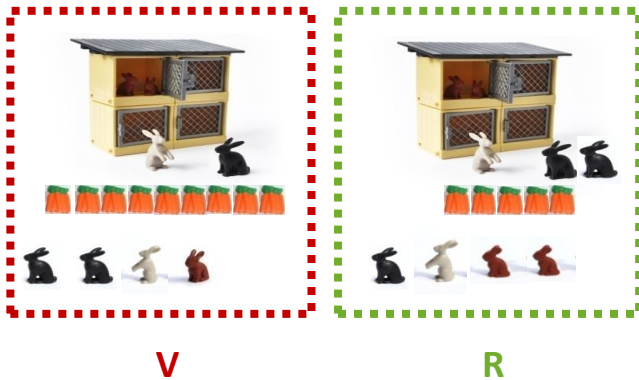
Drouilhet et al, JAS, 2016

→ Separate lines selected for different feed efficiency based on microbiota composition (DA-PC applied to OTU abundance matrix)



Genetic determinism

Within population



Bayesian estimation of variance components

Model **na**: no σ^2_a

Model **a**: σ^2_a

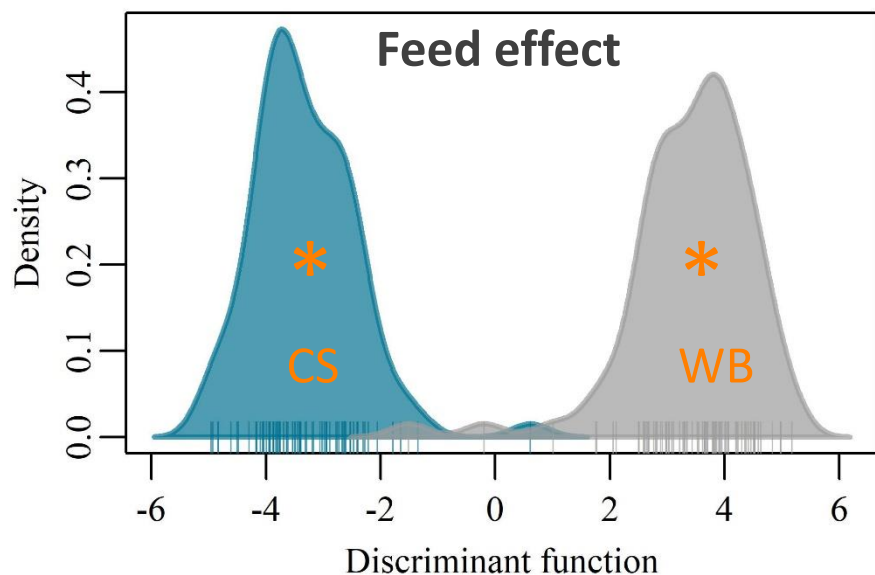
→ Deviance Information Criterion and BayesFactor computations

Trait	h^2
Phylum relative abundance	
Euryarcheota	0.13
Actinobacteria	0.10
Bacteroidetes	0.09
Cyanobacteria	0.11
Firmicutes	0.09
Proteobacteria	0.11
Tenericutes	0.08
Verrucomicrobia	0.08
Alpha index diversity	
#OTUs	0.17
Chao1	0.18
Shannon	0.11
Inverse Simpson	0.11
Principal components (PC)	
PC1	0.09
PC2	0.11



Adapting the **feed**, the **animal** and the **feeding techniques** to improve the efficiency and sustainability of monogastric livestock production systems

Feed effect



CS
~ 85 % Corn/Soybean meal
~ 10% By products



WB
~ 50 % Wheat/Barley
~ 45 % By products

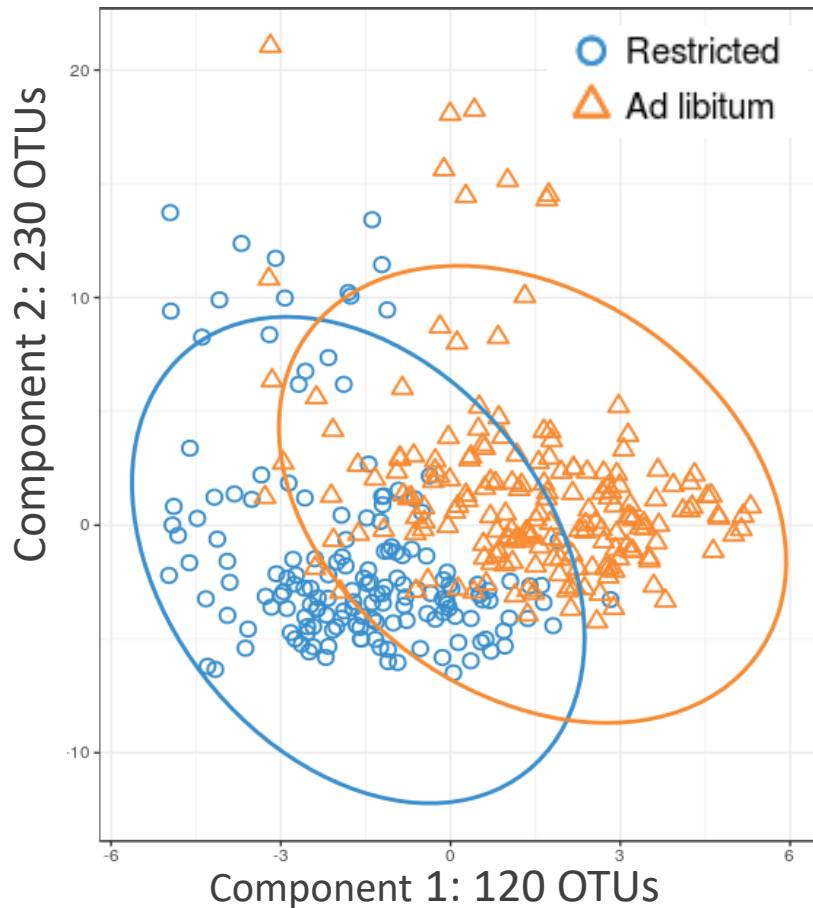


Day before slaughter

→ **Contrasted feed compositions highly affect fecal microbiota**



Feeding level effect



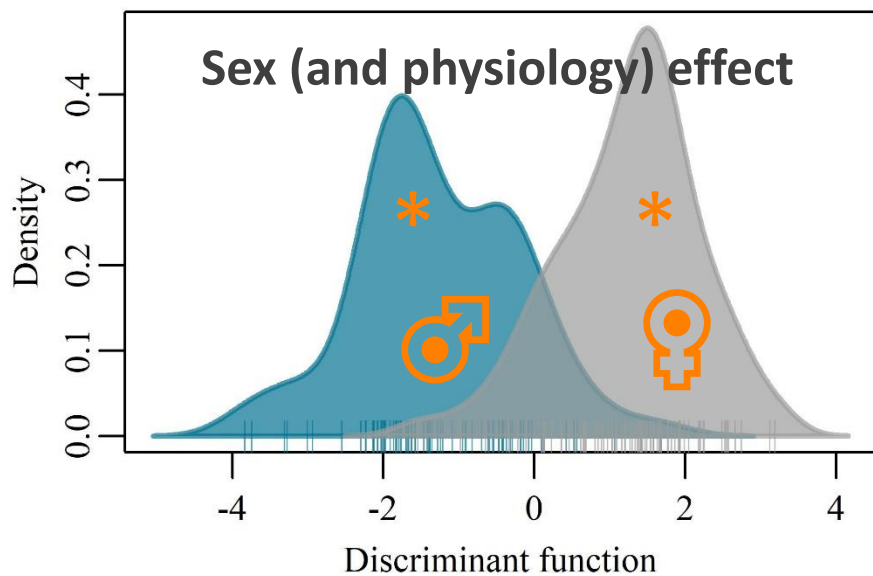
V

R

→ Feeding restricted or ad libitum affect fecal microbiota composition



Sex effect



CS
~ 85 % Corn/Soybean meal
~ 10% By products



WB
~ 50 % Wheat/Barley
~ 45 % By products



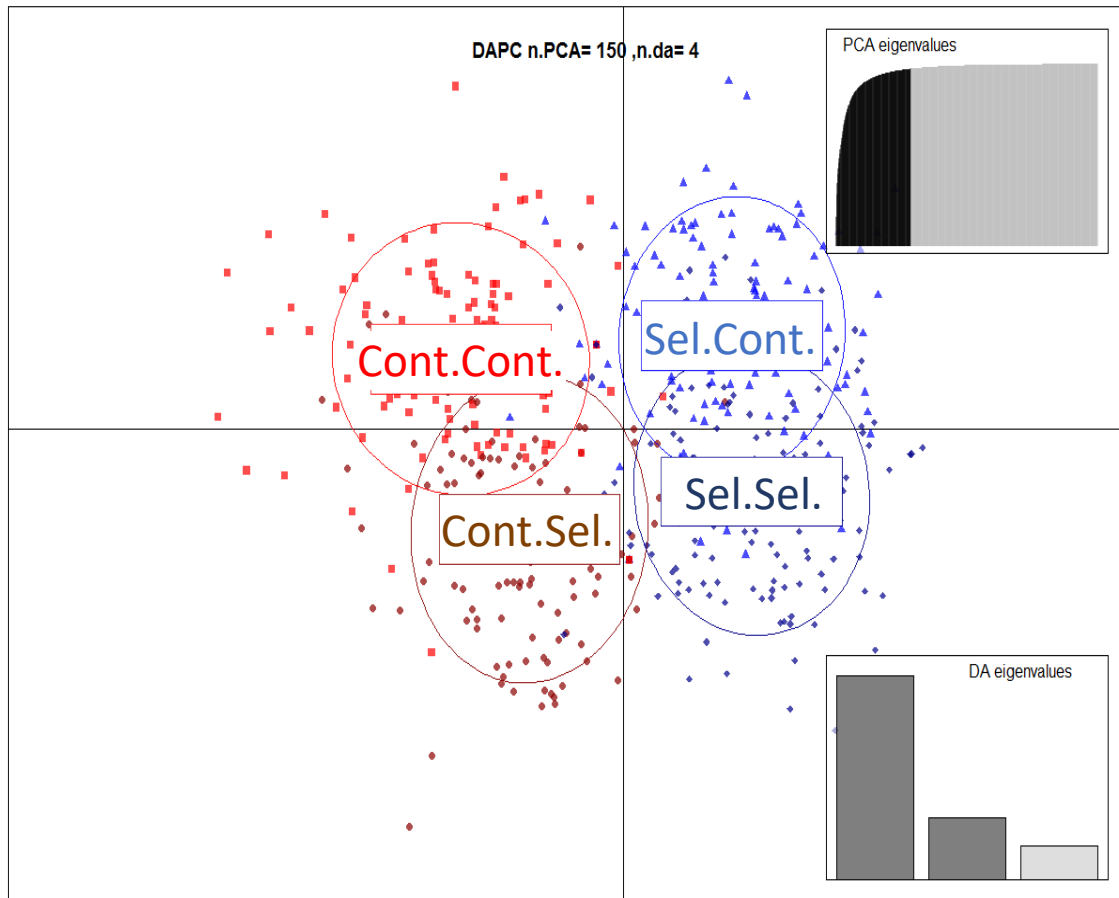
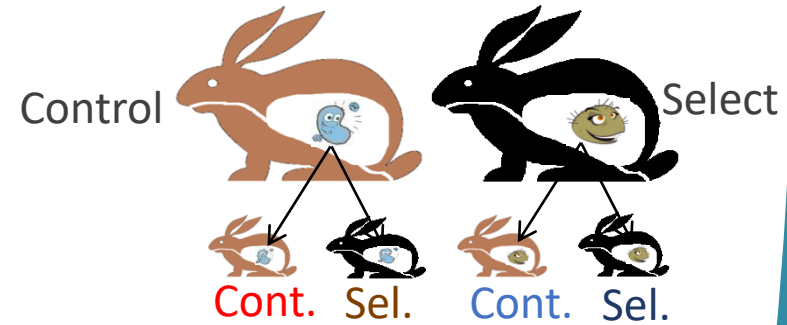
Day before slaughter

→ Sex, potentially via sexual maturity, affects gut microbiota composition



Maternal transmission

Cross-fostering experiment



→ The kit line is the primary effect, but the dam line also nicely separates the individuals



Production traits: **accounting for genetics**

1. Model ignoring the effect of microbial composition

$$y = X\beta + a + e$$

FIXED EFFECTS $X\beta$

RANDOM EFFECTS

- Additive direct genetic: $a \sim \text{NMV}(0, A\sigma_a^2)$

2. Model accounting for the effect of microbial composition

$$y = X\beta + a + b + e$$

RANDOM EFFECTS

- Additive direct genetic: $a \sim \text{NMV}(0, A\sigma_a^2)$
- Effect of the microbiome: $b \sim \text{NMV}(0, B\sigma_B^2)$

B = ?

microbiability $b^2 = \sigma_B^2 / \sigma_P^2$



Production traits models: **accounting for all confusion factors**

Model accounting for the effect of microbial composition

$$y = X\beta + a + c + m + j + b + e$$

RANDOM EFFECTS

- Additive direct genetic a
 - Maternal genetic m
 - Litter: $c \sim \text{NMV}(0, I\sigma_c^2)$
 - Pen: $j \sim \text{NMV}(0, I\sigma_j^2)$
 - Effect of the microbiome: $b \sim \text{NMV}(0, B\sigma_B^2)$
- $$\sim N\left(0, \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix} \otimes A\right)$$

a x b ?



Production traits models



V

R

$$\mathbf{b} \sim \text{NMV}(0, \mathbf{B}\sigma_B^2)$$

$$\mathbf{B} = \mathbf{f}(\mathbf{w} \text{Unifrac } \mathbf{d}_m)$$

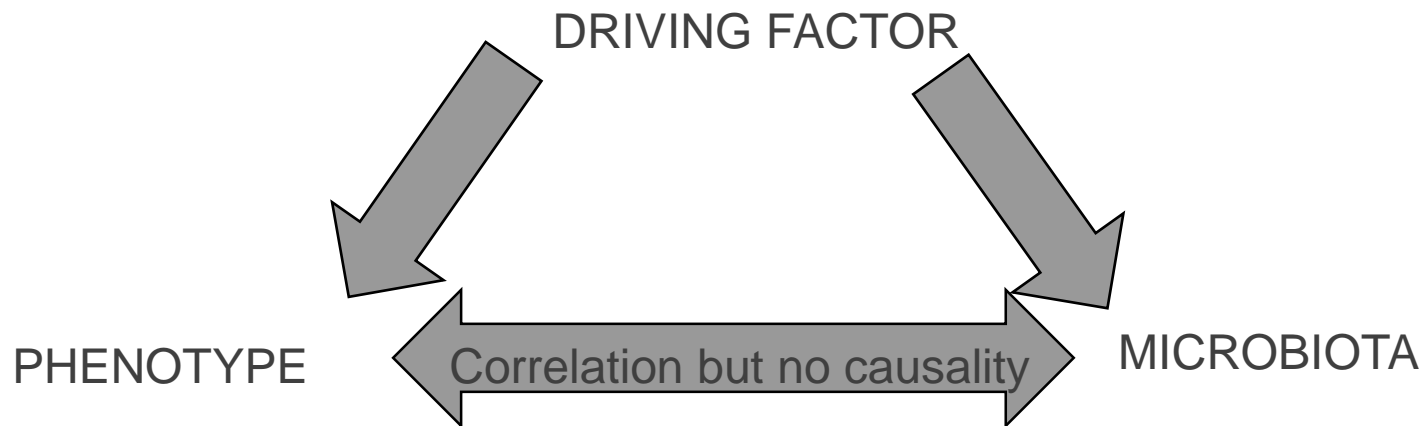
	w/o \mathbf{b}		with \mathbf{b}
\mathbf{h}^2	0.15 (0.04)	>	0.06 (0.03)
\mathbf{c}^2	0.26 (0.06)	>	0.14 (0.05)
\mathbf{b}^2	-		0.56 (0.11)
\mathbf{j}^2	0.12 (0.03)	>	0.05 (0.02)

→ An important % of the total phenotypic variance is explained by microbial composition



Summary

- ▶ Plenty of factors significantly affect gut microbiota composition → need to disentangle
- ▶ Some microbiota are related to production traits (statistical associations)
 - ▶ Causality? Joint effect of other factors?





Discussion

- ▶ Ignored the diversity of OTU tables (content and rules to obtain them)
- ▶ Ignore the diversity of **B**
- ▶ Plenty is missing, keep digging
- ▶ What can be used for livestock at the moment?
 - ▶ **For management?**
 - ▶ **For breeding?**

Genetics

Maternal transmission

Age

Contact with (others') faeces

Sex

Physiological status

use of anti-microbioals

feed

water

animal density

temperature and humidity (see Le Sciellour et al, Thursday morning)