EFFECT OF GUT MICROBIOTA ON PRODUCTION TRAITS, INTERACTION WITH GENETICS

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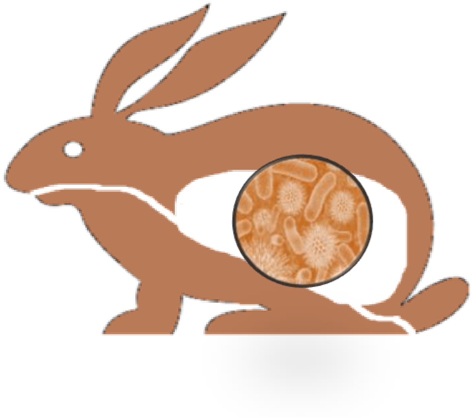
Between feed and meat

- Digestion = building a microbiota



Maternal transmission

Contact with (others') feces

Genetics

Age

Sex

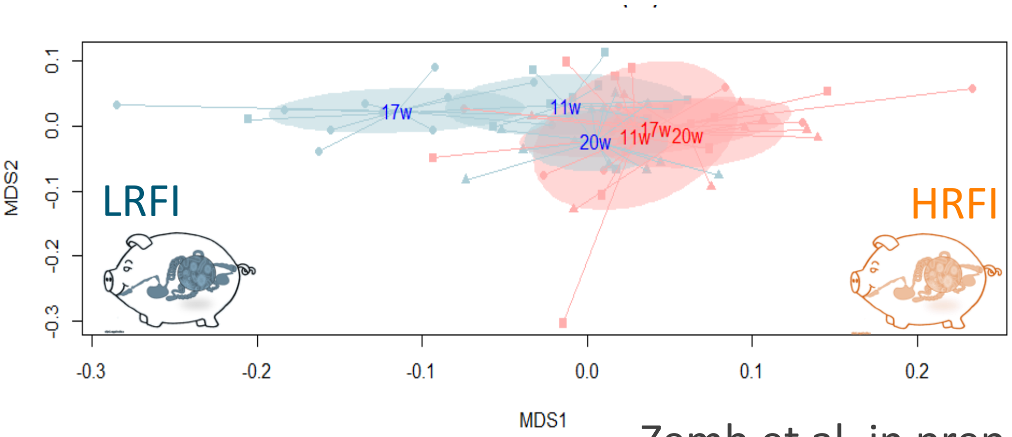
Physiological status

MANAGEMENT
- use of anti-microbials
- **feed**
- water
- animal density
- **temperature and humidity**
- …

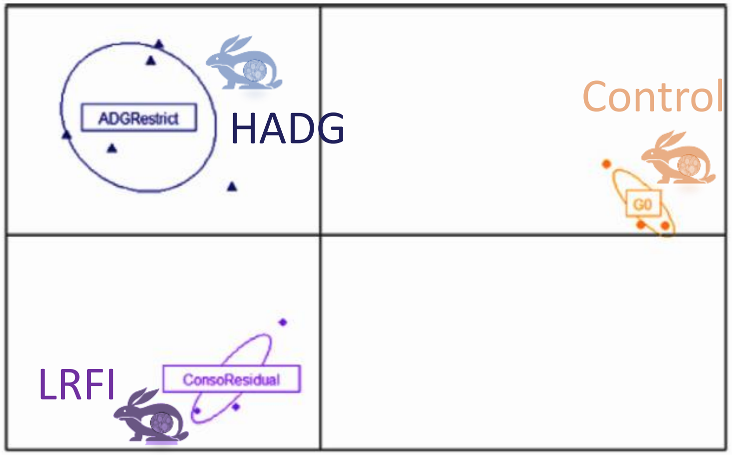
→ What should be accounted for to improve performances thanks to microbiota?
→ How to disentangle and test the effects of these factors?

Genetic determinism of microbiota composition

Based on selected lines



Zemb et al, in prep

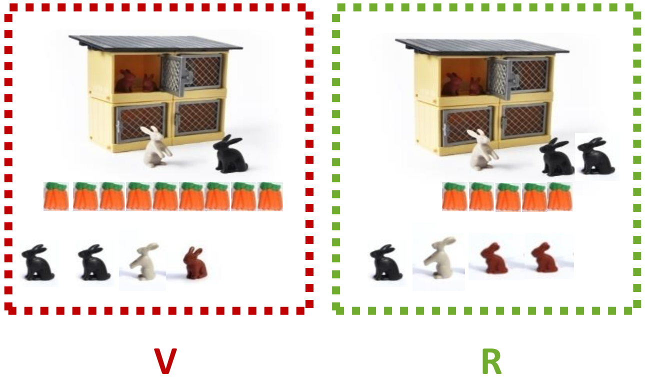


Drouilhet et al, JAS, 2016

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

Genetic determinism

Within population



Bayesian estimation of variance components

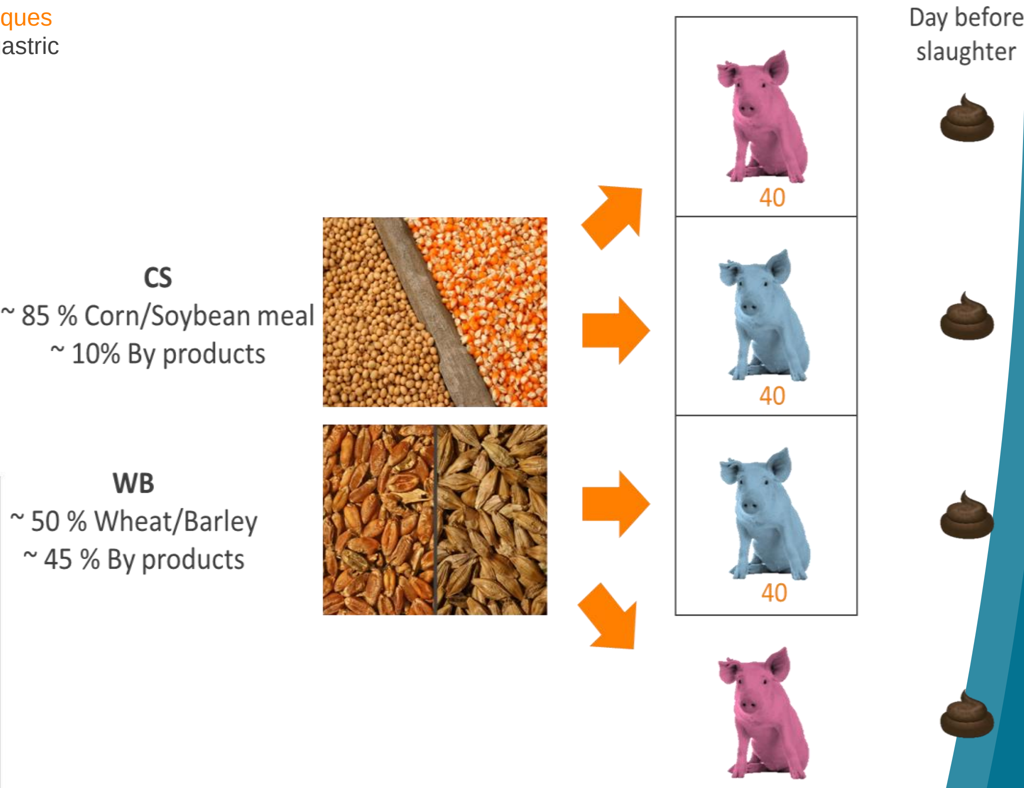
Model **na**: no $\sigma^2 a$
Model **a**: $\sigma^2 a$

→ Deviance Information Criterion and BayesFactor computations

Trait	h²
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**

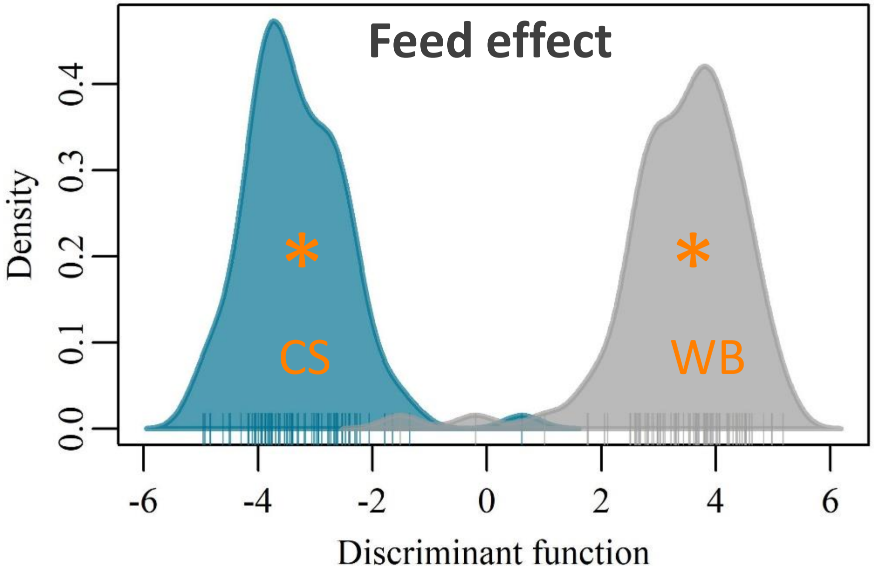
Velasco et al., León, 2018

Feed effect



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

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



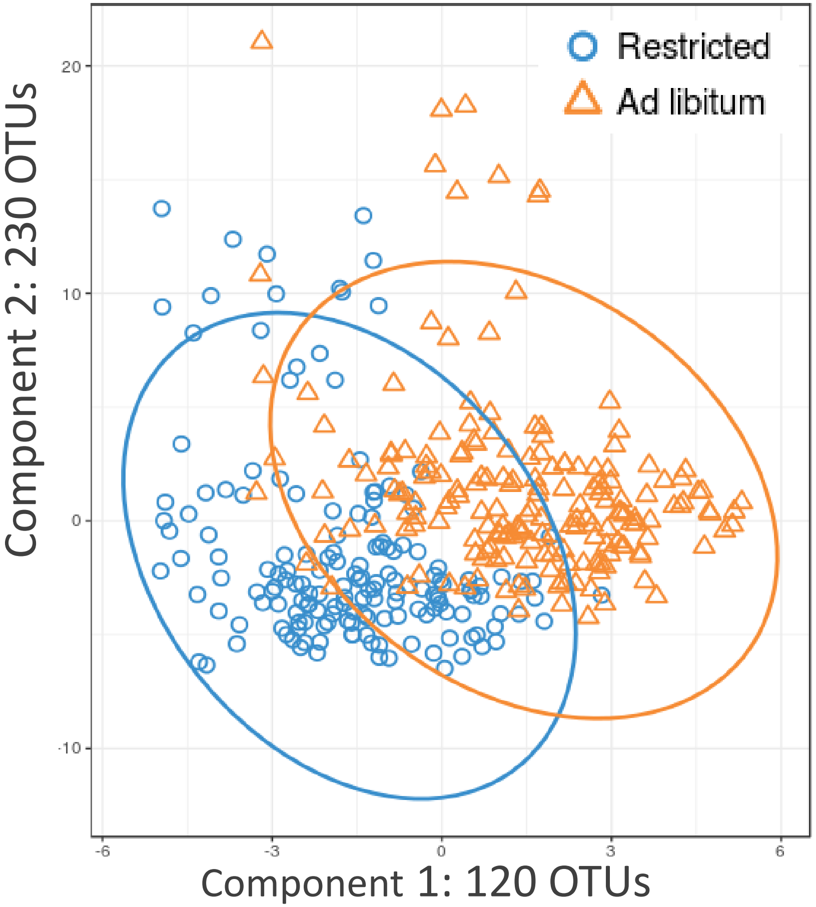
→ **Contrasted feed compositions highly affect fecal microbiota**

Verschuren et al, JAS, 2018

Feeding level effect

V

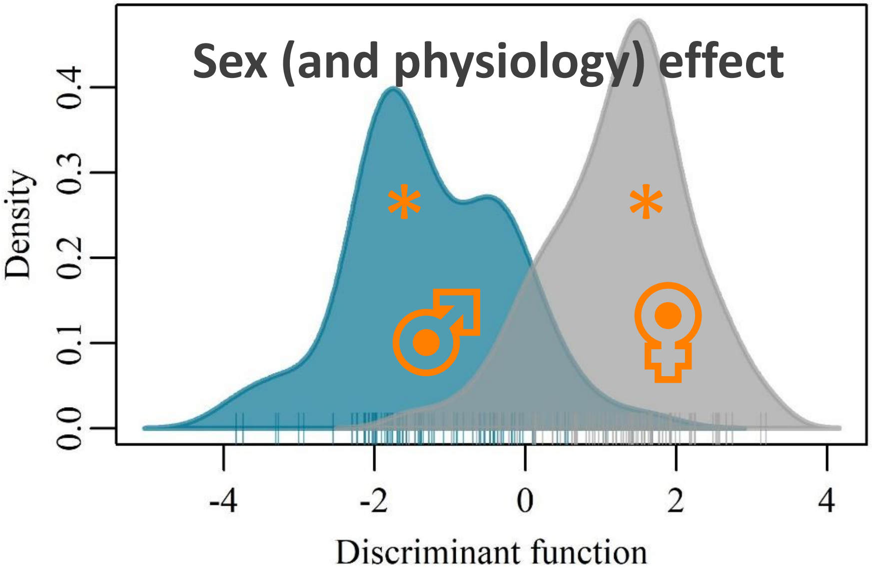
R

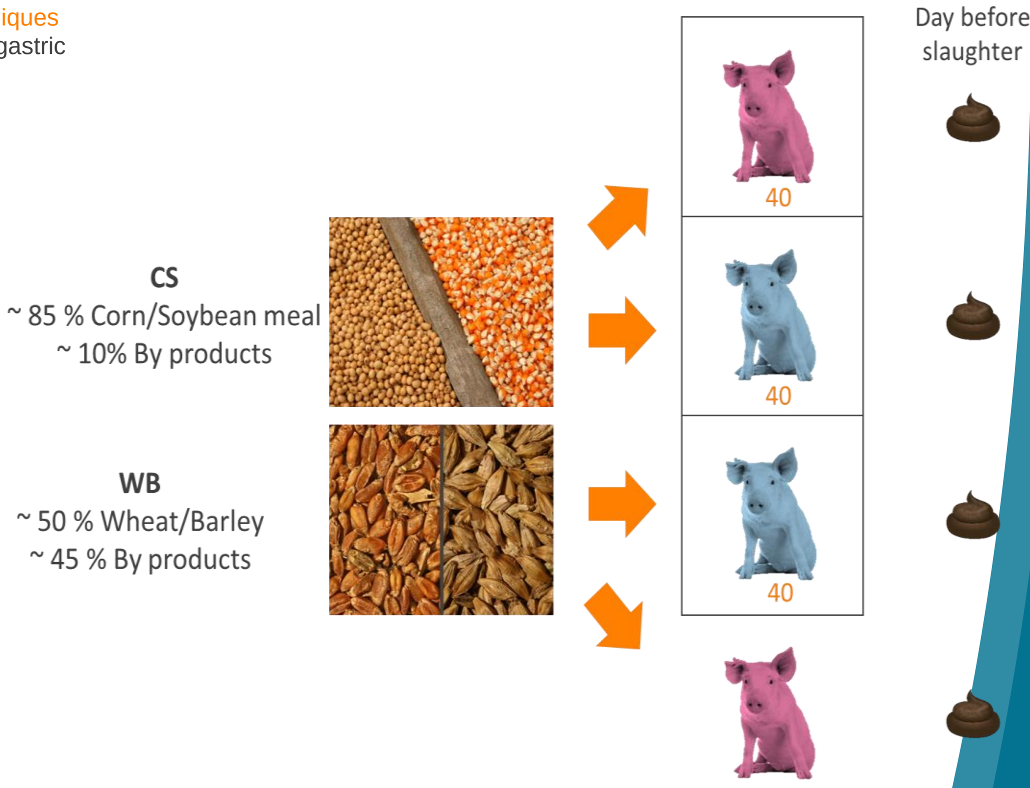


→ **Feeding restricted or ad libitum affect fecal microbiota composition**

Velasco et al., EAAP, 2017

Sex effect





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

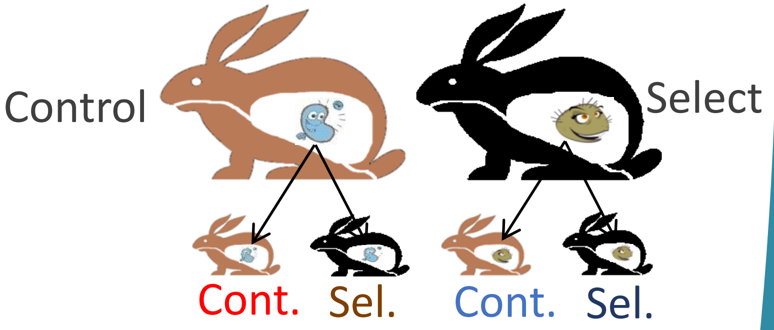
WB
~ 50 % Wheat/Barley
~ 45 % By products

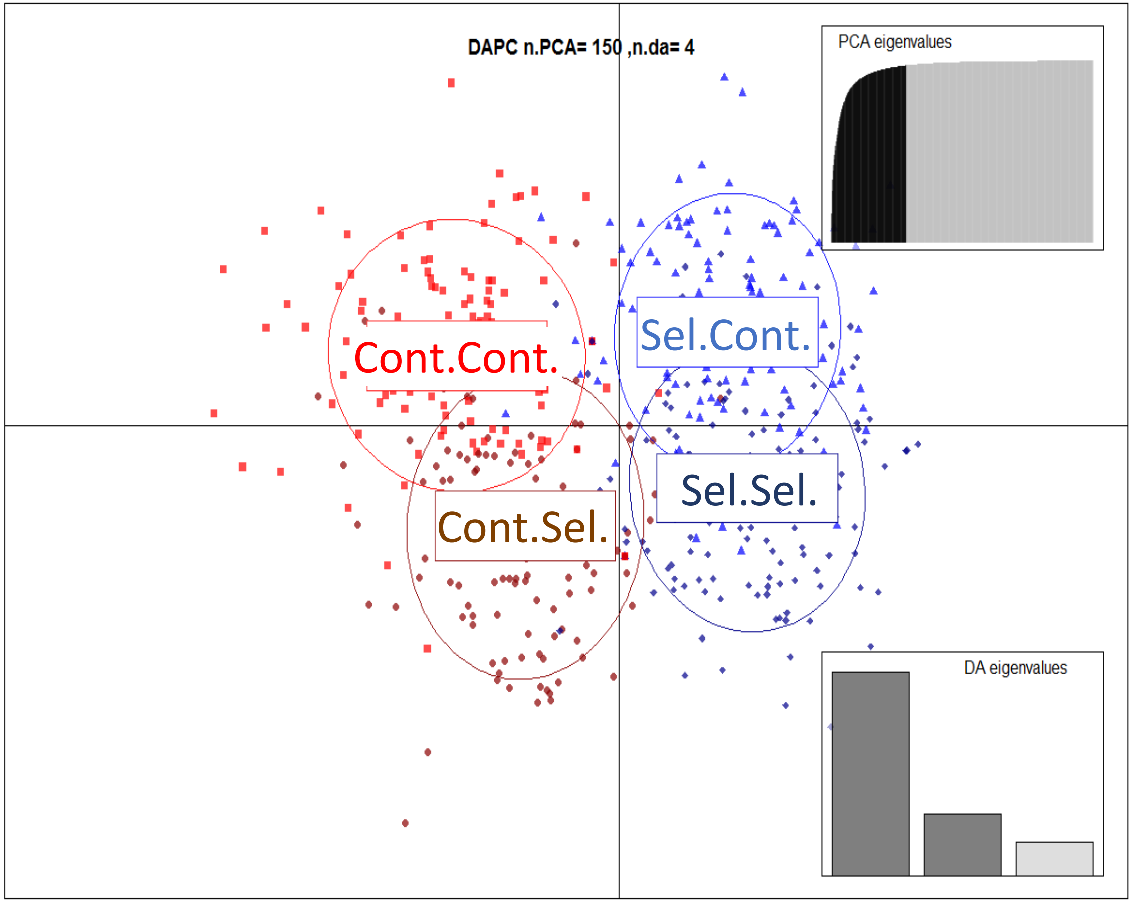
→ **Sex, potentially via sexual maturity, affects gut microbiota composition**

Verschuren et al, JAS, 2018

Maternal transmission

Cross-fostering experiment





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

Zemb et al, in prep

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: $\mathbf{a} \sim \text{NMV}(0, \mathbf{A}\sigma^2_a)$

2. Model accounting for the effect of microbial composition

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

RANDOM EFFECTS

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

B =?

microbiability $\mathbf{b^2} = \sigma^2_B / \sigma^2_P$

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

Model accounting for the effect of microbial composition

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

RANDOM EFFECTS

- Additive direct genetic
- Maternal genetic

$$\begin{matrix}\mathbf{a}\\ \mathbf{m}\end{matrix} \sim N\left(\begin{matrix}0\\0\end{matrix}, \begin{bmatrix}\sigma_a^2 & \sigma_{am}\\ \sigma_{am} & \sigma_m^2\end{bmatrix} \otimes \mathbf{A}\right)$$

- Litter: **c** ~ NMV (0, $\mathbf{I}\sigma^2_c$)
- Pen: **j** ~ NMV (0, $\mathbf{I}\sigma^2_j$)
- Effect of the microbiome: **b** ~ NMV (0, $\mathbf{B}\sigma^2_B$)

a x b ?

Production traits models

V

R

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

$\mathbf{b} \sim \mathrm{NMV}\,(0, \mathbf{B}\sigma^2_B)$

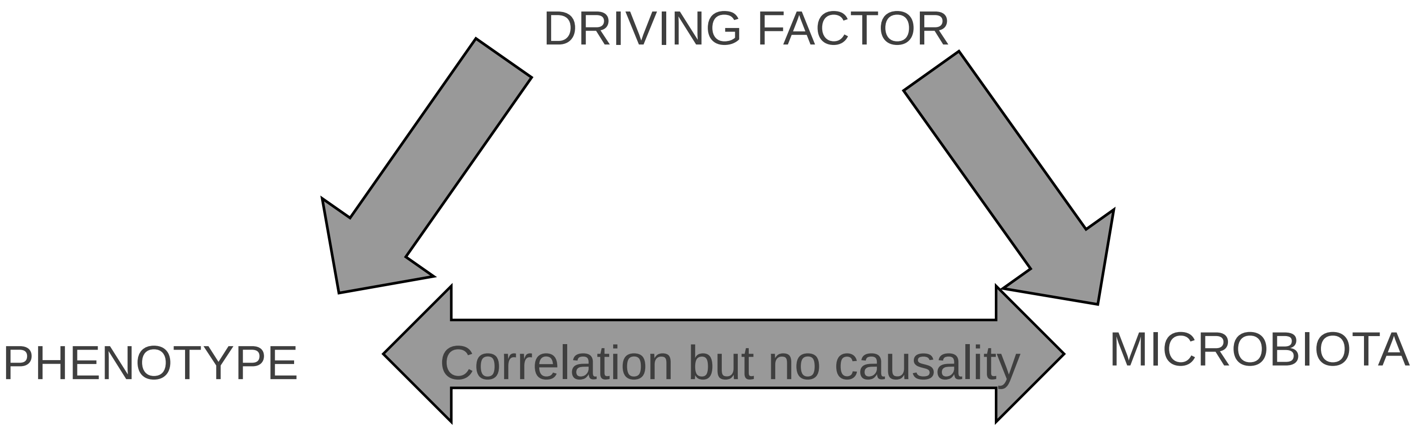
$\mathbf{B} = f(\mathrm{wUnifrac\ dm})$

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

Velasco et al., EAAP, 2017

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?



DRIVING FACTOR

PHENOTYPE

Correlation but no causality

MICROBIOTA

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)
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