Feed-a-Gene

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

Potential role of the fecal microbiome in breeding for feed efficiency

12 December 2019 | Lisanne Verschuren

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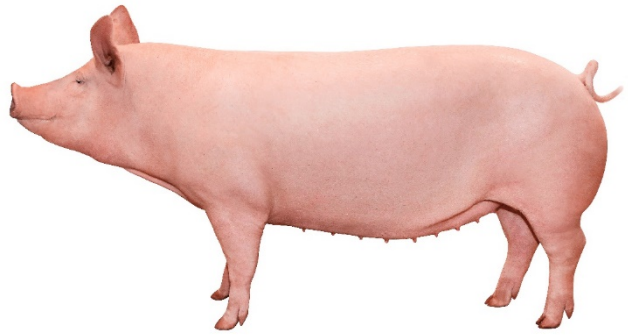

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Microbiota definition

Kerry Evans,. "In a microbial Fog". Labroots. 2015. Image Credit: Cardiff Student Media

"microbiome, to signify the ecological community of commensal, symbiotic, and pathogenic microorganisms that literally share our body space"

Lederberg J, McCray AT. 'Ome Sweet 'Omics—a genealogical treasury of words. The Scientist. 2001;15:8

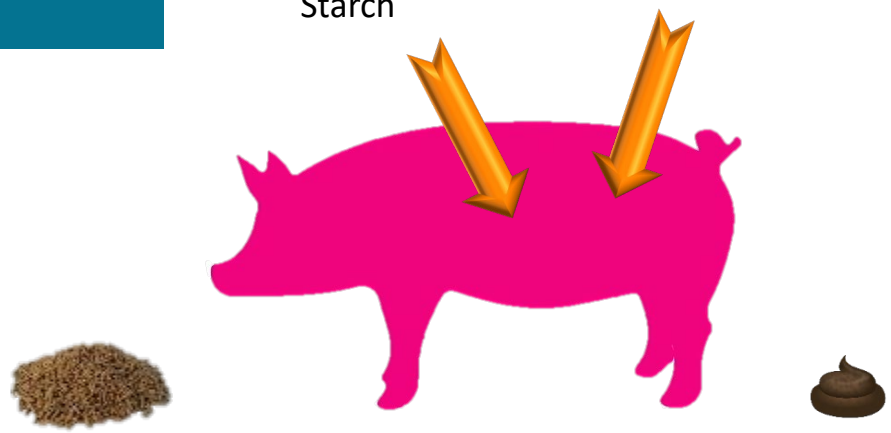
Feed efficiency

Nutrient metabolism

Protein
Fat
Starch

Microbial fermentation

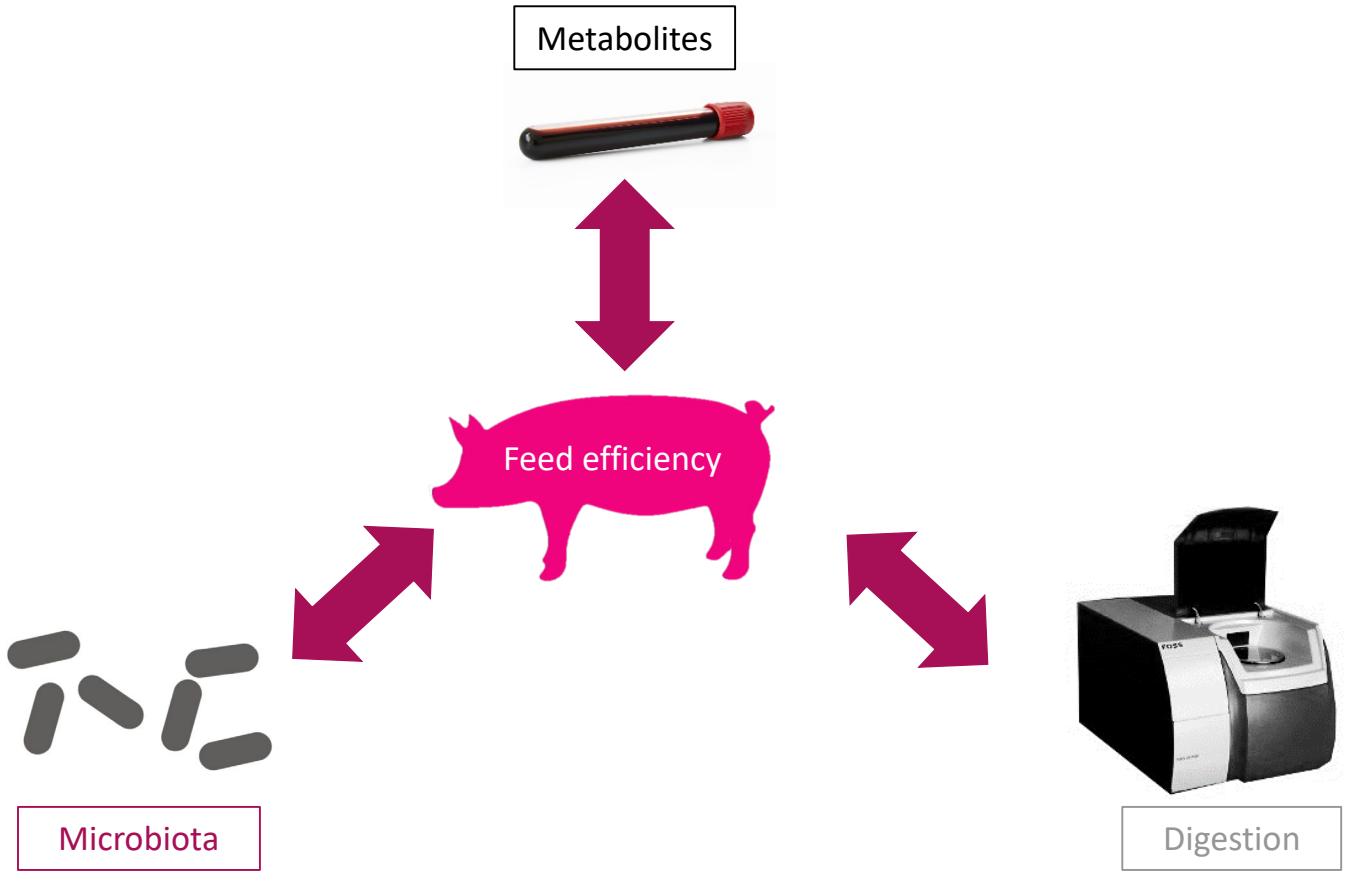
Fiber



Faecal nutrient digestibility
=
% of nutrients disappeared in the GIT

Higher
=
More nutrients for maintenance and growth

All connected



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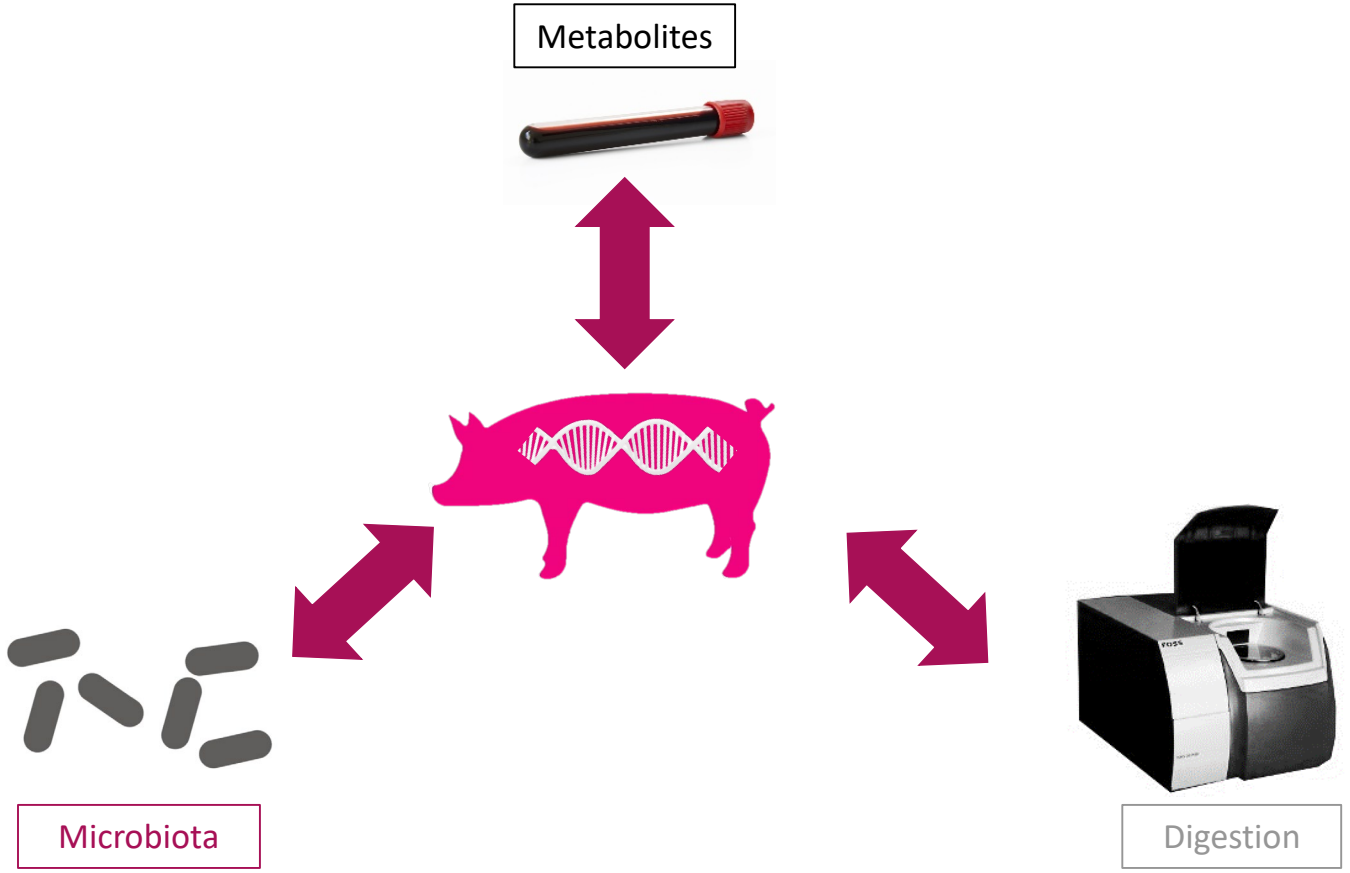

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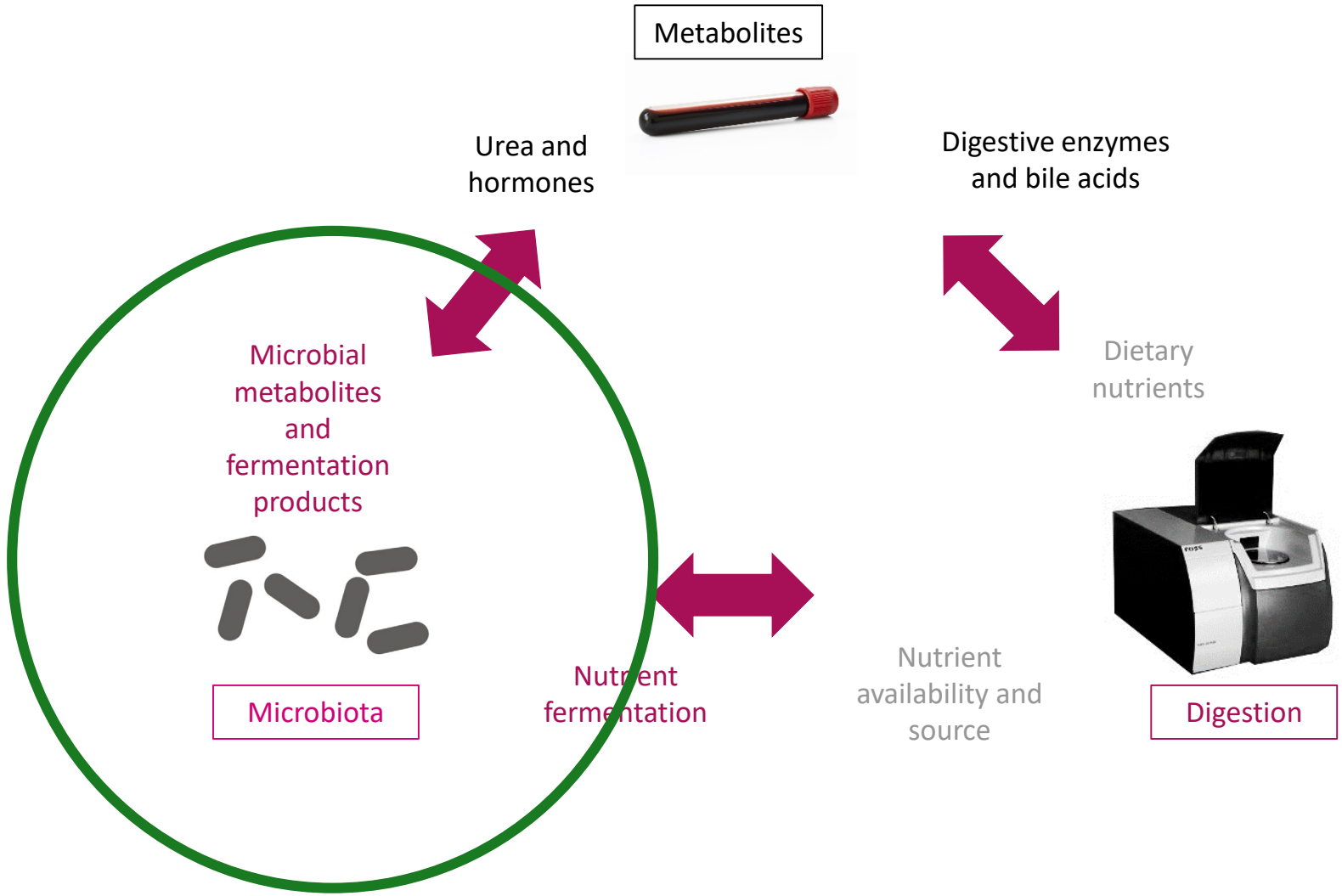

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Results Feed-a-Gene

Topigs Norsvin

Wageningen University & Research

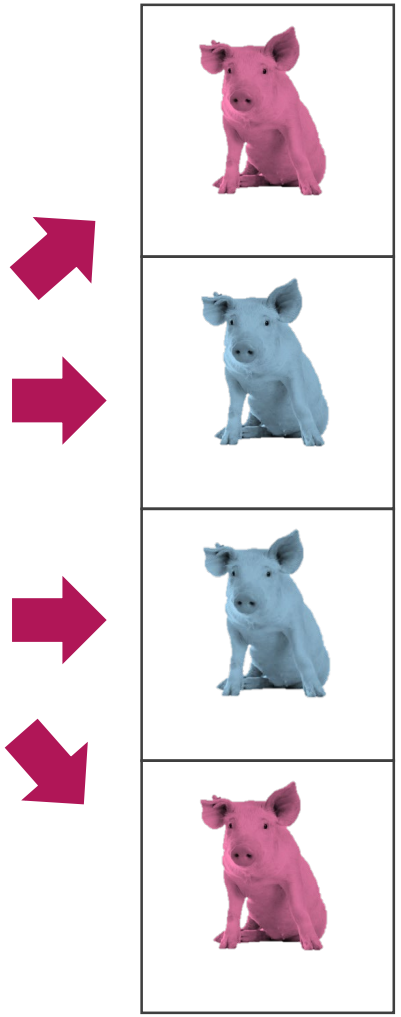
Institute National de la Recherche Agronomique

Experimental design

~160 pigs

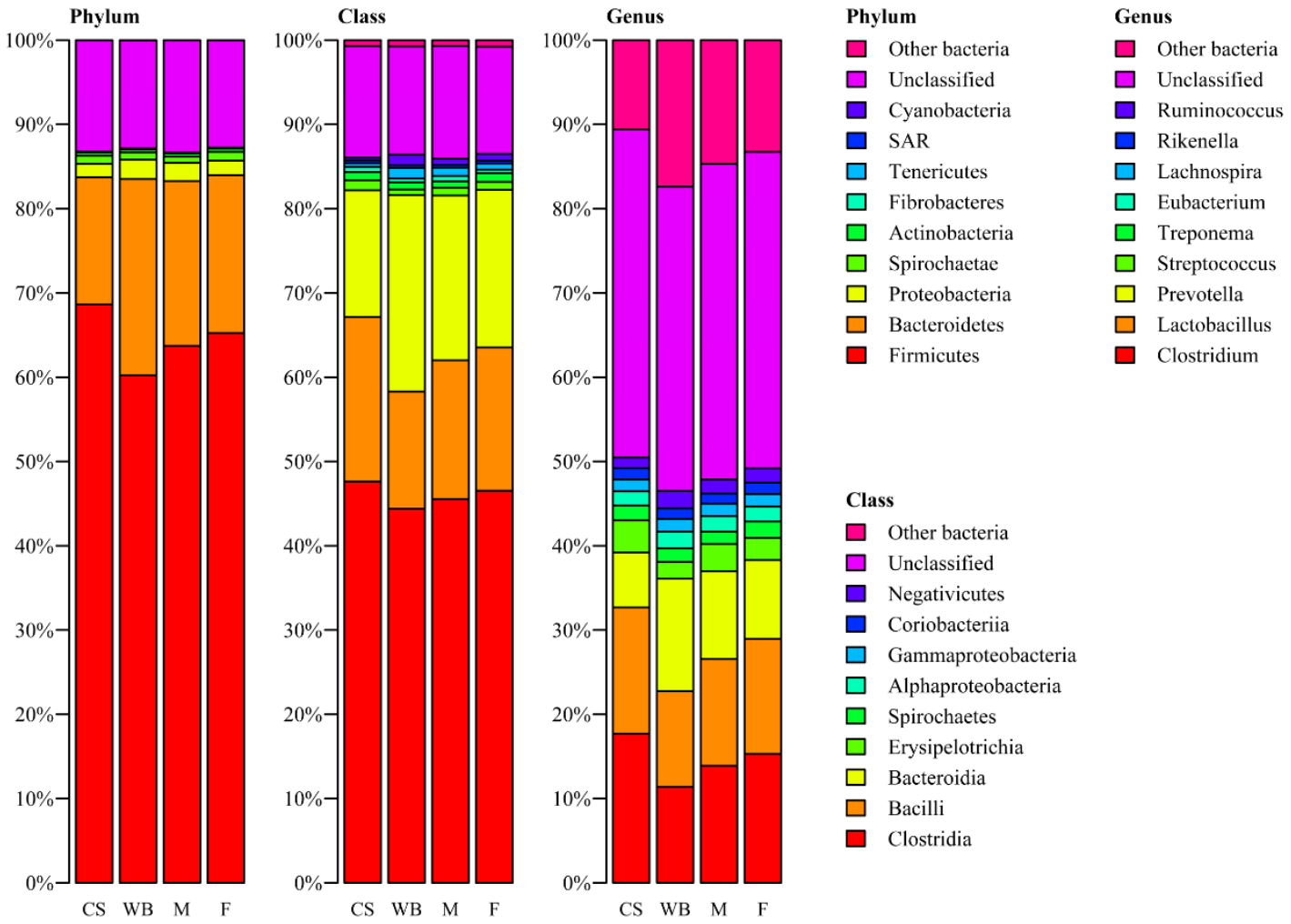
CS
~ 85 % Corn/Soybean meal
~ 10% By products

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



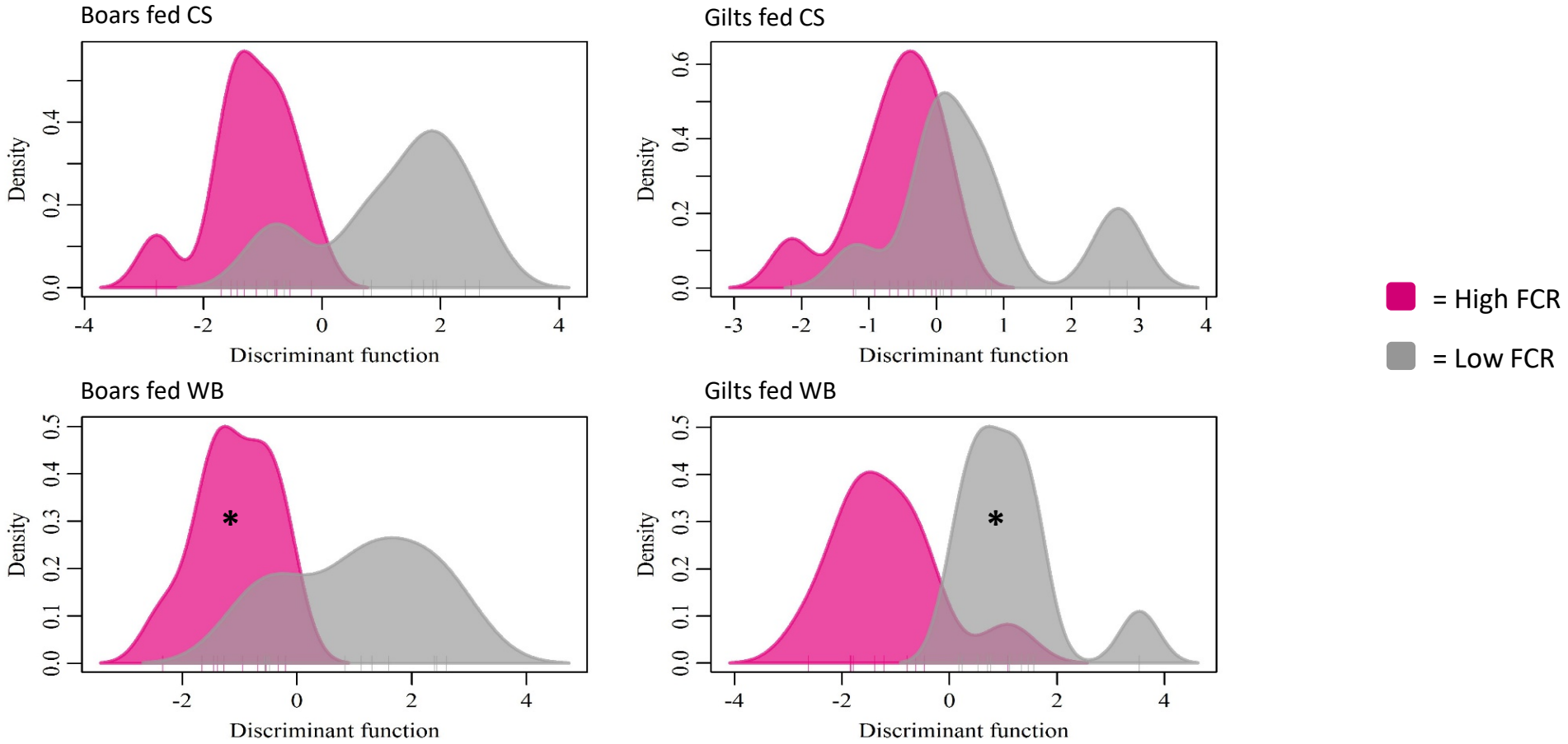
Verschuren et al., 2018

Fecal microbiota composition



Verschuren et al., 2018

Microbiota and feed efficiency extremes



Microbiability

The fraction of the phenotypic variance explained by the microbial variance (Difford et al., 2016).

In formula:

$$m^2 = \sigma^2_m / (\sigma^2_m + \sigma^2_e)$$

Compare to heritability:

$$h^2 = \sigma^2_g / (\sigma^2_g + \sigma^2_e)$$

Microbiability of feed efficiency

Microbiability for traits (corrected for sex, diet and pen):

ADG	m^2 = **0.46** (0.24)	
ADFI	m^2 = **0.42** (0.24)	
FCR	$\mathbf{m^2 = 0.81\ (0.21)}$	

When including common litter effect:

ADG	m^2 = **0.30** (0.22)	c^2 = **0.22** (0.10)
ADFI	m^2 = **0.20** (0.18)	c^2 = **0.39** (0.11)
FCR	$\mathbf{m^2 = 0.64\ (0.21)}$	c^2 = **0.17** (0.09)

Verschuren et al., 2019

Microbiability of nutrient digestibility

	m2 + c2			
Nutrient	m2	SE	c2	SE
Dry Matter	58.8	19.1	0.0	0.0
Organic Matter	58.1	18.9	0.0	0.0
Crude Protein	93.2	10.3	0.0	0.0
Crude Fat	37.4	23.7	12.3	11.6
Crude Fibre	65.3	19.1	0.0	0.0
NSP	66.4	19.8	0.0	0.0
Ash	1.3	10.0	2.2	9.0

Color coding:
Evidence for an association with microbiota profile
No evidence for an association with microbiota profile

Results Feed-a-Gene

Institute National de la Recherche Agronomique

Le Sciellour et al., 2018

Experimental design

- 60 pigs
- 3 breeds: Piétrain, Duroc, Large-White (from 3 different locations)
- 2 diets: low-fiber (LF) and high-fiber (HF)
  - In high-fiber: high diversity of fibers (soluble/insoluble)

		LF	HF
Ingredients (%)	**Corn**	34.58	17.77
	Barley	17.77	17.77
	Wheat	17.77	17.77
	Soybean meal	15.74	9.18
	Rapeseed meal	-	1.97
	Wheat bran	2.50	15.00
	Soybean hulls	-	10.00
	Sugar beet pulp	-	5.00
Chemical composition (%)	**Nitrogen**	2.3	2.3
	Crude fiber	2.8	7.7
	Neutral detergent fiber	10.0	20.0
	Acid detergent fiber	3.4	9.5
	Acid detergent lignin	0.7	1.4
	Gross energy (MJ/kg)	16	16
	Digestible Lysine / Net energy	0.86	0.86

Le Sciellour et al., 2018

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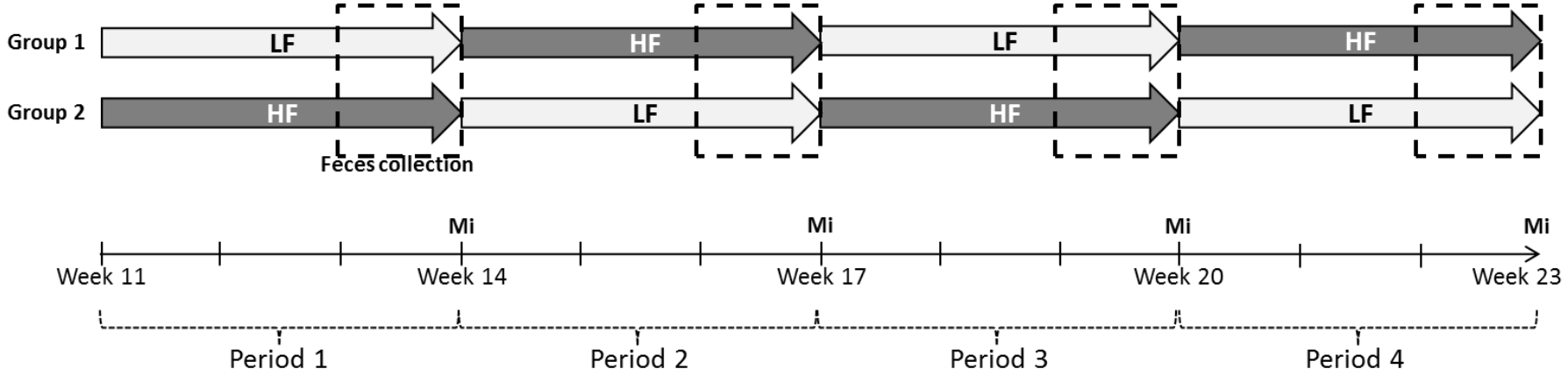
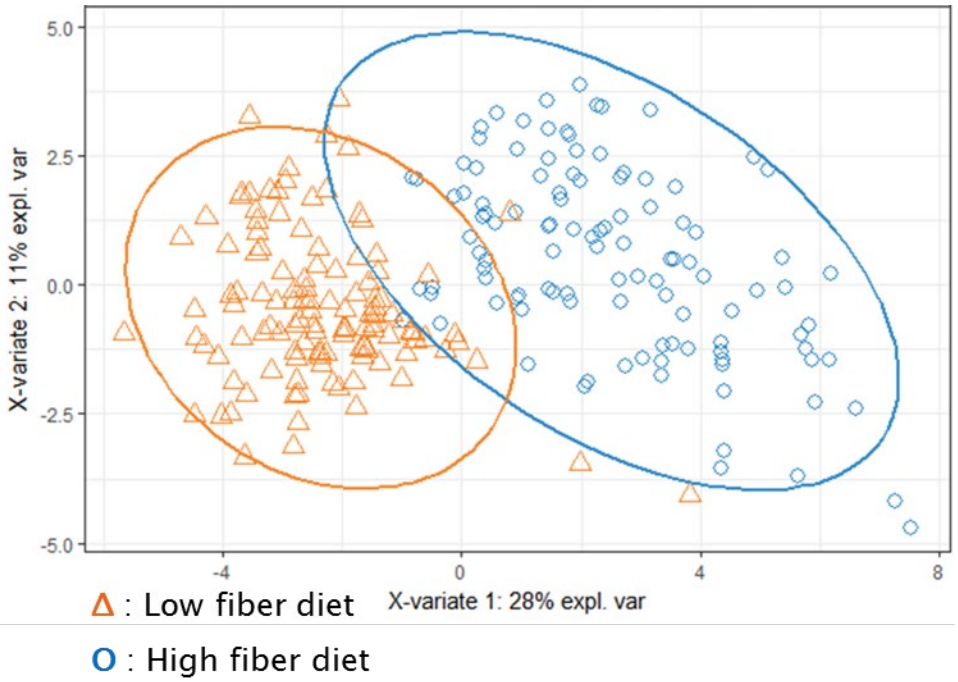


- Final data base:
  - Digestibility data: n = 240
  - Fecal samples for microbiota analyses: n = 229

Le Sciellour et al., 2018

Results

Diet discrimination



3,9% mean classification error-rate

31 OTUs in 90% of the cross-validation tests
→ « predictors »

More than half of the OTUs are differentially abundant between LF and HF

Diet discrimination

- **Whatever the period**
- **Whatever the previous diet**

Diet effect on microbiota
(Durmic et al., 1998; Heinritz et al., 2016)

Le Sciellour et al., 2018

Results

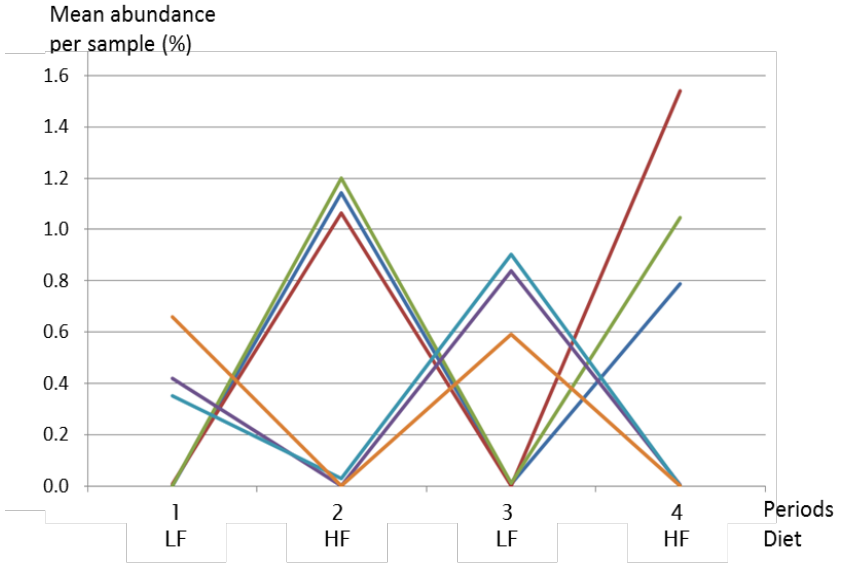
Diet discrimination

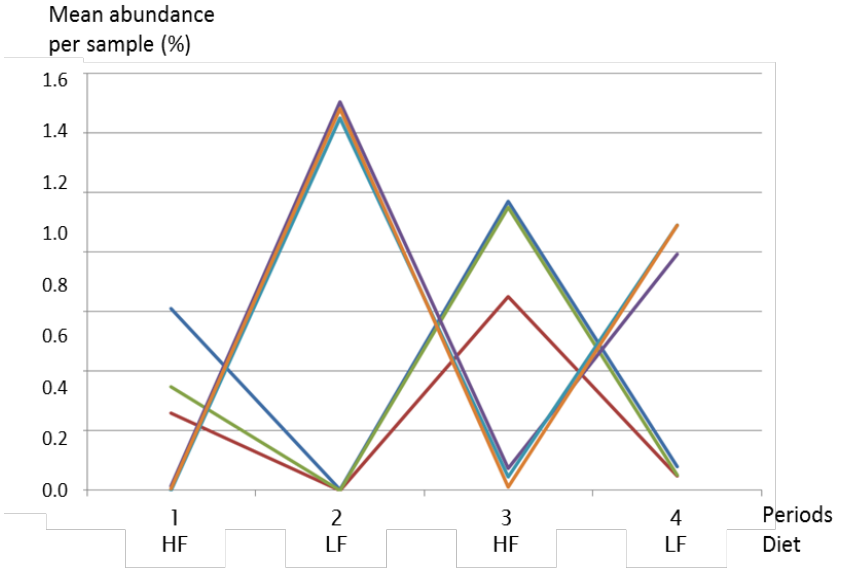
Appearance/disappearance

In 3 weeks, the predictors completely adapted to the new diet

→ resilience

3 weeks required to adapt to a new diet
(Tilocca et al., 2017)





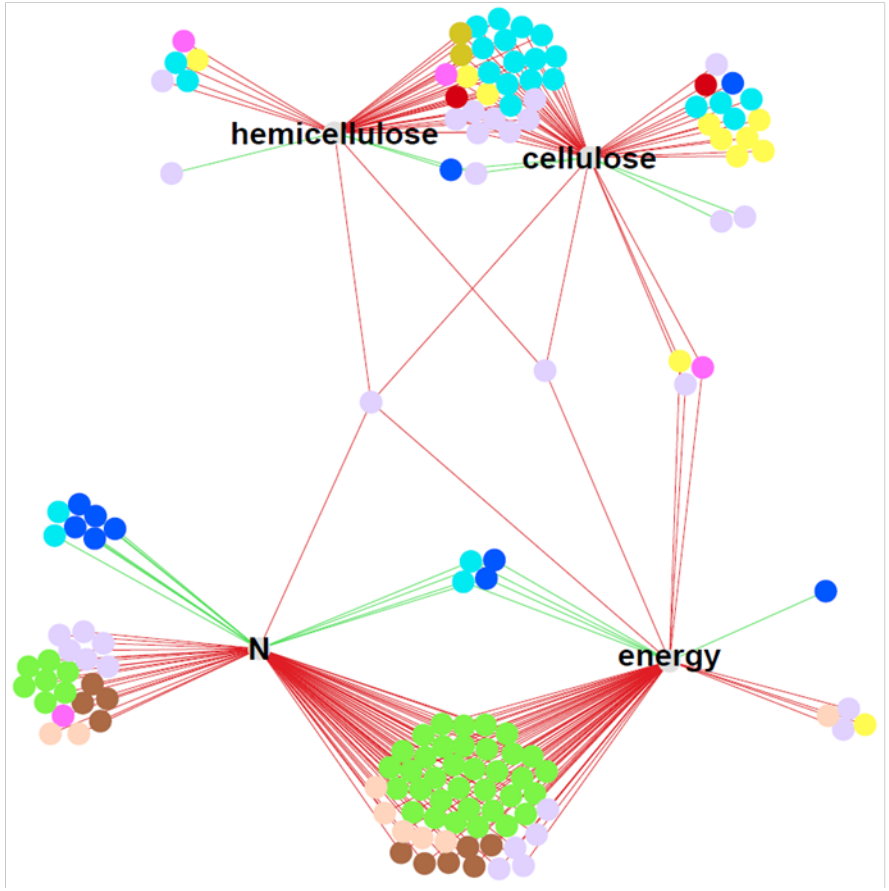
Le Sciellour et al., 2018

Results

Correlations microbiota – digestibility coefficients

Pearson correlations
p-value < 0,05

Positive correlation
Négative correlation



LF diet

- Unclassified
- Clostridiaceae 1
- Clostridiales Incertae Sedis XIII
- Erysipelotrichaceae
- Lachnospiraceae
- Lactobacillaceae
- Peptostreptococcaceae
- Prevotellaceae
- Ruminococcaceae
- Streptococcaceae

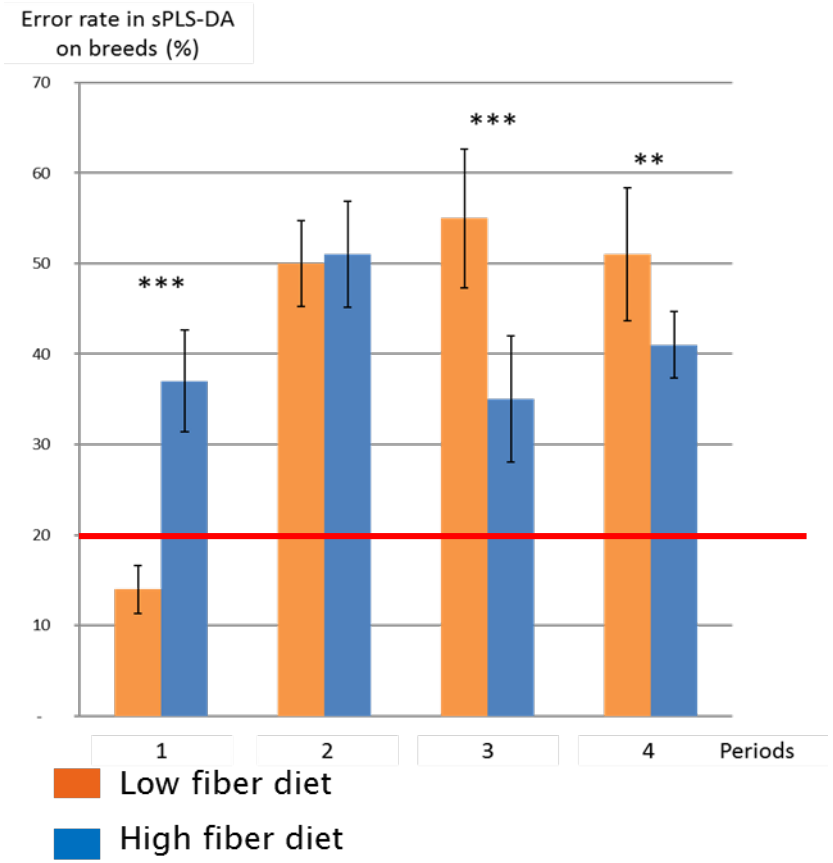
Favorable to a good digestibility
(Niu et al., 2015, Vigors et al., 2016)

- **No significant correlation in HF diet**
- **Difficulties in relating bacterial families to biological functions.**
  - **Contradictions in the literature.**
  - **Ex: Prevotella**

Le Sciellour et al., 2018

Results

Breed discrimination



- **Breed discrimination in LF, period 1**
- **Once the pigs fed a HF diet, the breeds cannot be discriminate**

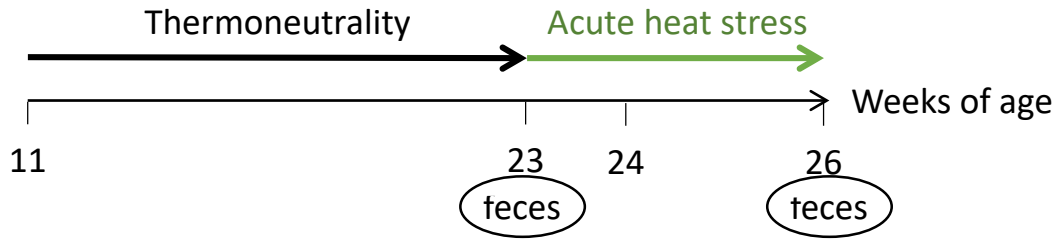
In mice:
diet effect > genotype
(Carmody et al., 2015)

Le Sciellour et al., 2019

Experimental design

Protocol

N = 558



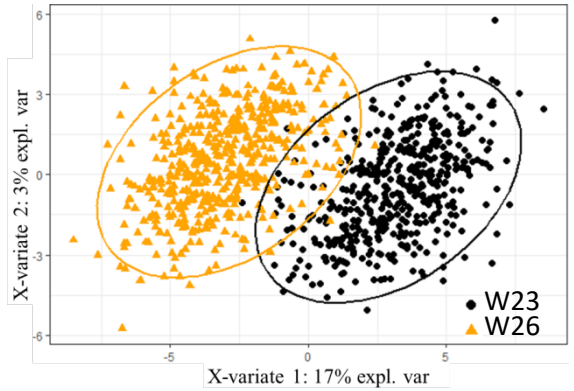
Objectives

- Microbiota composition differs before and after HS?
- Predict performances from microbiota before HS?

Le Sciellour et al., 2019

Results

Results



Great discrimination before and after HS using microbiota information (7% error-rate)

At W23 : each sample classified into an enterotype based on microbiota composition

Enterotype 1 vs 2:
↘*Lactobacillus*
↗*Turicibacter*, *Sarcina*, *Clostridium*

	E 1	E 2	RSD[2]
Short-term response (from 23 to 24 wk)			
ADG, g/d	590	600	390
Change in Skin Temperature, °C	2.20	2.11	0.98
Change in Rectal Temperature, °C	0.25[a]	0.34[b]	0.45
Long-term response (from 23 to 26 wk)			
ADG, g/d	579	589	157
Change in ST, °C	1.86	1.87	0.87
Change in RT, °C	0.09[a]	0.14[b]	0.43

Pigs in enterotype 1 → more robust to HS

Conclusions

Microbiota in pigs is related to

- Diet fed
- Feed efficiency
- Nutrient digestibility
- Breed
- Heat stress

→ Microbiota = indicator of environment

Added value of measuring microbiota?

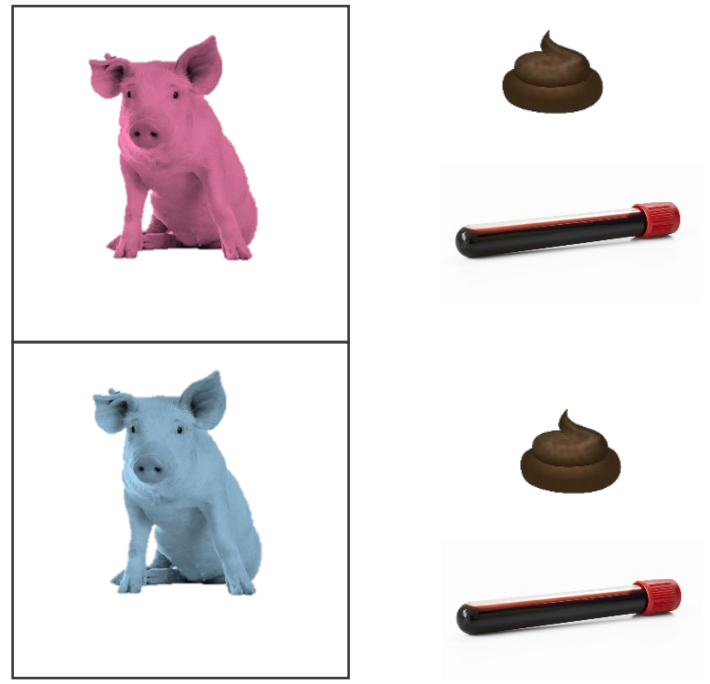
Currently under investigation

WB

~ 50 % Wheat/Barley

~ 45 % By products

Day before slaughter



→ Currently ~750 pigs under analysis for microbiota, digestibility and metabolites

→ Still collecting samples to get a total of ~3000 pigs

Publications

- Verschuren, L. M., Calus, M. P., Jansman, A. J., Bergsma, R., Knol, E. F., Gilbert, H., & Zemb, O. (2018). Fecal microbial composition associated with variation in feed efficiency in pigs depends on diet and sex. *Journal of Animal Science. 96*(4):1405-1418. doi:10.1093/jas/sky060.

- Le Sciellour, M., E. Labussière, O. Zemb, and D. Renaudeau. (2018). Effect of dietary fiber content on nutrient digestibility and fecal microbiota composition in growing-finishing pigs. *PLoS ONE*. 13:e0206159. doi:10.1371/journal.pone.0206159.

- Verschuren, L. M., Schokker, D., Bergsma, R., Jansman, A. J., Molist, F., & Calus, M. P. (2019). Prediction of nutrient digestibility in grower-finisher pigs based on faecal microbiota composition. *Journal of Animal Breeding and Genetics*. doi:10.1111/jbg.12433

- Le Sciellour, M., O. Zemb, I. Hochu, J. Riquet, H. Gilbert, M. Giorgi, Y. Billon, J.-L. Gourdine, and D. Renaudeau. 2019. Effect of chronic and acute heat challenges on fecal microbiota composition, production, and thermoregulation traits in growing pigs. *Journal of Animal Science*. 97(9):3845-3858. doi:10.1093/jas/skz222.

Thank you for your attention