

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

New animal traits for innovative livestock management strategies

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New traits related to feed efficiency

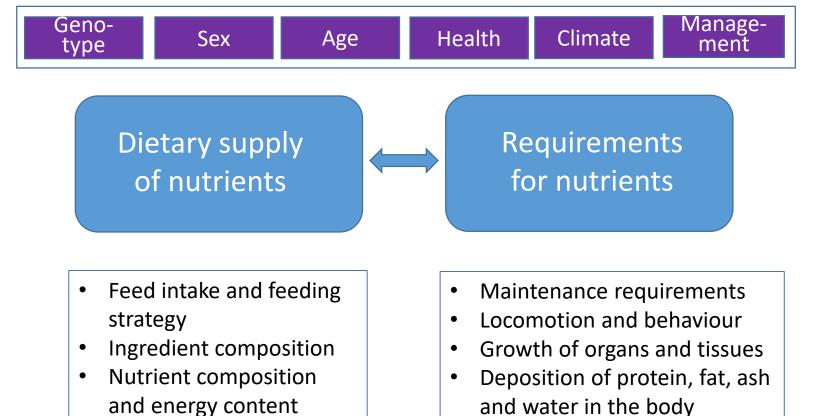
- Feed-a-Gene aimed is to explore and identify new animal traits directly or indirectly related to individual variation in the animal's response to feed and overall feed efficiency under different environmental conditions
- Traits to be used for new breeding and feeding strategies



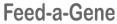
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Nutrient digestibility

Feeding and nutrient efficiency



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New animal traits for innovative feeding and breeding strategies

behaviour and welfare



image analysis serotonin, cortisol

individual feed intake



feed intake patterns feeding behavior

digestive efficiency



digestibility markers gut health microbiota metabolic efficiency



metabolomics



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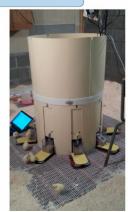
Individual feed intake in broilers and rabbits

Development of feed station

October-November 2016: 1st test of feed station

5 weeks Cobb birds Standard diet (corn+soy)











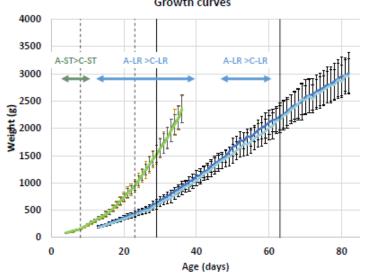
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Individual feed intake in broilers



BERGER Quentin, GUETTIER Elodie, URVOIX Séverine, LE BIHAN-DUVAL Elisabeth, MIGNON-GRASTEAU Sandrine





Berger et al. (2019)

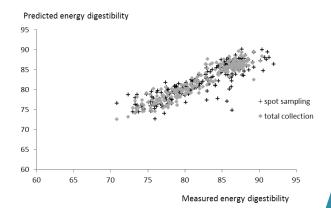
Growth curves



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NIRS determination in faeces for the rapid evaluation of variation in nutrient digestibility between pigs

- Goal: to predict digestibility of nutrients from faecal NIRS
- Calibration of the equations based on 246 faeces samples (FaG) and 500 samples (INRA trials)
 - Equations are good for digestibility of DM, OM, N and energy but poor for digestibility of fibre

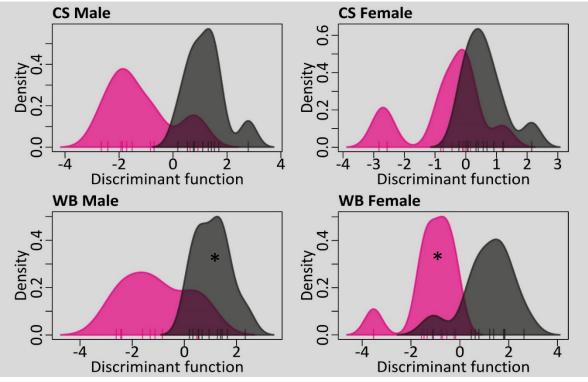


- Ability of the method to rank pigs for their digestive ability
- Heritability of DC of DM 0.4-0.6 and diet dependent



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Faecal microbiota composition as a trait to differentiate low and high FE pigs



Feed efficiency: * = *P* < 0.05

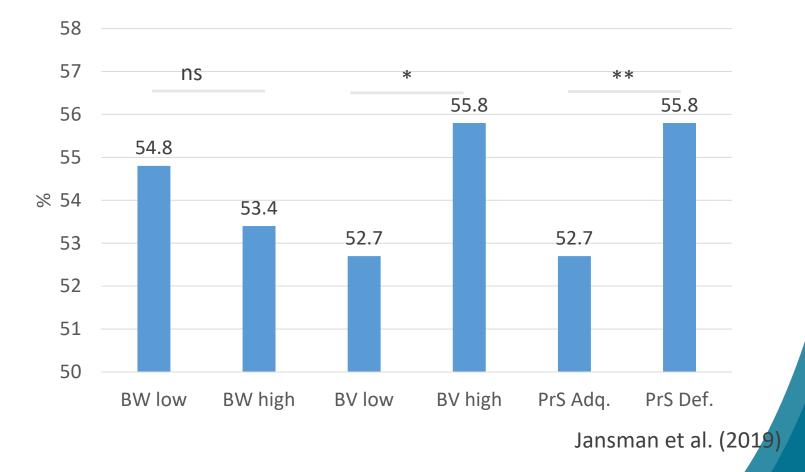
Pink = high feed efficient pigs, Black = low feed efficient pigs

Verschuren et al. (2018)



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Birth weight and breeding value for PD and N-efficiency (% of N-intake) in growing pigs

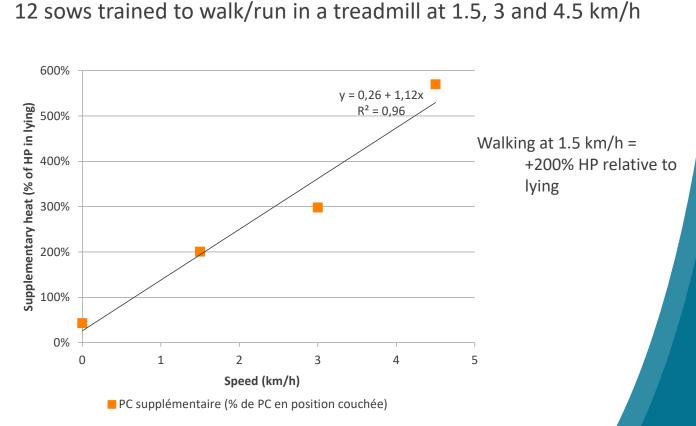




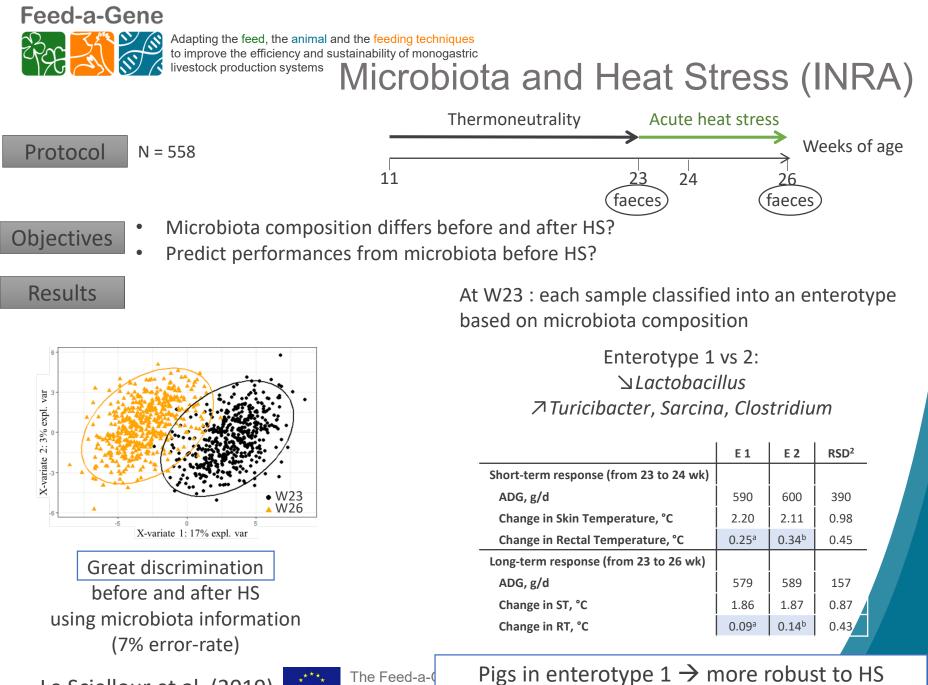
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High Level of Sow Physical Activity on Heat Production





Labussiere et al. (2019)



Le Sciellour et al. (2019)

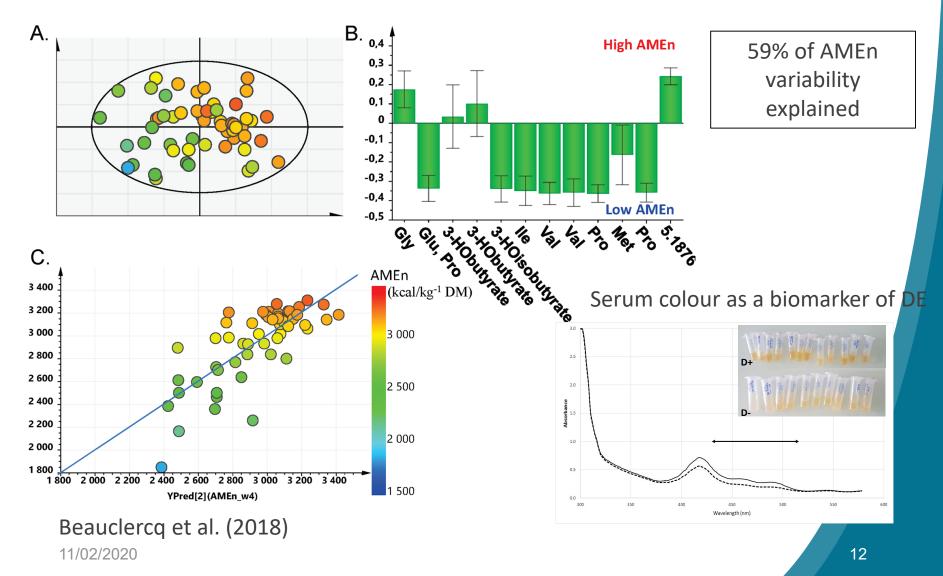


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Finding biomarkers in serum for AMEn in broilers





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Predictive biomarkers in muscle tissue and blood

 Table 2 Number of probes and encoded genes identified as

 VIP for feed efficiency traits

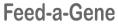
	Nb annotated probes	Nb unique genes	R ²	RMSE
RFI-BV	384	222	0.63	42.9
	280	161	0.64	39.6
	50	27	0.65	39.3
FCR	421	267	0.61	0.23
	88	52	0.70	0.22
	50	33	0.67	0.22
FCRe	318	218	0.49	2.2
	50	29	0.52	2.0
	7	6	0.52	2.0

Molecular indicators of feed efficiency in pigs as proposed by a meta-analysis of transcriptomics data in tissues and fluids

- Microarrays data were obtained from longissimus muscles or blood of two lines divergently selected for residual feed intake (RFI).
- Identification of ~50 biomarkers by feed efficiency traits (RFI, F:G, energy-based F:G) with machine learning methods validation of a subset of them by qPCR on the same (muscle) or other (blood) samples

Conclusion: It was possible to identify few genes expressed in muscle or blood that might be reliable predictors of feed efficiency.

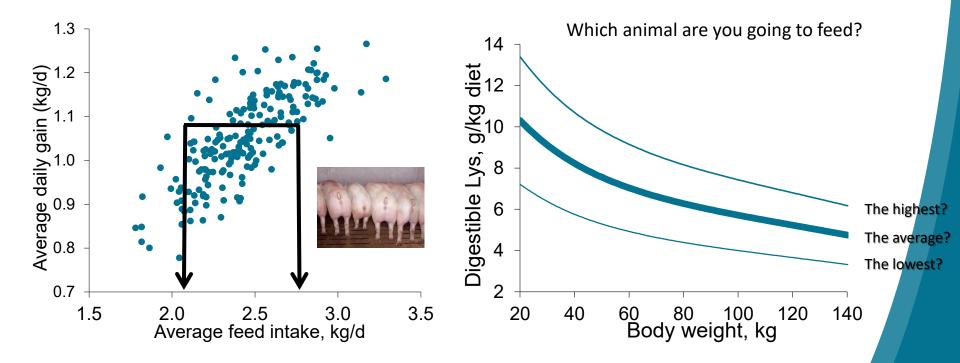
Perspective: The usefulness of genes as biomarkers for feed efficiency for other pig populations will be validated





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Managing variation among individuals through precision livestock feeding





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Conclusions

- Further understanding of responses of animals to feed and nutrient intake requires simultaneous measurement of data and information on the genotype, phenotype and the environment using novel, state of the art tools.
- New traits have been identified related to feed and nutrient efficiency in pigs, poultry and rabbits which can be used in new precision feeding concepts and future breeding programmes.
- Validation of the use of the traits and biomarkers requires further attention.





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Thank you for your attention and to all partners involved in FaG!

