

# Using digestive efficiency to improve feed efficiency in pig breeding schemes

Vanille Déru<sup>1,2</sup>, Marie-José Mercat<sup>3</sup>, David Picard<sup>3</sup>, Bruno Lignesche<sup>4</sup>, Loïc Flatrès-Grall<sup>5</sup>, Florence Ytournel<sup>6</sup>, Florian Herry<sup>6</sup>, Joël Bidanel<sup>3</sup>, Maxime Banville<sup>3</sup>, Hélène Gilbert<sup>2</sup>

[vanille.deru@inrae.fr](mailto:vanille.deru@inrae.fr)

<sup>1</sup> Alliance R&D, 35651 Le Rheu, France

<sup>2</sup> INRAE, 31320 Auzeville-Tolosane, France

<sup>3</sup> IFIP-Institut du Porc, 35651 Le Rheu, France

<sup>4</sup> Nucléus SAS, 35650 Le Rheu, France

<sup>5</sup> Axiom, 37310 Azay-sur-Indre, France

<sup>6</sup> Choice Genetics, 35170 Bruz, France

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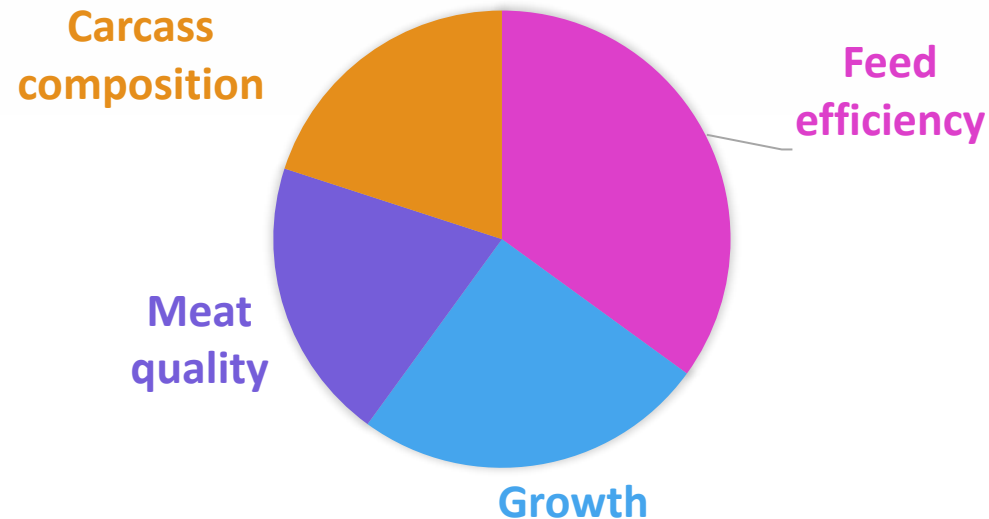


# Context of the study

## Improving **feed efficiency**:

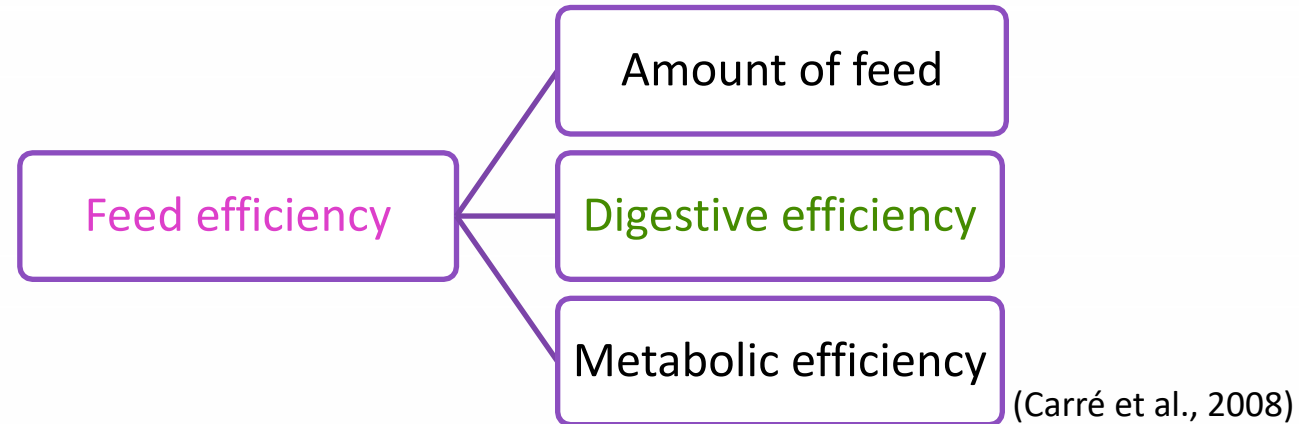
- » A critical topic for the sustainability of pig farms
- » Accounting for 30-50% of the selection objective in pig sire lines
- » Selection criterion is **Feed Conversion Ratio (FCR)**

*Traits weight in sire population objective:*





# Context of the study



**Digestive efficiency**, a trait to improve feed efficiency:

» Genetically correlated favorably with **feed efficiency traits** (Déru et al., 2021)

» Estimated here by **digestibility coefficients (DC)** obtained by near-infrared spectroscopy:

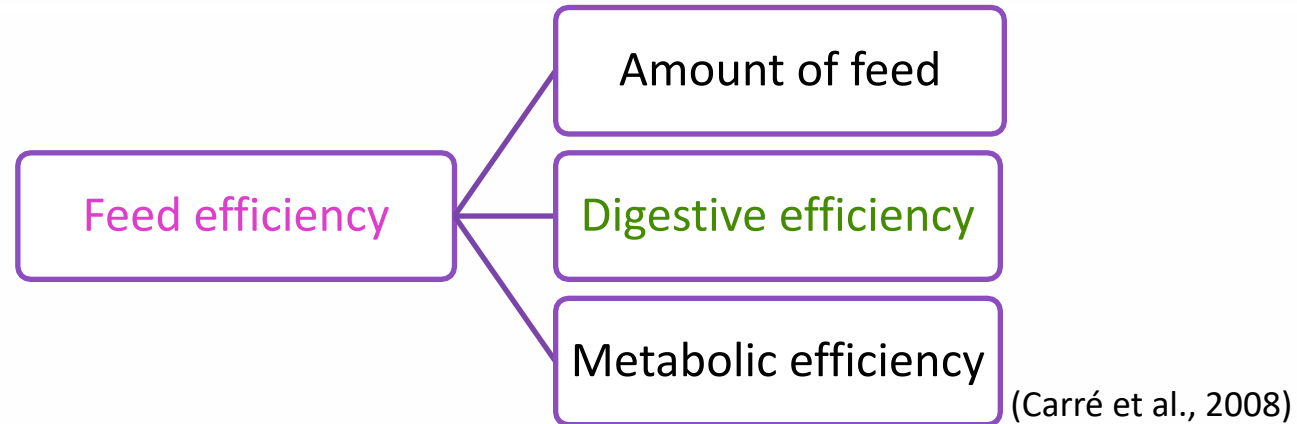
DC of organic matter

DC of energy

DC of nitrogen



# Context of the study



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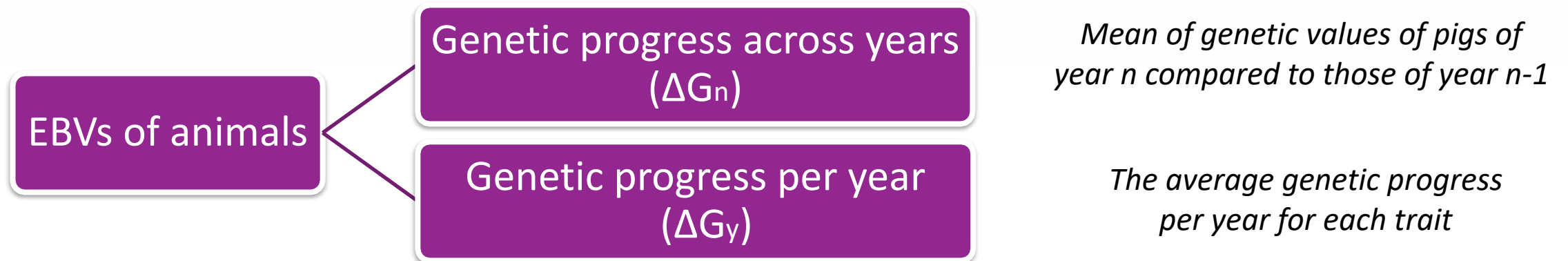
- » Genetically correlated favorably with **feed efficiency traits** (Déru et al., 2021)
- » Estimated here by **digestibility coefficients (DC)** obtained by near-infrared spectroscopy:

What strategy for integrating **DC** into sire population breeding schemes to improve **feed efficiency**?



# Parameters of simulations and indicators

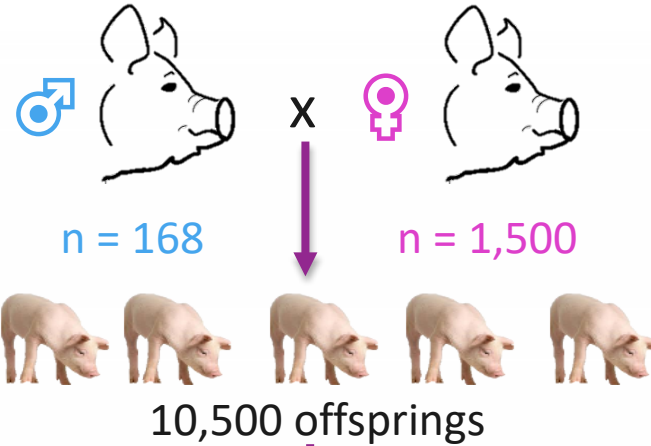
- » Breeding scheme simulated with **AlphaSimR** (Gaynor et al., 2021)
- » Five generations of funders selected on phenotypic traits
- » 8 generations
- » Stochastic simulations: 50 repetitions
- » Genetic and phenotypic parameters from a dataset previously available and literature
- » For each scenario: indicators were estimated:



*Expressed in genetic standard deviation units*



# Reference breeding scheme

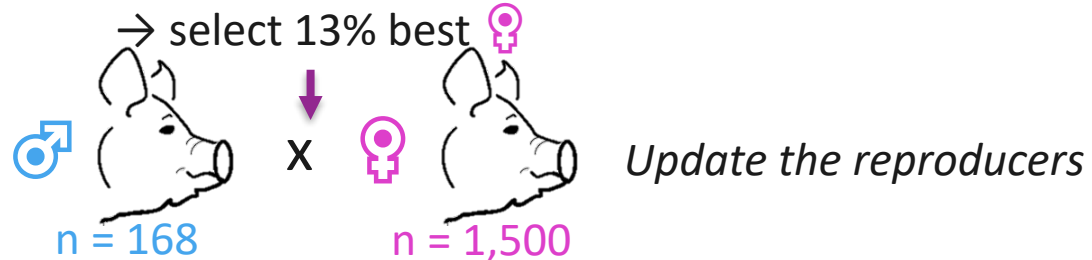


**BLUP genetic evaluation with BLUPF90** (Misztal *et al.*, 2018) **via the blupADC interface** (Mei *et al.*, 2021)

→ select 1% best ♂ without automatic feeders

→ select 2% best ♂ with automatic feeders

→ select 13% best ♀



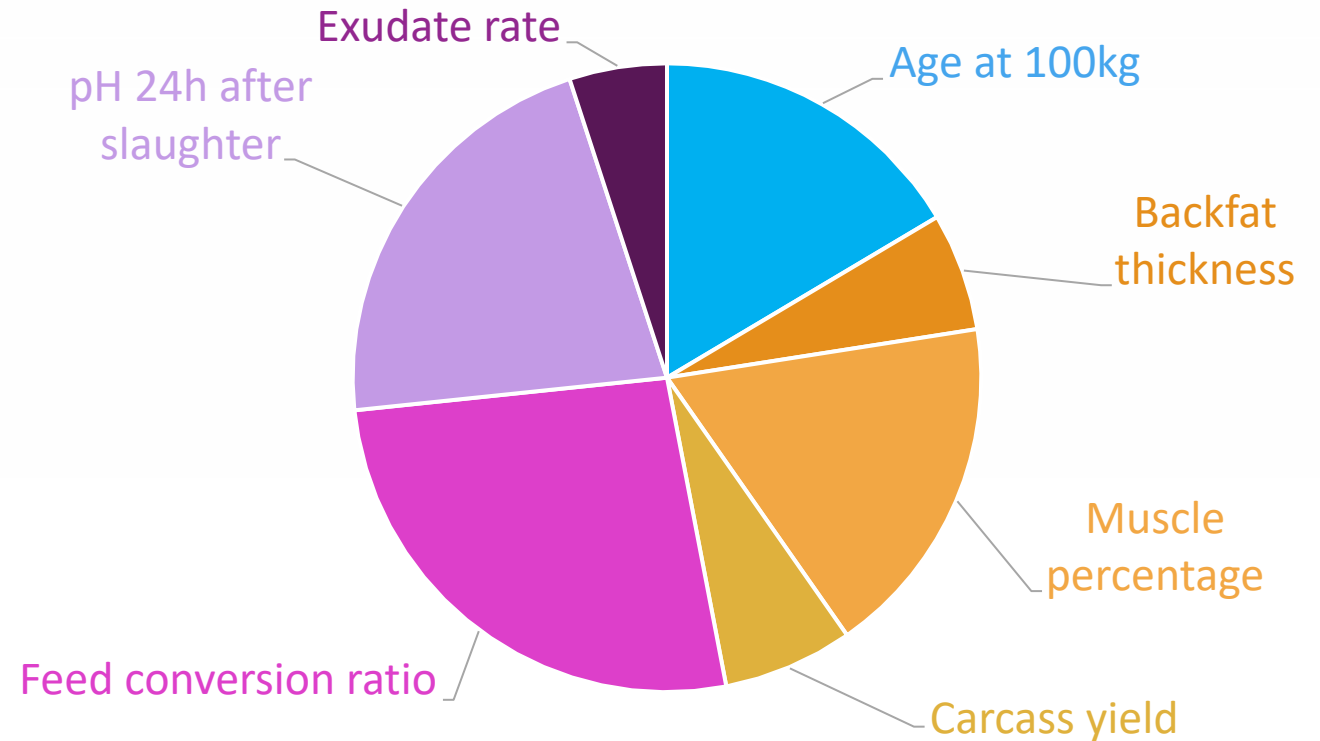


# Selection objective

» Consensus selection objective from the three French pig breeding companies for a pig sire line

» 7 traits included in the selection objective

*Trait weights in the selection objective:*





# Alternative breeding schemes

» Increase the **budget by 30%** compared to the reference breeding scheme



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Additional individuals phenotyped for digestive efficiency:

- » Proxy of feed efficiency ( $\text{cor}_g < -0,23$ )
- » Sample cost : 25 €
- » Using the three DC measures separately or together
- » Different scenarios constructed :

- +30%\_DCE
- +30%\_DCOM
- +30%\_DCN
- +30%\_3DC

25€/sample  
(+1,500 ♂)

15€/sample  
(+2,500 ♂)

- +30%\_DCE
- +30%\_DCOM
- +30%\_DCN
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- +30%\_DCOM
- +30%\_DCN
- +30%\_3DC

12€/sample  
(+2,500 ♂)

Additional individuals phenotyped for feed efficiency:

- » Sample cost : 50 €
- » One scenario constructed :

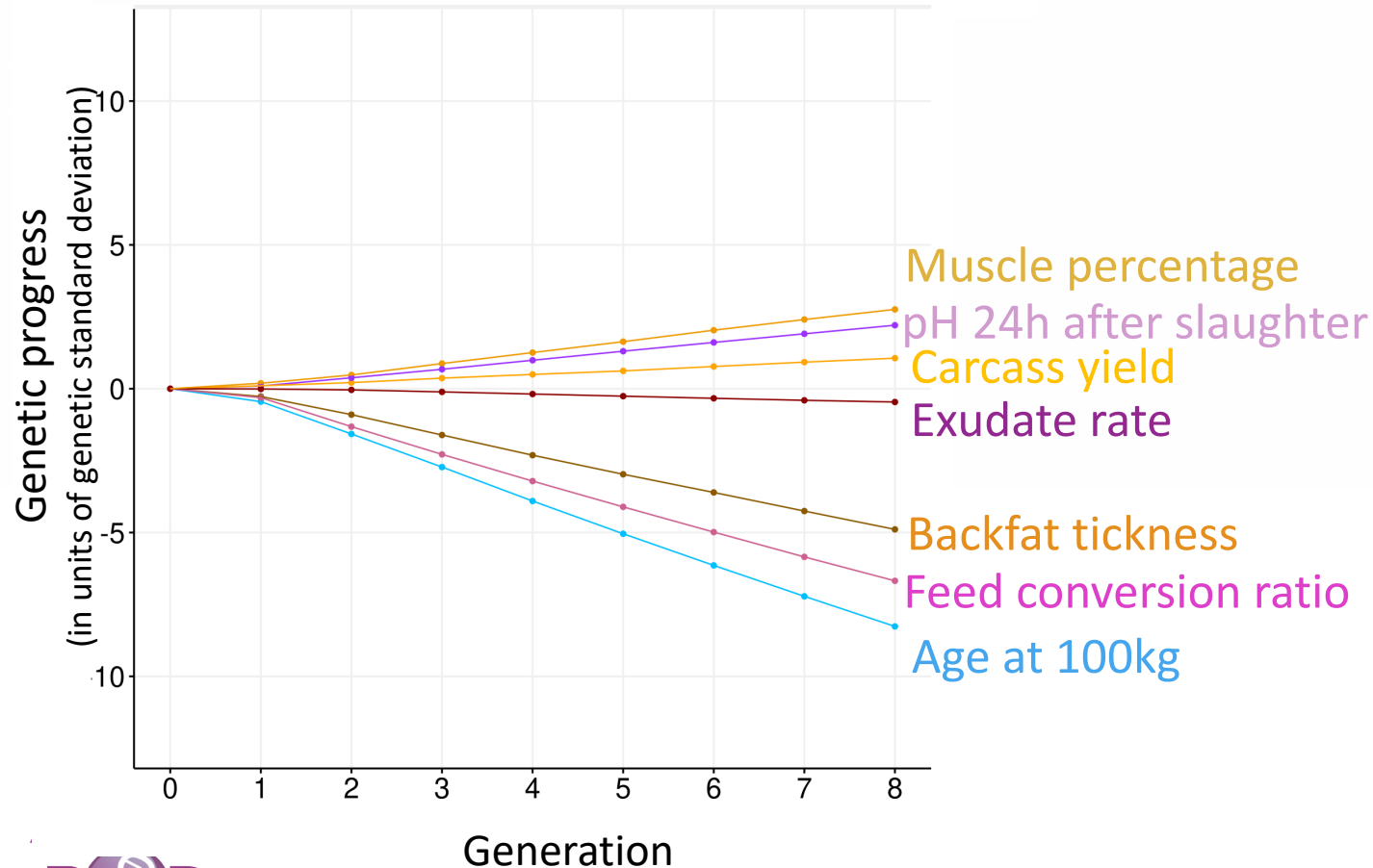
- +30%\_FCR

50€/sample  
(+ 750 ♂)



# Estimated genetic progress for traits in the reference breeding scheme

Evolution of  $\Delta G$  of traits included in the index over 8 generations:



Estimated annual genetic progress for *feed efficiency*:

Trait	$\Delta G_y^*$
Feed conversion ratio	-0.71

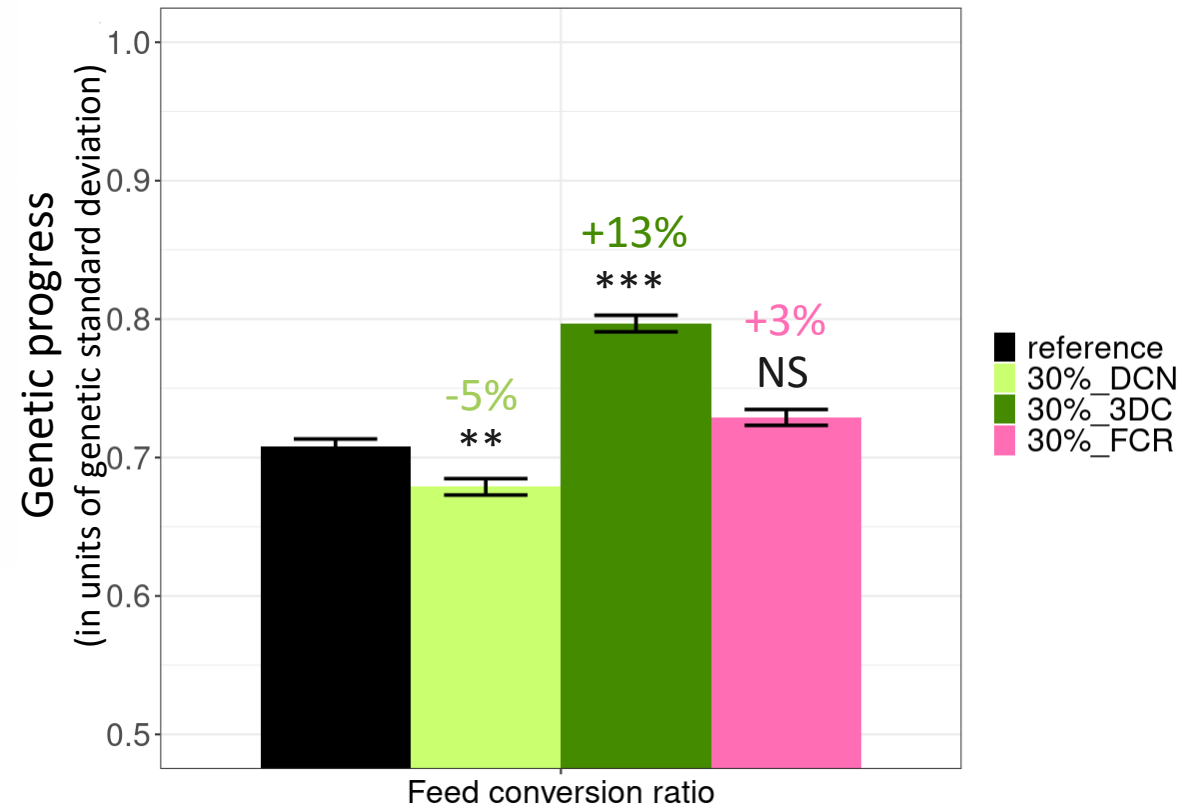
\* in units of genetic standard deviation



# Impact of an additional 30% phenotyping budget on the genetic gain of FCR

- » Price of digestibility sample: 25 €
- » No positive impact with DCN, DCE and DCOM separately
- » A significant positive effect on annual genetic progress of FCR with the three DC considered jointly

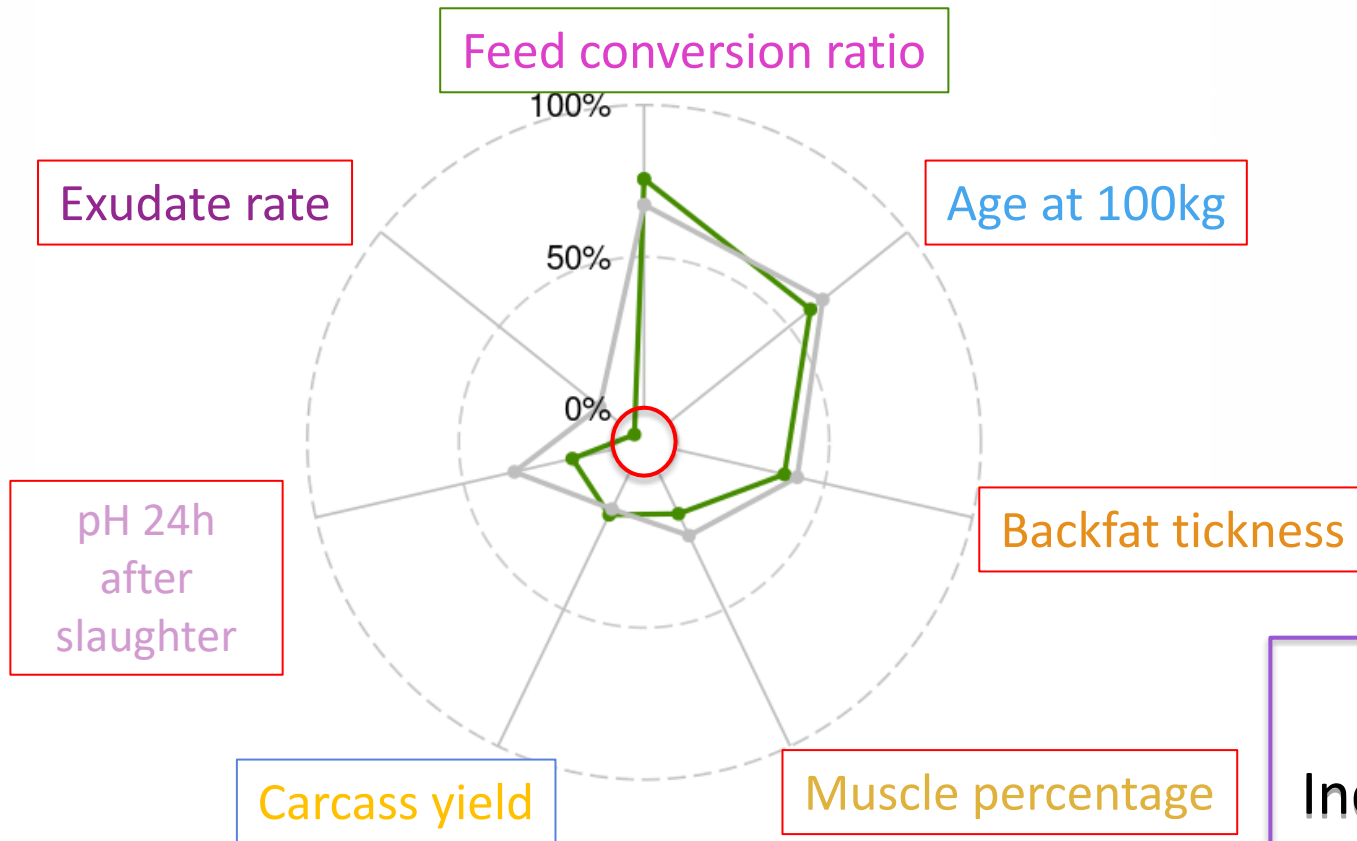
**Best scenario =  
Increase by 13% the genetic gain for FCR**



Mean comparison pairwise t-test between the alternative scenario and the reference scenario: \*\*\*:  $P < 0.001$ ; \*\*:  $P < 0.01$ ; NS: not significant



# Impact of an additional 30% phenotyping budget on the genetic gain of other traits



» Comparison of the reference breeding scheme (in grey) and the scenario +30%\_3DC

» Decrease of genetic gain of all traits, except carcass yield in comparison to the reference scenario

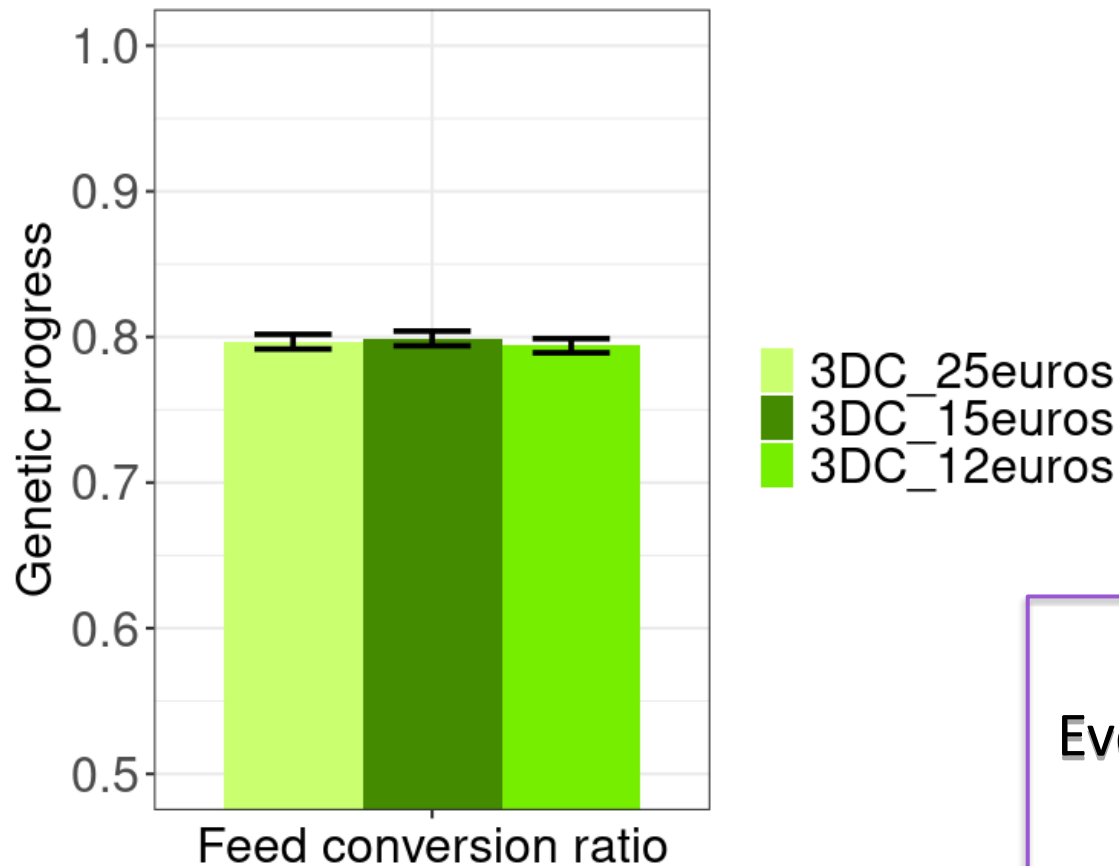
**Best scenario =  
Increase by 13% the genetic gain for FCR,  
but negative impact on the other traits**

*In grey : reference breeding scheme scenario*

*In green : +30%\_3DC scenario*



# Impact of the cost of measuring digestibility on annual genetic progress of FCR



» No significant impact of phenotyping more individuals on the three DC on  $\Delta G_y$  of FCR

» Assumption: Most families are represented and there is no additional interest in phenotyping more individuals.

**Even if the cost of digestibility measures decreases:  
not necessary to phenotype more individuals**



# Conclusion and perspectives

## Summary

- **Phenotyping supplementary individuals for the three DC: improves genetic gain on FCR**
- But negative impact on genetic progress of other traits: growth traits, carcass composition traits (except carcass yield) and meat quality traits
- Not necessary to phenotype more individuals

## What's next?

- **Find the best strategy:**
  - What type of animals to phenotype: females? males? Genetic connection?
  - Can we change the weights of the traits in the index to maintain the genetic progress of the other traits and still increase it on the FCR?



# Thank you for your attention !





# Appendix



## Selection objective

$$H = -1.5 \times \text{Age}_{100\text{kg}} - 4 \times \text{Backfat} + 5 \times \text{Muscle\%} - 225 \times \text{FCR} + 8 \times \text{Carcass}_y - 250 \times \text{pH24} - 4.7 \times \text{Exsudate\_rate}$$



# Annual genetic progress of all traits in all scenarios

Trait	Reference scheme	+30%_DCN	+30%_DCE	+30%_DCOM	+30%_3DC	+30%_FCR
Age 100kg	-0.87 <sup>a</sup>	-0.91 <sup>b</sup>	-0.94 <sup>c</sup>	-0.91 <sup>b</sup>	-0.80 <sup>d</sup>	-0.87 <sup>a</sup>
FCR	-0.71 <sup>a</sup>	-0.67 <sup>b</sup>	-0.57 <sup>c</sup>	-0.68 <sup>b</sup>	-0.80 <sup>d</sup>	-0.73 <sup>a</sup>
Backfat	-0.51 <sup>a</sup>	-0.49 <sup>b</sup>	-0.52 <sup>a</sup>	-0.44 <sup>c</sup>	-0.46 <sup>c</sup>	-0.52 <sup>a</sup>
Carcass yiel	0.11 <sup>a</sup>	0.13 <sup>b</sup>	0.18 <sup>c</sup>	0.17 <sup>c</sup>	0.12 <sup>a,b</sup>	0.12 <sup>a</sup>
Muscle %	0.29 <sup>a</sup>	0.17 <sup>b</sup>	0.22 <sup>c</sup>	0.18 <sup>b</sup>	0.19 <sup>b</sup>	0.18 <sup>b</sup>
pH24	0.23 <sup>a</sup>	0.19 <sup>b</sup>	0.21 <sup>a,b</sup>	0.20 <sup>b</sup>	0.09 <sup>c</sup>	0.15 <sup>d</sup>
Exsudate rate	-0.05 <sup>a</sup>	-0.02 <sup>b</sup>	-0.03 <sup>b</sup>	-0.01 <sup>b</sup>	0.05 <sup>c</sup>	0.02 <sup>d</sup>
DCE	0.30 <sup>a</sup>	0.33 <sup>b</sup>	0.25 <sup>c</sup>	0.23 <sup>c</sup>	0.31 <sup>b</sup>	0.33 <sup>b</sup>
DCN	0.30 <sup>a</sup>	0.32 <sup>b</sup>	0.24 <sup>c</sup>	0.23 <sup>c</sup>	0.32 <sup>b</sup>	0.33 <sup>b</sup>
DCOM	0.35 <sup>a</sup>	0.38 <sup>b</sup>	0.31 <sup>c</sup>	0.29 <sup>c</sup>	0.35 <sup>a</sup>	0.38 <sup>b</sup>



# Impact of an additional 30% phenotyping budget on the annual genetic progress of other traits in comparison to the reference scenario

*Green* = favorable impact on genetic progress  
*Red* = unfavorable impact on genetic progress  
*Blue* = no significant impact on genetic progress

