Feed-a-Gene

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

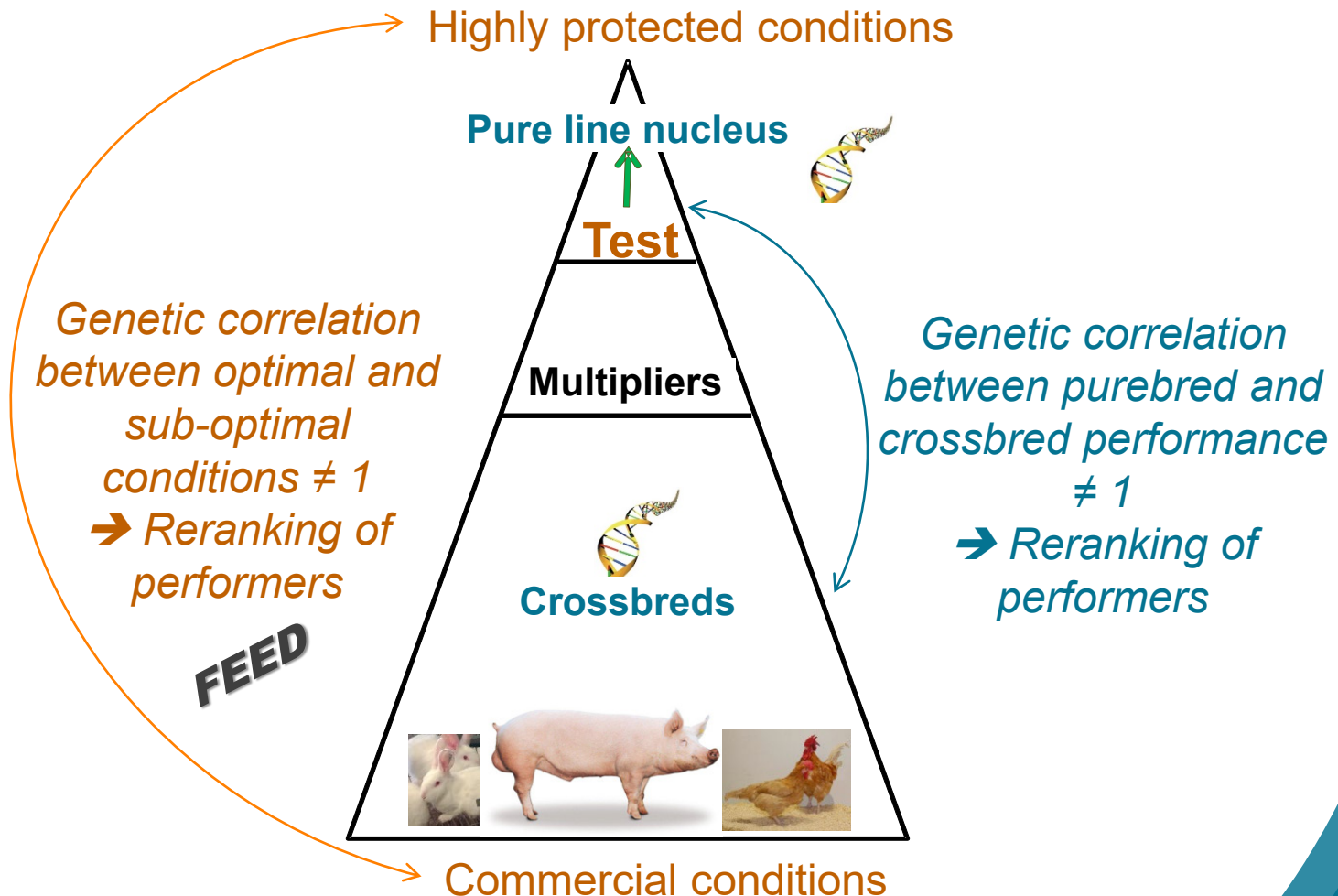# New traits and models for the genetic improvement of feed efficiency

Hélène GILBERT

INRAe

Selection in pigs, poultry and rabbits

Feed-a-Gene

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

Highly protected conditions

Pure line nucleus

Test

Multipliers

Crossbreds

Genetic correlation between optimal and sub-optimal conditions ≠ 1
➔ *Reranking of performers*

FEED

Genetic correlation between purebred and crossbred performance ≠ 1
➔ *Reranking of performers*

Commercial conditions

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

Challenges for Feed-a-Gene

▶ **Get more accurate predictions of crossbred feed efficiency?**

→ Increase breeding value (EBV) accuracies

  ▶ Via cheaper/easier measurements
  ▶ By accounting for crossbred information
  ▶ By including new components in genetic models (penmates influence, dominance, time)

▶ **Make animals more feed efficient when breeding conditions vary** (diets, feeding regimens, environment…)**?**

  ▶ By decomposing feed efficiency
  ▶ By understanding which components play a role in different situations
  ▶ By analysing the variability of the responses depending on the conditions

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Objectives in Feed-a-Gene

▶ Genetic transmission of new feed efficiency traits (previous talk) using classical and new genetic models

  ▶ Considering indicators of robustness, welfare, and product quality

▶ Obtain genomic and physiological indicators of feed efficiency (and its components) using high throughput methodologies

▶ Use new traits and models to propose new breeding strategies

▶ Test some for field validation

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New traits – at the animal level

Direct measures of feed intake

Broiler feed intake

Grasteau et al

Rabbit feed intake

Sanchez et al

Gestation and lactation feed intake

Sanchez et al

▶ Different responses on reproductive sows depending on management
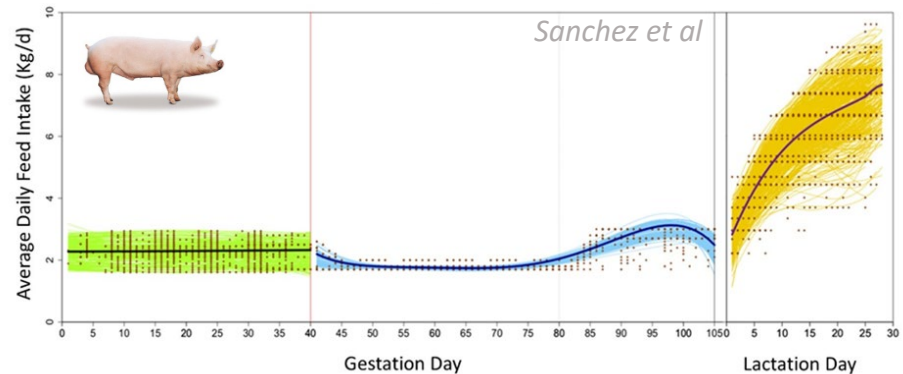
▶ Large gains from individual measures of growing animals

11/02/2020

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Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems
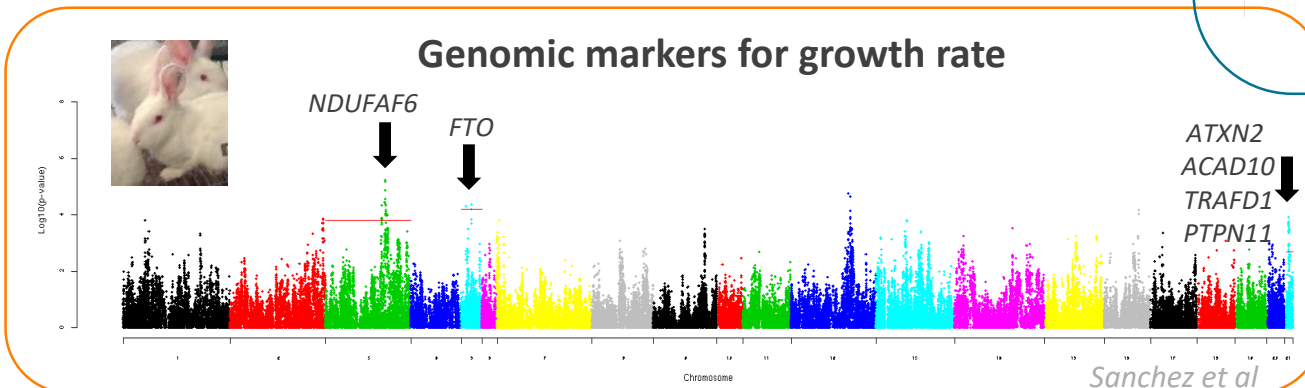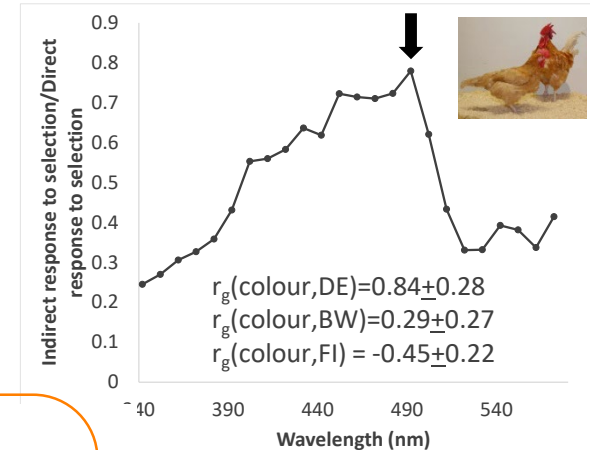
New traits – at the animal level

Molecular indicators of feed efficiency

Genome (SNP, sequence), transcription, metabolome: **candidates to validate**

Genomic markers of lines divergent for RFI
Selection signatures combined with gene expression

	SNP
Intergenic	4 282 102
Genic	3 750 023
Intronic	3 548 206
Exonic	201 817
5'UTR	13 396
CDS	108 342
3'UTR	55 110

Multi-tissues
RNA-seq
+
lipidomics &
metabolomics

Lagarrigue, Zerjal, Jehl et al
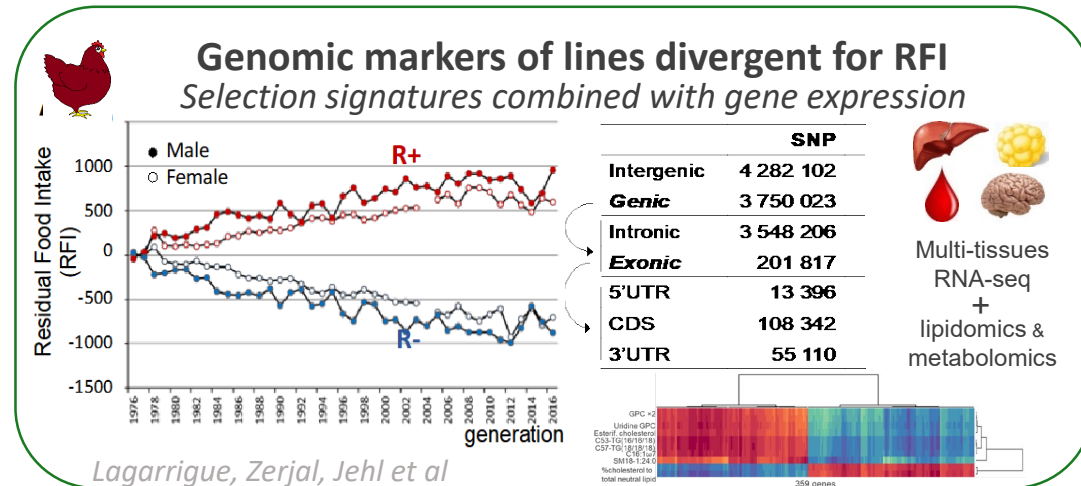
Genetic gain on efficiency with selection on colour of broiler serum

$r_g(colour,DE)=0.84\pm0.28$
$r_g(colour,BW)=0.29\pm0.27$
$r_g(colour,FI) = -0.45\pm0.22$

Grasteau et al

Genomic markers for growth rate

NDUFAF6
FTO
ATXN2
ACAD10
TRAFD1
PTPN11

Sanchez et al

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New traits – at the animal level

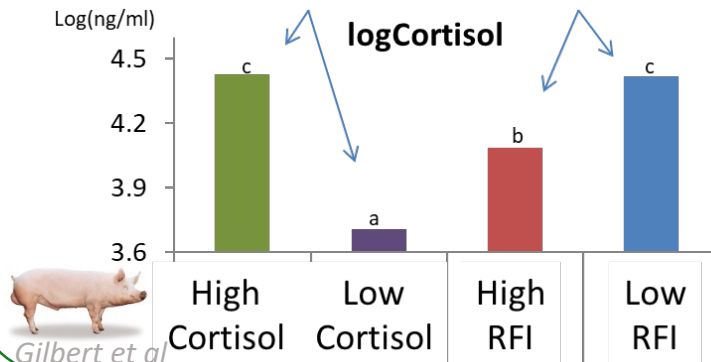## Measures of components of feed efficiency

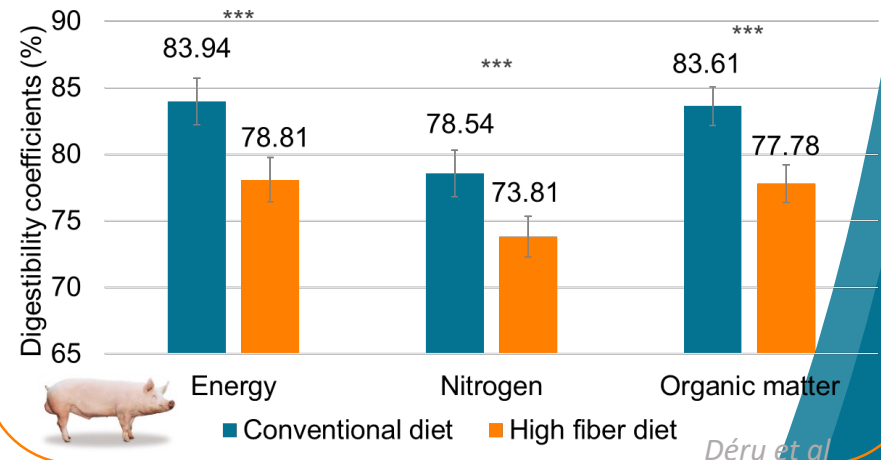Behaviour/aggressiveness - welfare/robustness - digestibility

DUROC LINE

Agha et al

Cortisol levels of lines divergent for RFI

Gilbert et al

▶ No adverse relationships with
behaviour or robustness indicators

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New traits – at the animal level

Measures of components of feed efficiency

Behaviour/aggressiveness - welfare/robustness - digestibility

DUROC LINE

Agha et al

Cortisol levels of lines divergent for RFI

Log(ng/ml)

logCortisol

	High Cortisol	Low Cortisol	High RFI	Low RFI
	c	a	b	c

Gilbert et al
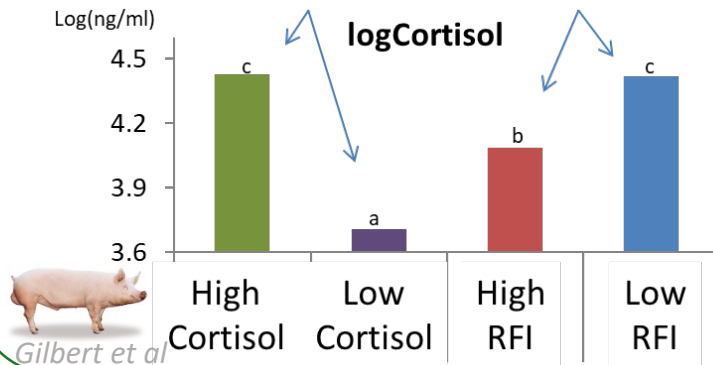
NIRS digestibility coefficients on farm

Digestibility coefficients (%)

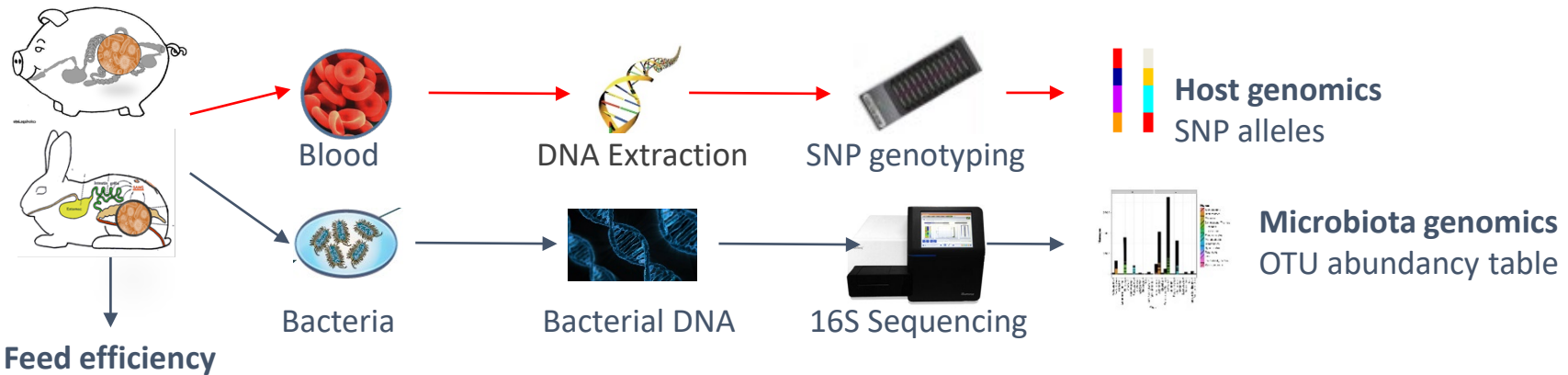|	Energy	Nitrogen	Organic matter
***	83.94 / 78.81	78.54 / 73.81 ***	83.61 / 77.78 ***

■ Conventional diet ■ High fiber diet

Déru et al

▸ No adverse relationships with behaviour or robustness indicators

▸ h² > 0.40 → selection for better digestion of dietary fibres is possible

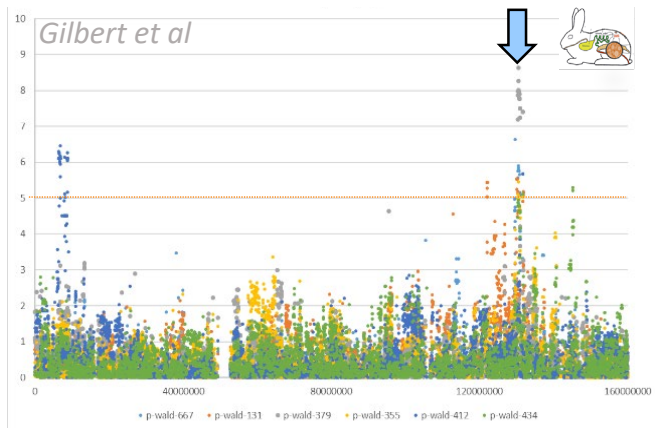# New traits – from microbiota

Feed efficiency
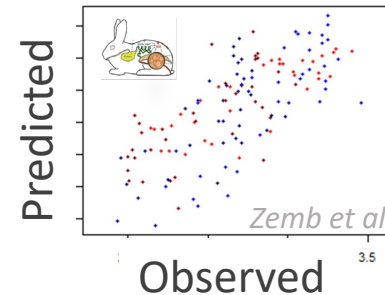
Blood → DNA Extraction → SNP genotyping → **Host genomics** SNP alleles

Bacteria → Bacterial DNA → 16S Sequencing → **Microbiota genomics** OTU abundancy table

Rabbit chr7 – 5 OTU with $h^2 > 0,15$ **associated with genome variants**

Gilbert et al

p·wald·667   p·wald·131   p·wald·379   p·wald·355   p·wald·412   p·wald·434

OTU to predict feed efficiency $R^2 = 0.53$

Predicted / Observed

Zemb et al

◗ Large sensitivity to external factors (feed, antibiotics, temperature…)

◗ Genetic control of gut microbiota

◗ Added value for prediction of feed efficiency?

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New statistical models

▶ Models to improve response on feed efficiency

  ▶ Analysis of feed efficiency over time

  ▶ Use of group records to select for feed efficiency

Huynh-Tran et al

% individual feed intake records

Herrera et al
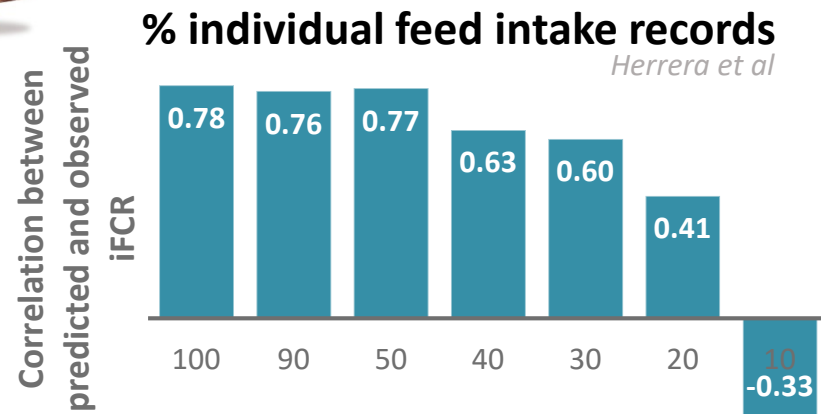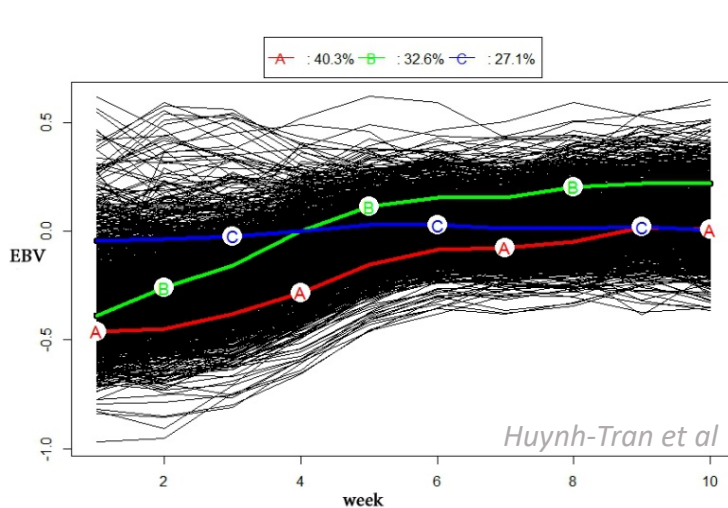
▶ Potential gains in identifying time dependent patterns of changes of feed efficiency

▶ Accurate feed efficiency predictions combinin group and individual feed intake records
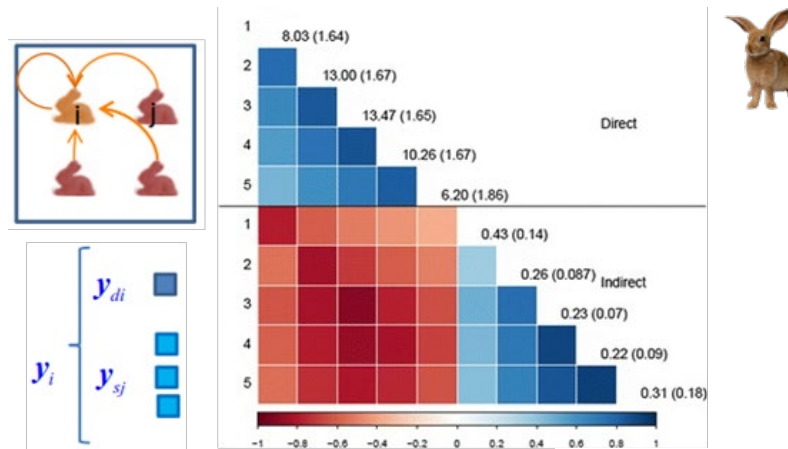
New statistical models

▶ Models to account for indirect genetic effects on feed efficiency

- Interaction between genetic and feeding for direct and indirect genetic effects
  Piles et al
- Use feeding behaviour to improve accuracy of indirect effects
  Ragab et al

David et al

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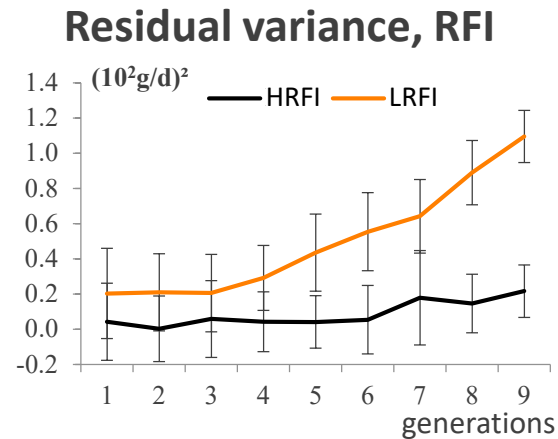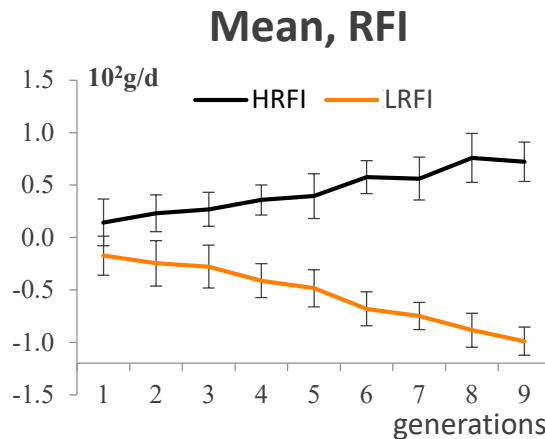
New statistical models

▶ Models to account for individual's environmental sensitivity

▶ Genetic analyses of residual variation for multiple traits suggest some common genetic basis of responses to environmental variability

Bodin et al

Mean, RFI — 10^2g/d — HRFI, LRFI — generations

Residual variance, RFI — $(10^2$g/d$)^2$ — HRFI, LRFI — generations

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Using crossbred (genomic) information
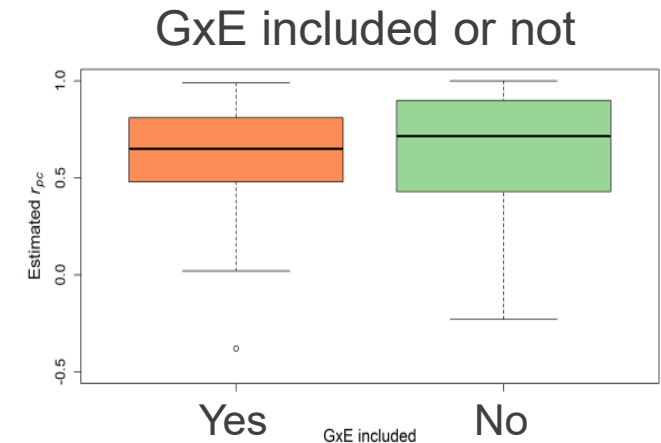
- Genetic architecture of the traits
  - Dominance contributes only to 9% to 12% of feed efficiency variability   *Tusell et al*

- Which model for genomic prediction?
  - Metafounders in crossbred genomic evaluation: same genetic gains, but can ease calculations   *van Grenvehof et al*

- Purebred-crossbred correlations
  - Difficult to disentangle purebred-crossbred interaction from genotype by environment interaction   *Wientjes and Calus*
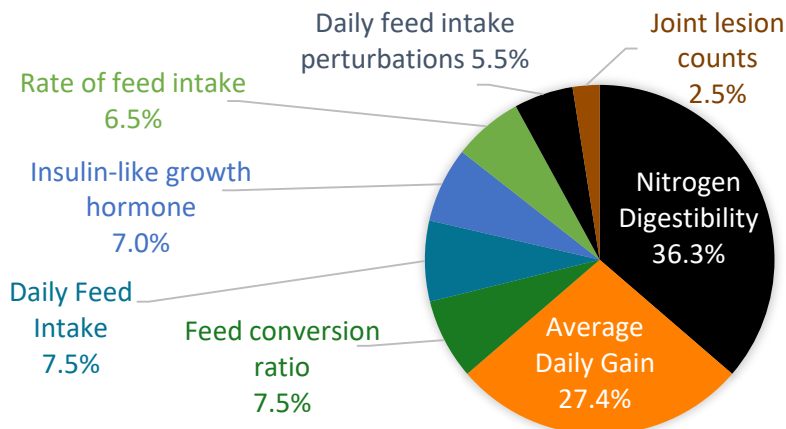

GxE included or not

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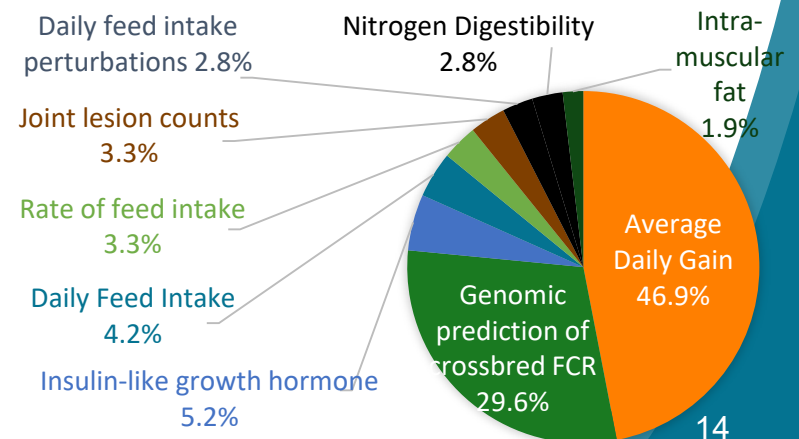
Using crossbred (genomic) information

◗ Evaluate genetic gain for feed efficiency with best indicators, including genomic prediction

- ◗ New traits can increase response to selection
- ◗ Recording is important: **+53% gross profit/generation**
- ◗ Including genomic prediction alone is beneficial: **+26% gross profit/generation**
- ◗ If possible record traits on crossbreds

Aldridge et al

New selection indexes, new records on purebred

without genomic prediction | **with genomic prediction**

Daily feed intake perturbations 5.5%
Joint lesion counts 2.5%
Rate of feed intake 6.5%
Insulin-like growth hormone 7.0%
Daily Feed Intake 7.5%
Feed conversion ratio 7.5%
Nitrogen Digestibility 36.3%
Average Daily Gain 27.4%

Daily feed intake perturbations 2.8%
Nitrogen Digestibility 2.8%
Intra-muscular fat 1.9%
Joint lesion counts 3.3%
Rate of feed intake 3.3%
Daily Feed Intake 4.2%
Insulin-like growth hormone 5.2%
Average Daily Gain 46.9%
Genomic prediction of crossbred FCR 29.6%

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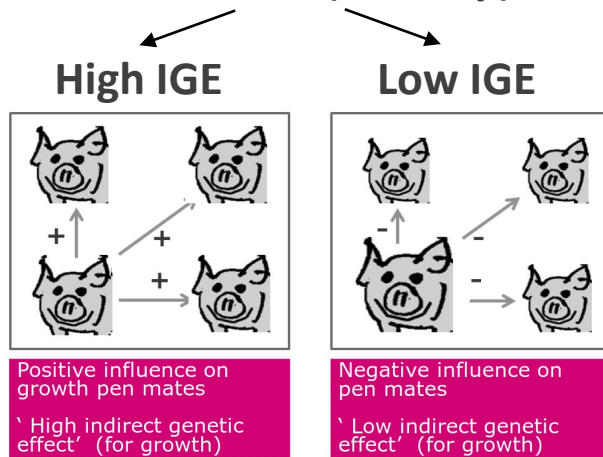to improve the efficiency and sustainability of monogastric
livestock production systems

Validation for selection

▶ Use of indirect genetic effects on crossbreds

Training population
+ few thousands CB with phenotypes and genotypes

High IGE   **Low IGE**

Positive influence on growth pen mates

' High indirect genetic effect' (for growth)

Negative influence on pen mates

' Low indirect genetic effect' (for growth)

➡ Limited performance differences between groups

Bergsma et al

▶ Use of group records versus individual records

indiv RFI   group RFI

➡

FCR - ad lib   FCR - restrict

■ indiv RFI   ■ group RFI   ■ ADG-Restr

Sanchez et al

15
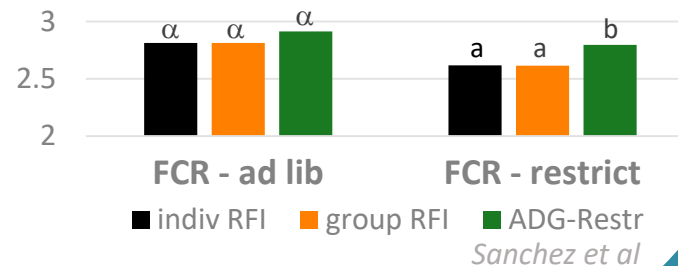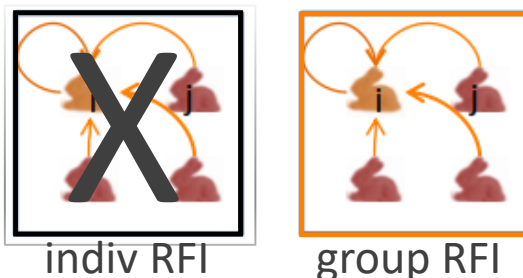
Looking forward

- Using new traits & measures:
  - Individual feeders in rabbits and poultry
  - Group records in pigs, to increase genetic gain at low cost
- Promising indicators of FE (further validation needed):
  - Digestibility measurements
  - Microbiota analyses
  - Biomarkers
- Recommendations to use the best indicators and genomic and crossbred information