New traits and models for the genetic improvement of feed efficiency

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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
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
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

Direct measures of feed intake

Broiler feed intake

Rabbit feed intake

Gestation and lactation feed intake

Different responses on reproductive sows depending on management

Large gains from individual measures of growing animals

11/02/2020
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

Genetic gain on efficiency with selection on colour of broiler serum

Genomic markers for growth rate

Lagarrigue, Zerjal, Jehl et al

Grasteau et al

Sanchez et al
New traits – at the animal level

Measures of components of feed efficiency

Behaviour/aggressiveness - welfare/robustness - digestibility

No adverse relationships with behaviour or robustness indicators
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

Measures of components of feed efficiency

Behaviour/aggressiveness - welfare/robustness - digestibility

No adverse relationships with behaviour or robustness indicators

\( h^2 > 0.40 \rightarrow \) selection for better digestion of dietary fibres is possible
Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems.

New traits – from microbiota

Blood → Bacteria → DNA Extraction → Bacterial DNA → 16S Sequencing → SNP genotyping → Host genomics

- SNP alleles
- Microbiota genomics
- OTU abundancy table

Feed efficiency

Rabbit chr7 – 5 OTU with $h^2 > 0.15$ associated with genome variants

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

- Large sensitivity to external factors (feed, antibiotics, temperature…)
- Genetic control of gut microbiota
- Added value for prediction of feed efficiency?

Gilbert et al

Zemb et al
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

Potential gains in identifying time dependent patterns of changes of feed efficiency

- Accurate feed efficiency predictions combining group and individual feed intake records

11/02/2020
New statistical models

- Models to account for indirect genetic effects on feed efficiency
  - Interaction between genetic and feeding for direct and indirect genetic effects
  - Use feeding behaviour to improve accuracy of indirect effects

David et al
Piles et al
Ragab et al
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.
Using crossbred (genomic) information

- **Genetic architecture of the traits**
  - Dominance contributes only to 9% to 12% of feed efficiency variability
    
- **Which model for genomic prediction?**
  - Metafounders in crossbred genomic evaluation: same genetic gains, but can ease calculations

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

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R. Tusell et al., van Grenvehof et al., Wientjes and Calus
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

**New selection indexes, new records on purebred**

**without genomic prediction**

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

**with genomic prediction**

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

Aldridge et al
Validation for selection

- Use of indirect genetic effects on crossbreds
  
  Training population
  + few thousands CB with phenotypes and genotypes

High IGE

Low IGE

Limited performance differences between groups

- Use of group records versus individual records

Indiv RFI

Group RFI

Sanchez et al

Bergsma et al
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