Genetic correlation between residual feed intake and easily measurable plasma parameters in early-fattening young bulls

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Context of the study

Feed is one of the main production costs on commercial farm (IDELE, 2019).

Significant individual variability exists for feed efficiency of fattening young bulls (from 5% to 14% CV for RFI; Cantalapiedra-Hijar *et al.*, 2020).

➡ **Identification of the least and most efficient animals is feasible.**

Knowing residual feed intake (RFI) early in life of growing cattle represents an interesting opportunity:

Precision feeding

Genetic selection

Measuring RFI is too expensive

Blood plasma biomarkers represent a cost-effective way to predict RFI and identify feed efficient cattle.

Candidate RFI plasma parameters identified between **extreme phenotypes** in young bulls **at the end of fattening period**:

- Creatinine
- Insulin
- Triglyceride
- Branched-chain amino acids (BCAA)
- …

Common and diet-specific metabolic pathways underlying residual feed intake in fattening Charolais yearling bulls

Ezequiel Jorge-Smeding[1], Muriel Bonnet[2], Gilles Renand[3], Sébastien Taussat[3,4], Benoit Graulet[2], Isabelle Ortigues-Marty[2] & Gonzalo Cantalapiedra-Hijar[2]✉

In Scientific Reports 11, 2021

Do plasma biomarkers of RFI previously identified during late fattening possess discriminatory ability during early fattening stages?

NUTRIMARKERS project

1. Confirm that biomarkers identify extreme animals **in early stage** (n=48)
   ➡ Aboshady et al., under revision in Animal

2. Test those biomarkers with **easily measurable and cheap methods** (n=48)

3. **RFI prediction model** in early stage of fattening (n=639):
   - ➢ **Proof of concept** that biomarker-assisted precision feeding may offer several benefits under field conditions: experimental trial from April 2024 to February 2025

   - ➢ Using this prediction for **genetic selection**

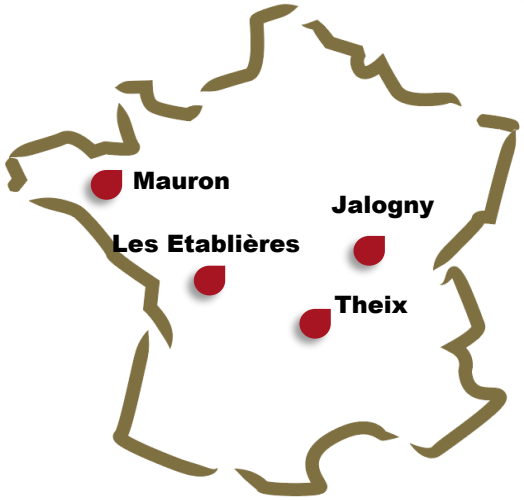
➡ **Is there any genetic relationship between RFI and plasma biomarkers?**

Objective of this study

The aim of this study is to estimate the genetic parameters of 13 easily measurable plasma parameters identified as biomarkers of RFI in early-fattening young bulls and assess their genetic correlations with RFI.

- **To understand the genetic determinism of RFI**
- **To observe if prediction model could be used in selection**

Young bull phenotyping



639 fattening Charolais young bulls on test from 2015 to 2020:

- Bought in commercial farms after weaning
- Entered in 4 experimental farms at 275 d of age
- Adapted to the conditions at least during 4 weeks
- Tested at least during 16 weeks
- Two contrasted diets:
  - **319 with corn silage** (high starch diet)
  - **320 with grass silage** (high fiber diet)

Traits used in this study

Residual feed intake

FI = diet*year*farm*pen + metabolic body weight + average daily gain + RFI

$R^2 = 0.64$

13 metabolites measured during early fattening:

- Creatinine
- Urea
- Non-esterified fatty acid (NEFA)
- Albumin
- Cholesterol
- Glucose
- Total plasma protein (Tprot)
- Triglycerides
- Aspartate aminotransferase (AST)
- Alanine aminotransferase (ALT)
- Alkaline phosphatase (ALP)

Statistical analysis

<u>Phenotypic and genetic parameter estimation:</u>

- Using Wombat software (Meyer, 2007)
- Animal model with:
  - Contemporary group and covariable of age at the start of the test
  - Random effects of birth farm*campaign, genetic, residual

Results

Traits	h^2
RFI	0.21
Creatinine	**0.33**
Urea	0.16
NEFA	0.02
Albumin	**0.31**
Cholesterol	**0.43**
Glucose	0.15
Tprot	0.15
Triglycerides	0.23
AST	0.27
ALT	0.21
ALP	**0.53**

Moderate heritability for RFI

Different heritability values depending on the metabolite:

- Lowest for NEFA
- Highest for creatinine, albumin, cholesterol and ALP

SE from 0.05 to 0.17

Results

Traits	h^2	Rp
RFI	0.21	
Creatinine	0.33	**-0.33***
Urea	0.16	0.03
NEFA	0.02	-0.04
Albumin	0.31	0.04
Cholesterol	0.43	-0.02
Glucose	0.15	0.04
Tprot	0.15	-0.01
Triglycerides	0.23	**-0.10***
AST	0.27	0.07
ALT	0.21	0.07
ALP	0.53	0.03

No strong phenotypic correlation observed with RFI

Negative relationships with **creatinine** and **triglycerides**

SE about 0.05

Results

Traits	h^2	Rp	Rg
RFI	0.21		
Creatinine	0.33	-0.33*	**-0.46**
Urea	0.16	0.03	-0.07
NEFA	0.02	-0.04	NA
Albumin	0.31	0.04	0.01
Cholesterol	0.43	-0.02	-0.19
Glucose	0.15	0.04	0.34
Tprot	0.15	-0.01	**-0.41**
Triglycerides	0.23	-0.10*	**-0.44**
AST	0.27	0.07	**0.50**
ALT	0.21	0.07	**0.89**
ALP	0.53	0.03	0.16

Moderate to strong genetic relationships observed:

- Negative with **creatinine, Tprot** and **triglycerides**
- Positive with **AST** and **ALT**

SE from 0.21 to 0.38

Discussion

Metabolites are heritable, except for NEFA.

Feed efficient animals (**low-RFI**) have:

- **Higher efficiency of protein use**: higher total plasma protein and lower concentration for both hepatic transaminases
- **Greater muscle mass and lower adiposity**: higher concentration of creatinine and triglycerides

Unfortunately precision of the estimates was low.

Conclusion

Our study highlighted genetic relationships between RFI and some biomarkers related to protein metabolism and body composition.

RFI prediction model based on biomarkers could be used in genetic selection.

<u>Perspectives:</u>

- Estimate genetic correlation between observed and predicted RFI by plasma biomarkers.
- Compare for sires the EBV estimated from observed and predicted RFI.
- Phenotypic prediction using model that integrates metabolites and genotypes.

Thank you for your attention

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