Rumen fatty acids linked to phenotypes in Romane lambs selected for feed efficiency

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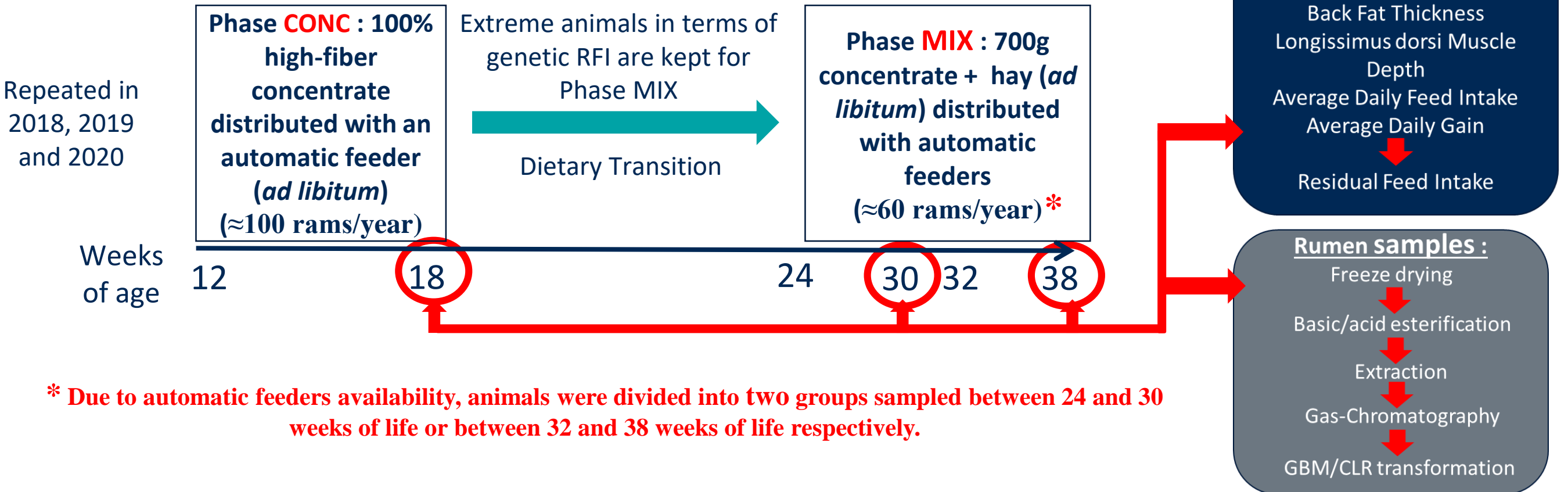
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1. Introduction

➢ Mechanisms underlying Feed Efficiency (FE) are not fully understood.

➢ Microbial metabolism of the dietary lipids is responsible for the formation of bioactive intermediates that could be involved in FE variability.

➢ Divergent selection on residual feed intake (RFI) is a good tool to investigate biological processes underlying feed efficiency : after 3 generations of selection under a 100% concentrate diet an important difference between **efficient (rfi –)** and **inefficient animals (rfi +)** was reached (~1.9 genetic standard deviation).

2. Experimental design

Repeated in 2018, 2019 and 2020

Phase **CONC** : 100% high-fiber concentrate distributed with an automatic feeder (*ad libitum*) (≈100 rams/year)

Extreme animals in terms of genetic RFI are kept for Phase MIX

Dietary Transition

Phase **MIX** : 700g concentrate + hay (*ad libitum*) distributed with automatic feeders (≈60 rams/year) *

Phenotypes :
End-Phase Metabolic Weight
Back Fat Thickness
Longissimus dorsi Muscle Depth
Average Daily Feed Intake
Average Daily Gain
Residual Feed Intake

Rumen samples :
Freeze drying
Basic/acid esterification
Extraction
Gas-Chromatography
GBM/CLR transformation

Weeks of age: 12 18 24 30 32 38

* Due to automatic feeders availability, animals were divided into two groups sampled between 24 and 30 weeks of life or between 32 and 38 weeks of life respectively.

→ Fatty Acid profiles and phenotypes were corrected for year and pen effects in phase CONC, and year, period and pen effects in phase MIX
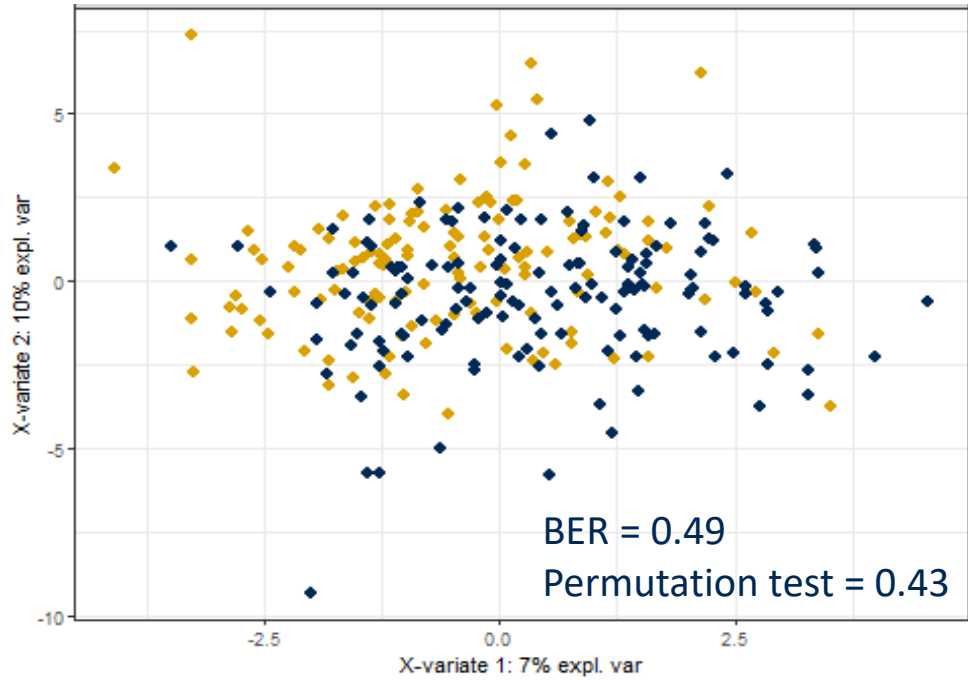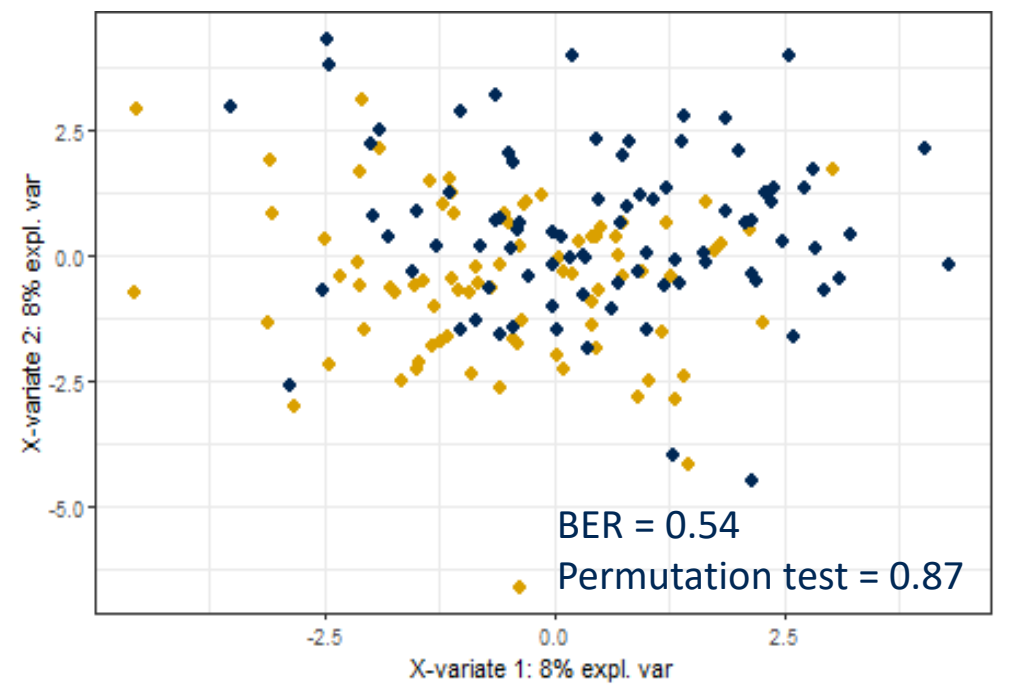
3. Results

CONC Phase | MIX Phase

Rumen fatty acid profiles are not modified by genetic selection on RFI
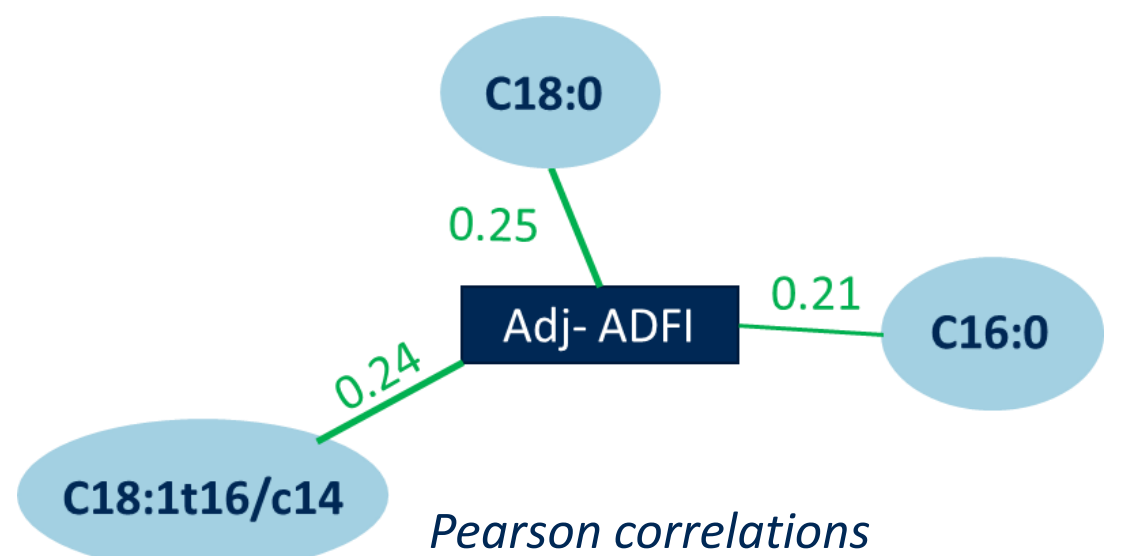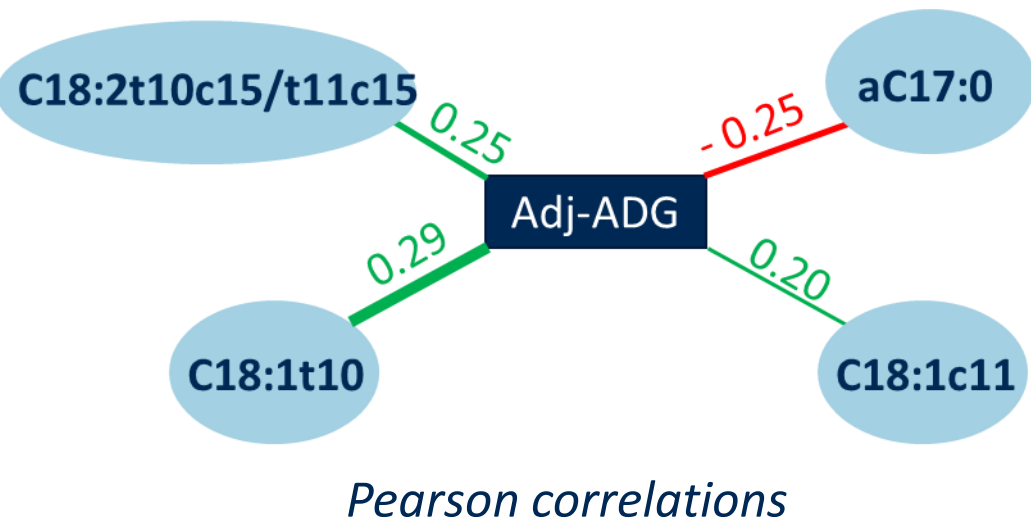
PLS-DA of CLR-transformed FA profiles by line

BER = 0.49
Permutation test = 0.43

PLS-DA of CLR-transformed FA profiles by line

BER = 0.54
Permutation test = 0.87

Line :
● rfi +
● rfi –

Rumen fatty acid profiles are weakly correlated to phenotypes whatever the diet

→ In phase CONC, the **PLS regression** identified ADG as the main phenotype variable linked to the fatty acid profile in the data set and C18:1 t10 as the main fatty acid linked to the phenotypes.

C18:2t10c15/t11c15 — 0.25 — aC17:0 (- 0.25) — Adj-ADG — C18:1t10 (0.29) — C18:1c11 (0.20)

Pearson correlations

→ In phase MIX, ADFI is the main phenotype highlighted in the **PLS regression** and is mostly correlated with C18:0.

C18:0 — 0.25 — Adj- ADFI — 0.21 — C16:0 — C18:1t16/c14 (0.24)

Pearson correlations