Divergent selection on residual feed intake influences gene and protein expressions in pig muscle

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Context

- **A need for feed efficient animals in the context of livestock production: it is essential to reduce feed cost and environmental impact**
- **Residual feed intake (RFI): a relevant criterion to measure feed efficiency**
- **Selection experiments have shown that reduced RFI is genetically correlated with higher carcass lean meat content (Gilbert et al., 2007)**

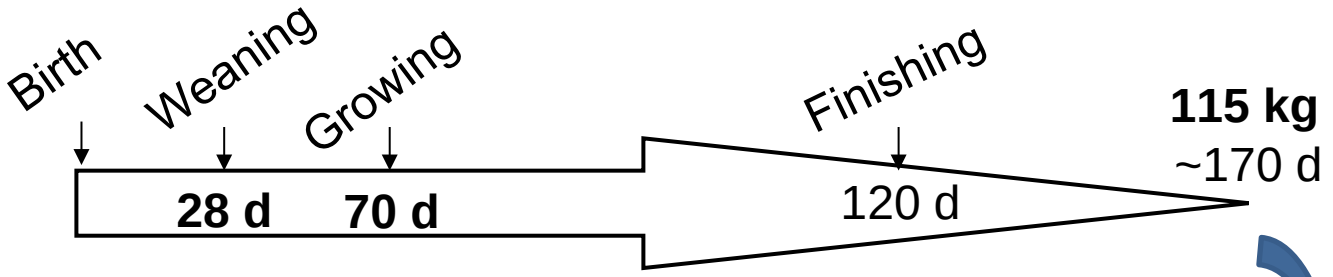
Objectives

- To determine the influence of divergent RFI selection on the transcriptome and proteome of skeletal muscle of 115 kg pigs

- To differentiate variations due to genetic orientation from those related to spontaneous feed intake level

Experimental design

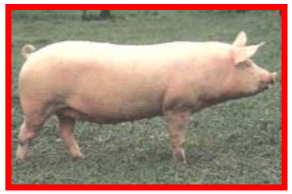
24 Large White females from 2 lines divergently selected for RFI during more than 7 generations; feeding with standard diets.



RFI-

n=8 — **Ad lib feeding**

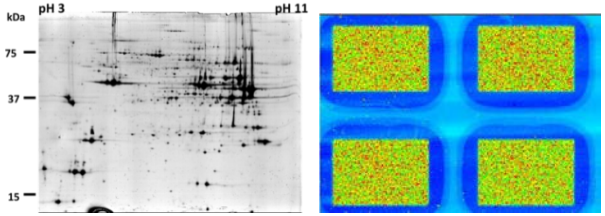
RFI+



n=8 — **Ad lib feeding**

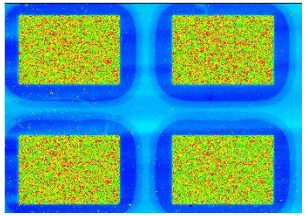
n=8 — **Pair-fed to daily feed intake of RFI-**

Body weight & feed consumption measurements



sample collection

Methodology



Total RNA

Agilent-026440 porcine oligo Microarray (V2, 44K)

H12 000 genes, one color-labeling

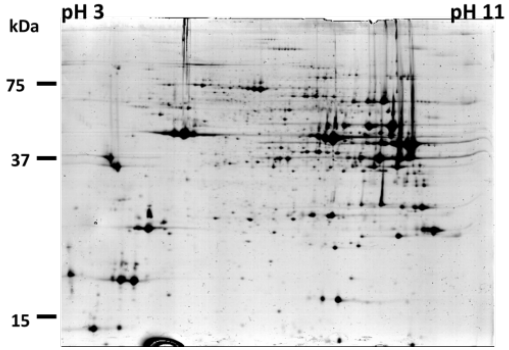
Scan & data extraction: Feature Extraction

Statistical analysis: R (limma, multtest)

Functional analysis

Methodology

Protein extraction



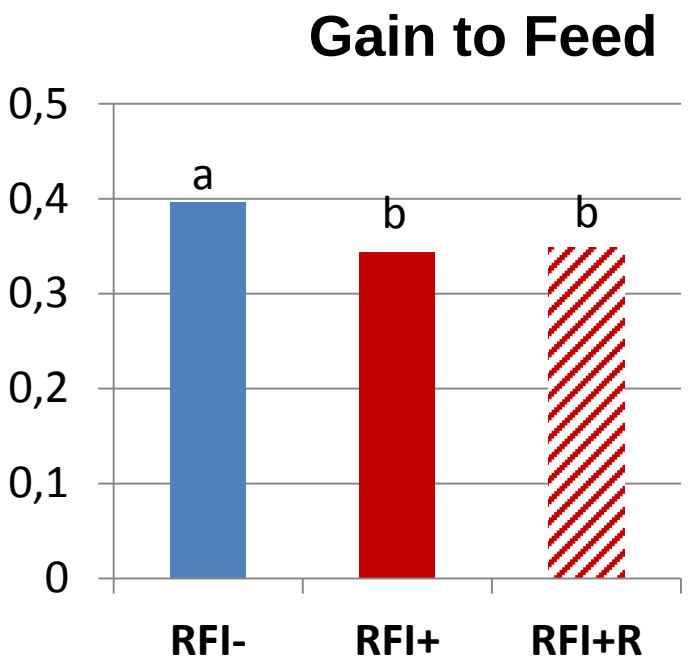
2D-PAGE + Silver blue staining

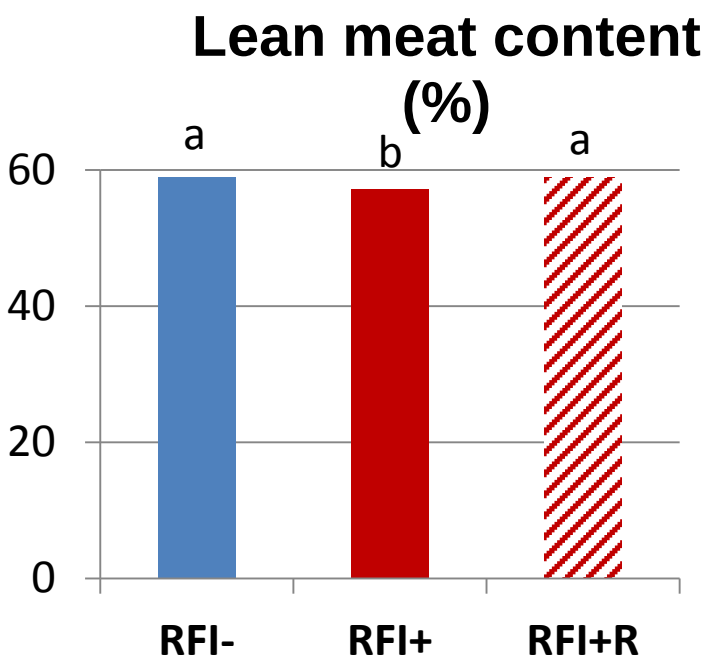
Mélanie 7.0., measurement of the relative protein abundance of each spot : % total volume

809 matched spots between gels

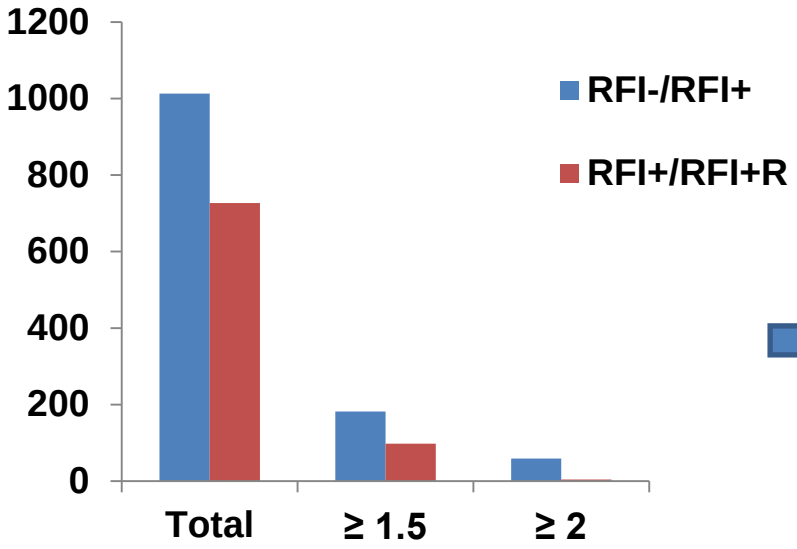
Statistical analysis

Growth performances





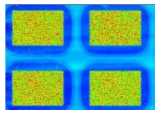
Number of probes differentially (P < 0.01) expressed in pigs divergently selected for RFI having either free (RFI^{-}, RFI^{+}) or restricted (RFI^{+R}) access to feed



More differences between RFI^{-}/RFI^{+} pigs than between RFI^{+}/RFI^{+R} pigs

A focus on the investigation of RFI^{-} and RFI^{+} pigs

Overrepresented GO terms of up-regulated genes in muscle of RFI$^-$ pigs



Translation (36)

EIF6, RPL18, RPL14, RPLP0, RPLP1, FAU, RPL10, RPL12, RPL36AL, EIF2B5, LOC645139, RPS18, RPS19, RPS12, UBA52, RPS26, RPL7, RPL6, RPL8, RPS20, RPS23, RPSA, EEF1A1, PAIP1, RPL23A, DENR, RPS6, COPS5, LOC100049695, RPS19P3, RPS3, EEF1G, RPS15A, RPL29, RPL23, RPL21

Ribonucleoprotein complex biogenesis (12)

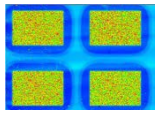
EIF6, GTPBP4, SNUPN, GNL3L LOC100049695, RPS6, SFRS5, RPS19, RPL7, RPLP0, POP4, TGS1

Muscle cell differentiation (9)

SYNE1, ACTA1, MAPK12, ERBB2, GLMN, SOX6, NEURL2, CAPN2, CACNA1S

Observed data consistent with ↑ protein synthesis in muscle of RFI$^-$ pigs

Overrepresented GO terms of up-regulated genes in muscle of RFI$^+$ pigs



Oxidation-reduction process (19)

ME1, ND1, ND4, LOC396756, NDUFB9, ND2, CYCS, MOSC2, IDH3A, SOD2, RDH11, SLC1A3, HSDL2, FMO1, GPX3, DLD, HSD17B4, LOC733694, ETFB

Generation of precursor metabolites and energy (10)

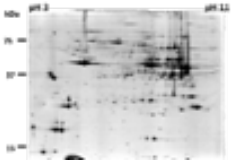
ND1, SLC1A3, ND4, LOC396756, PGAM4, NDUFB9, ND2, CYCS, ETFB, IDH3A

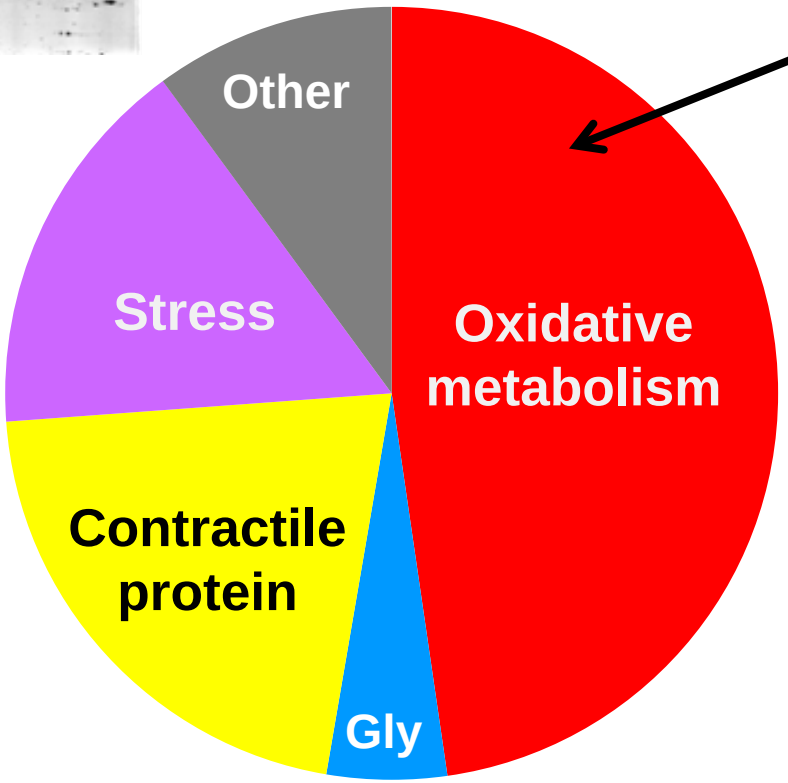
Electron transport chain (8)

ND1, SLC1A3, ND4, LOC396756, NDUFB9, ND2, CYCS, ETFB

Observed data consistent with ↑ oxidative metabolism in muscle of RFI$^+$ pigs

19 protein spots differently expressed (P < 0.05) between RFI^{-} and RFI^{+}



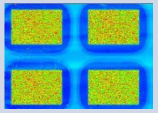
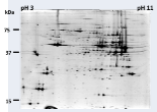


RFI^{-} < RFI^{+}

- Creatine kinase S-type, mitochondrial
- Aconitate hydratase, mitochondrial
- ATP synthase subunit alpha, mitochondrial
- Myoglobin
- Myozenin-1 (calcineurin signaling)
- Glycerol-3-phosphate dehydrogenase , cytoplasmic (glycerol phosphate shuttle)

NB: RFI^{+R} = RFI^{+} → Genetic effect

In summary

	RFI$^-$	RFI$^+$
	↑ expression of genes linked to protein synthesis	↑ expression of genes linked to oxidative metabolism
		↑ levels of 6 proteins associated with oxidative metabolism
Other data	No changes in activities of enzymes involved in protein catabolism (Le Naou et al., 2012)	↑ activity of HAD (Le Naou et al., 2012; Faure et al., 2013)

Conclusions

- **A specific impact of genetic selection on skeletal muscle features**

- **Compared with the less efficient pigs, the more efficient pigs exhibited:**
  - **↑ lean mass**
  - **↑ expression of genes associated with protein synthesis**
  - **↓ expression of genes and proteins linked to oxidative metabolism**

Thanks to

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  - UE1372 GenESI: divergent selection experiment

  - UMR1348, Pegase: animal care and animal slaughtering; laboratory analyses

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Thank you for your attention