Transcriptomic and DNA methylation response to feed intake in the duodenum in high- and low- feed efficiency pig lines

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1: GenPhySE, Université de Toulouse, INRAE, ENVT, 31326, Castanet Tolosan, France
2: INRAE, US 1426, GeT-PlaGe, Genotoul, Castanet-Tolosan, France
3: Pig phenotyping and Innovative breeding facility, GenESI, UE1372, INRAE, F-17700 Surgères, France

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Context

Feed efficiency is a complex trait of great interest in animal breeding, notably to reduce environmental impact of livestock herding and to reduce the cost of animal feed for the farmers. A successful divergent selection on feed efficiency was carried out in pigs for more than 10 generations at an INRAE experimental unit, establishing **lines of related good and poor feed efficiency large white pigs**. The objective of the present study was to identify the molecular mechanisms underlying the divergence in feed efficiency between the two pig lines at the intestinal level.

Method

Duodenum mucosal samples were collected in post-weaning pigs from the two divergent lines, in two groups: one after a 12 hours period of feed restriction, the other with a 10 hours period of feed restriction followed by a 2 hours period of ad libitum feed access (n=6 per group and per line). Transcritome and methylome of duodenal mucosa were analyzed by poly-A RNA sequencing (RNA-seq) and by methylated DNA precipitation followed by sequencing (MeDP-seq), respectively.

Key Results

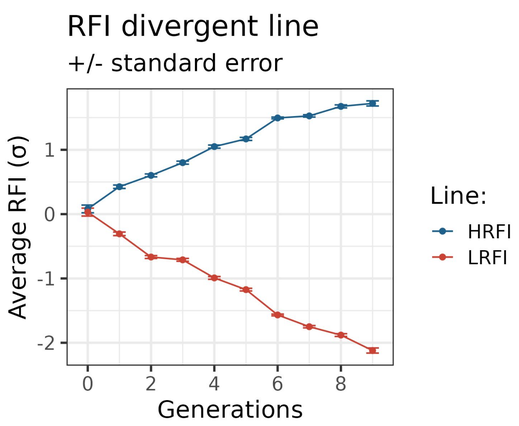
- 3 times as many genes differentially expressed due to feed intake than between the two pig lines.
- The duodenum transcriptomic response to feed intake is greater in the more efficient pig line.
- Duodenum DNA methylation profiles are barely affected by short-term feed intake.
- Duodenum DNA methylation profiles are distinct between the two pig lines.

Futur directions

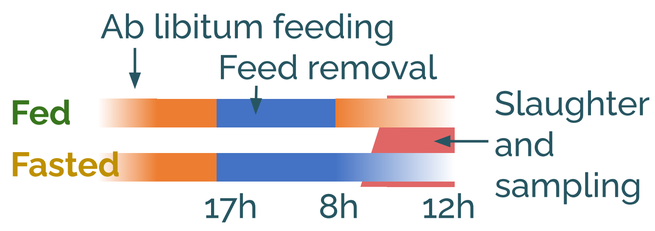
- Integration of transcriptomic and DNA methylation profiles to investigate if differences in DNA methylation might explain part of the different transcriptomic response between pig lines.
- Transcriptomic and DNA methylation profiling of the stomach mucosa.
- Cleaner identification of differentially methylated regions by focusing on unmethylated regions.

Sample production

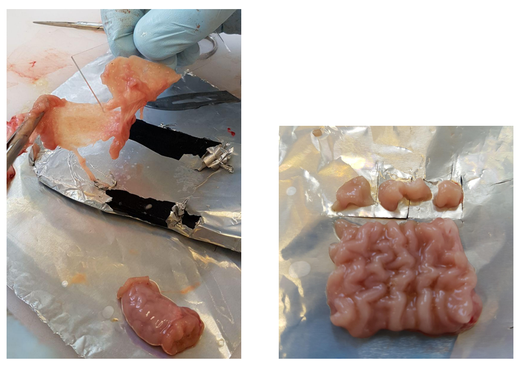
Divergent selection on Residual Feed Intake (RFI)



Experimentation on the 11th generation: 60 days-old **G11+** (HRFI, poor feed efficiency), and **G11-** (LRFI, good feed efficiency).



Duodenum mucosa dissection



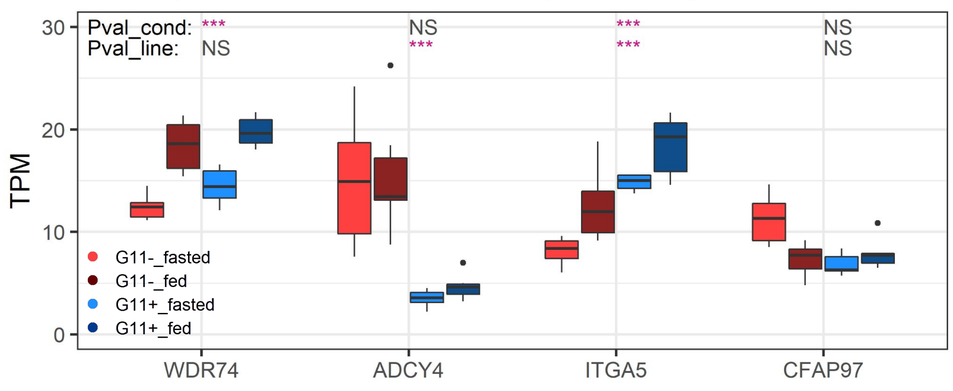
Balanced experimental groups:

- 24 pigs in total
- 12 G11+ and 12 G11-
- 12 fasted and 12 fed
- 13 castrated males and 11 females
- 4 pigs each from 3 litters per line

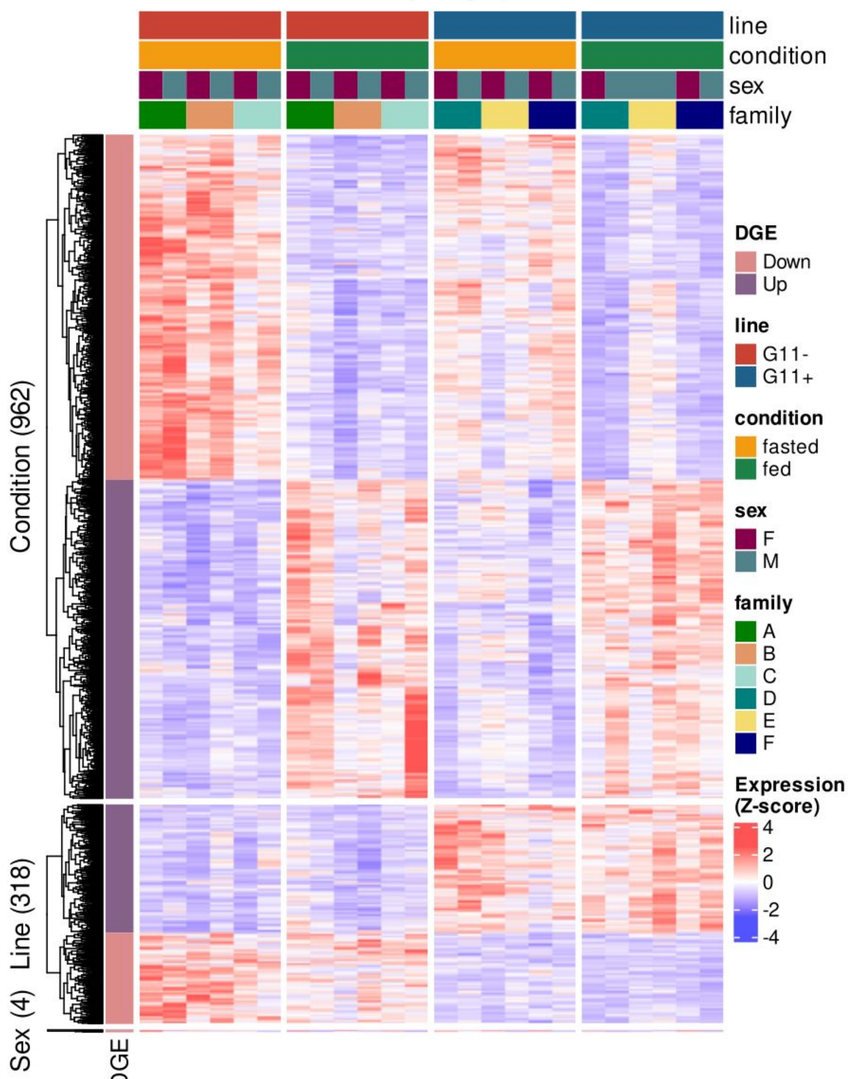
Differential gene expression (DGE) analysis

nf-core /rnaseq
Mapping and quantification: Salmon
DGE: limma-voom *Expression ~ Condition + Line + Sex*

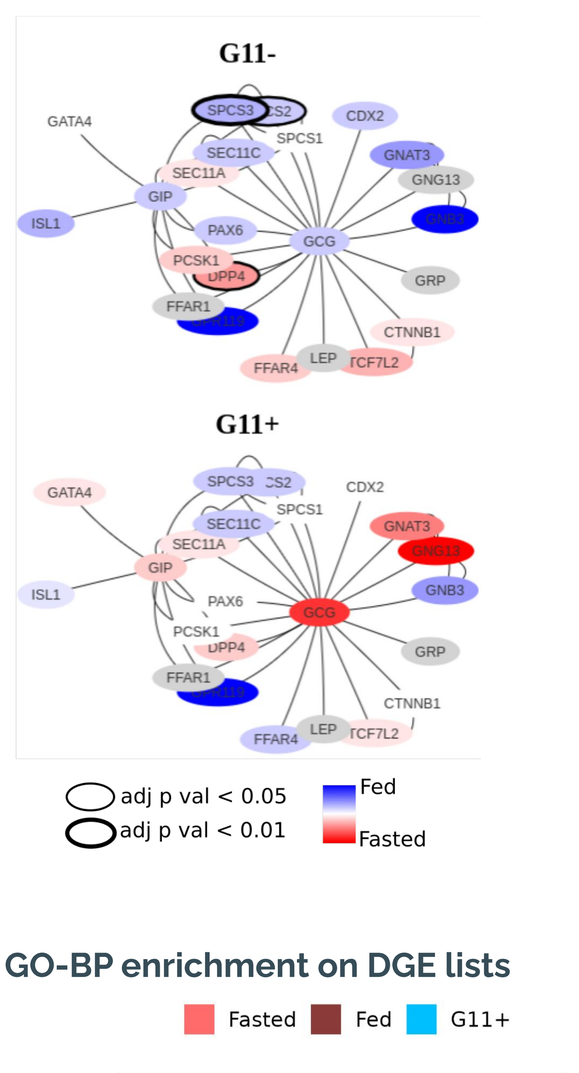
Examples of differentially expressed genes



Expression heatmap of DGE

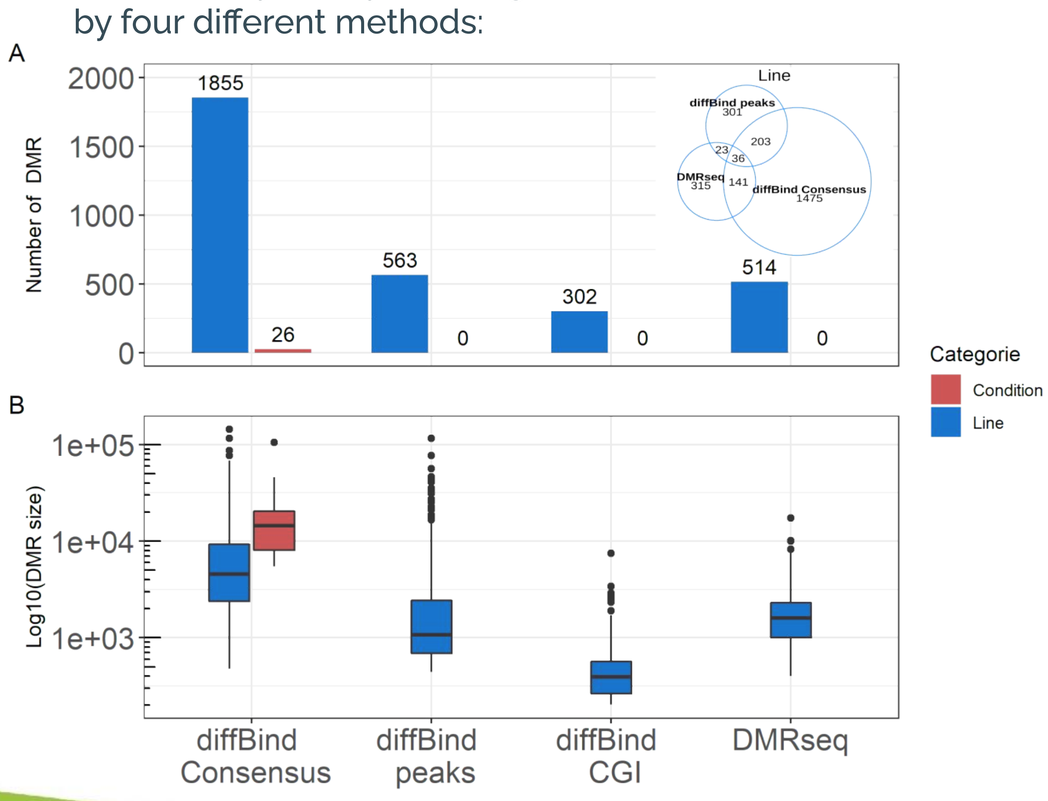


Focus on the Incretin pathway

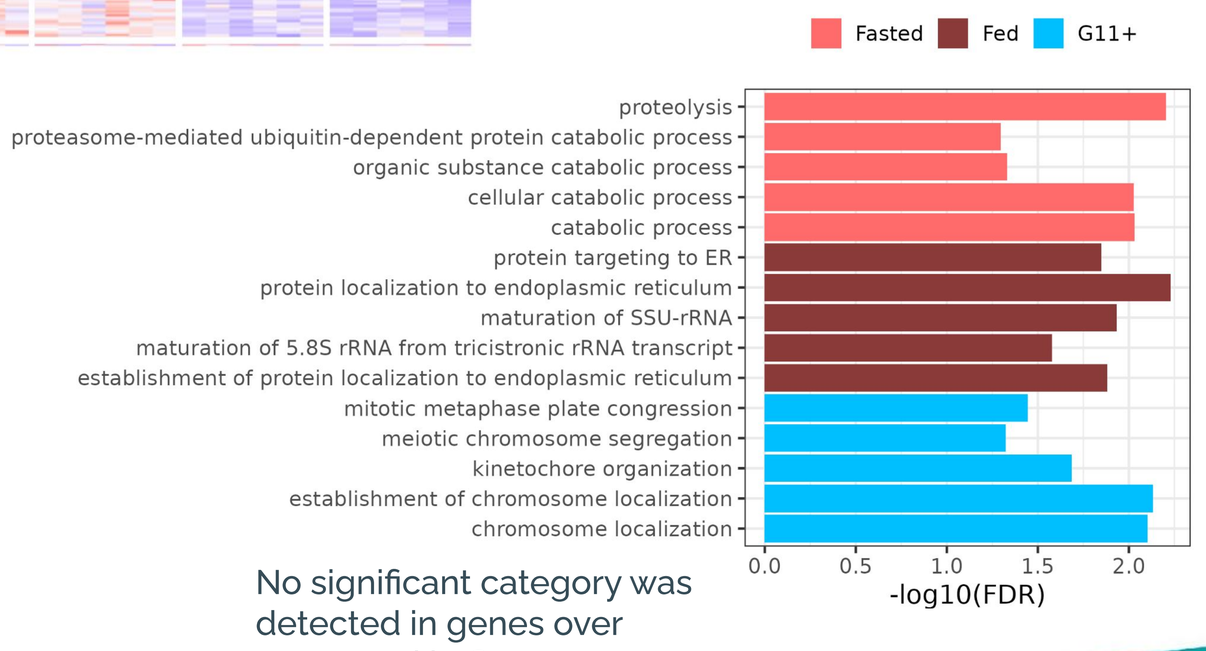


DNA methylation analysis

By methylated-DNA precipitation followed by high throughput sequencing (MeDP-seq).
Differentially methylated regions (DMR) identified by four different methods:



GO-BP enrichment on DGE lists



No significant category was detected in genes over expressed in G11-.

GenPhySE
Occitanie - Toulouse, France

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