

Influence of maternal diet on the liver and skeletal muscle epigenomes of fetal and young pigs

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The short chain fatty acids (SCFAs) produced by gut microbiota have emerged as one clear link between the non-digestible fibre content of the diet and the epigenetic regulation of host cells and tissues. Pregnancy is a critical period of genome plasticity during which maternal diet may have long-lasting impact on the growth and health of offspring into adulthood.

We aimed (i) to assess if varying fibre content in maternal diet influences the epigenome and the transcriptome in two target tissues (liver and skeletal muscle) of pig fetuses; and (ii) to explore the possible persistence of epigenetic marks through the weaning stage. Three isocaloric diets (high-fibre, pea fibre + acetate, and no-fibre control) were provided to three groups of sows (7 sows each) throughout gestation. Metadata, tissues and cell samples of all fetuses and piglets (2 males and 2 females per sow) were collected by FAANG protocols. Liver and skeletal muscle of 84 fetuses and 76 piglets were profiled for chromatin accessibility (ATAC-seq) and polyA+ RNA-seq.

The 632 ATAC-seq experiments (30 million 150bp paired-end reads) were processed with the nf-core ATAC-seq pipeline and results showed a very high mapping rate, a fraction of reads in peaks (FRIP) above 0.3 and an accumulation of mapped reads at the transcription start site (TSS) of known genes. Exploratory and differential analyses on the 245,452 peaks quantified in each sample are currently in progress.

This study is part of the GENE-SWitCH project (funded by European Union's Horizon 2020 Research and Innovation Programme under the Grant agreement n° 817998) and is part of EuroFAANG (<https://eurofaang.eu>).