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► To cite this version:

Agnès Bonnet, Sarah Maman, Laure Gress, Amandine Suin, Céline Bravo, et al.. Transcriptome of the feto-maternal interface in pigs in late gestation: part1fetal placenta. Joint International Congress on Animal Science (EEAP 2023), Aug 2023, Lyon, France. pp.37.20. hal-04193423

HAL Id: hal-04193423

<https://hal.science/hal-04193423v1>

Submitted on 1 Sep 2023

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Transcriptome of the feto-maternal interface in pigs in late gestation: part1-fetal placenta

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In pigs, selective breeding has led to a rise in neonatal mortality, in relation to a reduced maturity of newborn piglets. Piglet maturity and growth accelerate at the end of gestation and this requires considerable nutritional support. The process of maturation varies with fetal genome and uterine environment and depends upon placenta, the tissue that regulates feto-maternal allocation of resources.

To better understand the fetal maturation process, purebred and crossbred fetal genotypes were produced from 14 Large White (LW) and 14 Meishan (MS) sows differing for piglet maturity at birth and piglet survival. All the sows were inseminated with mixed semen from the two breeds. We compared the transcriptome in 224 placentas collected according to this four fetal genotypes and two days of gestation (D90-D110, term at 114 days). The transcriptome was obtained by RNAseq technology and processed by nf-core/rnaseq pipeline. Statistical analysis was performed using mixed linear models with sow as random effect followed by a correction for multiple testing (FDR < 0.001).

We documented the expression profile of 8,407 differential transcripts (DEGs) for gestational age, fetal genotype and their interaction. These DEGs reflect an important transcriptomic change that occurs between D90 and D110 in the endometrium (2,901 transcripts) and underline genes involved in pathways essential for normal placental development such as the insulin-signaling pathway. In addition, 1,543 transcripts were differentially expressed according to fetal genotype. Gene Ontology enrichment analysis of these DEGs highlighted the placental fatty acid β -oxidation pathway, which is proposed to be related to maternal nutrition and body composition. Other transcripts (561 DEGs) showed interactions between fetal genotype and gestational age. Biological interpretation is underway. This research is part of the ANR-20-CE20-0020-01 project COLOcATION.