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Transcriptome of the feto-maternal interface in pigs in late gestation: part2-sow endometrium

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In pigs, genetic progress has led to a rise in perinatal mortality, mostly due to a reduced piglet maturity. Piglet maturity acquisition and greater fetal growth occur at the end of gestation and require considerable nutritional support. These processes are closely related to the physiology and nutrition of the dam, as nutrients are transmitted from the endometrium to the fetus via the placenta. The endometrium is critical for implantation, placentation, embryonic and fetal development; many critical morphological and secretory changes occur throughout gestation.

In order to understand the role of endometrium during the fetal maturation process, we compared two breeds at two days of gestation (D90-D110, term at 114 days): Large White (LW) and Meishan (MS) with high and low neonatal mortality, respectively.

The transcriptome of 224 endometrial samples from the two breeds at two gestational stages was obtained by RNAseq technology and processed by Nextflow nf-core/rnaseq pipeline. Statistical analysis was performed using mixed linear models with sow as random effect (limma package) followed by a correction for multiple testing (Benjamini-Hochberg, FDR < 0.001).

We documented the expression profile of 10,080 differential transcripts (DEGs) for gestational age, mother breed and their interactions. These DEGs reflect an important transcriptomic difference between LW and MS breeds (2,721 transcripts) and underlined genes involved in protein binding and endocytosis pathways. A smaller transcriptomic change was observed between D90/D110 in the endometrium (607 transcripts), mainly reflecting an evolution in metabolic pathways. Moreover, 3,210 DEGs showed interactions between gestational age and breed. They correspond to eight clusters of expression profiles. Biological interpretation is underway. This research is part of the ANR-20-CE20-0020-01 project COLOCATION.