# Contribution of fetal genome and sex to late gestation endometrial gene expression

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**Title of the Abstract**

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**Body text of the Abstract**

Piglet maturity acquisition and greatest fetal and placenta growth occur at the end of gestation (90-110 days (D90-D110)) and require considerable nutritional support from the mother. A fine balance of feto-maternal allocation of resource is necessary to support pregnancy and results from interactions between maternal and fetal genetic potential, maternal nutrition and environment, endometrial and placental functions. Particularly, the imprinted genes have the role to drive the communication and regulate nutrient exchange between the mother and the fetus.
Considering this, we investigated the influence of fetal genome and sex on the expression of a subset of 42 putative imprinted genes at the maternal interface (endometrium) at D90 and D110. We used a genetic protocol that produced pure and reciprocal crossed fetuses using two extreme breeds for fetal maturity: Large White (LW; n=13) and Meishan (MS; n=11), showing substantial and low neonatal deaths respectively. Hence, in a same uterus, endometrium samples were associated with its purebred fetus or crossbred fetus. Relative expression was quantified using qRT-PCR and analyzed using linear mixed models (n=5-6 per genotype, n=5-6 per sex, n=2-7 per uterus).

Fifteen imprinted genes were differentially expressed in endometrium between the two breeds (FDR<0.05) that underlined differences in vascular development and permeability, nutrient transportation and energy store. Correlation networks (PLS, regression mode) at each gestational age associated genes expression with fetal biometric and placental measures.
At D90, we pointed out for the first time the influence of fetal genome on endometrial expression of eight genes (FDR<0.1). Fetal sex influenced the expression of three genes in MS endometrium associated to MS purebred fetuses and four genes in LW endometrium associated to their crossed fetuses (FDR<0.05).

These data suggest that particularly in crossbreeding schemes, fetal genome and sex may influence endometrial gene expression at the end of the gestation.