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Contribution of fetal genome and sex to fetal maturity, searching at the interface with sow endometrium

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Context

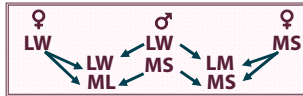
Maturity process occurs largely at the end of gestation (D90-D110, term at D114)

Endometrium ↔ Placenta key interface for the regulation of feto-maternal exchange of nutrients between mother and fetuses with implication of epigenetic mechanisms

Objectives

We investigate the influence of fetal genome and sex on the expression of a subset of 40 imprinted genes at the materno-fetal interface in late gestation (D90-D110)

Material

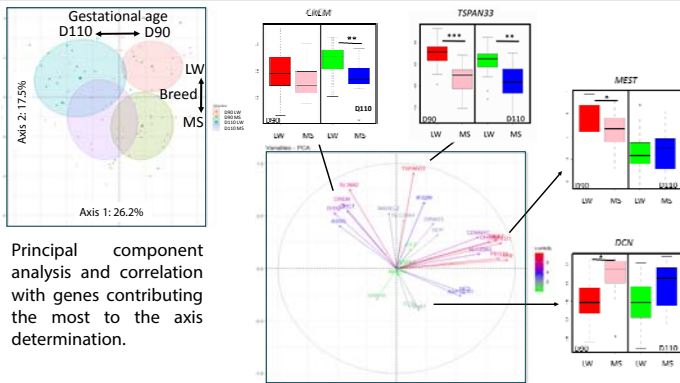


Experimental protocol (Canario et al., 2006, 2014)

4 fetal genotypes: Purebred (PB) Large White (LW) with reduced maturity and important mortality, purebred Meishan (MS) with naturally high maturity and few mortality, crossed bred fetuses (CB) MSxLW (ML) or LWxMS (LM)

Results

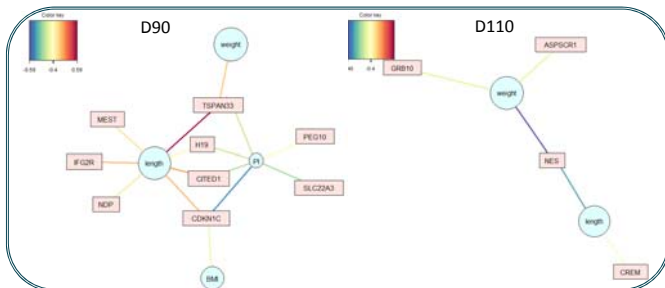
The main differences in endometrial imprinted gene expression between pregnant sows with extreme phenotypes for neonatal survey (LW and MS) are observed at D90 (15 genes; D110 (5 genes))



Principal component analysis and correlation with genes contributing the most to the axis determination.

TSPAN33-MEST: higher level of expression in LW than MS at D90
DCN: higher level of expression in MS than LW at D90
CREM: higher level of expression in LW than MS at D110

Imprinted gene expressions in endometrium are more associated with fetal maturity phenotypes at D90.

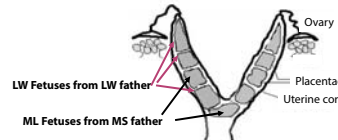
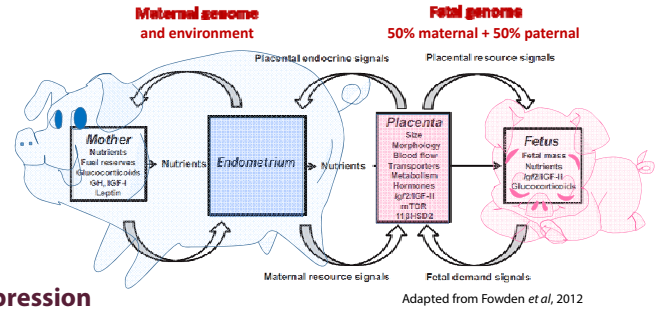


Networks of partial least square regression between endometrium gene expression and fetal biometric measurements (D90/D110): Length = body length ; weight = body weight BMI: Body mass index; PI: ponderal index The same threshold was used for the 2 networks.

Conclusion

Fetal genome and sex influence endometrium gene expression and suggest the participation of paternal alleles into the regulation of nutrient exchanges to fetuses

Genetic selection applied in swine led to a reduction of piglet maturity



The endometrium is juxtaposed to different placentae: example of a LW sow uterine tract

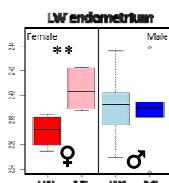
Methods

5 biological replicates
 Expression relative quantification by qPCR (BioMark HD)
 Statistical analyses with linear mixed models and Correction for multiple testing (FDR<0,05)

The genome of female fetuses affects gene expression in LW endometrium at D90
 PEG10, AMPD3, CITED1, ENPEP and H19

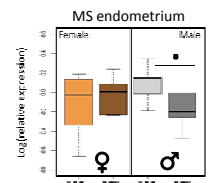
The genome of male fetuses affects gene expression in MS endometrium at D90
 PLAGL1 and TSPAN33

AMPD3



Lower *AMPD3* expression level in LW endometrium juxtaposed to female PB than other genotype x sexes. A lower placental *Gatm* abundance is described in human to be associated with intrauterine growth restriction (McMinn, J 2006).

PLAGL1

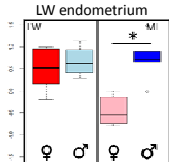


Lower *PLAGL1* expression level in MS endometrium juxtaposed to male PB than male CB (LM). *PLAGL1* protein has been shown to be a master coordinator of a genetic growth network in mice.

The sex of CB fetuses affects gene expression in LW endometrium at D90
 DHCR7, MEST, ASNS, CITED1, CREM and H19

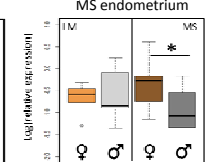
The sex of PB fetuses affects gene expression in MS endometrium at D90
 DHCR7, MEST, PEG10, CITED1 and H19

H19



The expression of *H19* and *PEG10* vary in LW and MS endometrium function the sex of respectively CB and PB fetuses. *H19* has a role in regulation of body weight and in cell proliferation. *PEG10* is important for embryonic development and the formation of placenta.

PEG10



Up to now, the expression of imprinted genes was hardly described in endometrium at the end of gestation.