Characterization of the endometrial metabolome in late gestation

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Title of the Abstract

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Body text of the Abstract

In pigs, genetic progress has led to a rise in perinatal mortality, mostly due to a reduced piglet maturity. The end of the gestation (90-110 days of gestation (dg)) plays a determinant role in the fetal maturity acquisition. Endometrium is crucial for its acquisition, as it delivers nutrients to the fetus through the placenta. To understand the role of the endometrium metabolome during late gestation, we compared two pure maternal breeds with contrasting birth survival (Large White (LW, higher birth mortality) and Meishan (MS, lower birth mortality)) inseminated with mixed semen from to generate extreme purebreds and reciprocal crossed fetuses in a same uterus environment.

Using 1H-NMR techniques, we acquired untargeted metabolomics measurements on 224 endometrial samples, each juxtaposed a fetal placenta from 28 sows. Metabolic quantification and identification were performed with the R package ASICS. Among the 191 available metabolites in the reference library of ASICS, approximately forty metabolites were identified.

Preliminary results using Orthogonal Partial Least Squares Discriminant Analyses were performed and discriminated the two stages of gestation and the mother genotype on the first component. Of 46 metabolites, 17 metabolites were found to be influential (Variables Influence on Projection >1) for the stage of gestation. These results are consistent with the results found via mixed linear models with sow as random effect models followed by a correction for multiple testing (FDR < 5%). As already known, fructose is more abundant at 90 dg than at 110 dg. Conversely, L-Glutathione-reduced was more concentrated at 110 dg than at 90 dg and more concentrated in MS than LW sows. These results are consistent with the previous analysis, performed in urine and amniotic fluid. In addition, Citrate and L-glycine were more concentrated in MS than LW sows at both stages of gestation. Further biological interpretation of metabolomic data is underway.