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Characterization of the endometrial metabolome in late gestation

Alyssa Imbert, Nathalie Marty-Gasset, Laure Gress, Cecile Bonnefont,
Nathalie Vialaneix, Laurence Liaubet, Agnès Bonnet

► **To cite this version:**

Alyssa Imbert, Nathalie Marty-Gasset, Laure Gress, Cecile Bonnefont, Nathalie Vialaneix, et al.. Characterization of the endometrial metabolome in late gestation. International Conference on Pig Reproduction 2023, Jun 2023, Gent, Belgium. hal-04126140

HAL Id: hal-04126140

<https://hal.inrae.fr/hal-04126140>

Submitted on 13 Jun 2023

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Submitting Author: Dr. Alyssa Imbert

Institution: INRAe

Country: France

Authors' preference: Poster

Topic allocated Pregnancy and mechanisms governing embryo and piglet survival/vitality

Emailaddress agnes.bonnet@inrae.fr

Submitted Keywords pregnancy / endometrium in late gestation / metabolome

Title of the Abstract

Characterization of the endometrial metabolome in late gestation

List of Authors of the Abstract

Imbert A. 1, Marty-Gasset N. 1, Gress L. 1, Bonnefont C. 1, Vialaneix N. 2, Liaubet L. 1, Bonnet A. 1

1 GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326, Castanet Tolosan, France

2 Université de Toulouse, INRAE, UR MIAT, Castanet-Tolosan F-31326, France.

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.