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► To cite this version:

Isabelle Louveau, Laurence Liaubet, Laurianne L. Canario, H el ene Quesnel, Pascal G.P. Martin, et al.. Understanding the development of adipose tissue of pure and crossbred fetuses from Meishan and Large White sows during the last month of pregnancy. 9th International Conference on Pig Reproduction, Jun 2013, Olsztyn, Poland. , 2013, 9th International Conference on Pig Reproduction : Program and Abstract Book. hal-01210458

HAL Id: hal-01210458

<https://hal.science/hal-01210458v1>

Submitted on 3 Jun 2020

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Understanding the development of adipose tissue of pure and crossbred fetuses from Meishan and Large White sows during the last month of pregnancy

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The Meishan (MS) breed exhibits higher piglet survival compared with commercial lean breeds such as the Large White (LW). Within a genotype, a positive relationship exists between lipid stores at birth and genetic merit for survival. White adipose tissue serves as an energy store; it may play a pivotal role in the adaptation to extra-uterine life by preventing heat loss or simply contributing to piglet maturity. This study aimed at a better understanding of the relationships between maturation of adipose tissue and neonatal vitality. It was based on the comparison of the progeny of two pure maternal breeds inseminated with mixed semen from the two breeds, so that 4 fetal genotypes were examined (MSxMS, LWxMS in MS sows; LWxLW, MSxLW in LW sows).

Subcutaneous adipose tissues were collected on second-parity fetuses sacrificed after caesarian at 90 or 110 days of gestation (GD) to evaluate gene and protein expressions (8 samples per GD and fetal genotype). The analyses involved a 60K porcine microarray, quantitative PCR on target genes, and two-dimensional differential gel electrophoresis of soluble protein extracts. Data were compared by ANOVA with fetal genotype, gestational age, and their interactions as main effects.

The numbers of transcripts and protein spots having a differential abundance in adipose tissue were found much greater when developmental stages were compared than when fetal genotypes were considered, which confirms the dynamics in adipose tissue maturation during this period. With respect to the gene expression, nearly 1500 oligonucleotides differed (FDR < 1%) between MSxMS and LWxLW fetuses at GD110. Expression level of DLK1/Pref1, a preadipocyte marker, decreased ($P < 0.05$) between GD90 and GD110; this reduction was more pronounced in MS and crossbred fetuses than in LW fetuses. Both FABP4, a marker of mature adipocyte, and LEPTIN, an indicator of the secretory function, were expressed more ($P < 0.05$) at GD110 than at GD90; they were expressed more in MSxMS than in LWxLW, and intermediate in crossbred fetuses at both stages. About 70 protein spots were affected ($P < 0.05$) by the fetal genotype. Vitality was evaluated on first-parity offspring of the same sows. After birth, MSxMS and LWxMS piglets had much higher mobility than LWxLW piglets; MSxLW ranked intermediate.

Thus, the genome of the fetus played an important role in adipose tissue development. These results suggest new strategies for genetic improvement or nutritional interventions to increase piglet survival through changes in their body composition.

Financially supported by the French project PORCINET, ANR09GENM005