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A multi-tissue analysis in fetal pigs to identify genes involved in the determinism of maturity and survival at birth

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Selection for prolificacy and lean growth rate in swine has been associated with a substantial increase in piglet mortality. The first 24–48 hours after birth represent the most critical period. A major determinant for early survival is piglet maturity at birth which relies strongly on the process of maturation during the last month of gestation.

The objective of the current study was to compare progeny from Large White (LW) and Meishan (MS) pigs which differ for piglet survival and vitality to identify new markers of maturity. The two pure MS and LW sows were inseminated with mixed semen from the 2 breeds, so that 4 fetal genotypes were examined (MSx-MS and LWxMS in MS sows, LWxLW and MSxLW in LW sows). Samples of skeletal muscle (Longissimus dorsi), adrenal glands, subcutaneous adipose tissue, small intestine, liver, and whole blood were collected on fetuses at 90 and 110 days of gestation. For gene expression analysis, a 60K microarray has been developed (Agilent Technology) from the 44K Porcine (V2) Gene Expression Microarray that was completed with 17,073 60-mers targeting genes expressed in the immune system, adipose tissue and muscle. A total of 384 hybridizations were obtained (8 fetuses x 4 genotypes x 2 stages of development x 6 tissues) and analyzed with a linear model and a FDR (False Discovery Rate) adjusted p-value of 1% to identify genes differentially expressed in the 4 fetal genotypes.

Between 90 and 110 days of gestation, from 8,000 (intestine) to 28,000 (muscle) transcripts were differentially expressed depending on the fetal genotype and 314 transcripts were common to the six tissues. The comparison between genotypes at each stage of gestation highlighted the difference between the two extreme fetuses (LWxLW versus MSxMS) with a mean of 3,700 and 8,000 transcripts differentially detected at 90 and 110 days, respectively. The contrast of expression between the two categories of crossbred piglets was more subtle with only a mean of 168 and 335 transcripts differentially detected at 90 and 110 days respectively; this may reveal the influence of the maternal and paternal genomes.

Biological interpretation of genomic data is underway. This genetic study will contribute to a better understanding of the molecular mechanisms involved in piglet maturity determinism and to the identification of biomarkers of maturity.

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