

25. Umbilical cord gene expression in newborn piglets with different birth body weight and lactation growth

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Introduction Modern hyperprolific sows must deal with large litters (> 16 piglets born) which may cause a significant reduction in mean piglet body weight (BW). Additionally, it increases the number of piglets being born with low BW that were exposed to different degrees of intrauterine growth restriction (Hansen *et al.*, 2019). The neonatal piglet survival and further piglet growth and efficiency may be determined by foetal programming, which takes place during gestation and leads to epigenetic changes. The aim of the present study was to investigate umbilical cord gene expression as a non-invasive method for understanding differences between piglets with varying birth weight and their growth performance during the suckling period.

Material and methods A total of 169 piglets [(Landrace x Yorkshire) x Pietrain] born from eight sows between first and sixth parity (3.6 ± 0.71) were individually weighed at birth. Umbilical cord samples were taken just after birth. A subset of 100 piglets with extreme birth BWs was selected for analysis. Firstly, piglets were classified into two categories based on their birth BW: small (SMALL; 0.9 ± 0.02 kg) if $BW \leq 1.15$ kg, or big (BIG; 1.5 ± 0.02 kg) if $BW > 1.15$ kg. At weaning (26 d), 52 piglets were individually weighed and re-classified as SMALL (4.3 ± 0.22 kg) if $BW \leq 5.15$ kg, or BIG (7.3 ± 0.20 kg) if $BW > 5.15$ kg (if SMALL at birth) or $BW > 8.00$ kg (if BIG at birth). Finally, piglets were divided into three groups ($n = 12$ piglets per group): SMALL-SMALL (SS), SMALL-BIG (SB) and BIG-BIG (BB). The BIG-SMALL group was not included in the study due to the small sample size for statistical analysis. The expression of 20 genes in umbilical cord tissue was analysed by RT-qPCR using a microfluidic dynamic array. After a logarithmic transformation, the gene expression data were analysed using linear mixed models with the BW piglet category as a main factor and the sow as a random effect (R, v4.2.3, R Foundation, Vienna, Austria).

Results Summary statistics and relative gene expression by group are provided in Table 1. At birth, vascular endothelial growth factor A (*VEGFA*) gene showed a log₂-fold change of 0.15, indicating a 0.15-fold upregulation in SMALL piglets compared to their heavier littermates ($P < 0.05$). A tendency for a higher gene expression of fms-related receptor tyrosine kinase 1 (*FLT1*) was also found in SS and SB piglets ($P < 0.10$). Considering that hypoxic conditions and vascular damage induce the expression of *VEGF* and its receptors (Vidal *et al.*, 2000), this result suggests that SMALL piglets may be associated with smaller placentas, which have slower blood flow or poorer permeability. The SS and SB piglets showed an upregulation of one gene involved in immune and inflammatory responses (interferon gamma receptor 1, *IFNGR1*), but also a downregulation of collagen type VIII alpha 1 chain (*COL8A1*) compared to the BB piglets ($P < 0.05$). Moreover, a tendency for an upregulation of bone morphogenetic protein 4 (*BMP4*) in BB piglets was observed ($P < 0.10$). *BMP4* is a protein-coding gene involved in a wide range of biological processes related to development and growth.

Table 1. Summary statistics for litter size (LS) at birth, birth body weight (BW), LS at weaning, weaning BW and average daily gain (ADG) during lactation for piglets classified as SMALL-SMALL, SMALL-BIG and BIG-BIG ($n = 12$ per group), and relative gene expression in SMALL-SMALL, SMALL-BIG and BIG-BIG piglets, where data are means of 12 piglets for each category.

Trait	SMALL-SMALL	SMALL-BIG	BIG-BIG	RSD	P value
	Mean	Mean	Mean		
LS at birth	23.3	23.3	24.3	3.63	0.76
Birth BW, kg	1.0 ^B	1.0 ^B	1.6 ^A	0.12	< 0.001
LS at weaning	13.2	13.0	12.8	1.39	0.75
Weaning BW, kg	4.2 ^C	6.1 ^B	8.9 ^A	0.79	< 0.001
ADG lactation, g	123 ^C	197 ^B	278 ^A	292	< 0.001
<i>IFNGR1</i>	0.00 ^A	0.00 ^A	-0.13 ^B	0.093	0.002
<i>COL8A1</i>	-0.06 ^{ab}	-0.15 ^b	0.09 ^a	0.225	0.037
<i>FLT1</i>	-0.02	-0.01	-0.17	0.168	0.051
<i>BMP4</i>	-0.04	0.02	0.09	0.125	0.055

^{A,B,C}Means within a row with different superscripts differ significantly ($P < 0.01$); ^{a,b}Means within a row with different superscripts differ significantly ($P < 0.05$); Gene expression values are indicated as the logarithmic transformation of the ratios of cycle relative threshold value for each gene normalised to that of the reference sample; RSD, residual standard deviation.

Conclusion and implications The gene expression of light piglets at birth reveals a major activation of angiogenesis and pro-inflammatory responses, suggesting that those piglets are the most compromised during gestation. The gene expression pattern of heavy body weight piglets at birth may be related to a greater potential for further growth performance compared to their lightweight littermates. Finally, the gene expression analysis of umbilical cord samples could help to characterise piglets at birth and understand the variations observed in their growth performance during the suckling period.

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References

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