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Effect of vitamin D supplementation on growth traits and gene expression in the intestine of pigs

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Vitamin D plays a key role in pig farming, affecting the health and performance of animals. In addition to its well-known effect on the skeletal system, it is known to stimulate the immune system to defend against infections. Better animal immunity can promote better growth and increase the profitability of breeding. Nevertheless the appropiate dosage of vitamin D in animal and human nutrition is still a question of debate. The aim of our study was to check whether the use of high doses of vitamin D can change gene expression patterns in the intestines of pigs – organ which is crucial in immune system. Also we wanted to check if these changes are accompanied by significant improve of the fattening performance characteristics of pigs. In the 90-day experiment, 30 pigs were divided into three groups depending on the dose of vitamin D; group A – 0 UI/Kg of vitamin D, group B – 5000 UI/Kg of vitamin D, group C – 10000 UI/kg of vitamin D. During fattening, animal growth and feed consumption were monitored, and half-carcasses were weighed at slaughter. Statistical analysis of the obtained results did not show a significant effect of vitamin D supplementation on fattening parameters and animal growth. Additionally we performed gene expression study, based on the RNA-seq and qPCR analysis of the jejunum and colon of pigs. We observed substantial activation of immune related genes in the jejeunum of pigs supplemented with 5000 and 10000 UI/Kg of vitamin D when compared with animals with no additional supplementation. Among the most activated genes, there were interferon stimulated genes like ISG 15, OASl, OASL2. In the jejunum, we also observed the activation of genes connected to protection against oxidative stress (SOD2, SIRT3, NOS2), while in the colon we noted significant increase in genes connected to cell cycle control (PLK1, KLIF4, KLIF3). This suggests that the currently used vitamin D dose of 2000 UI/Kg is optimal in terms of fattening characteristics of pigs, but higher doses of vitamin D may be helpful in improving animals' immunity during a dangerous period of increased infection rates in pig herds. Financed by National Science Center, Poland, grant no 2019/35/O/NZ9/03148 and NRiAP grant no 501-181-921

Transcriptomic differences in the adipose tissue of Krškopolje and modern hybrid pigs

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Compared to lean pig genotypes, the local Krškopolje pig is characterized by a greater capacity for lipid deposition. In the present study, we investigated differences in the adipose tissue transcriptome between Krškopolje pigs (n=7) and modern lean crossbreed (n=7). Starting at the same weight (27 kg), all animals were fattened in the indoor system with identical amounts of the same commercial feed for 179 days. After slaughter, adipose tissue samples were collected, and RNA was extracted. Samples were sequenced using the Illumina NovaSeq platform, generating 150 bp paired-end reads. Sequencing produced approximately 47.5 million paired-end reads, with over 94.6% mapping uniquely to the Sus scrofa 11.1 reference genome. Differential expression analysis identified 363 genes ($\log2FC > 1$; $P\text{-adj} < 0.05$), of which 182 were upregulated and 181 downregulated in Krškopolje pigs compared to the modern pig breed. The upregulated genes were involved in lipid and energy metabolism (e.g., ↑NR4A3, ↑ACBD7, ↑PTGS2, ↑CES1), adipocyte proliferation and differentiation (e.g., ↑IL-1A, ↑PAPPA2, ↑NR4A3, ↓TRPV4, ↓WNT10B), inflammation (e.g., chemokines ↑CXCL8, ↑CCL4, ↑CXCL2), and extracellular matrix composition (e.g., ↑COL6A5, ↓COL11A2). Gene ontology over-representation analysis highlighted biological processes such as the regulation of fat cell differentiation (GO:0045598), cell morphogenesis (GO:0000902), transmembrane transport (GO:0055085), and phosphatidylinositol-mediated signalling (GO:0048015). Enriched cellular components were the extracellular space (GO:0005615), insulin-like growth factor binding protein complex (GO:0016942), and growth factor complex (GO:0036454). The present RNA-seq comparative analysis represents the first high-throughput transcriptomic study on the Krškopolje pig, revealing several key processes responsible for the breed's high fat accumulation. Acknowledgements: Funding by Slovenian Research and Innovation Agency (grants P4-0133, P4-0053, J4-3094) is acknowledged. Key words: Krškopolje pig, lean hybrid pigs, adipose tissue, gene expression.