Book of Abstracts
of the 76th Annual Meeting of the European Federation of Animal Science

Book of Abstracts No. 39 (2025)
Innsbruck, Austria
25 - 29 August, 2025

Session 68 Poster 20

Influence of rearing systems on the liver transcriptome profile of krškopolje pigs: indoor vs. outdoor conditions

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Key words: local pig breed, RNA-sequencing, rearing system The Krškopolje pig is an autochthonous Slovenian breed, raised in various, mainly low-input production systems. To better understand, the impact of the rearing environment on this breed, this study aimed to characterize the liver transcriptome of Krškopolje pigs reared indoors (IND, n = 9) and outdoors (OUT, n = 10). At 331 days of age, the pigs were slaughtered, and liver samples were collected for RNA sequencing using the Illumina NovaSeq platform. On average, sequencing generated 45 million paired-end reads, with more than 88.4% uniquely mapped reads. Differential gene expression analysis identified 144 differentially expressed genes, including 85 upregulated and 59 downregulated in the OUT compared to the IND group. Genes upregulated in the OUT group were associated with neuronal development (e.g., UNC5D, PRTG, TENM4, BEND6), liver fibrosis via PFKFB3-mediated glycolysis (PFKFB3), hepatocyte regeneration and growth (FGF21, FGF14), and glucose metabolism (FGF21, RGS16). Additionally, the OUT group exhibited upregulation of GABRQ, which encodes gamma-aminobutyric acid receptor linked to lipid metabolism; DIO2 associated with adaptive thermogenesis, and gene TRARG1, a transport regulator of GLUT4. Among the downregulated genes, NNMT gene previously linked to fatty acid oxidation and liver fibrosis was detected. This study provides the first insights into the genetic regulation of the liver in Krškopolje pigs raised in different production systems, contributing to a deeper understanding of the breed's adaptability and metabolic responses.
Acknowledgements: Funding by Developmental Funding Pillar of Agricultural Institute of Slovenia, Slovenian Research and Innovation Agency (P4-0133, J4-3094 and Z4-60178) and project GEroNIMO (EU H2020 GA no. 101000236) are acknowledged.

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Tracing Transcriptomic Changes in Chicken Embryonic Blood: Multi-Generational Effects of In Ovo Stimulation with Nutriepigenetic Factors

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Epigenetic modifications regulate gene expression and are influenced by environmental factors, shaping phenotypic and clinical outcomes. These changes can persist across generations, though their stability can vary by tissue. This study aims to assess the effects of prenatal stimulation with nutriepigenetic factors on the transcriptome of embryonic blood across generations. Since primordial germ cells (PGCs) circulate in embryonic blood before settling in the gonads, this tissue likely represents both somatic and germline lineages. We established a novel in ovo model over three generations of Green- legged partridgelike with an added assessment of F4 embryos. Synbiotic PoultryStar and choline were injected in ovo on the 12th day of egg incubation. F1 embryos were divided into control (0.9% NaCl), synbiotic (SYN, 2 mg PS), and synbiotic + choline (SYNCH, 2 mg PS + 0.25 mg choline). In F2 and F3, SYN and SYNCH were split into two subgroups each: A) solely injected in F1 (SYNs and SYNCHs); and B) repeatedly injected in every generation (SYNr and SYNCHr). Fertilized eggs from all groups laid by F2 and F3 hens were incubated until HH stages 14–16, at which point embryonic blood was collected from the dorsal aorta of embryos. Embryos were sexed using PCR-based sex determination, and blood samples were pooled by sex. RNA was isolated from male samples for RNA sequencing. Our preliminary results revealed effects of in ovo stimulations on embryonic blood transcriptome in F3. However, the effect diminished in F4 embryos. Notably, synbiotic treatment primarily influenced cellular homeostasis, metabolic activity, and stress response mechanisms. The addition of choline further enhanced regulatory effects on gene expression and membrane-associated functions.
Funding: National Science Centre, Poland (2020/37/B/NZ9/00497). Bioinformatics analysis: Poznań Supercomputing and Networking Center resources.