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Poster Session Poster 32

Preliminary results on RNA-seq of Polish geese livers

A. Koseniuk[1], K. Połtowicz[2], G. Smołucha[1], J. Nowak[2], K. Kłos[3], B. Kmita[1]

[1] National Research Institute of Animal Production, Department of Animal Molecular Biology, 1, Krakowska Street, 32-083 Balice, Poland, [2] National Research Institute of Animal Production, Department of Poultry Breeding, 1, Krakowska Street, 32-083 Balice, Poland, [3] National Research Institute of Animal Production, Experimental Station of the National Research Institute of Animal Production, 1, Parkowa Street, 88-160 Kołuda Wielka, Poland

Over 98% of Poland's goose population consists of the White Kołuda® goose. The White Koluda ® is an oat-fed goose recognized on the Polish List of Traditional Products in the fresh meat and meat products category. On the contrary, the Pomorska is an old, native breed included in the Genetic Resources Programme in Poland. Both breeds significantly differed in their body mass. We conducted global RNA sequencing of the samples from the livers of both breeds, six samples from each breed. The study aimed to search for the genetic background of extraordinary body mass and meat performance, which featured the White Koluda ® breed. The sequencing was performed on the NovaSeq X Plus Series (Illumina, USA). The Differentially Expressed Genes analysis revealed 57 genes up and downregulated. The most expressed upregulated genes are HOGA1 (4-hydroxy-2-oxoglutarate aldolase 1) and ACP6 (acid phosphatase 6), and downregulated ones are SCD (stearoyl-CoA desaturase), and ASIC (acid-sensing ion channel subunit family member 4). Several genes among the 57 up and down-regulated genes are involved in processing fatty acids and energy metabolism. The most enriched molecular processes are found in the molecular function category (GO term: oxidoreductase activity) and biological process (GO term: small molecule biosynthesis process). The HOGA1 gene is involved in pyruvate synthase in mitochondria. SCD gene is involved in fatty acid biosynthesis, especially the synthesis of oleic acid. The ACP6 gene is involved in lipid raft modulation and balancing lipid composition within the cell. This gene, as well as others found in this study, has the potential to explain the extraordinary meatness of the White Koluda ®.

Poster Session Poster 33

Estimating the heritability of meat quality traits in Krškopolje pigs

K. Poklukar[1], M. Čandek-Potokar[1], M. J. Mercat[2], M. Banville[2], M. Škrlep[1]

[1] Agricultural Institute of Slovenia, Hacquetova 17, 1000 Ljubljana, Slovenia, [2] IFIP – Institut du Porc, 9 boulevard du Trieux, 35740 Pacé, France

The Krškopolje pig is the only autochthonous pig breed in Slovenia, characterized by high fat deposition, relatively low carcass leanness, and high quality meat suitable for the production of high-grade meat products. Despite these attributes, genetic parameters related to meat quality traits have not been previously studied, although such data are essential for developing an effective breeding program for breed. To address this gap, phenotypic data from 409 Krškopolje pigs under 500 days were collected for meat quality traits, along with pedigree data and genotypic data (N=518). Variance components and heritability were estimated using AIREMLF90. The model included fixed effects of the farm of origin and age, alongside random animal effects for additive genetic variance. Heritability estimates (±SE) derived solely from pedigree data were as follows: 0.39±0.15 for intramuscular fat content, 0.27±0.14 for backfat thickness, 0.42±0.15 for muscle L* CIE value, 0.55±0.16 for muscle a* CIE value, 0.25±0.14 for drip loss, and 0.54±0.16 for cooking loss. Incorporating single-step genomic best linear unbiased prediction increased heritability estimates (±SE) to 0.72±0.12, 0.63±0.15, 0.59±0.15, 0.62±0.13, 0.41±0.15, and 0.84±0.13 for intramuscular fat content, backfat thickness, muscle L* CIE value, muscle a* CIE value, drip loss, and cooking loss, respectively. Genetic correlations between meat quality traits suggested that selection for larger intramuscular fat content could decrease a* CIE value (-0.22), drip loss (-0.24) and cooking loss (-0.26). The findings highlight the potential for genetic selection to effectively enhance meat quality traits in local Krškopolje pig. Acknowledgements: Funding by Slovenian Agency of Research (grants P4-0133, Z4-60178, J4-3094) and project GEroNIMO (EU H2020 GA no. 101000236) are acknowledged. Key words: Krškopolje pig, genetic variance, breeding programme.