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Standardized ileal digestible Lysine needs based on growth performance, carcass and ham quality of pigs for dry-cured ham production

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This study aimed to assess the standardised ileal digestible lysine (SID-Lys) needs of ad libitum-fed pigs for dry-cured ham production. The trial included 96 gilts and barrows [45 ± 5 kg initial body weight (BW) at 90 days of age], divided into 4 treatment groups (2 pens/group) receiving feeds with different SID-Lys levels: Low (L), Medium-Low (ML), Medium-High (MH) and High (H). In each treatment, dietary SID-Lys decreased with age in growing (90-118 d), early finishing (119-132 d) and late finishing (133-233 d) periods. The SID-Lys contents (g/kg) were: 6.9, 6.0,4.2 for the L group; 7.8, 6.9, 5.2 for the ML; 8.3, 7.8, 6.0 for the MH; and 9.3, 8.3, 6.9 for H. Individual feed intake was measured with electronic feeders. BW and backfat thickness were recorded every two weeks. Pigs were slaughtered at 251 d (190 ± 15 kg BW). Growth, feed intake, gain-to-feed ratio, carcass and ham traits were analysed using a mixed model with treatment, sex and their interaction as fixed effects and pen within treatment as a random effect. No differences in growth performance, carcass and ham traits were found between ML and groups with higher SID-Lys (MH, H). However, the L pigs had lower final BW (197 vs 175 kg; $p = 0.016$), daily gain (985 vs 859 g/d, $p = 0.013$), gain:feed ratio (0.316 vs 0.283, $p = 0.004$), carcass weight (164 vs 146 kg, $p = 0.017$) fat cuts yield (234 vs 219 g/kg carcass, $p = 0.028$), and trimmed ham weight (14.8 vs 13.4 kg, $p = 0.030$) than ML pigs. Except for trimmed ham weight, no differences in ham quality traits were found. These findings indicate that the ML dietary SID-Lys levels optimize growth, feed efficiency and increase the carcass and ham weights, with minimal impact on carcass and ham quality traits. Research supported by 1) Agritech National Research Center, funded by the European Union Next–Generation EU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4-D.D. 1032 17/06/2022, CN00000022). 2) European Union, Next Generation EU, Mission 4, Component 1, CUP: C53D23005470006, Progetti di Rilevante Interesse Nazionale (PRIN), title project: NUTR-PIG grant.

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Genetic insights into backfat thickness and fatty acid composition in Krškopolje pig: Differential gene expression linked to genetic variants

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Key words: Local pig breed, adipose tissue, shallow DNA-sequencing, RNA-sequencing This study aimed to associate gene expression of the traits underlying backfat deposition, as well as palmitic and stearic acid content by linking RNA-sequencing with genetic variants. From a group of 15 Krškopolje pigs reared under the same conditions, extreme phenotypes ($n = 2\times5$) were chosen for backfat, palmitic and stearic acid content. DNA ($n=142$) and RNA ($n=2\times5$) were extracted and shallow DNA and RNA sequencing were performed to identify genetic variants and differentially expressed genes (DEG). DEG analysis highlighted 4 upregulated (e.g. PVALEF) and 5 downregulated genes (e.g. heat shock proteins, and ACSM5 involved in fatty acid synthesis) in pigs differing in backfat thickness. Pigs differing in palmitic acid content revealed 4 upregulated (e.g. LPN2 involved in lipid transport) and 5 downregulated genes (e.g. PAPPA2 being local regulator of IGF1 bioavailability, CYP26B1 involved in synthesis of cholesterol and lipids). DEG analysis of pigs diverging in stearic acid revealed 9 upregulated (e.g. PDK4 associated to fatty acid oxidation and glycolysis) and 10 downregulated genes (e.g. ABCD7 associated to energy expenditure). Using the WGS data, we identified variants in promoter regions, -1000 to +200 bp relative to transcription start site of genes that were differentially expressed in pigs with extreme phenotypes. Association analysis revealed a significant SNP in promoter region of PDK4 gene, associated with saturated fatty acid content. Given the PDK4 gene role in lipid metabolism, this variant may influence gene expression through transcriptional regulation. This preliminary study is the first to identify key genetic variants and genes associated with increased fat deposition and composition in the Krškopolje pig. Acknowledgement: Funding by Slovenian Agency of Research (grants P4-0133, P4-0220, J4-3094, Z4-60178) is acknowledged.