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Joel Gonzalez, Marta Gil, J. Jaume, Bénédicte Lebret, I. Diaz, Joan Tibau

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Majorcan Black Pig carcass, meat and fat quality parameters assessed by a standardised toolboxJ. Gonzalez¹, M. Gil¹, M.A. Oliver¹, J. Jaume², B. Lebre³, I. Díaz¹ and J. Tibau¹¹IRTA, Monells, 17121, Spain, ²SEMILLA-CAIB, C/ d'Eusebi Estada, 145, 07009 Palma, Spain, ³PEGASE INRA, Agrocampus-Ouest, 35042 Rennes, France; joan.tibau@irta.cat

TREASURE project aims to develop sustainable pork chains based on European local pig breeds. The Porc Negre Mallorquí (Majorcan Black Pig, MBP) is an untapped pig breed from Mallorca, in the Balearic Islands, included in the project due its high rusticity, adaptation to the environment and meat quality differentiation. Particularities of MBP are mostly unknown out from Mallorca, with only one representative meat product, the 'sobrassada de Mallorca de Porc Negre', a fat-rich cured sausage owning a PGI trademark. Carcass, meat and fat quality of MBP was evaluated, according to a standardised toolbox of parameters. The toolbox aimed for a harmonised knowledge of untapped breeds, made from the contribution of researcher's expertise and the literature. The mean values and standard deviation for carcass traits (n=29) were: 156.8±11.8 kg for live weight, 125.3±12.9 kg for carcass weight, 75.1±3.2% for carcass dressing, 88.7±3.7 cm for carcass length and 55.2±10.1 mm for ZP fat. The most remarkable results for the meat quality parameters toolbox (n=58) were an ultimate pH of 5.58±0.12 and electrical conductivity of 6.99±3.44 mS, a lightness value (L*) of 44.10±3.59, a drip loss of 1.49±1.46%, a shear force of 3.46±1.07 kg, and an intramuscular fat (IMF) content of 6.11±3.09%. The maximum value of IMF was 19%, a hint of the wide variability within this untapped breed, representing a disadvantage for the product standardisation in case of fresh meat, but not for 'sobrassada', mainly made of grounded ham, shoulder and loin. The results for the major fatty acid (FA) groups in back fat (n=48) samples were 41.00±1.42% of saturated FA, 51.27±1.64% monounsaturated FA and 6.88±0.71% polyunsaturated FA. 'Sobrassada' includes 40-50% of back fat, thus the FA composition is critical for product quality. The FA composition, with a high proportion of MUFA and low of PUFA contributes to an optimal technological quality of MBP back fat. Funded by European Union's H2020 RIA program (grant agreement no. 634476).

Adipose tissue transcriptome in Iberian and Duroc pigs fed different energy sourcesR. Benítez, B. Isabel, Y. Niñez, E. De Mercado, E. Gómez Izquierdo, J. García-Casco, C. López-Bote and C. Óvilo
INIA, UCM and ITACYL, Madrid, 28040, Spain; rmbenitez@inia.es

Diet and breed are main factors influencing animal body and tissue composition. In this study, we evaluated the effects of a diet supplemented with 6% high oleic sunflower oil (HO) or carbohydrates (CH) as energy source on subcutaneous ham fat composition and gene expression in growing Iberian and Duroc pigs. A comparative study of the ham subcutaneous fat transcriptome between animals fed with both diets was carried out in the two breeds. The study comprised 30 Iberian and 19 Duroc males. These animals were kept under identical management conditions and the two isocaloric and isoproteic diets were provided *ad libitum*, starting with 19.9 kg of average LW. All animals were slaughtered after 47 days of treatment, with 51.2 kg of average LW. Twelve animals of each breed were randomly selected for RNAseq analysis (six of each diet). In both breeds, the diet induced changes in the fatty acid composition of subcutaneous fat samples. The HO diet had higher monounsaturated fatty acids and oleic acid, and lower SFA than the CH diet. We detected 218 differentially expressed (DE) genes conditional on diet in Iberian pigs and 68 DE genes in Duroc pigs, 29 of these were common. Out of these, 27 genes were upregulated in HO diet in Duroc but upregulated in CH diet in Iberian (i.e. *PDLIM3*, *ANK1* and *PYGM*), one gene showed the opposite regulation (*SERPINE1*) and only one DE gene was upregulated in HO diet in both breeds (*CYP11A1*). These results indicate a strong interaction breed×diet on transcriptome. We performed a functional analysis (metabolic pathways and GO enrichment) of the 29 common genes, which showed the enrichment of functions related to carbohydrate metabolic process (digestion and absorption), starch and sucrose metabolism, insulin signalling pathway, glycogen catabolic process and purine nucleotide metabolic process. The bioinformatic analysis also allowed the prediction of potential regulators (such as *PPARGC1A*, *MEF2C*, *DMD*, *MYOCD*, or *MYO1D1*) for the expression differences observed. The results indicate the direct deposition of nutrients and a profound and different effect of the diet on adipose tissue gene expression between breeds, affecting relevant biological pathways.