

Identification of differentially expressed key genes of *Longissimus lumborum* samples from Portuguese Alentejano and Bísaro local pig breeds

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Most of the swine industry nowadays is about productive and profitable fast-growing lean breeds raised under intensive conditions leading to meat and fat rich in saturated fatty acids. The Portuguese local Alentejano (AL) and Bísaro (BI) pig breeds present high intramuscular fat (IMF) content which contributes to highly appreciated pork products. These breeds have different ancestors: AL belongs to the Iberian group, presenting lower growth rates and higher lipid accretion and unsaturated fatty acids level when compared to BI, which belongs to the Celtic group, sharing ancestors with leaner breeds such as Large White and Landrace. The goal of this work was to compare the muscle gene expression profiles of AL and BI pig breeds to better understand the influence of the genetic background in the main metabolic processes occurring in the *Longissimus lumborum* (LL) muscle, namely in terms of lipid synthesis, muscle tissue formation, protein synthesis and cell proliferation. LL samples were obtained at slaughter, from adult AL and BI pigs with ~150kg body weight. Total RNA was extracted and sequenced for a transcriptome comparison analysis. A total of 250 genes were found to be differentially expressed (DE) in LL samples ($q < 0.05$) conditional on breed, with 174 DE genes up-regulated in AL ($\log_2(\text{fold_change}) = 0.65$ to 7.03) and 76 in BI ($\log_2(\text{fold_change}) = 0.63$ to 4.53). Genes related to skeletal muscle development and function, such as *MYH3*, *MYH13* or *ACTN4*, were significantly up-regulated in BI when compared to AL, which is in agreement with the higher muscle mass of the former breed. Genes involved in lipid metabolism were up-regulated in AL, including *SCD* ($q = 0.05$), responsible for catalysing the reaction that introduces the first double bond into saturated fatty acyl-CoA substrates, which agrees with the higher unsaturation of fat tissues generally associated with the former breed. A functional enrichment analysis (metabolic pathways and GO enrichment) was performed for the DE genes and the identified functions included tissue development, cellular growth and proliferation, quantity of connective tissue and lipid metabolism. Potential regulators found that explain the observed gene expression changes in the dataset included molecules such as: *ADORA2A*, *CEBPA*, *SMAD3* and *PPARG* (predicted to be activated in AL); *HDAC* and *ASXL1* (predicted to be inhibited in AL).

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SNP association analyses for myoglobin content and water holding capacity in a purebred Iberian pig population

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The traditional Iberian pig production system *Montanera* linked to the genetic characteristics of the breed, have greatly influence in meat quality. In a previous study, a panel with SNPs mapped on candidate genes for meat quality traits was designed and relevant effects of SNPs located on *CAPN1*, *CASP9*, *PRKAG3* and *CTSL* genes on meat tenderness, instrumental color, thawing and cooking losses measured on Iberian purebred pigs were observed. The objective of the current study was to analyze the effects of the SNP panel on myoglobin content (MB) and centrifuge force water losses (CFL). A total of 32 SNPs were genotyped on 565 Iberian purebred individuals using TaqMan® OpenArray® Genotyping Plates and additive effects were estimated through univariate animal models with QXPAK software. Four out of the 32 SNPs were fixed in the typed individuals and one showed genotyping problems. The other 27 had a $MAF > 0.05$, and nine of them showed intermediate frequencies. Nineteen SNPs were used for association analyses since the remaining eight co-segregate. The association analyses revealed significant effects of SNPs mapped on *CASP9* and *PRKAG3* on the myoglobin content and mapped on *CAPN1*, *CTSL* and *PRKAG3* on CFL. The most relevant effects were observed for *CASP9_rs32430761* on MB ($a = 0.05 \pm 0.02$) and for *CAPN1_rs81358667* on CFL ($a = -0.68 \pm 0.20$). In the previous study, a significant effect of *CASP9_rs34618816* were observed on (a^*) instrumental color parameter (redness), which is related with myoglobin content and *CAPN1_rs81358667* SNP significantly affected tenderness and water losses traits, which are related with centrifuge force water losses. Although further analysis should be performed, these SNPs could be used for selecting sires in a selection scheme for meat quality traits.

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