Comparison of *longissimus lumborum* muscle transcriptomes in Romanov and Polish Merino sheep

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Meat quality is a complex trait, which is difficult to improve by applying only traditional breeding methods. Analysis of muscle tissue transcriptomes can enhance our understanding of the genes controlling meat quality in different sheep breeds. The study aimed to investigate the *longissimus lumborum* (LL) muscle transcriptomes in Romanov (ROM) and Polish Merino (PM) sheep to reveal differences in the expression of genes, including those associated with meat quality. The experiment was conducted on 3 ROM and 3 PM female lambs. Samples of LL muscle were collected immediately after commercial slaughter. Differential expression analysis was conducted using DESeq2 v.1.34.0 package. ClusterProfiler v4.2.2 software was applied for enrichment analysis of differentially expressed genes (DEG). A total of 381 mRNA transcripts, including 237 up- and 144 downregulated transcripts, were differentially expressed in ROM relative to PM lambs. The significant GO terms (Padj<0.05) for all DEGs included 9 GO terms in the category of a cellular component. Regarding the up-regulated genes dataset, a total of 7 GO terms were significantly enriched (Padj<0.05), including 5 and 2 GO terms in the categories of cellular component, and molecular function, respectively. The further enrichment analysis among the 381 DEGs revealed 23 significantly enriched (Padj<0.05) KEGG pathways. These results provide a foundation for identifying candidate genes and further develop the theoretical basis for new breeding strategies to optimize the production performance and meat quality of the two sheep breeds. Our outcomes provide also the foundation for further use of these breeds for crossbreeding. This work was supported by the Ministry of Science and Higher Education from the 'Innovation Incubator 2.0' programme (grant no. 8/1/2019/UTP) and by the Polish National Agency for Academic Exchange (grant no. PPI/APM/2019/1/00003).

SNP substitution effects for SCS changes across environmental gradients in Portuguese dairy cattle

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Several GWAS reports for milk related traits have been performed, however, the use of this approach in a context of G by E, is yet scarce. We aimed at identifying putative candidate genes associated with milk yield (MY) and somatic cell score (SCS) according to an environmental gradient (EG). A total of 4.6 million test-day records of MY and SCS from Portuguese Holstein cows were analysed. The data included 1,537 genotyped animals for 38,615 SNPs. First, the herd-test-day (HTD) effects were estimated using an autoregressive test-day model. Then, the solutions of HTD effect were used as an EG in a reaction norm model under ssGLBUP approach. The SNP effects for MY and SCS were calculated by back solving the genomic breeding values for each EG and the proportion of genetic variance explained by 100 kb SNP windows was also computed. For MY, the SNP effects were almost constant across EG, indicating the absence of SNP by environment interaction. Nevertheless, for SCS, higher changes in the magnitude of SNP effects were observed among EG. Based on significant SNP windows for MY and SCS between the extreme EG, candidate genes were mapped. For MY (SCS), we identified 25 (33) candidate genes unique for less favourable and 11 (10) candidate genes for more favourable EG. For SCS, candidate genes SOX14, HGF, and GPRIN1 were identified only in less favourable EG while NAALADL2, ELMO2, and ZNF830 were identified exclusively in more favourable EG. NAALADL2 gene for example, is related to response to bacterium and HGF is related to regulation of MAPK cascade, important in stress responses under pathological conditions. Meaningful differences in the genetic architecture of SCS across EG were revealed in this study and may contribute to a better understanding of the SCS genetic control, permitting the design of better strategies for genomic selection in specific dairy herd environments in Portugal.