

EXPRESSION QUANTITATIVE TRAIT LOCI ASSOCIATED WITH NELLORE MEAT PH

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Abstract:

Genomic studies make it possible to identify polymorphisms associated with quantitative characteristics of economic interest, such as meat pH, a factor that influences meat quality. Our goal was to identify gene expression regulatory variants (eQTLs) associated with meat pH in Nellore cattle. To identify the eQTLs, we used an imputed panel of SNPs containing genotypes from 778 progenies (BovineHDBeadChip 770k, Illumina), DNA-Sequencing of 26 unrelated Nellore sires, and transcribed SNPs called from RNA-Sequence data from muscle (Longissimus thoracis) of 192 progenies, resulting in a SNP panel of 4,522,914 SNPs. First, the imputed SNPs were filtered for our population subset of 192 animals, and we performed quality control of the variants keeping only SNPs with Minor allele frequency (MAF) > 5% and call rate > 95%, totaling 4,436,504 SNPs. Then, PLINK v. 1.07 was used to calculate linkage disequilibrium (LD) and pruning the variants ($r^2 = 0.8$). As a result, 553,581 tag-SNPs were used in further analyses. Before the analyses, population stratification was investigated by principal component analysis (PCA) using genotypes from the BovineHD 770k BeadChip and our population of 192 (eQTL mapping) and 374 animals (association analysis). The first two principal components (PC1 and PC2) were included as covariates in the statistical models. The eQTL identification was performed using the R package Matrix eQTL v. 2.3, with the expression of 12,991 muscle genes normalized in log2-CPM (Counts per million of mapped reads) and corrected for lane and flow cell effects; the genotype file containing the tag-SNPs; PC1, PC2, and contemporary group (CG - animals from the same farm, year, and slaughter date) as covariates in the model. The cis-eQTLs were defined in this study as SNPs located up to 1 Mb away from the regulated gene, while trans-eQTLs were SNPs located > 1 Mb away from the gene. In total, 51,324 eQTLs were identified (36,916 Cis and 14,408 Trans, FDR 5%). The association between eOTLs and the phenotype was performed in PLINK v. 1.07 software, using 374 animals, and considering a linear model with the effects of PC1, PC2, CG, and hot carcass weight as covariates in the model.SNPs associated with the phenotype with FDR <10% were considered significant. From these eQTIs, three (chr 4:77126175; chr 4:77010519; chr 4:77084998) were associated with meat pH 24 hours post mortem. All of them regulate the DNA Polymerase Mu (POLM) gene. Although the function of this gene in pH is still poorly understood, this gene has already been associated with oxidative stress, a factor that can interfere in meat pH. Other genes from the same family were also associated with meat traits. Therefore, in the current study we were able to identify regulatory polymorphisms associated with pH, helping to elucidate molecular mechanisms that participate in meat quality.

Palavras-chave: Cattle; gene; meat quality; ;