HAPLOTYPE IN THE LEPTIN GENE ASSOCIATED WITH CARCASS FINISHING SCORE IN SANTA INES SHEEP

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Leptin (LEP) gene play key role in energy metabolism and, therefore, it's a candidate gene in association studies with growth and carcass traits. Thus, this study aimed to identify association between haplotype in the LEP gene and carcass traits in Santa Ines sheep. A total of 192 lambs were genotyped for the 17 single nucleotide polymorphisms (SNPs) (g.92501356A>G, g.92501372G>A, g.92501407C>T, g.92501543A>G, g.92501808G>A, g.92502245A>G, g.92502283T>C, g.92502367C>T, g.92502623G>C, g.92502642A>G, g.92502663T>C, g.92502922G>T, g.92502947A>C, g.92503024G>A, g.92503025C>T, g.92503044A>G, g.92503086G>A) in the LEP gene and evaluated for ultrasound images of rib eye area (REA) and fat thickness (FT) in longissimus muscle between 12th and 13th ribs. In addition, all lambs were evaluated for carcass finish score (CFS), with values between 1 and 5. The haplotype block was found with haploview software and, then, a haplotype trend regression (HTR) analysis was performed, using a 5% significance level. The haplotype analysis found a block with 17 SNPs and seven haplotypes copies showed frequency higher than 4%. The most frequent haplotype copy was AGCGGATCGATGAGCAG with 41.9%, the other haplotype copies were GGTTAGGCCCATGAG (13.4%), GACAAATCGATTAGCGG (10.2%), GGCAATCGATTAGCG (9.1%), GGCAATCGATTAGCGG (4.6%), GGCAATCGATTAGCGG (4.6%) andGGCAAATTGATGAGCGG (4.0%). No haplotype effects (P>0.05) were found for REA and FT. However, the HTR analysis revealed an effect (P=0.042) on CFS, where to replace each copy of most frequent haplotype (AGCGGATCGATGAGCAG) by the haplotype GGCAATCGATTAGCGG reduced the CFS in -0.0828 ± 0.0404 scores. Therefore, a haplotype in LEP gene is associated with carcass finishing score in Santa Ines sheep, which may be sources of information for marker-assisted selection.

Keywords: fat, lamb, ovine, selection, SNP

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