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SNP in the Leptin gene associated with carcass trait in Santa Ines sheep

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This study was carried out with 185 Santa Ines lambs of approximately 240 days of age, which were evaluated for hot and cold carcass weights and yields, neck, leg, ribs, shoulder and loin weights, carcass external length, leg length, chest width, rump width, carcass conformation and fat scores. A fragment of Leptin gene was sequenced between the exons two and three and 16 single nucleotide polymorphisms (SNP) were identified in this segment. Statistical model used in the analysis was $Y_{ijklm} = u + F_i + Y_j + M_k + \alpha_{ijklm} BW + \alpha_{ijklm} Age + A_1 + D_m + e_{ijklm}$, where: Y_{ijklm} is the trait value; u is the average of this trait; F_i , Y_j and M_k are fixed effects of farm, year and month of birth, respectively; $\alpha_{ijk} BW$ and $\alpha_{ijklm} Age$ are the covariates body weight and slaughter age, respectively; A_1 and D_m are additive and dominance fixed effects, respectively; and e_{ijklm} is the residual random term. Significance level in the hypothesis tests was 0.035, obtained after multiple Bonferroni correction. The c.00+43G>A marker, located at position 92501372, had additive effect for neck weight (P=0.00556), the value of the additive effect and the standard error were 0.0964 and 0.0344, respectively. The marker c.100+214A>G, located at position 92501543, had additive effect for external carcass length (P=0.0150), cold carcass yield (P=0.0279) and hot carcass yield (P=0.0244). The additive effect value and standard errors were 0.9147 and 0.03731 for the external carcass length, 1.5374 and 0.7367 for cold carcass yield, and 1.6137 and 0.7469 for hot carcass yield. The SNP (c.101-144G>A, P=0.0129), located at position 92503024, had effect for fat score, with additive value and standard error of 0.1380 and 0.0654, respectively. The dominance effects were not significant for any SNP. The mechanism by which these polymorphisms affect these traits is still unclear, since the mutation found here was localized in intron. However, genes such as Leptin has exon region highly conserved in several domestic species and polymorphisms in this gene are more abundant in noncoding DNA regions. Several studies have already demonstrated that the DNA sequences in intron regions may be an alternative pathway of variation in the amino acid sequences of proteins. Several previous studies also showed that polymorphism in leptin gene were associated with body fat deposition, feed intake and body composition and other economic important traits in livestock animals, and the present study showed that polymorphisms in this gene have effects on carcass sheep traits too.

Keywords: Carcass quality, molecular markers, ovine, selection

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