00-12 Identification of a pleiotropic locus for beef quality and feed efficiency in cattle using bi-trait genome-wide association analysis

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The molecular mechanisms of pleiotropy indicate multiple functions of a single gene product and many consequences of a single molecular function related to animal breeding. However, single-trait GWAS are not per se suitable for systematically identifying such loci. In this study, we used a bi-trait GWAS for detecting pleiotropic effects between twenty beef quality and feed efficiency traits. Based on Illumina High-Density SNP-chip data for phenotyped population of 387 Nelore steers. Covariance components were estimated using the restricted maximum likelihood method under a mixed animal model, considering a genomic relationship matrix. Highlighted, we found one locus significantly associated with the sum of omega-3 (N-3) and relative growth rate (RGR). This locus resides in the gene encoding TBC1 Domain Family Member 5 (*TBC1D5*). In agreement with our results, recent studies show that *TBC1D5* regulates the activation of the Ras-related Rab-7, a protein that plays a pivotal role in the regulation of the autolysosome-mediated lipid degradation in fat cells. The detected SNP in *TBC1D5* explains up to 0.45% of the variance observed for N-3 and 3.77% for RGR. The locus identified in this study show pleiotropic effects suggesting a role in lipolysis in both phenotypes provides evidence for the genetic interrelation between omega-3 and relative growth rate and indicates candidate gene for future investigation of causal mutations.

Keywords: Fat/lipid, lipolysis, feed efficiency, pleiotropy, genome-wide association. This project was supported by FAPESP 2012/23638-8.