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Association analyses pointed the *TIPARP* as a potential candidate gene influencing residual feed intake variation in Nelore cattle.

Andressa O de Lima[1], Priscila SN de Oliveira[2], Polyana C Tizioto[2], Juliana Afonso*[1], Adriana L. Somavilla[3], Wellison J da S Diniz[1], Juliana V da Silva[1], Marina IP Rocha[1], Maurício A Mudadu[4], Luiz L Coutinho[5], Luciana C de A Regitano[2].

[1]Department of Genetics and Evolution, Federal University of São Carlos, São Carlos, SP, Brazil, [2]Embrapa Pecuaria Sudeste, São Carlos, SP, Brazil , [3]The Roslin Institute, Edinburgh, United Kingdom,[4]Embrapa Agriculture Informatics, Campinas, SP, Brazil,[5]Department of Animal Science, University of São Paulo, Piracicaba, SP, Brazil ,

Selection for residual feed intake (RFI), a measure of feed efficiency, can increase profitability of cattle herds besides potentially reduce methane emission, but it has late and costly measurements. Single nucleotide polymorphisms (SNPs) in both regulatory and coding regions can affect transcriptional and genetic variation related with RFI. Diverse studies of feed efficiency performed by our research group in a Nelore population, such as Genome-Wide Association (GWAS), Association weight matrix (AWM) and RNA-Seq analysis of skeletal muscle tissue, pointed that the *TIPARP* gene plays a role in RFI. In order to identify cis-regulatory variation for this gene, we analyzed a region starting two kb *upstream o*f the gene to its delimited 3' UTR. For this, we considered haplotypes consisting of SNPs presented in the *Illumina Bovine HD Bead Chip* available for 591 phenotyped steers. Genotype phasing and missing genotype imputation were performed using BEAGLE software, and the LDexplorer was used for haplotype block recognition. The association model included fixed effects of contemporary group, consisting of type of pen, birthplace and feedlot location; also, age of the animal was included as covariate. The genetic effects of haplotype were estimated by PLINK using a linear regression method. We identified one haplotype constituted of 37 SNPs, presenting six haplotype combinations but only one having a significant effect ($P \leq 0.05$) on RFI. This haplotype combination has 41.43% frequency was associated (pvalue= 0.04586) to lower RFI or more efficient animals ($\beta = -0.2516$). Moreover, the SNPs present in the haplotype were annotated using the *Variant Ensembl Predict* and we identified one SNP in an *upstream* region of the *TIPARP* gene that has a potential regulatory role. Our findings indicated this gene as a strong candidate to be considered by Nelore breeding programs that applies marker-assisted selection. Nevertheless, more studies considering variants in regulatory regions in this gene will be realized to understand better its effect on RFI. We would like to thank the Cnpq (grant number: 473091/2012-7 and 4491792/2014-7) and FAPESP (grant number: 2012/23638-8) for the founding.
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