00-13 Potential regulatory elements on *PCDH7* gene affecting residual feed intake in Nelore cattle

Andressa O. de Lima[1*], Polyana C. Tizioto[2], Priscila S.N. de Oliveira[3], Ludwig Geistlinger[3], Marina I.P. Rocha[1], Wellison J. da S. Diniz[1], Juliana Afonso[1], Carlos E. Buss[1], Juliana Petrini[2], Gerson B. Mourão[2], Luiz L Coutinho[2], Luciana C. de A. Regitano[3]

[1]*Departament of Genetic and Evolution, Federal University of São Carlos, São carlos, São Paulo, Brazil*
[2]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, São Paulo, Brazil*
[3]*Embrapa Southeast Livestock, São Carlos, São Paulo, Brazil*

Residual feed intake (RFI) is a measure of feed efficiency and can improve the profitability of cattle herds and potentially reduce methane emission, but it has late and costly measurements. Identify the causes of gene expression variation, like regulatory polymorphisms, can be helpful to understand the regulatory elements that affect residual feed intake and can be useful in animal breeding programs. Recent studies performed by our research group in a Nelore cattle population, such as Genome-wide association (GWAS), Association weight matrix (AWM) and RNA-Seq analysis of liver tissue revealed that the *PCDH7* gene plays a role in RFI. To identify regulatory elements and polymorphisms for this gene, we analyzed the promoter region of the *PCDH7* (*chr4:30716201bp–30722201bp*) described in Ensembl database for human (*GRCh38.p10*) at UCSC genome browser. This region is conserved among several species and has a binding affinity with the transcription factor *E2F1,* which is involved in regulation of fat cell proliferation and differentiation. We converted the human promoter region coordinates to the correspondent on the bovine genome *UMD 3.1* (*chr6:51530833bp-51537647bp*) using the lift genome annotation tool from UCSC genome browser. In this region, we identified nine SNPs of the 20 genome sires sequenced by Illumina Hiseq2500®. Briefly, after the sequencing, we performed BWA-MEM for alignment and GATK for variant calling. We annotated the SNPs using the Variant ensembl prediction (VEP), five of which are located in an upstream region of the *PCDH7*. We found one SNP located in a transcription factor binding site (TFBS) for *CCAAT/enhancer-binding protein beta (CEBPB)* and one SNP located in TFBS for *Neurofibromin (NF1)*. These Transcription factors (TFs) are related to regulation of brown fat cell differentiation and skeletal muscle tissue development, respectively. Our findings indicate putative regulatory elements in the *PCDH7* gene that could have a role in RFI variation. Nevertheless, more studies considering variants in regulatory regions in this gene will be performed to understand its effect on feed efficiency.

Keywords: Residual feed intake, promoter, transcription factor, SNPs.

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