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Cell cultures harbouring constructs of different pig promoter polymorphisms show different transcriptional efficiency in gene reporter systems

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ABSTRACT

Production traits variability among and within breeds, differences among developmental stages or the response to different environments are in part due to genetic factors that affect gene expression. Within the context of an Italian FIRB project, whose objective is to identify genes and molecular mechanisms affecting meat quality and production traits in pig, we studied the promoter regions of candidate genes selected on the basis of their physiological role in animal tissue development or composition. Genomic DNA was isolated from liver or muscle tissue of individuals belonging to Large White and Casertana breed. PCR primers were designed to amplify 5' upstream region of SCD (Stearoyl-CoA Desaturase), LDLR (Low Density Lipoprotein Receptor), LEP (Leptin), MSTN (Myostatin), ACTA1 (Alpha-actin) and HFABP (Heart Fatty Acid Binding Protein) genes using sequences available at NCBI. A total of 19 single nucleotide polymorphisms (SNPs) not previously described were characterised. Some haplotypes, harbouring SNPs located within, or closely flanking potential cis-acting elements, were used to carry out an *in vitro* analysis of the efficiency of promoter natural variants. Up to 1200 bases upstream the translation start codon were cloned in pGL3 basic vector in phase with the downstream luciferase reporter gene. The different luminescence intensities showed by constructs harbouring allelic variants suggest transcriptional efficiency influenced by polymorphism. The knowledge of a correlation between a different transcriptional activity and a particular haplotype could be a useful tool to identify variation at genes controlling important traits in pig.