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MOLECULAR CHARACTERIZATION OF *FIBROBLAST GROWTH FACTOR 5 (FGF5)* GENE IN ALPACA

Stefano Pallotti^{1*}, Dario Pediconi^{1*}, Dharaneedharan Subramanian^{2*}, María Gabriela Molina^{3*}, Marco Antonini^{4#}, Carlo Renieri^{1#}, Antonietta La Terza^{1#}

¹School of Bioscience and Veterinary Medicine, University of Camerino, Via Gentile III da Varano, 62032 Camerino (MC), Italy

²Department of Marine Life Science, Jeju National University, South Korea

³Facultad de Ciencias Agropecuarias .Universidad Nacional de Córdoba. Universidad Católica de Córdoba ,Argentina

⁴ENEA C.R. Casaccia Biotec-Agro, S.M. di Galeria, 00060 Roma, Italy

*these authors contributed equally to this work

#corresponding authors

Two coat phenotypes have been described in alpaca, Huacaya and Suri. The most common Huacaya type, is characterized by a crimped, dense fleeces, while the Suri type is characterized by a non-crimped, straight fleece. The genetic background of the two coat phenotypes has not been yet clearly defined. Results from segregation analysis provide statistical evidences that the Suri trait is possible inherited as a single dominant gene. The aim of our study was to molecularly characterize the *FGF5* as a possible candidate gene for hair length phenotype in Suri type because of its role in the regulation of the hair follicle growth cycle.

Currently, we have isolated and characterized two different cDNA clones encoding for *FGF5* obtained from total RNA purified from skin biopsies of Peruvian Suri type alpaca. Sequence analysis revealed two types of transcripts: a long form (*FGF5L*) containing an ORF of 498 bp encoding for a putative 166 amino-acid polypeptide, and a short form (*FGF5S*) of 375 bp encoding for a putative 125 amino-acid polypeptide. On the basis of the partial FGF5 genomic sequence data retrieved from the low-coverage 2.51X assembly of alpaca genome at the Ensembl database, the two transcript are produced by the alternative splicing of exon 5, which results in the loss of a fragment of 104 bases. Furthermore, RACE approaches specifically devised to characterize the 3' and 5' UTRs of *FGF5* transcripts, show that the *FGF5S* isoform possesses two 3'-UTRs of 713 and 542 bases respectively. Meanwhile a single 3'UTR has been so far identified for the *FGF5L* isoform. Work is in progress in our laboratory to better characterize the *FGF5* isoforms and their expression in the skin of Suri and Huacaya alpacas, and to identify mutations potentially involved in the fleece variations of alpaca.