

Evaluation of MC1R gene polymorphism in Vicugna pacos

Paola Crepaldi¹, Elisabetta Milanesi¹, Letizia Nicoloso¹, Vincenzo La Manna², Carlo Renieri²

¹Dipartimento di Scienze Animali - Sezione di Zootecnica Agraria – Università degli Studi di Milano, Italy ²Dipartimento di Scienze Ambientali - Università degli Studi di Camerino, Italy

INTRODUCTION



In alpaca (Vicugna pacos) fibre production and quality represent the most important characteristics from a market point of view and, as a consequence, current breeding programs are mainly based on these phenotypic traits.

The identification of genetic markers associated to coat color could lead to the set up of more reliable breeding programs, particularly aimed at the production of naturally colored fiber.

The genetic of pigmentation involved many genes at different level: melanocyte development, melanosome construction/protein routing, melanosome transport, eumelanin and pheomelanin synthesis (Bennet and Lamoreux, 2003).



Melanocortin 1 Receptor (MC1R) gene is known to play an important role in the regulation of eumelanin (brown/black) and pheomelanin red/yellow switch. Many polymorphisms in different mammal species are known. Some of these allow the differentiation of red versus black phenotypes (Klungland and Våge, 2003)

Aim of this work was the preliminary evaluation of polymorphism of MC1R gene in alpaca.

MATERIALS AND METHODS

Polymorphism of alpaca MC1R gene was evaluated by sequencing 1190 base pairs comprising the whole coding sequence and part of the UTR regions in 6 alpacas characterized by different coat color (2 solid black, 2 solid red, 1 brown-pied and 1 red-pied) shown in the photos reported below.



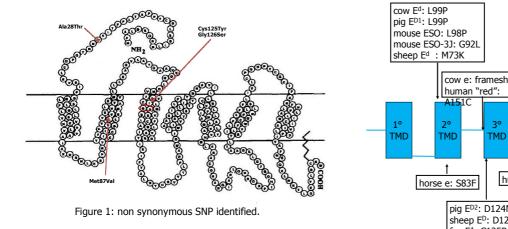
solid black

solid red

red-pied

RESULTS AND DISCUSSION

Sequence comparison revealed the presence of 8 SNPs, 6 of which in the coding sequence. Two of these were silent mutations, whereas 4 (A82G, A259G, A374G and A376G) resulted in amino acid changes (thr28ala, met87val, cys125tyr and gly126ser) in position NH₂ terminal, in the first, second and third trans-membrane and in the COOH terminal domain of the receptor, respectively (figure 1). Some of these SNP are in the same or nearby position of mutation with phenotypic effect in other species as reported in figure 2. Analysis of the genotypes revealed that the 3 animals characterized by a black/brown coat color were homozygous for the same allele at all the polymorphic loci, while the red animals showed an heterozygote status at all the polymorphic loci.



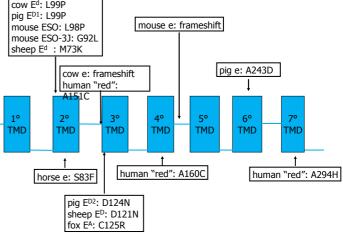


Figure 2: some known MC1R polymorphisms with coat colour effect in mammals (modified from Klungland and Våge, 2003).

These findings, although preliminary, agree with GenBank sequence data (EU135880 and EU220010) relative to alpacas described as "fawn" and "black/brown", and confirm the high level of polymorphism of alpaca MC1R gene described in a recent publication (Powell et al. , 2008).

Acknowledgement – The authors thank Dr. Berna for the samples provided.

References - Bennet D.C. and Lamoreux M.L. (2003). The color loci of mice - A Genetic Century. Pigment Cell Res 16:333-344. Klungland H. and Våge D.I. (2003). Pigmentary switches in domestic animal species. Annals of the New York Academy of Sciences 994: 331-338. Powell A.J., Moss M.J., Tegland Tree L., Roeder B.L., Carleton C.L., Campbell E., Kooyman D.L. (2008) Characterization of the effect of Melanocortin 1 Receptor, a member of the hair color genetic locus, in alpaca (Lama pacos) fleece color differentiation. Small Ruminant Res. 79: 183-187.