

GENETIC EVALUATION OF COAT COLOR PATTERN IN BRAZILIAN CREOLE SHEEP

Cavalcanti, LCG^{1,2}; Faria, DA²; McManus, CM¹; Souza, CJH³. Moraes JCF³; Paiva, SR⁴

¹Pós Graduação Ciências Animais, FAV, UnB, Brasília, DF, Brazil; ²Embrapa Recursos Genéticos e Biotecnologia, Brasília, DF, Brazil; ³Embrapa Pecuária Sul, Bagé, RS, Brazil; ⁴Embrapa Sede, Secretaria Relações Internacionais, Brasília, DF, Brazil

lilian1mel@gmail.com; samuel.paiva@embrapa.br

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Sheep breeding in Southern Brazil was characterized by the utilization of Brazilian Creole breed in the early twentieth century. Currently there are few breeders and for that reason Embrapa maintains a conservation nucleus, which includes, among its objectives, studies on the genetic mechanisms related to coat color. This trait is economic important, as the wool of these sheep is medulated and has been widely used in local crafts. Thus, identifying alleles that regulate patterns of color variation in this breed is strategic and can be used in selection programs, marketing the products made from naturally colored Creole sheep wool, while assisting in conservation of the breed. Two different types of melanin are involved in determining coat color of sheep, which is defined by the interaction and distribution of pigments; the eumelanin causes the expression of black color and white coat color originates from pheomelanin. In this study we sequenced 954 and 668 base pairs of MCR1 (Melanocortin 1 Receptor) and TYR (Tyrosinase) genes, respectively, in 35 samples to test the hypotheses of segregation of coat color. The animals used were kept in the breed nucleus in the Center for Conservation of Creole sheep in Embrapa Southern Region Animal Husbandry, Bage, Rio Grande do Sul State. After alignment of the sequences for the MC1R gene, five previously described single nucleotide polymorphisms (SNP) were found. Among these, 218T>A and 361G>A are mutations that determine changes in amino acid synthesis. SNPs T218 and G361 were observed at a frequency of 0.8, which suggests complete linkage. All parents in this case had black coats (at least one was heterozygote). All white animals were homozygotes for both markers confirming the usefulness of this haplotype for monitoring this trait. Two SNPs were identified in exon 1 of the gene TYRP G192C and C462T with frequencies equal to 0.825 for alleles G192 and C462 which also suggest the complete linkage of these markers. All white offspring were homozygous for these SNPs (G192 / C462), but animals of other coat colors were also observed for the same haplotype. This confirms that these SNPs may not act directly on the control of the dominant black phenotype but rather on the brown color. New experiments are being conducted both to increase the sample size as well as evaluate the action of more genes within the pathway of melanin production (eg ASIP). Therefore, we expect to validate a specific diagnostic panel to assist in the selection of animals to be used in controlled matings and in identifying donors for the Germplasm Bank of the Conservation Program for Animal Genetic Resources coordinated by Embrapa and partner institutions. Financial Support: CNPq and Embrapa