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Genetic parameters for fiber diameter at different shearings

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Alpaca is the most important fiber producer of South American camelid species, being an important income for the Andean communities. Nowadays, the fiber diameter is considered as the main selection objective in alpaca populations all over the world. However, fiber diameter increases with age of animals, and its value at consecutive shearings might be affected by different genetic and environmental conditions. The goal of this study was to estimate the genetic parameters for fiber diameter depending on the age of the animal. The data set consisted of a pedigree of 4,173 individuals of Huacaya breed, and 8,405 records of fiber diameter corresponding to 3,257 individuals. Shearing for four age groups (one year old animals, two years old, between three and four years old, and five or more years old) were defined. The model for each group includes age in days as a covariable, sex, fiber color, and month-year as fixed effects, as well as a permanent environmental effect (for the second group onwards), and additive genetic effect as random effects. REML estimates were obtained using VCE6 program under a multitrait procedure. Heritabilities ranged from 0.54 to 0.70, and were higher than that estimated when all shearings were considered as a unique trait. The highest heritability was estimated for two years old animals, indicating that shearing at two years of age is the best showing the genetic value of the animal. Environmental permanent variance was only relevant for the last group with a ratio of 0.11. Genetic correlations ranged between 0.76 and 0.98 but those involving the first shearing were lower and decreased as the time elapsed between shearings increased. First shearing seemed to be the worst to represent the fiber diameter of the animal along its life.

A deletion in exon 9 of the LIPH gene is responsible for the rex hair coat phenotype in rabbits

Diribarne, M.¹, Mata, X.¹, Chantry-Darmon, C.¹, Vaiman, A.¹, Auvinet, G.², Bouet, S.¹, Deretz, S.², Cribiu, E.P.¹, Rochambeau, H.³, Allain, D.³ and Guérin, G.¹, ¹INRA, UMR1313, GABI, Domaine de Vilvert, 78350 Jouy en Josas, France, ²INRA, UE967, GEPA, Le Magneraud, 17700 Surgères, France, ³INRA, UR631, SAGA, BP 52627, 31326 Castanet Tolosan, France; daniel.allain@toulouse.inra.fr

Hair follicles are complex structures which naturally play an essential role in the protection of mammals against climatic variations. In addition, it is of utmost importance in certain domestic species bred for the quality their coat such as in rabbit. Among these is the rex coat which confers to rabbits a soft plush-like fur of high economic value. The coat of common rabbits is made of 3 types of hair differing in length and diameter while that of rex animals is essentially made up of amazingly soft down-hair. Rex short hair coat phenotype in rabbits was shown to be controlled by a mutation segregating at an autosomal-recessive locus. A positional candidate gene approach was used to identify and primo-localized the rex gene within a 40 cM region on rabbit chromosome 14 by linkage analysis in large experimental families. Then, fine mapping refined the first defined interval region by genotyping 359 offspring for 94 microsatellites. Comparative mapping pointed the LIPH (Lipase Member H) as a candidate gene. The rabbit gene structure was established and a deletion of a single nucleotide was found in LIPH exon 9 of rex rabbits (1362delA). This mutation results in a frameshift and introduces a premature stop codon potentially shortening the protein by 19 amino acids. The association between this deletion and the rex phenotype was complete as determined by its presence among a panel of 60 rex and its absence in all 60 non-rex rabbits. This strongly suggests that this deletion, in a homozygous state, is responsible for the rex phenotype in rabbits. This result represents for breeders a good marker for introgressing this character in other rabbit strains for quality pelt improvement.