
Genetic improvement programmes of alpaca in Caylloma province - PROMEGE

C. Pacheco¹, C. Renieri², M. Antonini³, A. Valvonesi²,
W. Frank⁴ & N. Mamani¹

¹Desco Studies Center and Promotion of Development Arequipa, Perú

²Camerino University, Department of Veterinary Science, Matelica, Italy

³ENEA Casaccia, Bistec AGRO, S. Maria di Galeria, Rome, Italy

⁴Catholic University of Cordoba, SUPPRAD Program, Cordoba, Argentina

The breeding program that develops in the Caylloma province, Arequipa Region, Peru, aims to improve qualitatively and quantitatively the production of alpaca fiber. His intervention strategy se basa en un esquema selection of core open, with single-core and 15 multipliers whom have records pedigree and productivity of their animals. The reproductive management of animals kernel is done under the system apareamientos scheduled between males and females in the same race and color but distant in terms of kinship (circular matings), the selection of animals is developed based on qualitative criteria (Fleece type and color) and quantitative (assessment mean diameter fiber, coefficient of variability means of fiber diameters and total weight of the fleece of the first shearing) through which determines their selection indices.

The intensity of selection in the nucleus and herds of planteleros is high, for this reason breeders with purely qualitative selection criteria are not required to keep records of their production or herd animals. The spread and replacement players will take place from the core toward the planteleros, creating a genetic relationship between those with and through the transfer of players and vice versa. Keeping the necessary genetic differential. Also, the relationship between the core and Planteleros a system governed reproductive rate move "circular matings" in which every two years plantelero receive a player from a family genetically diverse and distant from that existing in the core, thus will create a genetic relationship between effective and controlled planteleros inbreeding..

Key word: Genetic improvement, Selection, Index, Core.

This document presents the experience of genetic selection of alpacas in the province of Caylloma in Peru; this objective is driven through a cooperative effort between the Center of Studies and Promotion of Development (DESCO) - Peru, the Department of Environmental Science at the University of Camerino - Italy, the Center for New Technology, Energy and Environment Jan - Italy and Program SUPPRAD of the Catholic University of Cordoba, Argentina.

Summary

Introduction

The PROMEGE (program of genetic improvement) utilizes the selection of the open core of alpacas managed by desco- Center for Development of Alpacas Tocra (CEDAT) which included 15 multipliers (approximately 1 500 animals) and more than 150 of the breeding base of farming families (15 000 animals in total).

The total alpaca population of the Caylloma province is estimated at 200 000 animals, 90% huacaya, 10% suri, 60% of white alpacas, and 40% of color (Gonzales and Renieri, 1998).

The breeding program began in 1985 with the creation of desco's Rural Development Colca Canyon Program and expanded in 1996 with the establishment of the CEDAT. In 1998, a breeding plan was developed, and later, in 2005, started its full operation following the results of two research programs of development financed by the European Union (EU. INCO), SUPREME (1997-2000), DECAMA (2002-2006) enabling the acquirement of the necessary genetic information. PROMEGE is the first breeding program developed to operate in the alpaca and llama populations in the Andean highlands.

PROMEGE

The specified characteristics of the selection objectives are as follows:

1. Qualitative characteristics.
 - o Type fleece: Huacaya and Suri.
 - o The color of fleece, in this case, the selection is:
 - In favor of white, non-albino.
 - Color fleece (Black, brown, wild, and LF).
 - Against the fleece of two colors and irregular spots.
2. Quantitative Features.
 - o Number of fiber produced.
 - o Fineness of fiber (diameter).
 - o Variability Coefficient of the fiber diameter.

The selection criteria can be summarised as follow:

- Direct observation of animals at birth, by type and color of the fleece.
- Weight of the produced fiber in the first shearing at age one with a confidence interval of ± 2 months (Antonini *et al.*, 2004).
- Average diameter of fiber and the coefficient of variation obtained during the first shearing through a sample on the left side of the alpaca.

Genetic basis of the characteristics

Suri vs. Huacaya

Various theories have been raised concerning the hereditary mechanism of the suri in respect to huacaya (Velasco, 1980; Street Escobar, 1884, Ponzoni *et al.*, 1997, Baychelier, 2000). The analysis of data from a large, private breeding farm in Peru demonstrates information of 588 alpacas (62 families of half paternal brothers) born as a result of the mating between suri x suri and 2 126 alpacas (177 families of half paternal brothers) born as a result of mating between huacaya x huacaya (Renieri *et al.*, 2008, unpublished). Of the animals born into the 21 suri x suri families (of whom was born at least one sample of a huacaya alpaca), four assumptions have been tested for a model of two phenotypes:

1. The hypothesis of a single dominant gene (tested hypotheses, 7 suri: 1 huacaya) and three epistatic scenarios.
2. Double dominant epitasis (15 suri: 1 huacaya).
3. Double recessive epitasis (9 huacaya: 1 suri).
4. Dominant and recessive epitasis (13 suri: 3 huacaya).

Only the hypothesis of a single dominant gene adequately explains the segregation between suri and huacaya ($G_{adj} = 0,347$, $P = 0,556$). Using the modified method Single Jackknife Estimator (MSJE), the frequency of the recessive gene huacaya is estimated at 0.295; while the frequency of the dominant gene for suri is 0.705 (Huet and Murphy, 1980). The heterozygote frequency in the suri population has equally resulted to the entire population at 0.416 and 0.455, with a "carrier" suri/huacaya of 4.780.

The location selection for the suri must be one that seeks to remove heterozygous for the homozygous dominant.

Between 2 126 (1 009 females and 1 117 males) huacaya x huacaya in 177 families of half paternal brothers, 2 123 huacaya and 3 suris were born into three different families. Since the parents belong to several generations of the huacaya line, a classification error by mothers is unlikely to exist. Therefore, this phenomenon is a result of new mutations on gene expression (reverse mutation) of the gametes level lines of the parents. The gene responsible for the synthesis of huacaya and suri would be the result of a recurrent mutation appearing with a constant rate of mutation in each generation. The rate of mutation would be equal to $3 / (2126) = 0.001411101$. The birth of suri as a result of mating between huacaya x huacaya explains why sometimes it is considered recessive. Some authors describe the existence of an intermediate type called chili (anonymous, 1994: C Tuckwel, personal communication and Ponzoni *et al.*, 1997) also described in the llama (Frank *et al.*, 2001).

The favorite colors for selection include the non-albino white and the pigmentation model of black and brown (Renieri *et al.*, 1994 a, b; Renieri, 1995). White signifies the absence of pigmentation. The cells that produce pigments are not found only on the skin of animals fitted with coverage pilífera (melanocytes follicular), but also in the eye, in the inner ear, in the meninges and other internal organs; for clarification, the white is non-albino. This white color is obtained through a mutation which includes the loss of gene function involved in embryonic melanoblasts and the migration of neural crest of the hair follicle in the local development of the animals (Bennet and Lamoreaux 2003). This mutation is identified and cloned in mammals of 22 genes involved in the function (Baxter *et al.*, 2004); however, most mutations associated with white in such loci behave as lethal. In three cases of the reverse for the loci mITF (microphthalmia), C - Kit (Dominant Spottting) and SCF demonstrated the possibility to obtain completely white individuals which may involved these genes within the process.

The black fleece stems from the eumelanina prevalence in the fleece of the animal (Renieri *et al.*, 1991, Renieri *et al.*, 1995; Cecchi *et al.*; 2006). Within the black eumelaninas, a net prevalence of DHI (Dihidroindo) monomer is present which characterizes the heteropolimero. On the other hand, the prevalence of the opposite acidified form (DHICA) produces the brown eumelaninas. Genetically speaking, the black derives from two origins: 1) a mutation due to the loss of function to Agouti locus which, as a result, behaves like a recessive trait regarding other models of pigmentation, 2) mutations in the gene expression on locus MC1R which is dominant (Lauvergne *et al.*, 1996). These results of data segregation exhibit a

Fleece color

recessive trait in the black alpaca. Nevertheless, it is not possible to exclude the existence of a dominant black. Many mutations are identified in the locus without MC1R function definition (Powell *et al.*, 2007).

The brown represents an eumelanico model with the prevalence of brown eumelaninas due to the presence of brown eumelanosomas (Cozzali *et al.*, 2001); genetically, brown stems from a mutation with loss of function of locus TYRP1 (Brown) alleles while allowing the expression of wild black (Castrignano *et al.*, 2001).

Quantitative characteristics

The quantitative characteristic selection considers the weight of the fleece, the diameter of fleece, and the variability coefficient (VC) of the first shearing. Data of these characteristics have been gathered from 293 male and female alpacas born in Tocra in 2004 and 2005.

The non-genetic factors (type of fleece, age, sex, color fleece) were significant to the analysis of variance, the influence of the birth year on the diameter, as well as a key type of fleece on the variability coefficient of the diameter. The phenotypic correlation is equal to 0.179 between the weight of the fleece and its diameter, 0.091 between the weight of fleece and VC of the diameter, and 0.124 between the diameter and the VC of the diameter. The genetic correlations were equal to 0.230 ($P = 0.001$) between the weight and diameter of fleece, 0.377 ($P = 0.001$) between the weight of fleece and VC of diameter, and 0.324 ($P = 0.001$) between the diameter and VC of diameter; these results are rarely seen in the literature, given the great variability (Frank *et al.*, 2006).

Table 1. Heritability (diagonal), genetic correlation (on the diagonal) and phenotypic correlation of the fleece weight (below the diagonal), of the fineness and of the VC of finesse.

Characteristic	Hair weight	Fineness	VC of Fineness
Hair Weight	0.84	0.230 ¹	0.377 *
Fineness	0.179 *	0.32	0.324 *
VC of Fineness	0.091	0.124	0.46

¹ $P < 0.001$.

Selection method and identification of reproducers

Using the test performance method, alpacas are evaluated for their quantitative characteristics. The basis of genetic parameters of the considered characteristics has proposed a synthetic index estimated with the Multiple Trait model and MTDFREML software (Multiple Trait Derivate Restricted Free Maximum Likelihood), 50% of the fiber diameter, 40% of VC diameter, and 10% of the fleece weight. Of the 293 alpacas born between January-April of 2005, 2006 and 2007, 154 (53%) had positive selection index; the reliability of this estimate varies between 0.503 and 0.783, with an average of 0.733. Of the 154 alpacas with a positive index, 126 hold values higher than average reliability.

The core of Toccra - CEDAT is organized into 14 huacaya alpaca families and 4 suri alpaca families. These families have been created based on their same phenotype and in relation to the degree of its members, ranging from offspring up to first cousins. Each family includes 2 or 3 males and 20-30 females. The 14 huacaya families comprise 9 white families, 3 brown families, and 2 black families while the 4 suri families are white. The reproductive management of the 9 white huacaya families and 4 white suri families was achieved using the "circular mating" scheme (Wright, 1921, 1931; Kimura and Crow, 1963) or circular breeding season, involving the passage of the native family reproducers to distant kinship. Through this mating system, each family reproduces yearly: the male reproducer, the genetically best for mating in the internal core and 2 male breeders transfer to the multipliers. Replacement core reproducers must be done every two years; the females with positive selection index born into each family will be used by substitution, internal family replacement, or transferred to multipliers. The black and brown huacaya families function as a cooperative core with the multipliers due to their limited number.

The multipliers must register phenotype data relating to the fleece weight, fiber diameter, and VC diameter. From this year, the data used will serve to estimate the genetic indexes of the alpacas. The multipliers will receive core breeders which changes every three years. The multipliers will transfer the offspring of breeders to the core or commercial breeders. The value of multiplication must be equal to 5 male breeders per year for every core male received.

Contrary to what is most important within this alpaca genetic improvement program, limitations for the operation do not seem to be environmental in nature (complexity of the Andean environment) or an economic, if not essentially cultural.

A program of genetic improvement requires a well-defined population of where to apply such a program.

The existing alpaca breeds are essential of the primary type, resulting of the first division of the genetic pool assembling the domestication and the effect of genetic drift caused by the shock of conquest (Renieri *et al.*, 2007). The breeds of relatives are classically characterized by a high phenotypic variability of qualitative characteristics (color, type of fleece) and quantitative characteristics (parameter, biometrics, production); the closeness of the selection requires particular impact options within the same population.

An erroneous approach has led to the effects of genetic combination (Incrocio) to those of selection. This particular selection has been highly valued in Peru. From the creation of a Libro Genealogico (L.G.) national allowing the entry of animals belonging to any population stems the idea that a breeder can behave in a manner in any population where it reproduces.

Organization of the core selection in Toccra

Transfer of core reproducers to multipliers

Conclusion

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