

# Phenotypes Resulting From Huacaya by Huacaya, Suri by Huacaya and Suri by Suri Alpaca Crossings

R.W Ponzoni(1), D.J. Hubbard(2), R.V. Kenyon1, C.D. Tuckwell(2), B.A. McGregor(3), Andrea Howse(3), I. Carmichael(4), and G.J. Judson(4)

- 1. South Australian Research and Development Institute, GPO box 397, Adelaide, South Australia 5001
- 2. Primary Industries South Australia, c/o The University of Adelaide, Roseworthy, South Australia 5371
- 3. Victorian Institute of Animal Science, Attwood, Victoria 3049
- 4. Central Veterinary Laboratories, Primary Industries South Australia, Glenside, South Australia 5065

## SUMMARY

Data on 145 huacaya sire by huacaya dam, 24 suri sire by huacaya dam and 35 suri sire by suri dam mating records (and their corresponding progeny) were used to determine the mode of inheritance of the huacaya and suri feature in alpacas. The results indicated control by a single gene (or by an haplotype), and dominance of the allele responsible for the suri type (AIFS) over that responsible for the huacaya type (AIFh).

Keywords: alpaca, huacaya, suri, crosses, inheritance.

## INTRODUCTION

Two distinct phenotypes can be identified among alpacas (*Lama pacos*), the huacaya and the suri (Calle Escobar 1984, Bustinza Choque 1985, Wheeler 1991, Novoa and Wilson 1992). Most (~90 per cent) alpacas belong to the huacaya type. Huacayas can be distinguished from suris by their fleece characteristics. The huacaya's fibre is sometimes crimped, and may be described as similar to that of Corriedale or of strong wool Merino sheep. The staples grow perpendicular to the skin surface. By contrast, the suri fleece has a longer and lustrous fibre, which 'hangs' from the skin surface as in Lincoln sheep or Angora goats. The suri staples show ringlet formations characteristic of Angora goats, and these part along the back of the animal exposing the skin.

When crosses are made between huacaya and suri alpacas the progeny distinctly fall into one or the other type (Calle Escobar 1984). This suggests the presence of a major gene influencing the trait. Novoa and Wilson (1992) indicate that suri could be dominant over huacaya, whereas Calle Escobar (1984) suggests that the opposite could be true. Both references stress that further matings should be rigorously studied. Note that there is anecdotal information (e.g. Anonymous 1994, C. Tuckwell – personal communication) about a third type (Chili), which is not well documented and is not dealt with here.

In this paper we report results from an alpaca research project described by Tuckwell et al. (1996). It is suggested that the trait is controlled by a single gene (or by an haplotype) and that the suri allele is dominant over the huacaya allele.

## MATERIALS AND METHODS

The data analysed here are part of a broader alpaca study involving five cooperating producers (Tuckwell et al. 1996). Full pedigrees were kept on the animals involved in the project, and the phenotype (huacaya or suri) of progeny and of both parents was recorded. A total of 204 mating records (and their corresponding progeny) were available for analysis. The mating combinations were: 145 huacaya sire by huacaya dam, 24 suri sire by huacaya dam, and 35 suri sire by suri dam. There were no huacaya sire by suri dam matings.

Initially, sex of the progeny and the interaction of sex with mating combination were included in a linear model to ascertain whether there was significant sex effect, and (or) a significant sex by mating combination interaction on progeny phenotype. Both effects were non significant ( $P>0.6$ ) and were ignored in all later analyses.

A single gene (AIF, for alpaca fleece) mode of inheritance was postulated, with two alleles: AIFh and AIFS, the latter being dominant over the former. Deviations from the expected phenotypic ratios among the progeny resulting from the different mating combinations were tested by chi-square (corrected for continuity). [Ed. Chi-square: method of comparing observed and theoretical values in statistics].

## RESULTS

Huacaya sire by huacaya dam matings resulted in 145 huacaya and no suri progeny. A single phenotype among the progeny suggests that the parents are homozygous. Also, because no suri phenotypes were produced from huacaya sire by huacaya dam matings one may assume that the AIFh allele is recessive. The results fit with the hypothesis of a single gene and dominance of the AIFS allele over the AIFh allele.

Suri sire by huacaya dam matings resulted in 13 huacaya and 11 suri progeny. These numbers do not deviate significantly ( $\chi^2$  1 df = 0.21,  $P=0.65$ ) from a 1:1 ratio. A 1:1 ratio suggests control by a single gene and that one of the parents (the suri sires in this case) is heterozygous.

Suri sire by suri dam matings resulted in 6 huacaya and 29 suri progeny. These numbers do not deviate significantly ( $\chi^2$  1 df = 1.4,  $P=0.24$ ) from a 1:3 ratio. A 1:3 ratio suggests control by a single gene and that both parents (suri sires and dams) are heterozygous.

We examined the progeny of each suri sire in our data base. Under the postulated mode of inheritance, a single huacaya progeny from a suri sire would be proof that the sire is heterozygous (i.e. carrier of the AIFh gene). Out of a total of 11 suri sires in our data base, 9 could be deemed heterozygous using this criterion. The other 2 sires had too few (1 and 3) progeny to be classified as homozygous or heterozygous.

Suri dams had insufficient number of progeny to ascertain their genotype, but one may assume that among them the gene frequency is similar to that among sires (i.e. most, if not all, dams are heterozygous). Heterozygosity among suris could be due to frequent crossing with huacaya or to heterozygous advantage. We know that crosses between the two phenotypes are frequent, but we are not aware of evidence regarding the possibility of heterozygous advantage.

## DISCUSSION

Results from huacaya by suri matings have been reported by Novoa and Wilson (1992) and by Flint (1996). Although we lack depth of knowledge about the data sets involved, some comparisons may be made with our findings. Huacaya by huacaya matings only produced huacaya offspring in Novoa and Wilson's study, which is in agreement with our findings. However, out of 8446 such matings Flint (1996) reports that 0.45 per cent produce suri progeny. This is not consistent with our hypothesis that huacayas are homozygous recessive, but such a small percentage of suri progeny could be accounted for by errors in recording parental and progeny phenotypes, or when entering the data for analysis. Suri by huacaya matings result in a 1:1 ratio in Flint's data ( $\chi^2$  1 df = 0.06,  $P=0.8$ ), but the deviation from the expected values borders significance ( $\chi^2$  1 df = 3.08,  $P=0.08$ ) in Novoa and Wilson's report. Note, however, that in the latter case there are only 12 progeny resulting from this mating combination. In both, Flint's and Novoa and Wilson's reports there is a significant ( $P<0.01$ ) departure from a 1:3 ratio among progeny from suri by suri matings, due to an excess of suri phenotypes. Unfortunately, neither study attempts to ascertain the genotypes of the parents, and the results could be simply due to the presence of a fraction of homozygous suri parents. In summary, the results presented by Novoa and Wilson (1992) and by Flint (1996) are not in complete agreement with ours, but the discrepancies have possible explanations and the evidence is not sufficient to disprove our hypothesis.

We conclude that our results are consistent with the postulated mode of inheritance (a single gene and two alleles, AIFS dominant over AIFh). The model was chosen because it is the simplest possible one. Note, however, that the same results could be obtained if the trait were not controlled by a single gene, but by a group of very closely linked genes (haplotype) that were inherited together. Further analyses of data should contribute to a greater understanding of the genetic mechanisms involved in the expression of the huacaya and suri phenotypes.

In the meantime, rules and regulations drawn up by the Australian Alpaca Association regarding the registration and status of huacaya and suri animals resulting from different mating combinations should take into account current knowledge about the inheritance of this alpaca feature.

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