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Genetic parameters for different types of medullated fibre in Alpacas

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Abstract

The quality of alpaca textile fibre has great potential, especially if objectionable fibres (coarse and medullated fibres) that cause itching are reduced, considering that objectionable fibres can be identified by diameter and medullation types. The objective of this study was to estimate genetic parameters for medullar types and their respective diameters to evaluate the possibility of incorporating them as selection criteria in alpaca breeding programmes. The research used 3149 alpaca fibre samples collected from 2020 to 2022, from a population of 1626 Huacaya type alpacas. The heritability and correlations of the percentages of non-medullated (NM), fragmented medulle (FM), uncontinuous medullated (UM), continuous medullated (CM), and strongly medullated (SM) fibres were analysed, also the fibre diameter (FD) for each of the medullation types. The heritability estimated for medullation types were 0.25 ± 0.01, 0.18 ± 0.01, 0.10 ± 0.01, 0.20 ± 0.01 and 0.11 ± 0.01 for NM, FM, UM, CM and SM, respectively. The genetic correlations for medullation categories ranged from 0.15 ± 0.03 to 0.66 ± 0.02 (in absolute values). The heritabilility estimated for fibre diameter (FD) of each of the medullation types were 0.29 ± 0.03, 0.27 ± 0.02, 0.35 ± 0.02, 0.30 ± 0.02, 0.25 ± 0.02 and 0.10 ± 0.02 for FD, FD_NM, FD_FM, FD_UM, FD_CM and FD_SM, respectively. The genetic correlations for fibre diameter of the medullation types ranged from 0.04 ± 0.04 to 0.97 ± 0.01. FD, NM and FM are the main traits to be used as selection criteria under a genetic index, since they would reduce fibre diameter, and also increase NM and FM, and, in addition reducing indirectly CM, SM, and SM_FD. Therefore, the quality of alpaca fibre could be improved.

KEYWORDS

camelid, compositional data, heritability, medullation type, objectionable fibre

1 | INTRODUCTION

The main objective of alpaca (*Vicugna pacos*) breeding programmes is to increase fibre production and quality (Gutiérrez et al., 2009). However, the alpaca textile industry has commercial limitations, because the fleece has hairs that stand out from the main fleece (coloured fibre and coarse medullated fibre) known as objectionable fibres (Frank et al., 2014; Hunter, 1993; McGregor, 2006). When the medulla occupies an area more than 60% of the fibre, it is catalogued as strongly medullated (Lupton & Pfeiffer, 1998; Wildman, 1954), which in camelids may be confused with kemp despite camelids not produce this type of fibre.

Strongly medullated fibres pose an additional concern for alpaca fibre production because medullation modifies the internal structure of the hair (Mucha & Janeczek, 2018), and increasing its stiffness (Frank et al., 2014), which is related to the prickle factor (Cruz et al., 2019; Quispe, Quispe, et al., 2022). Besides causing an unpleasant sensation when in contact with the skin, the stiffness of these objectionable fibres also reduces the softness of the garments (Frank, 2008). The decrease in softness can also be attributed to fibre thickness, known as comfort factor defined as the percentage of fibres below 30 μm in diameter (Naylor, 1992) and less than 3% of objectionable fibres with a diameter greater than 32 μm (Naylor & Phillips, 1997).

There are different grades of medullation in fibres, they can be classified in five categories, non-medullated (NM), fragmented medulle (FM), uncontinuous medullated (UM), continuous medullated (CM) and strongly medullated (SM) as reported by Frank et al. (2011) for llamas by Pinares et al. (2018), Quispe, Quispe, et al. (2022) and Quispe et al. (2023) for alpacas. Similar grouping has been defined for goats and sheep (Hunter et al., 2013; McGregor, 2012). Pinares et al. (2018) proposed including medullation as a selection criteria in alpacas, quantifying the diameter and medulla category for 600 fibres each from 36 animals by using a projection microscope, also they reported the difficulties of measuring these traits in a wider alpaca population. The Fiber Med device has recently been developed (Quispe et al., 2023;Quispe, Quispe, et al., 2022; Quispe, Serrano-Arriezu, et al., 2022) by applying artificial intelligence methodology for the automatic identification and classification of the medullation classes, allowing to determine the incidence of medullation in animal fibres, considering the types of medullation, in absolute and relative values. Additionally, the device provides the general average of the fibre diameter (FD) and the mean of diameter by medullation categories (Quispe, Quispe, et al., 2022; Quispe, Serrano-Arriezu, et al., 2022).

Analysing compositional data (data that describes the parts of a whole, referring to the data that depend on each other to express a final value) presents challenges because the sum of categories is one and the increase in one of the categories necessarily corresponds to a decrease in the remaining categories, creating a spurious correlation between medullated fibre types (Aitchison, 1982). Thus raw data must not be analysed as such, but they need to be transformed (Aitchison & Egozcue, 2005; Egozcue & Pawlowsky-Glahn, 2011). The centered log-ratio (CLR, Aitchison, 1986), addresses these issues by expressing the compositional data as proportional to the geometric mean. There are still correlations among the transformed traits, which is also given by the sum-to-zero constraint. This is necessarily so because an increase in one of the categories will lead to a decrease in one or more of the remaining categories.

The quality of the alpaca textile fibre could improve if objectionable fibres are reduced or eliminated. This improvement in quality would give greater commercial opportunities in international markets, increasing its commercial value, competing with other fibres of high economic value, and improving the economic income of the entire alpaca production chain (Frank et al., 2017). The objective of this study was to estimate genetic parameters of the medullation types and their respective diameters in order to evaluate the possibility of incorporating them as selection criteria in alpaca breeding programmes.

2 | MATERIALS AND METHODS

2.1 | Population and data collection

The information was obtained from PacoPro v5.10 dataset belonging to the Pacomarca Scientific Station, located southeast of Peru, in the climatic zone classified as Very Humid Paramo–Subalpine-Subtropical (pmh-SaS), with an average annual temperature of 11°C and an average annual precipitation of 1178 mm/year. The data of medullation types corresponds to 3149 samples from 1626 Huacaya alpacas (mean 1.94 records per animal), measured in three consecutive years, 2020, 2021 and 2022, alpacas age were between 1 and 16 years old. The pedigree consisted of 14,457 individuals with up to 7 generations, born from 1992 to 2022.

Fibre samples were taken at the shearing time by the farm manager from the mid side of alpacas (McGregor et al., 2012), around 10 gr. The preparation of each sample to be analysed followed the procedure described in IWTO-8-2011 (IWTO-8, 2011). Diameter and medulla category were measured using the Fiber Med device (Quispe et al., 2023; Quispe, Serrano-Arriezu, et al., 2022). The analysed traits for each individual were: Medullation types (NM, FM, UM, CM and SM) expressed in percentage, the global mean of the fibre diameter (FD) and the mean for each type of medullation (NM_FD, FM_FD, UM_FD, CM_FD and SM_FD). The descriptive statistics for all traits are shown in Table 1.

2.2 | Methods

Prior to the estimation of the variance components, the traits referring to medulla type, were transformed using the CLR method proposed by Aitchison (1986), using the following expression:

$$\mathrm{CLR}(x) = \ln\left(\frac{x_1}{g(x)}, \frac{x_2}{g(x)}, \ldots, \frac{x_D}{g(x)}\right),$$

where $g(x)$ is $\mathbf{g}(\boldsymbol{x}) = \left(\prod_{i=1}^{D} \boldsymbol{x}_i\right)^{\frac{1}{D}}$, D is the number of components, five in this case. $\mathrm{CLR}_i(X) = \ln\left(\frac{x_i}{g(x)}\right)$ are known as logarithmic-contrasts, that is the coefficients sum to zero (Egozcue & Pawlowsky-Glahn, 2011). When one of the categories was zero, it was assigned to a very low value (0.01) and this value reduced from the adjacent category.

Variance components were estimated in the traits referring to the medullation categories using the data transformed to CLR, the traits referring to the fibre diameters for each type of medullation were estimated using the raw data. The genetic parameters were estimated via a multi-trait restricted maximum likelihood procedure applied to mixed models. The analysis was performed by grouping the traits into 3 groups, the first group analysed the medullation categories (NM, FM, UM, CM and SM), the second group analysed the general average of fibre diameter and the diameters of the medullation types (FD, NM_FD, FM_FD, UM_FD, CM_FD and SM_FD), and the third group analysed all traits to estimate the genetic and phenotypic correlations between medullation types and their respective fibre diameters. The model was:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wp} + \mathbf{e},$$

in the matrix notation is

$$\begin{pmatrix} \mathbf{u} \\ \mathbf{p} \\ \mathbf{e} \end{pmatrix} \sim \mathbf{N}\left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{A} \otimes \mathbf{G_0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I_p} \otimes \mathbf{P_0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I_e} \otimes \mathbf{R_0} \end{bmatrix}\right), \text{ where}$$

y is the vector of observations, **b** is the vector of fixed effects, **u** is the vector representing the additive genetic effects, **p** is the vector of permanent environments of individuals for fibre traits, **e** is the vector of residuals; **X, Z** and **W** the incidence matrices for fixed, direct genetic and permanent environmental effect, respectively, **A** the numerator relationship matrix, $\mathbf{G_0}$ the covariance matrix for additive genetic effects, $\mathbf{I_p}$ the identity matrix of equal order to the number of permanent environmental subclasses, $\mathbf{P_0}$ the covariance matrix for permanent environmental effects, $\mathbf{I_e}$ the identity matrix of equal order to the number of records, $\mathbf{R_0}$ the residual covariance matrix among measurements on the same animal and $\otimes$ the Kronecker product, where the dimension of the matrices $\mathbf{G_0}$, $\mathbf{P_0}$ and $\mathbf{R_0}$ depended according to the number of traits within each analysis group. Only animals from Pacomarca farm were analysed and were treated as a single genetic group. Fixed effects previously showing significant

TABLE 1 Minimum, maximum, mean, and standard deviations of the percentage of medullation and fibre diameter for medullation types in 3149 alpaca records.

Traits	Frequency	Minimum	Maximum	Mean	Standard deviations
NM (%)	3149	0.88	98.72	63.18	24.60
FM (%)	3147	0.01	57.47	18.16	11.0
UM (%)	3148	0.01	45.37	7.86	7.49
CM (%)	3149	0.12	95.28	10.46	12.30
SM (%)	2009	0.01	10.54	0.34	0.89
FD (µm)	3149	14.92	34.00	20.78	2.85
NM_FD (µm)	3149	14.42	30.18	18.88	1.99
FM_FD (µm)	3147	17.82	32.25	22.15	1.90
UM_FD (µm)	3148	18.58	39.99	24.57	1.88
CM_FD (µm)	3149	22.73	50.92	28.10	2.48
SM_FD (µm)	2009	23.00	89.68	45.96	10.90

Abbreviations: CM, continuous medullated; CM_FD, continuous medullated fibre diameter; FD, general mean of the fibre diameter; FM, fragmented medulle; FM_FD, fragmented medullated fibre diameter; NM, non-medullated; NM_FD, non-medullated fibre diameter; SM, strongly medullated; SM_FD, strongly medullated fibre diameter; UM, uncontinuous medullated; UM_FD, uncontinuous medullated fibre diameter.

influence on these traits (Cruz et al., 2019, 2021; Gutierrez et al., 2023). These fixed effects were the colour in two levels (white and cream), sex in two levels (male and female), year of sampling (3 levels) and age as linear and quadratic covariate.

Approximate standard errors for phenotypic correlations (se_r) were calculated using the following formula $se_r = \sqrt{\frac{(1-r^2)}{(n-2)}}$, where r = phenotypic correlation, n = number of samples. Likewise, to calculate the standard errors for repeatability (se$R$) was used the following formula $seR = \sqrt{\left(se_{h^2}\right)^2 + \left(se_{C^2}\right)^2}$, where se_{h^2} = standard error of the heritability and se_{C^2} = standard error of the permanent environmental variance ratio. The pedigree recodification was done using the Endog v4.8 program (Gutierrez & Goyache, 2005). The statistical descriptive and figures were done with the *stack* and *tidyverse* packages in R language (R Core Team, 2020). Genetic parameters were estimated using the VCE 6.0 program (Neumaier & Groeneveld, 1998).

3 | RESULTS

The distribution of the data of fibre by medullation types in relation to the age of the alpacas, considering one shearing per year is shown in Figure 1. Figure 1a shows that the percentage of NM fibre tends to decrease with age. While the percentage of medullated fibre (Figure 1: charts b–e) tends to increase with age.

Figure 2 shows the histogram of the fibre diameter according to the type of medullation, showing how the fibre diameter with a structure classified as SM is separated. The 3149 samples, 63.80% present this type of medullation SM, while the difference corresponds to samples whose fibre analysis does not present fibre with SM. Likewise, it is shown how the diameter in this type of medullation (SM) has the widest range in comparison with the other diameters of the other categories.

The estimated variance components were the additive genetic variance, permanent environment variance and the residual variance, as shown in Table 2. The estimated genetic parameters for medullation types and their respective standard errors (in brackets) and the phenotypic correlations are shown in Table 3. The heritability was moderate between 0.10 and 0.25. The permanent environmental ratios were from very low to moderate between 0.01 to 0.18. The repeatability was moderate between 0.12 to 0.35, the genetic correlations were from moderate to high between 0.15 and 0.66 (in absolute value), and the phenotypic correlations were from moderate to high between 0.18 to 0.78 (in absolute value).

The estimated heritability for the FD and fibre diameter according medullation types, the permanent environmental ratios, the repeatability and the genetic correlations between traits, with their respective standard errors in brackets are shown in Table 4. The heritability was moderate between 0.10 and 0.35. The permanent environmental ratios were moderate between 0.18 and 0.26. The repeatability was moderate to high between 0.29 and 0.58. While, the genetic correlations between traits were

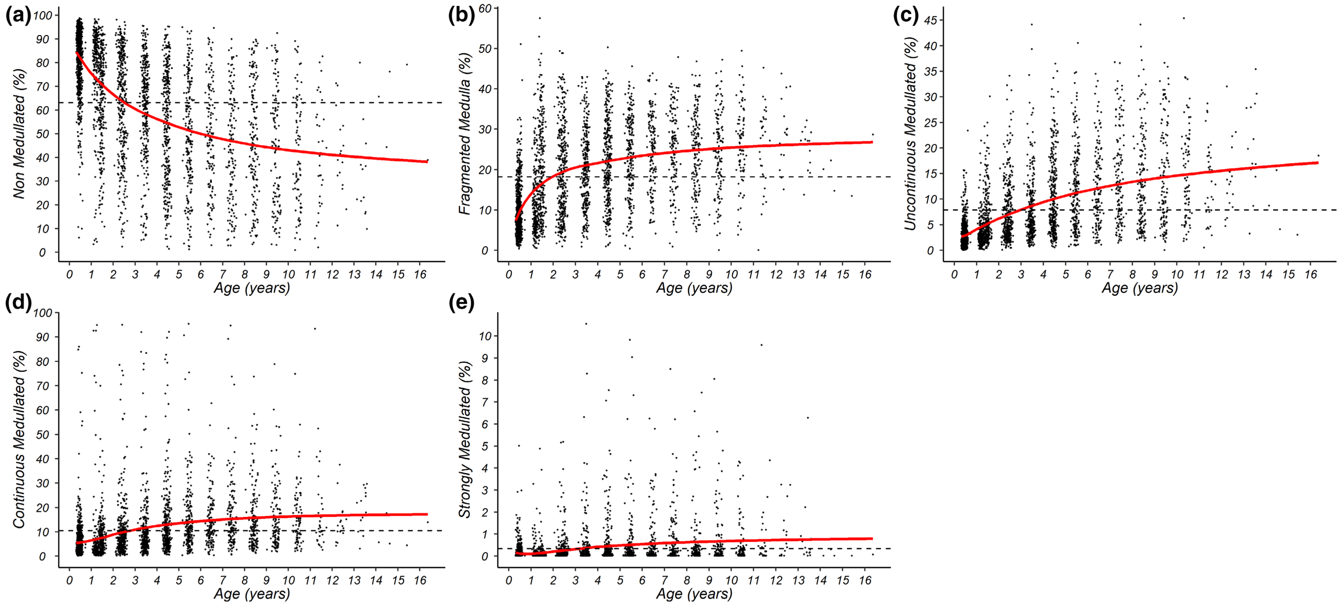

FIGURE 1 Distribution of medullation types according to age in alpacas, red line shows the phenotypic trend and the black line shows the average of the category. (a) non medullated; (b) fragmented medulle; (c) uncontinuous medullated; (d) continous medullated; (e) strongly medullated.

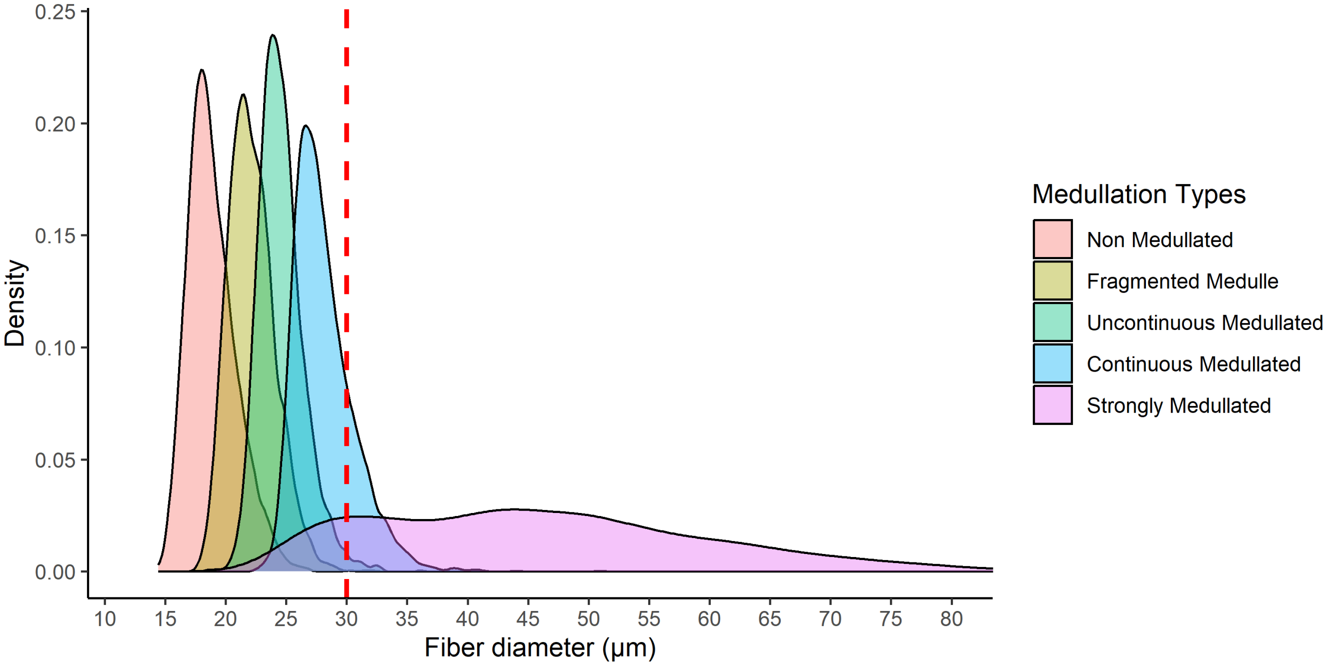

FIGURE 2 Histogram showing fibre diameter according to medullation types and the comfort factor threshold (red line) in Huacaya alpacas.

TABLE 2 Estimates of additive genetic variance (σ^2_A), permanent environment variance, (σ^2_{perm}) and residual variance (σ^2_e) of the medullation categories and their respective fibre diameter in alpacas.

Traits	σ^2_A	σ^2_{perm}	σ^2_e
NM	0.065	0.023	0.170
FM	0.021	0.018	0.077
UM	0.013	0.023	0.089
CM	0.027	0.022	0.093
SM	0.073	0.063	0.525
FD	1.378	0.999	2.400
NM_FD	0.730	0.494	1.460
FM_FD	1.088	0.705	1.324
UM_FD	0.952	0.656	1.523
CM_FD	1.474	1.553	2.908
SM_FD	15.439	30.001	109.062

from very low to high between 0.04 and 0.97 in absolute value and the phenotypic correlations were high between 0.32 and 0.85, except the SM_FD with the rest of fibre traits with values very low (0.01–0.11).

The genetic correlations between medullation types and their respective fibre diameter according to medullation type ranged from very low to high between 0.01 to 0.77 (in absolute values). The important correlations are between FD and medullation types (except the FD and SM 0.13), NM_FD–CM (0.33) and CM_FD – CM (−0.42), as shown in the Table 5.

The phenotypic correlations between the transformed medullation categories and their respective diameters ranged between FD and the different categories of medullation (0.06–0.79), NM_FD and the different categories of medullation (0.03–0.51) and SM_FD and the different categories of medullation (0.06–0.76), the phenotypic correlations among the remaining traits were close to zero, as shown in Table 6.

4 | DISCUSSION

Reducing the percentage of objectionable fibres in alpaca fleece would lead to important economic benefits (Quispe, Grabiel, et al., 2022; Quispe, Quispe, et al., 2022; Quispe, Serrano-Arriezu, et al., 2022) that ultimately might be transferred to all the stakeholders of the fibre textile chain, and particularly to the producers (Gutierrez et al., 2023). From the point of view of the customer, it would reduce the itching and thus improving the softness and quality of the garments (Cruz et al., 2019). To our knowledge, this is the first study that uses direct information of the medullation categories with their respective diameters to evaluate their incorporation as selection criteria in alpaca breeding programmes. To date, medullation has been usually assessed by using a unique measure of percentage of medullation (PM) provided by OFDA100 (Cruz

TABLE 3 Heritability (in the diagonal), between traits genetic correlations (above the diagonal), permanent environmental variances ratio (c^2), and their corresponding standard errors (in brackets), repeatability (R), and phenotypic correlations (below diagonal) for medullation categories.

	NM	FM	UM	CM	SM
NM	0.25 (0.01)	0.23 (0.02)	−0.29 (0.03)	**−0.65** (0.02)	**−0.57** (0.02)
FM	**0.33** (0.02)	0.18 (0.01)	**0.60** (0.03)	**−0.45** (0.02)	**−0.66** (0.02)
UM	−0.26 (0.02)	**0.57** (0.01)	0.10 (0.01)	0.15 (0.03)	**−0.51** (0.02)
CM	**−0.49** (0.02)	−0.18 (0.02)	**0.40** (0.02)	0.20 (0.01)	0.15 (0.03)
SM	**−0.42** (0.02)	**−0.78** (0.01)	**−0.69** (0.02)	−0.26 (0.02)	0.11 (0.01)
c^2	0.09 (0.01)	0.16 (0.01)	0.18 (0.01)	0.16 (0.01)	0.01 (0.01)
R	**0.34** (0.01)	**0.34** (0.01)	0.28 (0.01)	**0.35** (0.01)	0.12 (0.01)

Note: Heritability and genetic correlations higher than 0.30 in absolute value are provided in bold.

Abbreviations: CM, continuous medullated; FM, fragmented medulle; NM, non-medullated; SM, strongly medullated; UM, uncontinuous medullated.

TABLE 4 Heritability (in the diagonal), between traits genetic correlations (above the diagonal), permanent environmental variances ratio (c^2), and their corresponding standard errors (in brackets), repeatability (R), and phenotypic correlations (below the diagonal) for fibre diameter according to the medullation categories in alpacas.

	FD	NM_FD	FM_FD	UM_FD	CM_FD	SM_FD
FD	0.29 (0.03)	**0.81** (0.02)	**0.41** (0.03)	0.22 (0.03)	0.04 (0.04)	0.06 (0.06)
NM_FD	**0.85** (0.01)	0.27 (0.02)	**0.81** (0.02)	**0.66** (0.03)	**0.55** (0.04)	0.06 (0.07)
FM_FD	**0.63** (0.01)	**0.81** (0.01)	**0.35** (0.02)	**0.94** (0.01)	**0.86** (0.03)	−0.28 (0.09)
UM_FD	**0.50** (0.02)	**0.66** (0.01)	**0.85** (0. 01)	**0.30** (0.02)	**0.97** (0.01)	−0.21 (0.09)
CM_FD	**0.32** (0.02)	**0.46** (0.02)	**0.66** (0.01)	**0.70** (0.01)	0.25 (0.02)	−0.10 (0.11)
SM_FD	0.07 (0.02)	0.04 (0.02)	−0.02 (0.02)	0.01 (0.02)	0.11 (0.02)	0.10 (0.02)
c^2	0.21 (0.02)	0.18 (0.02)	0.23 (0.02)	0.21 (0.02)	0.26 (0.02)	0.19 (0.02)
R	**0.50** (0.03)	**0.45** (0.03)	**0.58** (0.03)	**0.51** (0.03)	**0.51** (0.03)	0.29 (0.03)

Note: All heritability and genetic correlations higher than 0.30 in absolute value are provided in bold.

Abbreviations: CM_FD, continuous medullated fibre diameter; FD, general mean of the fibre diameter; FM_FD, fragmented medullated fibre diameter; NM_FD, non-medullated fibre diameter; SM_FD, strongly medullated fibre diameter; UM_FD, uncontinuous medullated fibre diameter.

TABLE 5 Genetic correlations and standard errors (in brackets) between medullation categories and their respective fibre diameter for medullation categories in alpacas.

	FD	NM_FD	FM_FD	UM_FD	CM_FD	SM_FD
NM	**−0.75** (0.03)	−0.26 (0.04)	0.22 (0.03)	0.22 (0.03)	0.29 (0.03)	−0.08 (0.03)
FM	**−0.31** (0.05)	−0.09 (0.04)	−0.06 (0.04)	0.13 (0.03)	0.19 (0.03)	0.08 (0.03)
UM	**0.49** (0.04)	0.20 (0.04)	−0.23 (0.04)	−0.14 (0.03)	−0.19 (0.03)	0.15 (0.03)
CM	**0.77** (0.03)	**0.33** (0.04)	−0.14 (0.04)	−0.27 (0.03)	**−0.42** (0.03)	−0.12 (0.03)
SM	0.13 (0.06)	−0.02 (0.04)	0.03 (0.04)	−0.04 (0.03)	−0.01 (0.03)	0.03 (0.04)

Note: All genetic correlations higher than 0.30 in absolute value are provided in bold.

Abbreviations: CM, continuous medullated; CM_FD, continuous medullated fibre diameter; FD, general mean of the fibre diameter; FM, fragmented medulle; FM_FD, fragmented medullated fibre diameter; NM, non-medullated; NM_FD, non-medullated fibre diameter; SM, strongly medullated; SM_FD, strongly medullated fibre diameter; UM, uncontinuous medullated; UM_FD, uncontinuous medullated fibre diameter.

et al., 2019; Mancisidor et al., 2021; Pinares et al., 2018), and it should be noted that PM is defined as the sum of the percentages of all the medullation categories with some degree of medullation (FM, UM, CM and SM) except for NM fibres such that NM = 100 − PM. As such, PM and NM can be conceptually considered as opposite traits with the same heritability.

Table 1 shows that the percentage of NM (63.18%) was similar to that of 62.69% reported by Cruz et al. (2019) using OFDA100 as measurement device, but considerably

TABLE 6 Phenotypic correlations between medullation categories and their respective fibre diameter for medullation categories in alpacas.

	FD	NM_FD	FM_FD	UM_FD	CM_FD	SM_FD
NM	**−0.79** (0.01)	**−0.51** (0.01)	−0.03 (0.02)	−0.04 (0.02)	0.03 (0.02)	**−0.45** (0.02)
FM	−0.06 (0.02)	0.03 (0.02)	0.22 (0.02)	0.14 (0.02)	0.09 (0.02)	**−0.50** (0.01)
UM	**0.46** (0.02)	**0.32** (0.02)	0.09 (0.02)	0.10 (0.02)	−0.05 (0.02)	−0.27 (0.02)
CM	**0.45** (0.02)	0.28 (0.02)	−0.17 (0.02)	−0.12 (0.02)	−0.21 (0.02)	−0.06 (0.02)
SM	0.28 (0.02)	0.14 (0.02)	−0.04 (0.02)	−0.01 (0.02)	0.06 (0.02)	**0.76** (0.01)

Note: All phenotypic correlations higher than 0.30 in absolute value are provided in bold.

Abbreviations: CM, continuous medullated; CM_FD, continuous medullated fibre diameter; FD, general mean of the fibre diameter; FM, fragmented medulle; FM_FD, fragmented medullated fibre diameter; NM, non-medullated; NM_FD, non-medullated fibre diameter; SM, strongly medullated; SM_FD, strongly medullated fibre diameter; UM, uncontinuous medullated; UM_FD, uncontinuous medullated fibre diameter.

higher than that of 32.56% reported by Pinares et al. (2018) for small populations (36 selected males) both in the same Pacomarca population, but it measured with a projection microscope. Much of these discrepancies could be attributed to the different methodology, sample size and the number of fibres per sample used to assess the categories. Note that OFDA100 bases on opacity inference, while the Fiber Med uses the artificial intelligence to recognize the types of fibre medullation, being an automated objective method, but the projection microscope is a manual objective method. However, when comparing the results using the same methodology with a population with similar highlands conditions such as that of Huancavelica (Berolatti et al., 2021; Quispe, Quispe, et al., 2022), which has not been subjected to intense selection pressure for fibre diameter, the percentage of medullation were lower in favour of Pacomarca. Analysing a different population, Wang et al. (2005) reported a wide range of percentage of medullation between 72% and 33% for Australian alpacas. Regarding objectionable fibres (SM), working with 15 samples only Berolatti et al. (2021) reported sixfold (2.10%) that reported here (0.34%) in a Huancavelica aged population. However, Quispe, Quispe, et al. (2022) found similar percentages for Huancavelica and Pacomarca (0.72% and 0.74%, respectively), although with respect to total medullation, in alpacas from Huancavelica, they found a higher incidence than in Pacomarca (55.52% and 33.49%, respectively).

The distribution of the percentage of medullation according to category shows that age has relevant influence (Figure 1). NM fibre (Figure 1a) shows a trend by age similar to the distribution of fibre diameter reported by Gutierrez et al. (2011), it has also been reported that the tendency of wool thickening may be influenced by the number of shearings as reported in sheep (Quispe, Grabiel, et al., 2022). However, as the medullation grade increases towards a strongly medullated fibre type the trend tends to be independent as shown in Figure 1e, similar to that reported in llamas (Iñiguez et al., 1998). In Figure 2, the diameter distribution with respect to medullation types are similar to that reported by Pinares et al. (2018) and Quispe, Quispe, et al. (2022). However, here the independence of FD_SM is shown to be much less pronounced than the rest of the categories, because there are 1140 fibre samples that do not have this type of medullation (Table 1).

Fortunately, the genetic parameters are consistent with other works for this type of textile traits (Cruz et al., 2019; Gutierrez et al., 2023), even though the systematization of genealogical and productive records in Peru has begun approximately three decades ago. The concern in this type of analysis is the small number of generations contained in the pedigree could show inconsistent results. Likewise, the results of other works for this type of traits support the reliability of its use with a similar size and depth of the pedigree (Cruz et al., 2023; Mancisidor et al., 2021; More et al., 2023).

The heritability found for the different types of medullation show that the NM fibre in alpacas values are similar (0.24 and 0.25) to those reported by Pinares et al. (2018) and Cruz et al. (2019) respectively, and lower (0.37) than those reported in sheep (Sánchez et al., 2016). The heritability of the different medullation categories have lower values limiting the use in genetic improvement programmes (of textile traits) especially UM and SM fibre. Likewise, the repeatability show that SM fibre has a very low value than the other traits, showing that there is a negligible permanent environmental effect with low heritability. However, the genetic correlations of NM fibre shows favourable, especially for reducing CM (−0.65) and SM (−0.57) which are the fibres that exceed the comfort factor threshold (Figure 2), which would be the undesirable fibres to the textile sector in the implementation of a genetic programme, which seeks to produce fine fibres with the lowest degree of itchiness, under a genetic index as proposed by Cruz et al. (2023). The positive genetic correlation was found for NM and FM fibre (0.23). This genetic relationship could be considered favourable since FM fibres exhibit good fineness, less weight (due to lower specific weight) and better thermal capacity (Czaplicki, 2012) to fabrics and garments made with them. It would be more practical select directly for NM fibres as it would directly lead to a decrease in UM, CM, and SM. However, it could lead to an increase in FM which may not be as undesirable as the rest, but that is positively correlated with undesirable fibres.

In goats and sheep, the study of the genetic parameters of objectionable fibres has been limited to the study of pigmented fibre, medullation and kemp (Allain & Roguet, 2003; Sánchez et al., 2016), ignoring the types of medullation due to the difficulty of automatic measurement.

The heritability of diameter by medullation obtained were similar to the heritability and repeatability found for fibre diameter regardless of medullation type in alpacas (Cruz et al., 2019, 2021; Mancisidor et al., 2021), sheep (Di et al., 2011), and goats (Visser et al., 2009). The genetic correlations between the general average of the FD and the other diameters reduces as the degree of medullation increases. However, the FD_SM is independent of the other fibre diameters, similar to that reported by Martinez et al. (1997), which shows that the NM is finer (22.7 μm) than the medullated fibre as SM (40.8 μm). Phenotypic correlations are larger than genetic correlations. Fibre diameter FD_SM does not follow the trend of the rest of the traits, showing very low values for all genetic parameters.

Regarding genetic correlations of the medullation types with their respective fibre diameters was observed that the overall average FD of the fibre was the trait showing the most favourable correlations with the medullation types (except with UM). The correlation between FD and NM (−0.75) is higher than the reported by Cruz et al. (2019), who analysed the medullation percentage in a single category (0.55). Selecting for decreased fibre diameter will also decrease UM (0.49) and CM (0.77) fibre percentage. This validates the genetic improvement programmes that are currently being developed (Cruz et al., 2017, 2021; Mancisidor et al., 2021) that use fibre diameter and percentage of NM (or PM) as the main selection criteria. Cruz et al. (2023) reported that when these two traits are used under appropriate weight a favourable response to selection to improve alpaca fibre quality can be obtained. The relationship between CM and NM_FD showed a favourable genetic correlation (0.33), while CM and CM_FD showed an unfavourable genetic correlation (−0.42). A priori, the CM reduction and the diameter reduction are interpreted as something favourable since all efforts are focused on reducing both traits, and vice versa if the opposite occurs. However, by reducing the percentage of continuous type medullation, in this category its diameter would increase, a priori this correlation is detrimental, but the difference in diameters within the types of medullation would help greater differentiation of this type of fibre, and could give rise to mechanical dehairing processes, which base their success on the differentiation of the diameter within the fibre samples. The remaining of the genetic correlations show very low values, especially for SM and SM_FD with the remaining traits in the medullation categories and their respective diameters.

The phenotypic correlations between FD and medullation (NM) were similar (−0.79), to those reported for alpacas by Quispe, Quispe, et al. (2022), McGregor (2006) and Pinares et al. (2019), who found phenotypic correlations between 0.68 and 0.80. In contrast, phenotypic correlations between FD and the other medullation types were slightly higher (0.46, 0.45 for FD and UM, FD and CM, respectively) than those reported by Quispe, Quispe, et al. (2022). Likewise, SM_FD has important phenotypic correlations with NM fibre, FM (−0.45 and −0.50 respectively) and especially with SM (0.76). Similarly, phenotypic correlations between FD and SM fibre showed lower correlations (0.28) than those by Berolatti et al. (2021) and Quispe, Quispe, et al. (2022), who reported correlations between 0.41 and 0.45 for tuis and adult alpacas, respectively.

5 | CONCLUSION

From the analysis of the genetic parameters for the medullation types, it has been deduced that FD, NM and FM are the main traits to be used as selection criteria under a genetic index, since the FD reduces fibre diameter, and also increases NM and FM and in addition reduces in indirect way CM, SM, and SM_FD.

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CONFLICT OF INTEREST STATEMENT

The authors declare that there are no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

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