

V I R T U A L

International Symposium on

Sustainable Animal Production and Health

Current Status and Way Forward

BOOK OF SYNOPSES

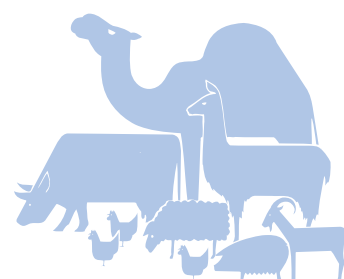


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COMPARISON OF BREEDING VALUES' ACCURACY USING BLUP AND SS-GBLUP METHODOLOGY IN PERUVIAN ALPACAS

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Introduction

The textile industry places exceptionally high-quality demands on alpaca fiber to be competitive on the international market. Therefore, reducing the fiber diameter and reducing the percentage of medullation are economically important breeding goals to reduce the itching factor (Gutiérrez et al., 2009). To date, no national breeding program has been established in Peru, but there are several local genetic improvement initiatives carried out (Gutiérrez et al., 2018). Best Linear Unbiased Prediction model (BLUP) is the standard method for estimating breeding values. Recently, a SNP-chip for alpacas has been developed, and possible use in genomic selection is discussed (Calderon et al., 2020).

This study aims to evaluate the possible advantage of including genomic information in estimating breeding values. Therefore, accuracies of estimated breeding values for three different fiber traits (fiber diameter (FD), standard deviation (SD), and percent of medullation (PM)) using two different methods, namely BLUP and ssGBLUP, are compared.

Material and methods

The data were obtained from the PacoPro v5.10 software from the Pacamarca scientific research experimental station, which contains pedigree information from 1992 to 2020 and phenotypic data collected from 2001 to 2019. The fiber traits were FD and SD described by Gutiérrez et al. (2009) and PM described by Cruz et al. (2019). Table 1 provides an overview of the number of observations for each trait.

Table 1. Traits and number of observations recorded

	Animals (n)	Total records		
		FD	SD	PM
Full pedigree	7,012			
Animal with records	6,889	24,169	24,169	8,386
Genotyped animals	431	2,774	2,774	1,767

FD=fiber diameter, SD=standard deviation of fiber diameter, PM=percentage of medullation

Genotyping data of 431 animals from the project N° 028-2016-INIA-PNIA/UPMSI/IE of the National Agrarian University - La Molina was used. The quality control was carried out using the R language. All SNPs with a genotyping rate lower than 95% and minor allelic frequency (MAF) ≤ 0.05 were removed, leaving 60,624 SNP markers.

Two methods to determine the accuracy of breeding values of three fiber traits were used, a traditional BLUP method with phenotypic data and pedigree-based relationship matrix (A), and ss-GBLUP based on a combined matrix (H) constructed from a matrix A and a genomic relationship matrix (G).

The model fitted for FD, SD and PM was: $y = Xb + Zu + Wp + e$

where **y** is the vector of observations, **b** is the vector of fixed effects, **u** is the vector representing the additive genetic effects, **p** corresponds to the vector of permanent environments, and **e** is the vector of residuals; **X**, **Z**, and **W** are the incidence matrices for respectively fixed, genetic and permanent effects. The fixed effects included: coat color (9 levels), combined effects sex and physiological state of lactation (3 levels), year of recording as a contemporary group (19 levels), and age as a linear and quadratic covariate. Breeding values (EBV) were estimated using BLUPF90 family of programs as RENUM, REML and BLUP (Miszta et al., 2015). The computing procedures for genetic evaluation, including phenotypic, full pedigree, and genomic information, where a numerator relationship matrix (**A**) can be modified to a matrix (**H**) that includes both pedigree-based relationships and differences between pedigree-based and genomic-based relationships, were applied (Miszta et al., 2009).

The calculation of the accuracy of the genetic and genomic values was carried out in the following steps: First, the de-regressed mean of the phenotypic data was calculated, adjusting for the effects of the contemporary group, age, coat color, and the combination of the effects of the sex and physiological status of the females, for this the *lm* function of the R package was used. Second, 10 times random samples of 100 animals were taken from the 431 animals. For each run the phenotypic information was dispensed from each animal. Third, the prediction of genetic accuracy was calculated as a correlation between the predicted genetic value estimated by the BLUP methodology and the de-regressed mean, assuming it as the true value. Fourth, the prediction of genomic accuracy was calculated as a correlation between the predicted genomic value estimated by the ss-GBLUP methodology and the de-regressed mean, assuming the later as the true value.

Results and discussion

Table 2 shows the accuracy (scale 0 to 1) of estimates of 10 runs for the three fiber traits using BLUP and ss-GBLUP method. The BLUP method's average accuracy estimates were 0.452, 0.351, and 0.371 for FD, SD, and PM, respectively. The average accuracy estimates using ss-GBLUP method were 0.490, 0.436, and 0.465 for FD, SD, and PM, respectively. The differences between BLUP and ss-GBLUP methods were 9.8%, 29.8%, and 29.1% for FD, SD, and PM, respectively, in favor of the method using additional information from molecular markers.

Table 2. Accuracy of the genetic values (BLUP) and genomic values (ss-GBLUP) and the difference of accuracy between both methods in alpacas

BLUP	p1	p2	p3	p4	p5	p6	p7	p8	p9	p10	Mean
FD	0.547	0.408	0.450	0.507	0.291	0.475	0.584	0.474	0.367	0.422	0.452
SD	0.463	0.382	0.204	0.310	0.376	0.381	0.376	0.402	0.291	0.321	0.351
PM	0.327	0.385	0.332	0.504	0.352	0.282	0.375	0.579	0.230	0.343	0.371
ss-GBLUP											
FD	0.577	0.495	0.508	0.523	0.386	0.472	0.575	0.479	0.407	0.474	0.490
SD	0.518	0.470	0.451	0.355	0.432	0.447	0.417	0.418	0.404	0.454	0.436
PM	0.459	0.522	0.512	0.515	0.462	0.399	0.397	0.572	0.315	0.495	0.465
Difference between BLUP- ssGBLUP (%)											
FD	5.3	21.5	12.9	3.2	33.0	-0.7	-1.6	1.1	11.1	12.3	9.8
SD	12.0	22.9	121.0	14.3	14.9	17.5	10.6	3.9	39.0	41.4	29.8
PM	40.5	35.7	53.9	2.2	31.0	41.6	5.8	-1.2	37.3	44.0	29.1

BLUP= Best linear Unbiased Prediction methodology, ssGBLUP= single step genomic best linear unbiased prediction methodology, FD= fiber diameter, SD= standard deviations, PM= percentage of medullation, p1-p10: runs.

Our results are in line with studies for other livestock species. For carcass traits in sheep an increase of accuracy of 33.3% was reported (Daetwyler et al., 2012). While in dairy sheep an increase of 47.98% was found (Legarra et al., 2014), only an improvement of 5-7% was described in dairy goats (Teissier et al., 2018). The use of genomic information (ss-GBLUP) generates greater accuracy than the traditional BLUP since genomic relationships are more accurate than relationships based on pedigree (Meuwissen et al., 2016), and it can detect small genetic variations since it can integrate the phenotypic, genomic and pedigree information (Gao et al., 2019). Genomic selection is considerably more precise than the traditional BLUP methodology, especially for a low heritability trait (Calus et al., 2008) such as percentage of medullation.

Conclusion

The study could demonstrate that the additional use of genomic information for breeding value estimation increases the accuracy. This result is particularly interesting for traits with low heritability. However, to implement genomic selection on a larger scale, the necessary conditions, such as animal identification, comprehensive field data collection of production and reproduction traits, must first be created. In addition, the number of genotyped animals has to be increased to take full advantage of the technology.

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