

Genomic selection improves genetic gain for fiber traits in a breeding program for alpacas

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ABSTRACT

The implementation of genetic improvement programs including genomic information leads to higher genetic and economic gains in animal production. So far, genomic selection in alpacas is still at an early stage and its response for fiber quality traits has not been studied. Therefore, this study aimed to evaluate the genetic gains for fiber diameter (FD) and percentage of medullation (PM) using BLUP (Best Linear Unbiased Prediction) and ssGBLUP (single-step Genomic BLUP) under five selection index scenarios. The ZPLAN+ software was used to simulate for FD and PM annual genetic gain and standardized genetic gain, and also a total standardized genetic gain for a selection index. Input parameters were taken from field data of the Pacamarca Scientific Station in the Highlands of Peru. The respective weights given for FD and PM in the selection indexes were as follows: -1 and 0 (Scenario 1); -0.75 and -0.25 (Scenario 2); -0.5 and -0.5 (Scenario 3); -0.25 and -0.75 (Scenario 4); and 0 and -1 (Scenario 5). Total standardized genetic gain from the alpaca breeding program based on ssGBLUP in scenario 2 was higher compared to other scenarios. In all scenarios the genetic gain using ssGBLUP were higher than those from BLUP. Therefore, the use of genomic breeding values could have a favorable impact on genetic gains for FD and PM in alpacas.

1. Introduction

The main objective of alpaca breeding is to improve fiber quality and production (Gutiérrez et al., 2009). To this end, efforts have been focused on producing finer fiber to increase comfort of alpaca fiber garments (McGregor, 1997; Gutiérrez et al., 2009; Quispe et al., 2013). A recent study in Peru showed that farmers focus on fiber quality as the main breeding objective by reducing fiber diameter. In addition, many farmers would like to maintain or even increase fleece weight. Other traits such as fertility, fitness and functional traits are not considered as breeding goals, but animals which don't meet the producers' expectations are discarded from the herd (Wurzinger and Gutiérrez, 2022). Also, it was postulated that a high percentage of medullated fibers is related to lower comfort in alpaca fiber garments due to itching (Pinares et al., 2018; Cruz et al., 2019). Fiber diameter (FD) and the percentage of medullated fiber (PM) has a favorable genetic correlation (Cruz et al.,

2019) for reducing both traits simultaneously by using selection index. However, the emphasis for each trait on the breeding goal needs to be studied to improve the comfort of alpaca garments (Gutiérrez et al., 2014).

There is no national breeding program in alpacas to improve their textile quality (Gutiérrez et al., 2018; Cruz et al., 2021). Currently, isolated initiatives of private companies (Aguilar et al., 2019; Cruz et al., 2021), non-governmental organizations (Quina et al., 2015) and breeders associations (Gutiérrez et al., 2019) are working to reduce the fiber diameter, and others such as Pacamarca Scientific Station is working to reduce the percentage of medullation (Pinares et al., 2018; Cruz et al., 2019). Some of these breeding initiatives have carried out genetic evaluation using classical BLUP (Best Linear Unbiased Prediction) methodology, which utilizes pedigree and phenotypic information to predict the genetic merit of alpacas.

The use of genomic BLUP (GBLUP) for genetic evaluation has many

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advantages compared to BLUP methodology (Goddard and Hayes, 2007), such as increased genetic gain and decreased generation interval, leading to higher economic income (VanRaden, 2008; VanRaden et al., 2009; Thomasen et al., 2014). Furthermore, a single-step genomic BLUP method (ssGBLUP) has been developed, which allows the combination of information from genotyped and non-genotyped animals in genomic evaluations (Legarra et al., 2009; Aguilar et al., 2010). ssGBLUP has previously been used successfully in different species, such as sheep (Van Der Werf, 2009), cattle (Silva et al., 2014), pigs (Knol et al., 2016), chickens (Gao et al., 2019b), fish (Lu et al., 2020), and goats (Molina et al., 2018).

A microarray of 76K Single Nucleotide Polymorphisms (SNP) has been developed for Huacaya alpacas. This SNP microarray, covers 90.5% of genome length with a density of about 39 SNPs/Mb (Calderon et al., 2021), so it enables the application of genomic selection in alpacas. However, the feasibility of applying genomic selection in alpacas has not been further studied (Mancisidor et al., 2021). Different authors argue (Ducrocq et al., 2018; Mrode et al., 2018a) that there is a need to increase the number of genotyped animals and to establish a sound size of training population in local breeds of developing countries.

Simulation has been used as a tool for predicting genetic and economic gains when field data is unavailable (Lillehammer et al., 2016; Gao et al., 2019a; Stock et al., 2021). Therefore, this research aimed to simulate the genetic gains in fiber diameter (FD) and percentage of medullation (PM) using BLUP and ssGBLUP Estimated Breeding Values (EBVs) under five breeding goal scenarios.

2. Materials and methods

2.1. Traits, performance records, pedigree data and animals genotyped

The pedigree records from 12,431 alpacas were collected between 1992 and 2019 at Pacamarca Scientific Station. The number of records were different for FD (24,169 from 2001 to 2019) and PM (8,386 from 2015 to 2019). The FD and PM trait were described by Gutiérrez et al. (2009) and Cruz et al. (2019) respectively. The mean (standard deviation) assumed for these traits were $22.83 \mu\text{m} \pm 4.07$ and $37.31\% \pm 29.70$ with a respective range between $12.02 \mu\text{m}$ and $43.56 \mu\text{m}$, and between 0% and 100% for FD and PM respectively Cruz et al. (2019).

Generation interval was calculated from the pedigree using ENDOG v4.8 (Gutierrez and Goyache, 2005). Genotyping data from the 76K SNP microarray for alpacas (Calderon et al., 2021) was obtained from 431 animals. The quality control of data included a call rate $\geq 95\%$ and minor allele frequency $\geq 5\%$. Hardy-Weinberg equilibrium was not considered as quality control parameter because the simulated population is not structured and in order to avoid removing markers potentially linked to the traits of interest (Hao and Storey, 2019). Applying from Hardy-Weinberg proportions deviations thresholds as quality controls has been proved to remove a little number of loci actually carrying genotyping errors due to technical issues to the cost of the removal of an undesirable number of truly informative loci (Fardo et al., 2009; Arias et al., 2022). After quality control, 60,624 SNP markers (Mancisidor et al., 2021) were used to calculate the accuracy of the genomic EBVs in fiber diameter and percentage of medullation.

2.2. Breeding goal scenarios

Genetic gains and standardized genetic gain for average fiber diameter (FD) and percentage of medullation (PM) were calculated simulating five different breeding goal scenarios (Table 1) and using EBVs from BLUP or ssGBLUP (Legarra et al., 2009) in the selection index.

2.3. Simulation

The ZPLAN+ program (Täubert et al., 2010) was used for the simulation. This program uses the conventional gene flow method (Hill,

Table 1

Weights for fiber diameter (FD) and percentage of medullation (PM) under five breeding goal scenarios.

Scenario 1	Scenario 2	Scenario 3	Scenario 4	Scenario 5
FD= -1	FD= -0.75	FD= -0.5	FD= -0.25	FD= 0
PM= 0	PM= -0.25	PM= -0.5	PM= -0.75	PM= -1

1974) and the selection index for predicting genetic merit and its accuracy (Hazel and Lush, 1942).

The breeding structure was one tier with 300 female and 43 male adult white Huacaya alpacas, reflecting the current management scheme of the Pacamarca Scientific Station. All adult females (3 years old) mate with adult males (4 years old), and 80% of young females (2 years old, first service) mate with young males (3 years old, first service) and the remaining 20% mate with adult males. The number of selection candidates for both sex was calculated using the following information: 85% of fertility, 6% of embryonic absorption rate and abortions, 1:1 sex ratio at birth, 10% of offspring mortality and 25% of culling due to undesirable morphological traits. The number of selected young alpacas were calculated choosing the best 10% males and the best 37% females. Therefore 8 young males and 30 young females serve as replacements each year.

The biological parameters came from a white Huacaya alpaca population raised at the Pacamarca Scientific Station. The age at first mating was 2 years in females and 3 years in males, and the age at first offspring were 3 and 4 years for females and males, respectively. The productive life was 10 years in both sexes, and the reproductive life were 7 and 6 years for females and males, respectively. The average calving interval was of 1.3 years (Cruz et al., 2015).

Performance records from parents, grandparents, half-siblings and progeny were included as information sources in the ZPLAN+ program for all scenarios using BLUP. In addition, genomic EBV from males was considered as additional information source for all scenarios using ssGBLUP.

Accuracy of breeding values for genomic prediction was empirically computed via ssGBLUP, using field data, to be included in ZPLAN+ with values of 0.72 for FD and 0.56 for PM. These values were calculated using a bivariate repeatability animal model (Legarra et al., 2009). The equation was $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{Wp} + \mathbf{e}$, where \mathbf{y} is FD or PM, \mathbf{X} , \mathbf{Z} , \mathbf{W} represent the incidence matrices of the fixed effects, direct genetic effects and permanent effects respectively, \mathbf{b} represents the vector of the fixed effects, \mathbf{u} is the vector representing the additive genetic effect, \mathbf{p} is the vector of the permanent environment and \mathbf{e} represents the residual vector. Year of shearing (19 levels for FD and 4 levels for PM), color (9 levels) having at least 7 records within level, and a combined effect of sex and lactation (3 levels) were considered as fixed effects; age in days as linear and quadratic covariates was also fitted. The RENUMF90, REMLF90 and BLUPF90 programs (Miszta et al., 2015) were used to estimate additive genetic variance (VG_A) and predicted error variance ($e.v$). Then, the accuracy (r) of genomic breeding values for FD or PM was calculated from:

$$r = \sqrt{1 - \frac{(e.v)^2}{VG_A}}$$

Standardized genetic gains (SGG) were calculated from the following expression $SGG = \frac{GG}{SD_g}$ where GG is the annual genetic gain of the trait and SD_g is the genetic standard deviation. The total SGG is the sum of SGG for FD and SGG for PM.

2.4. Genetic and phenotypic parameters

Heritability values of 0.347 for FD and 0.225 for PM, genetic correlation between FD and PM of 0.552 and repeatability of 0.478 and 0.556 for FD and PM were applied respectively (Cruz et al., 2019).

Phenotypic standard deviation of 4.07 μm for FD and 29.7% for PM, and the phenotypic correlation between DF and PM of 0.443 were used as inputs for the simulation (Cruz et al., 2019).

3. Results

The annual genetic gain for FD was higher when the trait was used as a breeding goal and selection criterion (Scenario 1), showing genetic gains of -0.21 μm and -0.25 μm for BLUP and ssGBLUP respectively. Also, the annual genetic gain of FD decreased to almost half when no weight was applied to this trait (Scenario 5).

Genetic gains and standardized genetic gains predicted using ssGBLUP for FD and PM were better than those predicted using BLUP in all breeding goal scenarios (Table 2). As expected, genetic gains and standardized genetic gains for each trait decreased as its weight decreased regardless of using BLUP or ssGBLUP. However, the highest total standardized genetic gain was observed in scenario 2 (FD = -0.75 and PM = -0.25), with values of 0.23 and 0.27 for BLUP and ssGBLUP respectively.

The selection index accuracy decreased as the FD weighting decreases, in both methodologies. However, the accuracy of the ssGBLUP methodology was higher than the accuracy of BLUP methodology in all scenarios, as shown in Fig. 1.

The average generation interval using pedigree data was 6.8 years, while the average generation interval of the simulation has a value of 8.07 years (ZPLAN+ program) for all scenarios.

Genetic gains were compared over a period of 14 years (~ 2 generations) by both BLUP and ssGBLUP methods. The initial phenotypic means were 22.83 μm for FD and 37.31% of PM as reported by Cruz et al. (2019). Fig. 2a and b display the improvement of investigated traits over time for the scenario with the highest observed genetic gains (Scenario 2).

4. Discussion

This is the first simulation study of genetic gains for textile traits (FD and PM) using genomic selection in alpacas. The information used for the simulation was obtained from a Peruvian alpaca ranch, where

Table 2

Annual genetic gain and standardized genetic gain predicted for fiber diameter (FD) and percentage of medullation (PM), total standardized genetic gain, under five breeding goals scenarios, with BLUP and ssGBLUP in Huacaya alpacas.

	Scenario 1 FD=-1, PM=0	Scenario 2 FD=-0.75, PM=-0.25	Scenario 3 FD=-0.50, PM=-0.50	Scenario 4 FD=-0.25, PM=-0.75	Scenario 5 FD=0, PM=-1
BLUP					
Genetic gain FD (μm)	-0.21	-0.18	-0.15	-0.14	-0.13
Genetic gain PM (%)	-0.68	-1.02	-1.06	-1.04	-1.07
FD SGG	0.12	0.10	0.08	0.08	0.07
PM SGG	0.08	0.12	0.13	0.13	0.13
Total SGG	0.20	0.23	0.21	0.21	0.20
ssGBLUP					
Genetic gain FD (μm)	-0.25	-0.21	-0.19	-0.17	-0.16
Genetic gain PM (%)	-0.85	-1.21	-1.25	-1.26	-1.26
FD SGG	0.14	0.12	0.11	0.10	0.09
PM SGG	0.10	0.15	0.15	0.15	0.15
Total SGG	0.24	0.27	0.26	0.25	0.24

BLUP= Best Linear Unbiased Prediction, ssGBLUP= single-step Genomic BLUP, SGG= standardized genetic gain.

alpacas have been selected using estimated breeding values by BLUP (Cruz et al., 2017).

The annual genetic gain for FD for both BLUP and ssGBLUP (scenario 1), were slightly higher (-0.21 and -0.25), compared to the other scenarios. The response to selection depends on the traits weight used in elaborating the selection index (Gutiérrez et al., 2014). In this case, the scenario 1 uses 100% of the weighting for FD, as reported by Quispe et al. (2008), who predicted annual genetic gains between -0.17 μm and -0.23 μm for FD in alpacas under an open nucleus scheme. The genetic gains for FD found by both BLUP and ssGBLUP methodologies were higher than when using bio-economic selection indexes (-0.14 μm) as reported for FD in alpacas (León-Velarde and Guerrero, 2001). However, the genetic gains for FD using ssGBLUP were similar to those reported for FD in Merino sheep, in a simulation with 2,500 genotyped animals, which predicted annual genetic gains of -0.25 μm and -0.26 μm for FD by using genomic selection (Van Der Werf, 2009). This demonstrates that the use of genomic information increases genetic gains, even when there is a small number of genotyped animals.

Genetic gain for PM was highest when only this trait was used as breeding goal and selection criterion (Scenario 5) for both methodologies (-1.07% and -1.26%). On the other hand, the lowest genetic gain for PM was found when the PM were not included as breeding goal (Scenario 1). PM is a relatively new trait that has been considered to be included in alpaca breeding programs (Pinares et al., 2018; Cruz et al., 2019). As shown in Table 2, in order to speed up the reduction of PM, this trait must be included as a breeding goal. The most relevant differences were found between Scenario 1 and 5, with genetic gains of 63.55% for the BLUP methodology and 67.46% for the ssGBLUP methodology.

Despite being a difficult trait to measure, it is important to include PM in the breeding goal to further improve the fiber quality in alpacas. It is necessary to take this into account, when comparing the standardized genetic gain for each trait FD and PM in the five scenarios for BLUP and ssGBLUP methodologies, very small differences were observed. The PM had some disadvantages, such as fewer records, a lower heritability and less accuracy of breeding value than the FD. However, higher standardized genetic gain for PM than for FD was found in the scenarios where PM was included as breeding goal in both methodologies. This result could be attributed to the greater genetic and phenotypic variation for PM than FD (Cruz et al., 2019), since a direct selection for reducing PM started about 5 years ago at the Pacamarca Scientific Station.

For a better interpretation of genetic gains, they have been standardized as shown in Table 2. Here it is observed that the total SGG in ssGBLUP is higher than in BLUP regardless of the scenarios. The total SGG are similar within BLUP (0.20) or ssGBLUP (0.24) when a single trait is used as the breeding goal (scenario 1 and 5). However, when weighting the selection index construct (scenario 2 to 4), scenario 2 has the highest total SGG in BLUP (0.23) and ssGBLUP (0.27). This is because the genetic gains depend also on the heritability and accuracy of each trait and the genetic correlation between those traits. Therefore, the heritabilities and accuracies for FD (0.347 and 0.72) are higher than those for PM (0.225 and 0.56) in Scenario 2. Then, in the construction of the index it is necessary to take advantage of the genetic correlation between both traits (0.552), but it is more accurate to use the FD as the main trait within the weighting (FD = -0.75 and PM = -0.25).

It was found, that ssGBLUP showed higher accuracy for all scenarios. Likewise, the highest accuracies were obtained when fiber diameter was considered as the only trait in the breeding goal and as selection criterion (Scenario 1) in both BLUP (0.69) and ssGBLUP (0.76) methodologies as a consequence of its higher heritability (Fig. 1). Moreover, the greatest gain in accuracy was obtained in Scenario 4, which increases from 0.59 (BLUP) to 0.68 (ssGBLUP), representing an increase of 15% due to the use of genomic information. Similar results for FD were found for increasing the accuracy of genetic merit in a simulated study using ssGBLUP (Mamani et al., 2022). This increase in accuracy with the use of

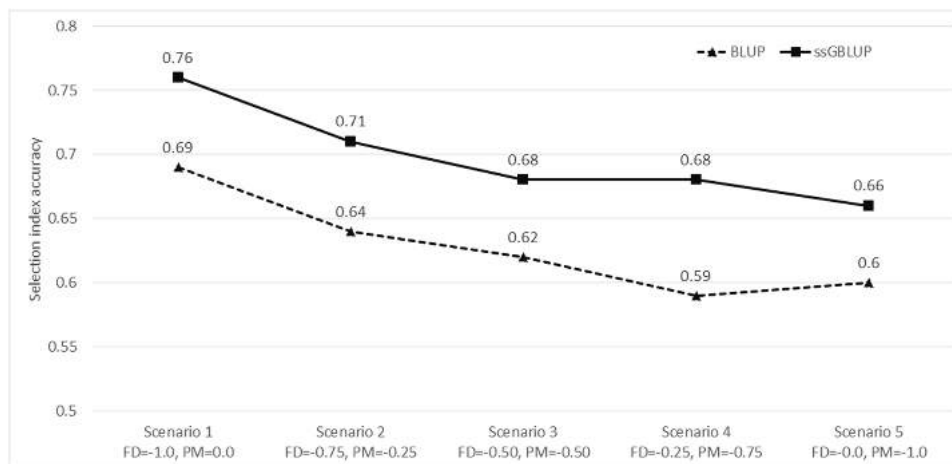


Fig. 1. Selection index accuracy under five breeding goal scenarios, using in the simulation BLUP and ssGBLUP methodologies.

genomic information was also reported in alpacas, although the increase was much lower, with 2.623% and 1.471% for FD and PM respectively, under a multi-trait animal model (Mancisidor et al., 2021). Also, the accuracies of the selection index using genomic information were very similar to those reported in sheep, showing values from 0.43 to 0.79 for wool diameter using genomic selection (Daetwyler et al., 2010).

The use of genomic selection resulted in higher genetic gains for FD and PM compared to those obtained using BLUP methodology. For traits as PM, which are more difficult to measure and have lower heritability, genomic selection can be beneficial and lead to higher genetic gains compared with a BLUP methodology. It could even be interesting to evaluate the impact of genomic selection on traits with very low heritabilities (such as reproductive traits) or others that have not yet been addressed in alpacas, such as resistance to diseases and parasites (Mrode et al., 2018b). On the other hand, genomic information has been reported to increase the accuracy of the genetic merit, when selection is based on a single trait (Lourenco et al., 2014), as shown in Scenario 1 for FD and Scenario 5 for PM.

The FD in an interval of ~ 2 generations can be reduced by 2.52 μm (11.04% of starting value) and 2.94 μm (12.88%) using BLUP and ssGBLUP methodologies respectively. These values are higher than reported by León-Velarde and Guerrero (2001), who estimated values around 1 μm for a similar period. Likewise, the same tendency can be observed for PM with a reduction of 14.28% and 16.94% in ~ 2 generations. This represents 38.27% and 45.40% of genetic gain above the average at the beginning of the program, using BLUP and ssGBLUP methodologies respectively. The genomic information leads to a higher reduction (7.13%) of PM compared to BLUP methodology.

The applicability of genomic selection for genetic improvement programs in alpacas is still limited, due to the scarcity of pedigree and phenotypic records in most of the alpaca ranches in Peru. The reliability of the use of genomic information in domestic species depends on factors such as the percentage of genome covered by molecular markers, linkage disequilibrium between markers and loci, effective population size and population size (Muir, 2007; Hayes et al., 2009; Daetwyler et al., 2012). In this study a low number of alpacas genotyped ($n = 431$) were used to predict genetic gains for both BLUP and ssGBLUP. Therefore, it is necessary to increase the size of the reference population in order to implement genomic evaluation as a tool in alpaca breeding. A strategy for increasing the number of genotyped alpacas is needed and performance control must be greatly spread across the alpaca ranches. In dairy cattle a number 1,000 genotyped animals was considered appropriate to provide relevant information for applying genomic selection (VanRaden et al., 2009).

Genomic selection would not only allow better genetic gains, but also economic gains for the alpaca fiber production chain, because, by

decreasing the FD, much lighter and softer garments can be produced (Naylor et al., 1997; Allain and Renieri, 2010). Moreover, reducing the PM would decrease the itchinness of alpaca fiber (Pinares et al., 2018; Cruz et al., 2019; Pinares et al., 2019), and consequently the alpaca fiber would achieve a better position in the international market, triggering economic improvements along the manufacturing up to the producer. These economic improvements would be expected to motivate the farmers to implement genetic improvement programs for textile purposes in the future. This change, from traditional management to implementation within an integral program, needs economic resources. Genetic programs should go through a gradual process of implementation, especially in Peru, since this sector (producers and animals) have been relegated to the most adverse farming conditions in the highland. However, most of the different producers are willing to implement them in their herds (Wurzinger and Gutiérrez, 2022). However, this change from traditional management to an integrated program needs to adapt the guidelines, standardize criteria for pedigree and productive records (Cruz et al., 2021), and finally complement it with genomic information (Wurzinger and Gutiérrez, 2022). Fortunately the market is transforming, improving marketing channels, moving from paying only by fleece weight to paying for a combination of fiber weight and quality (Cruz, 2017).

Although results showed relative genetic gains with the use of genomic information, intensive implementation is hampered by the current high cost of genotyping of approximately \$120 per animal. At the same time, the annual fiber production generates an income of approximately \$17 per animal. Under these economic conditions, the implementation of genomic selection in a larger alpaca population is not feasible. As the costs for genotyping might decline in the coming years (e.g. using low-density genotyping, sequencing), it might become attractive for farmers to implement genotyping at least of male animals on a regular basis.

One option may be to genotype only the male alpaca population, as males generally serve as the major disseminators of genetic improvement (González-Recio et al., 2009). Pedigree analysis of the population under study shows that the average offspring on the male side is 28.27 ± 34.34 offspring, with a maximum of 193 offspring, while females have on average only 4.01 ± 2.84 offspring in their reproductive life with a maximum of 17 offspring. However, pedigree and phenotypic information cannot be dispensed with, as it has been shown that there is a higher genetic response when all available information is used for genomic selection (Gao et al., 2019a).

The average generation interval was 8.07 years for all scenarios in both methodologies, since the same input parameters such as the age at reproduction in males and females, calving interval, ratio of fertility, ratio of mortality, percent of selection were used in all scenarios.

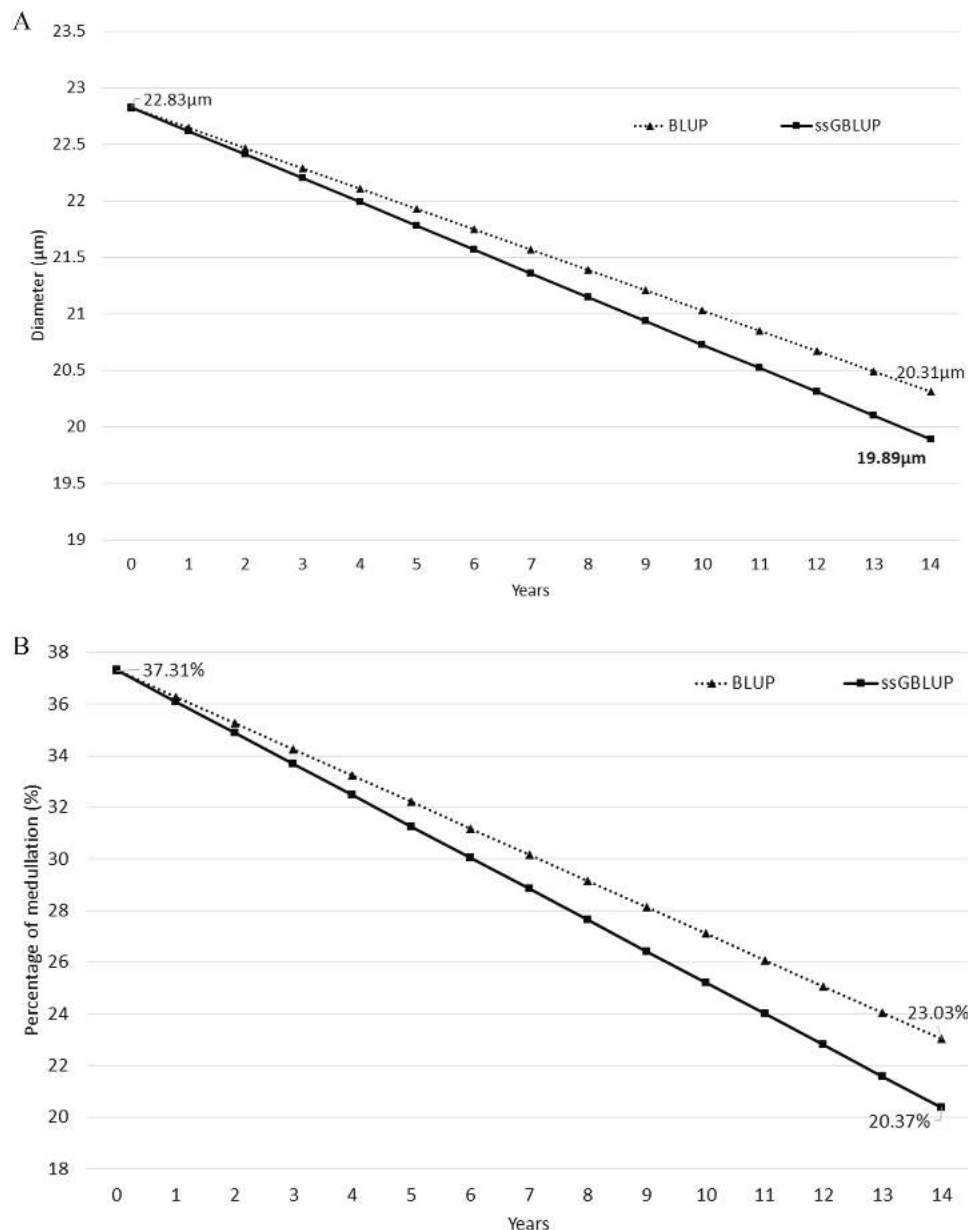


Fig. 2. a and b) Simulated genetic gains of scenario 2 for fiber diameter (FD) and percentage of medullation (PM), using a BLUP (Best Linear Unbiased Prediction) and ssGBLUP (single-step Genomic BLUP) methodology.

However, the generation interval was higher than estimated with the pedigree (6.8 years), this could be due to the fact that in this simulation only the statistical mean of the calving interval, which is 1.3 ± 0.6 years, was used (Cruz et al., 2015). In dairy cattle, genomic selection facilitates the shortening of generation interval without detrimentally affecting accuracy values (Boichard et al., 2016). The reduction of generation interval in alpacas is not possible as artificial insemination is not yet readily available for commercial farms.

The semen of the alpaca has physical and chemical peculiarities that are little understood, which help ovulation in females (Ratto et al., 2006) but prevent semen refrigeration and cryopreservation (Adams et al., 2009; García et al., 2017). Consequently, artificial insemination is currently impractical to implement in commercial alpaca breeding. Therefore, the scarce use of artificial insemination in alpacas affects the selection intensity of males leading to lower genetic gains. This limitation needs to be overcome in the future, since artificial insemination and embryo transfer are biotechnological tools that accelerate genetic progress, as proposed in genetic improvement programs focused on

textile production, such as in wool sheep programs (Van Der Werf, 2009; Auvray et al., 2014), and as proposed for small ruminants, which have breeding characteristics similar to camelids (Mrode et al., 2018b).

5. Conclusions

Genomic selection using ssGBLUP had a higher genetic gain than BLUP method for both fiber diameter and percentage of medullation in alpacas in all breeding scenarios. A selection index with weights of -0.75 and -0.25 for fiber diameter and percentage of medullation is recommended due to the higher genetic gain observed when compared to other investigated scenarios. For the construction of the selection index for textile purposes in alpaca fiber, both traits should be considered as a breeding goal.

Author statement

We confirm that the manuscript has been read and approved by all

named authors and that there are no other persons who satisfied the criteria for authorship but are not listed. We further confirm that the order of authors listed in the manuscript has been approved by all of us.

We confirm that we have given due consideration to the protection of intellectual property associated with this work and that there are no impediments to publication, including the timing of publication, with respect to intellectual property. In so doing we confirm that we have followed the regulations of our institutions concerning intellectual property.

We understand that the Corresponding Author is the sole contact for the Editorial process (including Editorial Manager and direct communications with the office). He is responsible for communicating with the other authors about progress, submissions of revisions and final approval of proofs. We confirm that we have provided a current, correct email address which is accessible by the Corresponding Author and which has been configured to accept email from Alan Cruz E-Mail: alancruz@outlook.com

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CRediT authorship contribution statement

Alan Cruz: Conceptualization, Validation, Formal analysis, Investigation, Writing – original draft, Writing – review & editing. **Jorge Sedano:** Investigation, Formal analysis. **Alonso Burgos:** Data curation. **Juan Pablo Gutiérrez:** Validation, Writing – review & editing, Visualization, Supervision. **María Wurzinger:** Conceptualization, Methodology, Writing – review & editing, Visualization, Supervision. **Gustavo Gutiérrez-Reynoso:** Conceptualization, Methodology, Validation, Writing – review & editing.

Declaration of Competing Interest

There is no conflict of interest for this paper.

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