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Genetic parameters for gastrointestinal parasitosis resistance traits in Junín sheep

Parâmetros genéticos para características de resistência à parasitose gastrointestinal em ovinos Junín

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ABSTRACT

The Junín sheep contribute to livestock production in the Peruvian Andes, but face problems related to gastrointestinal parasitism. In this study, we estimated the heritability and repeatability of traits associated with resistance to gastrointestinal parasitism in the genetic nucleus of Junín sheep raised at altitudes above 3600 m. For this purpose, fecal and blood samples were collected from 101 female lambs and 88 male lambs (4–6 months old) during the rainy and dry seasons. The data on live weight (LW), the FAMACHA score (FS), blood hematocrit (HCT), and the fecal egg count (FEC) were analyzed using a repeated multiple-trait animal model; the variance components and genetic parameters were estimated using a Bayesian inferential approach. The results showed that heritability estimates ranged from 0.09 (FS) to 0.27 (LW), with 95% high posterior density intervals (HPD95%) between [0.02–0.19] and [0.12–0.43], respectively. The repeatability ranged from 0.15 (FS) [HPD95%: 0.04–0.27] to 0.74 (LW) [HPD95%: 0.67–0.81]. The genetic correlations were moderate to low, with HPD95% intervals including zero. This indicated that, at least based on the data collected, no clear relationships occurred between traits that were selected for application in a breeding program. However, focusing the breeding program on the FEC, with a heritability of 0.16 [HPD95%: 0.05–0.28], could be a viable strategy to increase resistance to parasitism. Additional data on other traits are also needed to achieve more precise estimates for this population.

Index terms: Fecal egg count; FAMACHA score; hematocrit; heritability; repeatability.

RESUMO

As ovelhas da raça Junín contribuem para a produção pecuária nos Andes peruanos, mas enfrentam problemas relacionados ao parasitismo gastrointestinal. Neste estudo, estimamos a herdabilidade e a repetibilidade de características associadas à resistência ao parasitismo gastrointestinal no núcleo genético de ovinos da raça Junín criados a altitudes superiores a 3600 m. Para isso, foram coletadas amostras de fezes e sangue de 101 cordeiras e 88 cordeiros (com idades entre 4 e 6 meses) durante as estações chuvosa e seca. Os dados de peso vivo (LW), escore FAMACHA (FS), hematócrito sanguíneo (HCT) e contagem de ovos nas fezes (FEC) foram analisados usando um modelo animal multicaracterística de medidas repetidas, os componentes de variância e os parâmetros genéticos foram estimados por meio de uma abordagem inferencial bayesiana. Os resultados mostraram que as estimativas de herdabilidade variaram de 0,09 (FS) a 0,27 (LW), com intervalos de densidade posterior alta de 95% (HPD95%) entre [0,02–0,19] e [0,12–0,43], respectivamente. A repetibilidade variou de 0,15 (FS) [HPD95%: 0,04–0,27] a 0,74 (LW) [HPD95%: 0,67–0,81]. As correlações genéticas foram moderadas a baixas, com intervalos HPD95% incluindo zero. Isso indicou que, pelo menos com base nos dados coletados, não ocorreram relações claras entre as características selecionadas para aplicação em um programa de melhoramento genético. No entanto, focar o programa de melhoramento na FEC, com herdabilidade de 0,16 [HPD95%: 0,05–0,28], pode ser uma estratégia viável para aumentar a resistência ao parasitismo. Dados adicionais sobre outras características também são necessários para alcançar estimativas mais precisas para esta população.

Termos para indexação: Contagem de ovos nas fezes; escore FAMACHA; hematócrito; herdabilidade; repetibilidade.

Introduction

The sheep sector is extremely important in Peru and has reached a certain level of development, especially in the Peruvian highlands (Pantoja Aliaga et al., 2022). Among the main sheep breeds that are used in the country, the Junín breed, which specializes in wool and meat production, is of particular interest. Junín sheep are adapted to the harsh climatic conditions of the rugged areas of the Peruvian highlands (Burfening & Carpio, 1993). However, a major problem affecting the productivity of this breed is its susceptibility to gastrointestinal parasitosis.

The control of parasitic diseases is a big challenge, as parasites can cause significant productive and economic losses. Many studies have focused on addressing the problem of gastrointestinal parasitosis in terms of the response to different drugs or changes in management (Antunes et al., 2022; Castagna et al., 2022).

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Another promising strategy for alleviating gastrointestinal parasitosis involves the development of genetically resistant populations through genetic selection. Various traits are used in genetic improvement programs to enhance resistance to parasites. Commonly used traits in sheep include the fecal egg count (FEC), FAMACHA score (FS), blood hematocrit content (HCT), live weight (LW), and body condition (Balconi, Goldberg, & Ciappesoni, 2020; Poli et al., 2023; Williamson et al., 1995).

The FEC is the most commonly used trait, as it is directly correlated with gastrointestinal nematode infections. A low FEC count is generally associated with greater host resistance to parasitic infection (Amarante et al., 2004, 2009). The other traits are indirect indicators of gastrointestinal parasitosis in sheep. Ocular conjunctiva staining is often assessed by the FAMACHA© method, which analyzes the intensity of redness using a scoring system. A high FS indicates anemia, suggesting a parasitic cause and the necessity for selective anthelmintic treatment (Rodríguez et al., 2015). Similarly, parasites such as intestinal helminths can induce anemia in the host by either feeding on its blood or causing damage in the gastrointestinal tract, thus decreasing hematocrit (Kaur et al., 2018). Consequently, HCT also serves as an indirect indicator of parasitic infections. Finally, the LW is used as an indirect indicator not of infection but of resistance, as resistant animals maintain higher productive performance under comparable levels of infection (Amarante et al., 2009). Moreover, assessing the body condition can help detect weight loss in sheep, and this loss may be related to parasite load (Rodrigues et al., 2021).

The genetic parameters for these traits, including heritability, repeatability, and genetic correlations, need to be evaluated for designing effective breeding programs. Genetic parameters for FEC, FS, HCT, and LW traits have been extensively estimated across various sheep populations (Medrado, Pedrosa, & Pinto, 2021; Rodrigues et al., 2021). However, these parameters may exhibit significant variability among populations due to differences in gene frequency, genetic structure, management practices, and environmental conditions, making them population-specific (Medrado, Pedrosa, & Pinto, 2021).

As the Junín breed is important for livestock production in Peruvian highlands and is susceptible to gastrointestinal parasitosis, we conducted a field study on a specific genetic nucleus of Junín sheep raised at altitudes above 3600 m. This study represents the first attempt to estimate the genetic parameters of traits related to parasite resistance in this particular population.

Material and Methods

Study population

The population investigated was a selection nucleus of the Junín sheep breed, owned by the Pachacayo Production Unit of the Agricultural Society of Social Interest "Túpac Amaru" (SAIS, for its acronym in Spanish). The study was conducted in Canchayllo district, province of Jauja, Junín Region, Peru, at an altitude of 3600–4700 m above sea level.

Phenotypes for traits related to parasite resistance were recorded from a group in the selection nucleus in May and October 2023, corresponding to the dry and rainy seasons, respectively. This group initially consisted of 125 ewe lambs and 110 ram lambs aged 4–6 months, with an average LW of 42.1 ±4.13 kg. These animals exclusively grazed on native pastures, predominantly consisting of species from the genera *Festuca*, *Calamagrostis*, and *Stipa*, with no access to stable or supplemental feeding.

An analog hanging scale (capacity 500 g/100 kg) was used to measure the LW of the animals. Additionally, the level of anemia was assessed using the FS on a scale from 1 to 5 (Van & Bath, 2002). To complement these data, blood samples were collected from the cephalic vein in vacutainer tubes with EDTA, and fecal samples were collected directly from the rectum of each animal. These samples were transported in thermal boxes to the Microbiology Laboratory of the Faculty of Animal Science at the Universidad Nacional del Centro del Perú, where they were processed and analyzed. HCT was measured in the blood samples using the microhaematocrit technique (Farrand, 1976), whereas the parasite load in the fecal samples was evaluated by determining FEC using the modified McMaster method (Pugh & Baird, 2002). The larvae were subsequently identified using the modified Corticelli and Lai technique (Luck Montero et al., 2018). LW and FS data, along with fecal and blood samples, were recorded on the same day and only once during each season.

The data were subsequently filtered to exclude animals with unknown ancestors or with incomplete records. After filtering, the database included 189 animals, consisting of 101 ewe lambs and 88 ram lambs, each with two records for traits. Additionally, a genealogical database was established comprising data on 356 animals, including the registered animals, their parents (17 rams and 150 sheep), and the ancestors connecting them.

Statistical analysis

The data were edited using the statistical software R v. 4.3.2 (R Core Team, 2023). The FEC values were adjusted by adding 1 before being log-transformed to base 10 (L_{10}FEC) to normalize their distribution. The LW and HCT values were adjusted to follow a normal distribution.

Before fitting a model, the fixed effects were preliminarily assessed. The data were subsequently fitted using a multiple-trait repeated animal model (Mrode, 2014). The multiple-trait animal model combined specific models for each trait in a single formulation. The general equation of the specific models used for the traits L_{10}FEC, HCT, and LW, in matrix notation, was given by Equation 1.

$$y_i = X\beta + Zu_i + Wpe_i + e_i \quad (1)$$

Here, y_i indicates the vector containing the two observations of each individual for the i^{th} trait (i = {L_{10}FEC, HCT, LW}), X indicates the incidence matrix of the fixed effects vector, β indicates sex, season, and sex × season interaction, Z indicates the incidence matrix of the vector of additive genetic effects or genetic values for the i^{th} trait, u_i, W indicates the incidence matrix of the vector of permanent environmental effects (pe_i), and e_i indicates the vector of random errors associated with each observation.

In contrast, due to its categorical nature, a threshold model was fitted for the FS trait (Mrode, 2014). In this model, the category in which an individual is registered is attributed to the existence of an underlying trait (termed "liability") that follows a normal distribution. The mean of the distribution of this underlying trait is modeled as a linear function of fixed effects, genetic values, and permanent environmental effects. In the threshold model, the error variance cannot be estimated, and a standard procedure involves assigning a value of one to this parameter to guarantee the identifiability of the parameters (Sorensen & Gianola, 2002).

Let u be a vector that stacks the vectors of additive genetic effects of each trait, as shown in Equation 2.

$$u = [u_{L_{10}FEC}\ u_{HCT}\ u_{LW}\ u_{FS}]^T \quad (2)$$

Then, this vector is assumed to follow the distribution described below (Equation 3).

$$u \sim N\left(0, \sum_u \otimes A\right) \quad (3)$$

Here, Σ_u represents the 4 × 4 order (co)variance matrix of genetic parameters and A represents the additive relationship matrix derived from the pedigree (Henderson, 1984). The vector that stacks the permanent environmental effects is distributed as $pe \sim N\left(0, Diag\left\{\sigma^2_{ep}\right\} \otimes I\right)$, where I represents an identity matrix and $Diag\left\{\sigma^2_{ep}\right\}$ represents a diagonal matrix of order 4 × 4 that contains the permanent environmental variance parameter. Finally, the random vector e, which stacks the errors of each model, is distributed as $e \sim N\left(0, R_0 \otimes I\right)$, where R_0 represents the (co)variance matrix of the errors of order 4 × 4.

Strict sense heritabilities ($\hat{h}^2$) and repeatabilities ($\hat{R}$) were estimated for each trait, as shown in Equations 4 and 5, respectively.

$$\hat{R}_i = \frac{\hat{\sigma}^2_{u_i} + \hat{\sigma}^2_{ep_i}}{\hat{\sigma}^2_{u_i} + \hat{\sigma}^2_{ep_i} + \hat{\sigma}^2_{e_i}} \quad (4)$$

and

$$\hat{h}^2_i = \frac{\hat{\sigma}^2_{u_i}}{\hat{\sigma}^2_{u_i} + \hat{\sigma}^2_{ep_i} + \hat{\sigma}^2_{e_i}} \quad (5)$$

Here, $\hat{\sigma}^2_{u_i}$ represents the estimated additive genetic variance for the evaluated trait i, $\hat{\sigma}^2_{ep_i}$ represents the permanent environmental variance of the evaluated trait i, and $\hat{\sigma}^2_{e_i}$ represents the estimated error variance of the trait. The genetic ($\hat{r}_{A_{ij}}$) and phenotypic correlations ($\hat{r}_{P_{ij}}$) between traits i and j were estimated as shown in Equations 6 and 7, respectively.

$$\hat{r}_{A_{ij}} = \frac{\hat{\sigma}_{u_{ij}}}{\sqrt{\hat{\sigma}_{u_{ii}} \times \hat{\sigma}_{u_{jj}}}} \quad (6)$$

and

$$\hat{r}_{P_{ij}} = \frac{\hat{\sigma}_{P_{ij}}}{\sqrt{\hat{\sigma}_{P_{ii}} \times \hat{\sigma}_{P_{jj}}}} \quad (7)$$

Here, $\hat{\sigma}_{u_{ij}}$ and $\hat{\sigma}_{P_{ij}}$ represent the estimated additive genetic and phenotypic covariances between traits i and j, respectively.

A Bayesian inferential approach (Sorensen & Gianola, 2002) was used to estimate the variance components and, from them, the genetic parameters of the L_{10}FEC, FS, HCT, and LW traits were obtained. Specifically, a Gibbs sampling algorithm implemented through gibbsf90+ software (Misztal et al., 2002) was used. A chain of 4,000,000 samples was generated for each parameter, and the first 2,000,000 samples were discarded as burn-in. For the remaining 2,000,000 samples, one sample per 200 was stored, and descriptive statistics were assessed. Specifically, the average over the resulting 10,000 samples was interpreted as the point estimate of the parameters of interest, and 95% high posterior density intervals (HPD) were derived from the 0.025 and 0.975 quantiles of the empirical distribution of these samples. A non-informative a priori distribution was assumed for all model parameters.

To evaluate the convergence of the sampled chain from the posterior distribution of the parameters of interest, the Geweke diagnostic test was performed (Du et al., 2022; Geweke, 1992), and the Monte Carlo error (MCE) was computed using the postgibbsf90 program (Misztal et al., 2002). The square root of the MCE approximates the standard deviation of the error associated with the size of the chain (Van Tassell & Van Vleck, 1996).

Results and Discussion

Data description

The coproparasitological results revealed a predominance of *Nematodirus* spp. (45%) (ranging from 39% to 52%), followed by *Trichostrongylus* spp. (29%), *Ostertagia* spp. (20%), and *Cooperia* and *Oesophagostomum* genus. (6% each). Although these genera are not directly associated with anemia,

as *Haemonchus* spp., they can indirectly contribute to anemia by affecting nutrient absorption in the host (Al-Gaabary et al., 2012). *Haemonchus* spp. were absent probably because of their exclusive occurrence in tropical regions (Amarante et al., 2009), which are far away from the study area.

Summary statistics for the traits under evaluation are presented in Table 1. FEC values were highly variable across the assessed animals, with a range of 8,500 and a mean of 1,082. However, the distribution was highly skewed, with a modal value of 250, a threshold that is assumed by some researchers to indicate moderate infestation (Morales et al., 2010). The average FEC was greater in females than in males (1,215 vs. 967, $p \leq 0.05$). Additionally, a slight difference in gastrointestinal parasite infestation was found between the rainy and dry seasons (1128 vs. 1037), but this difference was not statistically significant. Sissay, Uggla, and Waller (2007) also reported differences in FEC between seasons, attributing these differences to the favorable environmental conditions for the development and viability of gastrointestinal nematode larvae during the rainy season compared to the dry season.

The distributions of LW and HCT were unimodal and symmetrical. No difference was recorded between the average and modal values for both traits (Table 1). The average LW recorded was greater than that reported by Burfening and Carpio (1993). This difference was observed for animals of a similar age and the same breed and under a similar management system. The higher weight recorded in our study may be attributed to the fact that the lambs recorded belonged to a selection nucleus.

Regarding FS, 75% of the total observations comprised scores of 2 and 3 (Table 2). FS reliably indicates the degree of anemia in animals, particularly in cases of heavy infestation with hematophagous gastrointestinal parasites, such as those of the genus *Haemonchus* (Van & Bath, 2002). However, while a considerable percentage of the animals had an FS of 3, we cannot confidently attribute anemia to other gastrointestinal parasites, as *Haemonchus contortus* was not predominant (Moors & Gauly, 2009). These findings suggested that the elevated FS might be related to other factors, such as nutritional status.

The HCT values recorded in this study (Table 1) were considerably higher than those reported by Rodrigues et al. (2021). However, these results should be considered referential, as the research conducted by Rodríguez et al. (2015) was performed in a different location and involved a different breed. The absence of hematophagous parasites from the genus *Haemonchus*, the low phenotypic correlation with FEC (–0.13), and the magnitude of the average found indicated that HCT may be influenced by the altitude of the study area. Low oxygen availability at higher altitudes triggers an increase in HCT and hemoglobin levels to facilitate efficient oxygen transport. However, at altitudes above 4500 m, the body naturally adjusts HCT and hemoglobin concentrations to prevent pulmonary hypertension and optimize oxygen exchange between the air and blood. This is achieved by increasing the available surface area for gas exchange and adjusting the partial pressure of the oxygen required to achieve optimal oxygen saturation. This adaptation enhances the efficiency of oxygen transfer to the tissues (Zhao et al., 2022).

Genetic parameter estimation

The Gibbs sampler was implemented, satisfying the convergence criteria established (Du et al., 2022; Geweke, 1992; Van Tassell & Van Vleck, 1996). The point estimates of the genetic parameters for the traits under evaluation, along with dispersion measures and the corresponding convergence values are presented in Table 3. The Geweke statistic and the MCE approached zero, indicating good convergence.

The heritability ranged from 0.09 for FS to 0.27 for LW (Table 3). The heritability for L_{10}FEC was 0.16, suggesting the potential to increase resistance through genetic selection. FEC is a widely studied trait for evaluating genetic resistance to parasitism, with heritability estimates ranging from 0.23 to 0.34 (Castells, 2005). However, heritability is a population parameter and can vary between populations depending on the breed, age of the animals at the time of recording, and environmental factors (Eady et al., 1996). This study was conducted about 4,000 m above sea level, and the feeding regimen (primarily natural grasses without supplementation) might have influenced the results. Greater control over environmental factors can reduce environmental variance, thereby increasing the proportion of phenotypic variance attributed to additive genetic variance (Assenza et al., 2014).

Table 1: Descriptive statistics for the traits associated with parasite resistance in the evaluated Junín sheep population.

Trait	Mean	Mode	SD	CV	Minimum	Maximum	Range
FEC	1082.0	250.0	1116.73	103.2	0.0	8500.0	8500.0
L_{10}FEC	2.87	2.40	0.38	13.09	1.708	3.929	2.221
HCT	40.4	40.0	2.57	6.4	30.0	50.0	20.0
LW	41.9	42.0	5.90	14.8	27.0	62.0	35.0

SD: standard deviation; CV: coefficient of variation (%); FEC: fecal egg count; L10FEC: decimal logarithm of (FEC + 1); HCT: blood hematocrit content (%); LW: live weight (kg).

Table 2: Frequency distribution of FAMACHA Score (FS) in the Junín sheep population.

Score	Frequency
1	0.08
2	0.37
3	0.38
4	0.15
5	0.00

The repeatability values ranged between 0.15 for FS and 0.74 for LW, whereas, for L_{10}FEC, they were of moderate magnitude, relatively lower than those reported by Snyman and Fisher (2019) and Vanimisetti et al. (2004). L_{10}FEC is a trait that greatly affects the life of animals since it is strongly influenced by environmental factors (Doligalska, Moskwa, & Niznikowski, 1997).

The genetic and phenotypic correlations among the evaluated traits are shown in Table 4. The genetic correlations obtained were lower than those reported by Rodrigues et al. (2021) and Woolaston and Piper (1996) for the studied traits in other sheep breeds. As genetic parameters are influenced by the specific population being studied, differences in values may be attributed to genetic, geographic, and/or management factors.

As shown in the Table 4, most of the genetic and phenotypic correlations had small values, suggesting a weak relationship between the traits studied. The 95% HPD intervals (HPD95%) indicated that these correlations may not be significant. Given the small size and specificity of the study population, these correlations may not accurately reflect the true relationships between the traits, potentially masking the results and leading to inaccurate conclusions.

The correlation between FS and HCT was notable. This finding indicated that an increase in one of these traits (genetic and phenotypic) is associated with a decrease in the other. This correlation was similar to that reported by Rodrigues et al. (2021) and Van and Bath (2002) only in direction but not in magnitude. However, in the absence of the genus *Haemonchus*, this correlation cannot be directly attributed to parasitism. These findings suggested that FS may not be a reliable indicator of the relationship between FS and gastrointestinal parasites in this specific population (Moors & Gauly, 2009).

Given the aforementioned limitations, L_{10}FEC is a more reliable indicator of parasite resistance in a genetic improvement program, whereas other more easily measurable criteria need to be carefully evaluated.

Table 3: Estimates of genetic parameters for traits associated with parasite resistance in the evaluated Junín sheep population.

Trait	$h^2 \pm SD[HPD]$	$R \pm SD[HPD]$	Geweke	MCE
L_{10}FEC	0.16 ±0.06 [0.05 – 0.28]	0.29 ±0.07 [0.11 – 0.40]	-0.03	0.006
FS	0.09 ±0.05 [0.02 – 0.19]	0.15 ±0.06 [0.04 – 0.27]	0.04	0.005
HCT	0.13 ±0.04 [0.05 – 0.20]	0.25 ±0.05 [0.14 – 0.35]	-0.05	0.005
LW	0.27 ±0.07 [0.12 – 0.43]	0.74 ±0.04 [0.67 – 0.81]	-0.04	0.006

h^2 heritability; *R*: repeatability; SD: standard deviation; HPD: 95% high posterior density interval; MCE: Monte Carlo error; L_{10}FEC: decimal logarithm (FEC + 1); FS: FAMACHA score; HCT: hematocrit; LW; live weight.

Table 4: Genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal) among traits associated with parasite resistance in the evaluated Junín sheep population. The values are presented as the mean ± standard deviation, with the 95% HPD interval shown in brackets.

Trait	L_{10}FEC	FS	HCT	LW
L_{10}FEC	-	0.14 ± 0.08 [-0.04 – 0.30]	-0.07 ± 0.03 [-0.14 – 0.00]	0.09 ± 0.05 [-0.01 – 0.19]
FS	0.07 ± 0.05 [-0.06 – 0.18]	-	-0.08 ± 0.05 [-0.17 – 0.02]	0.11 ± 0.04 [0.02 – 0.20]
HCT	-0.13 ± 0.05 [-0.24 – –0.01]	-0.40 ± 0.05 [-0.50 – –0.28]	-	0.07 ± 0.09 [-0.11 – 0.23]
LW	-0. 06 ± 0.06 [-0.18 – 0.06]	0. 05 ± 0.07 [-0.09 – 0.19]	0.03 ± 0.06 [-0.09 – 0.15]	-

L_{10}FEC: decimal logarithm (FEC + 1); FS: FAMACHA score; HCT: hematocrit; LW: live weight.

Conclusions

In this study, considering that L_{10}FEC had a heritability of 0.16 [HPD95%: 0.05–0.28] and a repeatability of 0.29 [HPD95%: 0.11–0.40], it may be used as a selection criterion in a genetic improvement program for resistance to parasites in the Junín sheep population. Although variance components and correlations were estimated for other traits, such as LW, FS, and HCT, conclusions based on these traits are not recommended due to the limited population size, these traits may be integrated in future studies with more data.

Author Contributions

Conceptual idea: Cruz, D.J.; Arauco-Villar, F.; Methodology design: Arauco-Villar, F.; Cruz, D.J.; Mayorga, N.; Solano, J.C.; Data collection: Unchupaico, I.; Solano, J.C.; Mayorga, N.; Data analysis and interpretation: Cruz, D.J.; Munilla, S.; Arauco-Villar, F., and Writing and editing: Cruz, D.J.; Munilla, S.

References

Al-Gaabary, M. H. et al. (2012). Studies on gastrointestinal nematodes infection in sheep with special reference to *Haemonchus contortus*. *Assiut Veterinary Medical Journal*, *58*(133):31-40.

Amarante, A. F. T. et al. (2004). Resistance of Santa Ines, suffolk and Ile de France sheep to naturally acquired gastrointestinal nematode infections. *Veterinary Parasitology*, *120*(1-2):91-106.

Amarante, A. F. T. et al. (2009). Resistance of Santa Ines and crossbred ewes to naturally acquired gastrointestinal nematode infections. *Veterinary Parasitology*, *165*(3):273-280.

Antunes, M. I. et al. (2022). Anthelmintic efficacy in sheep and goats under different management and deworming systems in the region of Lisbon and Tagus Valley, Portugal. *Pathogens*, *11*(12):1457.

Assenza, F. et al. (2014). Genetic parameters for growth and faecal worm egg count following Haemonchus contortus experimental infestations using pedigree and molecular information. *Genetics Selection Evolution*, *46*(13):1-9.

Balconi, C., Goldberg, V., & Ciappesoni, G. (2020). Genetic parameters for production traits, resistance and resilience to Nematode parasites under different worm burden challenges in Corriedale sheep. *Veterinary Parasitology*, *287*:109272.

Burfening, P. J., & Carpio, M. P. (1993). Genetic and environmental factors affecting growth rate and survival of junin sheep in the central highlands of Peru. *Small Ruminant Research*, *11*(3):275-287.

Castagna, F. et al. (2022). Potential new therapeutic approaches based on *Punica granatum* fruits compared to synthetic anthelmintics for the sustainable control of gastrointestinal nematodes in sheep. *Animals*, *12*(20):2883.

Castells, D. (2005). Adaptación de genotipos a ambientes adversos: Resistencia genética de los ovinos a parásitos gastrointestinales. *Agrociencia*, *9*(1-2):587-593.

Doligalska, M., Moskwa, B., & Niznikowski, R. (1997). The repeatability of faecal egg counts in Polish Wrzosówka sheep. *Veterinary Parasitology*, *70*(4):241-246.

Du, H. et al. (2022). The performances of gelman-rubin and geweke's convergence diagnostics of monte carlo markov chains in bayesian analysis. *Journal of Behavioral Data Science*, *2*(2):47-72.

Eady, S. L. et al. (1996). Resistance to nematode parasites in Merino sheep: sources of genetic variation. *Australian Journal of Agricultural Research*, *47*(6):895-915.

Farrand, L. L. (1976). The microhematocrit: Technique and applications. *Nurse Practitioner*, *1*(5):19-20.

Geweke, J. (1992). Evaluating the accuracy of sampling-based approaches to the calculation of posterior moments. In J. M. Bernardo. et al. *Bayesian statistics 4*. Oxford: Oxford University Press, (pp.169-193).

Henderson, C. R. (1984). *Applications of linear models in animal breeding.* University of Guelph, Ontario, Canada. Available in: <https://learnanimalbreeding.com/files/Henderson_1984.pdf>.

Kaur, T. et al. (2018). Gastrointestinal parasitaemia and its correlation with anemia a study in small ruminants. *Intas Polivet*, *19*(2):336-341.

Luck Montero, R. et al. (2018). Actividad ovicida y larvicida de extractos acuosos de *Pluchea sericea* y *Artemisia* tridentata en *Haemonchus contortus*. *Ecosistemas y Recursos Agropecuarios*, *5*(13):149-156.

Medrado, B. D., Pedrosa, V. B., & Pinto, L. F. B. (2021). Meta-analysis of genetic parameters for economic traits in sheep. *Livestock Science*, *247*:104477.

Pantoja Aliaga, C. et al. (2022). Parámetros tecnológicos de la lana de ovinos en razas importadas obtenidas mediante transferencia de embriones, criados bajo las condiciones de la sierra central del Perú. *Revista de Investigaciones Veterinarias del Perú*, *33*(3):e21249.

Misztal, I. et al. (2002). *BLUPF90 and related programs (BGF90)*. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production.

Moors, E., & Gauly, M. (2009). Is the FAMACHA© chart suitable for every breed? Correlations between FAMACHA© scores and different traits of mucosa colour in naturally parasite infected sheep breeds. *Veterinary Parasitology*, *166*(1-3):108-111.

Morales, G. et al. (2010). Clasificación por el método Famacha y su relación con el valor de hematocrito y recuento de h.p.g. de ovinos criados en condiciones de pastoreo. *Zootecnia Tropical*, *28*(4):545-555.

Mrode, A. R. (2014). *Linear models for the prediction of animal breeding values*. London. UK.: CABI, 343p.

Poli, M. A. et al. (2023). Genetic resistance to gastrointestinal parasites in sheep. *CABI Reviews*, *18*:1.

Pugh, D. G., & Baird, A. N. (2002). *Sheep and goat medicine*. Second edition. Maryland Heights, Missouri, United States: W.B. Saunders, 621p.

R Core Team. (2023). *R: The R project for statistical computing*. Available in: <https://www.r-project.org/>.

Rodrigues, F. et al. (2021). Genetic parameters for worm resistance in Santa Inês sheep using the Bayesian animal model. *Animal Bioscience*, *34*(2):185-191.

Rodríguez, J. G. et al. (2015). Antihelmínticos, resistencia y método FAMACHA. experiencia cubana en ovinos. *Revista Salud Animal*, *37*(1):57-63.

Sissay, M. M., Uggla, A., & Waller, P. J. (2007). Prevalence and seasonal incidence of nematode parasites and fluke infections of sheep and goats in eastern Ethiopia. *Tropical Animal Health and Production*, *39*(7):521-531.

Snyman, M. A., & Fisher, A. D. (2019). Genetic parameters for traits associated with resistance to *Haemonchus contortus* in a South African Dohne Merino sheep flock. *Small Ruminant Research*, *176*:76-88.

Sorensen, D., & Gianola, D. (2002). *Likelihood, bayesian, and MCMC methods in quantitative genetics*. New York, NY: Springer New York, 740p.

Van Tassell, C. P., & Van Vleck, L. D. (1996). Multiple-trait Gibbs sampler for animal models: Flexible programs for Bayesian and likelihood-based (co)variance component inference. *Journal of Animal Science*, *74*(11):2586-2597.

Van, W. J. A. & Bath, G. F. (2002). The FAMACHA system for managing haemonchosis in sheep and goats by clinically identifying individual animals for treatment. *Veterinary Research*, *33*(5):509-529.

Vanimisetti, H. B. et al. (2004). Inheritance of fecal egg count and packed cell volume and their relationship with production traits in sheep infected with *Haemonchus contortus*. *Journal of Animal Science*, *82*(6):1602-1611.

Williamson, J. F. et al. (1995). Parasitism and production in fleece-weight-selected and control sheep. *New Zealand Journal of Agricultural Research*, *38*(3):381-387.

Woolaston, R. R., & Piper, L. R. (1996). Selection of Merino sheep for resistance to *Haemonchus contortus*: Genetic variation. *Animal Science*, *62*(03):451-460.

Zhao, P. et al. (2022). Physiology and proteomic basis of lung adaptation to high-altitude hypoxia in tibetan sheep. *Animals*, *12*(16):2134.