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RESEARCH ARTICLE

Population and genetic characterization of Blackbelly sheep in the Amazonian Savanna

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Abstract

Locally adapted sheep breeds represent valuable genetic resources for livestock under tropical climatic, nutritional, and health constraints. This study characterized the population structure and estimated genetic parameters for birth weight and FAMACHA (FAffa MAIn CHArt) score in Blackbelly sheep maintained in a conservation nucleus in the Amazonian Savanna of northern Brazil. Pedigree records from 371 animals and phenotypic records for birth weight ($n = 274$) and repeated FAMACHA scores ($n = 482$) were analyzed. Population structure parameters were estimated from genealogical data, and genetic parameters were obtained using Bayesian single-trait animal models. The pedigree was shallow (1.24 equivalent generations), with an effective population size of 40.76 and an average relatedness coefficient of 3.40%. Mean inbreeding was 0.80% but increased by 0.63% per generation. Birth weight and FAMACHA score averaged 2.36 kg and 3.15, respectively. Heritability was high for birth weight (0.47) and low for FAMACHA score (0.14). These findings underscore the importance of improving pedigree recording and implementing targeted mating strategies to mitigate inbreeding, preserve genetic diversity, and ensure the long-term sustainability of Blackbelly sheep in tropical systems of the Amazonian Savanna.

Keywords: birth weight; FAMACHA; heritability; inbreeding; relationship; variability.

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1. Introduction

Sheep play an important role in global food security and the production of animal-derived protein (Wanjala et al., 2025). Locally adapted breeds represent valuable genetic resources in tropical regions, where climatic and nutritional constraints often limit the performance of highly specialized breeds (McManus et al., 2020). Their resilience to these conditions makes local sheep populations particularly relevant for improving meat production while preserving important adaptive traits (Al-Bial & Alkubaibi, 2026). Usually, these animals are primarily managed under extensive systems, making them more susceptible to the impacts of climate change (Wanjala et al., 2025). Sheep are raised across diverse ecosystems in Brazil and exhibit different patterns of heat tolerance associated with variation in skin and coat traits,

heart rate, and respiratory rate, associated with differences in skin and coat traits, as well as heart and breathing rates (Paim et al., 2022; Bayraktar et al., 2026; Saravanan et al., 2026).

Blackbelly sheep originated on the Caribbean island of Barbados and are currently distributed across the Americas, including Brazil, Venezuela, Mexico, and Guyana (Almeida, 2017; Braga & Mendonça, 2018; Paim et al., 2022). The breed is characterized by black pigmentation on the ventral region and by adaptive attributes typical of tropical hair sheep, including tolerance to hot and humid conditions, ability to use low-quality forage, and resilience to gastrointestinal parasite challenge (Almeida, 2017; Braga & Mendonça, 2018). High fertility, prolificacy, maternal ability, and relatively lean carcasses further support the use of Blackbelly sheep in tropical meat production systems (Hernandez et al., 2022).

Since the 1980s, Embrapa Roraima has maintained a Blackbelly conservation flock within the Brazilian Program for the Conservation of Animal Genetic Resources (Braga & Mendonça, 2018). The flock is raised in the Amazonian Savanna, locally known as *Lavrado*, an ecosystem characterized by native grasslands of low nutritional value and pronounced seasonal variation in forage availability (Gonçalves et al., 2021). These edaphoclimatic conditions impose constraints on sheep production, requiring animals to develop adaptive traits such as feed efficiency, parasite resistance, and tolerance to heat stress (Wanjala et al., 2023). Consequently, understanding the genetic characteristics of locally adapted sheep breeds is essential, as they result from long-term processes of adaptation and selection, often associated with reduced genetic variability or the fixation of specific traits (Eydivandi et al., 2021). Conservation populations maintained under these conditions can preserve locally useful alleles, but their small size and restricted use of breeders may accelerate loss of genetic diversity and increase inbreeding (Rafter et al., 2022). Pedigree-based estimates of completeness, effective population size, relatedness, and inbreeding therefore provide practical information for mating design and long-term conservation management. Genetic evaluation of productive and health-related traits can complement population monitoring in locally adapted breeds (Abebe et al., 2025).

Birth weight is an early indicator of growth and neonatal performance (Gautam & Tyasi, 2025). The FAMACHA system (Malan & Van Wyk, 1992) uses conjunctival color as a field indicator of anemia and is widely applied to support targeted control of *Haemonchus contortus* in sheep (Cunha et al., 2024). However, the population structure and genetic variability of Blackbelly sheep maintained in Roraima remain poorly documented. Therefore, this study aimed to characterize pedigree structure and estimate genetic parameters for birth weight and FAMACHA score in a Blackbelly conservation flock raised in the Amazonian Savanna.

2. Methodology

2.1 Dataset

This study used retrospective genealogical and phenotypic records from the Blackbelly conservation flock maintained by the Brazilian Agricultural Research Corporation in Roraima (Embrapa Roraima). The flock is located at the Água Boa Experimental Station, approximately 30 km from Boa

Vista, Roraima, Brazil (02°39'00"-02°41'10" N and 60°49'40"- 60°52'20" W). The 1,200-ha experimental area receives approximately 1,500 - 2,000 mm of annual rainfall, irregularly distributed throughout the year. Animals were managed in a semi-intensive system, with daytime rotational grazing, free access to water and mineral supplement, and nighttime housing with a concentrate based on soybean meal and corn.

Records collected from 2012 to 2024 included birth weight and repeated FAMACHA scores. The FAMACHA method evaluates the color of the ocular conjunctiva by comparison with a five-category laminated chart: 1 = red (non-anemic), 2 = red-pink (non-anemic), 3 = pink (mildly anemic), 4 = pink-white (anemic), and 5 = white (severely anemic) (Kaplan et al., 2004). Lower scores indicate less severe anemia and are desirable in the context of *Haemonchus contortus* challenge, although other parasitic and non-parasitic conditions may also affect conjunctival color. Animals scored as 4 or 5 were immediately treated with anthelmintic.

Exploratory analyses were conducted in the R software (R Core Team, 2024). Records were checked for biological consistency, and potential outliers were removed before analysis. Descriptive statistics included the number of observations, mean, standard deviation, coefficient of variation, and minimum and maximum values for each trait.

2.2 Population structure analysis

Population structure was characterized by using pedigree depth, pedigree completeness index, effective population size (N_e), average relatedness (AR), and inbreeding coefficient (F). Pedigree-depth and relatedness metrics were obtained with the optiSel package in R software (R Core Team, 2024), and individual inbreeding coefficients were calculated with INBUPGF90 (Misztal et al., 2019). The inbreeding trend was assessed by linear regression according to model: $y_{ij} = \mu + b(x_{ij} - \bar{x}) + e_{ij}$, where y_{ij} is the inbreeding coefficient of the j th animal in the i th generation; μ is the intercept; b is the regression coefficient; x_{ij} is the generation number of the j th animal; $\bar{x}$ is the mean generation number; and e_{ij} is the residual.

The effect of inbreeding on each phenotype was evaluated using the same linear-regression structure, replacing the response with the phenotypic record and the explanatory variable with the individual inbreeding coefficient. Regression analyses were performed in the R software (R Core Team, 2024), using a 5% significance level.

2.3 Genetic analysis

Single-trait animal models were fitted for birth weight and FAMACHA score. Birth weight was analyzed using the model: $y = Xb + Za + e$, where y is the vector of observation, b is the vector of systematic effects (contemporary groups), a is the vector of random additive genetic effects, X and Z are the corresponding incidence matrices, and e is the vector of residual effects. Contemporary groups combined sex and birth season (rainy and dry). Because FAMACHA score was recorded repeatedly and is ordinal, it was analyzed using a threshold animal model including additive genetic effects and permanent environmental effects. Variance components were estimated by Bayesian inference using GIBBSF90+ software (Misztal et al., 2019). A Markov chain of 500,000 iterations was generated; the first 50,000 iterations were discarded as burn-in, and every tenth sample was retained. Convergence was evaluated with the Geweke diagnostic (Geweke, 1992) implemented in the BOA package in R software (R Core Team, 2024). Posterior means, standard deviations, and 95% highest posterior density (HPD) intervals were used to summarize the estimates.

3. Results and discussion

3.1 Population structure

After data editing, the pedigree comprised 371 Blackbelly sheep from the conservation flock at the Água Boa Experimental Station. The pedigree showed an unbalanced breeding structure, with a sire-to-dam ratio of approximately 1:4.6 and only 60.6% of animals having both parents identified (Table 1). The larger proportion of missing paternal records may reflect incomplete sire recording and/or the use of a limited number of breeding males, both of which can reduce the precision of pedigree-based relationship estimates.

Pedigree depth was limited, with fewer than two equivalent generations and less than one complete generation recorded on average (Table 2). Maternal ancestry was more complete than paternal ancestry, but completeness declined markedly beyond the parental and grandparental generations (Figure 1). This asymmetry indicates that historical recording was more consistent for dams than for sires and highlights the need for systematic identification of both parents.

Table 1
Pedigree structure and completeness of genealogical records of Blackbelly sheep in the Amazonian Savanna

Pedigree structure	Number of animals	%
Size of population	371	100.00%
Number of dams	105	28.30%
Number of sires	23	6.20%
Animals with only sire known	0	0.00%
Animals with only dam known	67	18.06%
Animals with both parents known	225	60.64%
Animals with unknown sire	146	39.35%
Animals with unknown dam	79	21.29%
Number of known females	182	49.06%
Number of known males	113	30.46%

Table 2
Population and pedigree parameters of Blackbelly sheep in the Amazonian Savanna

Parameter	Value
Pedigree depth	
Average number of equivalent generations	1.24
Average number of complete generations	0.79
Average number of maximum generations	2.06
Population structure	
Number of founding animals	79
Inbreeding	
Average inbreeding (F)	0.80%
Inbreeding rate in equivalent generations	0.47%
Inbreeding rate in complete generations	0.71%
Inbreeding rate in maximum generations	0.28%
Relatedness	
Average relatedness coefficient (AR)	3.40%
Average sire-dam relatedness	4.00%

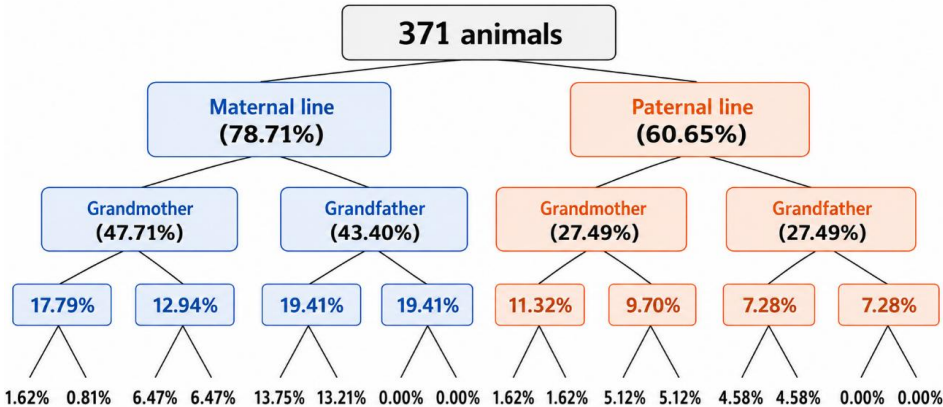


Figure 1. Pedigree completeness of Blackbelly sheep in the Amazonian Savanna. Values represent the percentage of known ancestors.

The effective population size was sensitive to the pedigree-depth criterion (**Figure 2**). Estimates based on complete and equivalent generations were below the FAO reference value of 50 (FAO, 1998), whereas the estimate based on maximum generations only slightly exceeded it. This pattern indicates a restricted effective breeding population and potential vulnerability to future loss of genetic diversity, despite the presence of 79 founders.

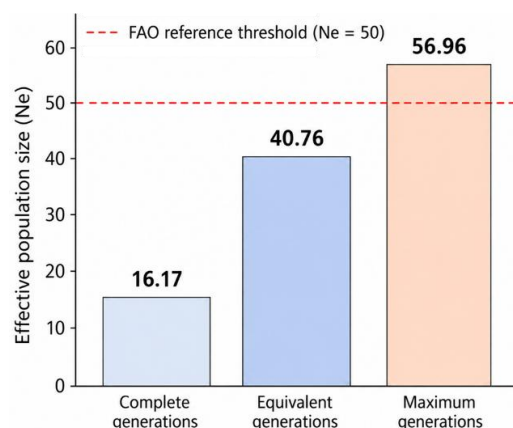


Figure 2. Effective population size across pedigree depth estimates of Blackbelly sheep in the Amazonian Savanna.

Average relatedness was low at the population level (3.40%), but mean sire-dam relatedness was higher (4.00%), and individual mating pairs reached values consistent with close relationships. Such matings can generate highly inbred offspring even when the population mean remains low. Similar concerns have been reported in pedigree analyses of small sheep populations, in which unequal breeder contribution and incomplete parentage increase the probability of related matings (Barros et al., 2017; Cortellari et al., 2022).

The pedigree completeness diagram (**Figure 1**) shows higher information recording in the maternal lineage (78.71%) than in the paternal lineage (60.65%). Pedigree completeness increased by an estimated 5.6 percentage points per generation, indicating improvement in recent recording. In addition, only 60.64% of animals had both parents identified, reflecting moderate pedigree completeness compared with values reported for Santa Inês (74.36%) and Dorper sheep (81.80%) (Barbosa et al., 2020; Kiya et al., 2019). More complete parentage recording would improve estimates of relationship and inbreeding and enable mating plans that better preserve founder contributions (Kiya et al., 2019; Justinski et al., 2023). Collectively, the pedigree indicators characterize a conservation flock with moderate parental completeness but restricted ancestral depth. The structure is comparable to that

reported for other Brazilian and international sheep populations under conservation or early-stage breeding programs, where incomplete pedigrees remain a major obstacle to accurate genetic management (Barbosa et al., 2020; Kiya et al., 2019). Mean inbreeding was low (0.80%), and most animals were non-inbred (**Table 3**). However, 33 animals were inbred, and individual coefficients reached 25%, indicating that close-relative matings occurred in part of the pedigree. Therefore, the low population mean should not be interpreted as absence of risk. In small populations, a limited number of breeding animals can rapidly increase homozygosity and expose deleterious recessive alleles, with potential consequences for health, fertility, and performance (Cortellari et al., 2022; Rafter et al., 2022).

Table 3
Pedigree-based inbreeding coefficients (F) of Blackbelly sheep in the Amazonian Savanna

F (%)	N	%
F = 0	338	91.11
0 < F ≤ 6.25	17	4.58
6.25 < F ≤ 12.50	13	3.50
12.50 < F ≤ 18.75	0	0.00
18.75 < F ≤ 25.00	3	0.81
F > 25.00	0	0.00

The estimated inbreeding trend was 0.63% per generation, indicating gradual accumulation of relatedness in the Blackbelly conservation flock. No significant association between inbreeding and the evaluated traits was detected, possibly because few animals were inbred and the available phenotypic sample was limited. The absence of detectable effect does not exclude inbreeding depression, which has been reported for growth traits in other sheep populations (Hashemi & Hossein-Zadeh, 2020). In small populations, inbreeding becomes particularly critical because the limited number of breeding animals increases the probability of related matings (Rafter et al., 2022). Continuous monitoring and mating plans that minimize relatedness among breeders are therefore necessary to maintain genetic diversity.

3.2 Genetic parameters

Descriptive statistics for the evaluated traits in the Blackbelly sheep are presented in **Table 4**. The mean birth weight (2.36 kg) was lower than values reported for Blackbelly (2.97 kg) and Pelibuey (3.05 kg) populations in Mexico (Hernandez et al., 2022). FAMACHA score (3.15) was higher than that reported for Santa Inês sheep (1.90) by Bem et al. (2023). Differences among studies may reflect breed composition, environmental conditions, parasite exposure, and management practices.

Table 4

Descriptive statistics for birth weight and FAMACHA score of Blackbelly sheep in the Amazonian Savanna

Trait	N	Mean	Standard deviation	Coefficient of variation %	Minimum value	Maximum value
Birth weight (kg)	274	2.36	0.65	27.62	0.92	5.27
FAMACHA	482	3.15	1.01	32.02	1	5

Table 5

Posterior means, standard deviation (SD), and 95% highest posterior density (95% HPD) intervals for variance components and heritability of birth weight and FAMACHA score of Blackbelly sheep in the Amazonian Savanna

Trait*	$\sigma_a^2 \pm \text{SD}$ [95% HPD]	$\sigma_{pe}^2 \pm \text{SD}$ [95% HPD]	$\sigma_e^2 \pm \text{SD}$ [95% HPD]	$\sigma_p^2 \pm \text{SD}$ [95% HPD]	$h^2 \pm \text{SD}$ [95% HPD]
Birth weight (kg)	0.207±0.064 [0.089;0.335]	-	0.229±0.046 [0.142;0.322]	0.436±0.043 [0.354;0.522]	0.470±0.117 [0.243;0.695]
FAMACHA	0.173±0.070 [0.044;0.313]	0.077±0.046 [0.0003;0.152]	0.963±0.235 [0.513;1.430]	1.214±0.251 [0.732;1.715]	0.145±0.058 [0.039;0.264]

* σ_a^2 = additive genetic variance; σ_{pe}^2 = permanent environmental variance; σ_e^2 = residual variance; σ_p^2 = phenotypic variance; h^2 = heritability.

The estimates of variance components and genetic parameters of evaluated traits are presented in **Table 5**. Birth weight showed heritability of 0.47, indicating substantial additive genetic variation and potential response to selection. Heritability estimates for birth weight vary among sheep breeds, as shown by values of 0.40 for Dorper and 0.24 for Red Maasai sheep reported by **Oyiang et al. (2022)**, and 0.33 for Garut sheep by **Nurfaridah (2022)**. Lower estimates have been reported for Bonga (0.11) and Central Anatolian Merino sheep (0.22) (**Canaza-Cayo et al., 2024; Behrem, 2021**). This variation suggests that both genetic and environmental factors play an important role in determining birth weight (**Tesema et al., 2022; Amarilho-Silveira et al., 2021**).

Heritability for FAMACHA score was low (0.14), indicating that most variation was associated with environmental effects (**Table 5**). Similar estimates have been reported for Santa Inês sheep, 0.19 by **Bern et al. (2023)** and 0.21 by **Oliveira et al. (2018)**. Genetic progress is therefore expected to be gradual, and FAMACHA based selection should be integrated with parasite monitoring, nutrition, and targeted selective treatment. Parasitic infections also negatively affect productivity, causing significant economic losses through increased treatment costs, reduced daily weight gain, decreased immunity, anemia, and, in severe cases, animal mortality (**Burke et al., 2022; Snyman & Fisher, 2019**). Long-term selection for favorable health indicators may reduce dependence on anthelmintics and contribute to more sustainable parasite control (**Burke et al., 2022; Costa et al., 2025**).

4. Conclusions

The Blackbelly conservation flock showed moderate parental pedigree completeness but shallow ancestral depth and a restricted effective population size. Although mean inbreeding was low, its positive generational trend and the occurrence of close-related matings indicate a need for preventive genetic

management. Birth weight had sufficient additive genetic variation to support selection, whereas the low heritability of FAMACHA score indicates that genetic improvement should be combined with health and nutritional management. More complete pedigree recording, balanced use of sires, and mating plans based on minimum relatedness are immediate practical priorities. Future studies should integrate genomic information and larger longitudinal datasets to improve estimates of diversity, inbreeding, and parasite-related resilience. These measures can strengthen the conservation and sustainable productive use of Blackbelly sheep in the Amazonian Savanna.

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Author contributions

J. T. Paiva: Conceptualization, Methodology, Validation, Formal analysis, Investigation, Resources, Data curation, Writing - original draft, Writing - review & editing, Visualization, Supervision, Project administration. **J. C. Senger:** Methodology, Validation, Formal analysis, Investigation, Data curation, Writing - original draft, Writing - review & editing, Visualization. **R. M. Braga:** Methodology, Investigation, Resources, Writing - original draft, Supervision. **K. M. A. S. C. Morais:** Formal analysis. **E. Z. L. D'suze:** Formal analysis. **G. M. Fagundes:** Investigation, Writing - original draft. **N. D. S. Lima:** Investigation, Writing - original draft. All authors read and approved the final manuscript.

Declaration of Competing Interest

The authors declare that there is no conflict of interest.

Ethical statement

This study used retrospective pedigree and phenotypic records from an existing database; therefore, approval by an animal ethics committee was not required under the applicable institutional procedures.

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