



Short communication

Genetic parameters for growth and reproductive traits of Morada Nova sheep kept by smallholder in semi-arid Brazil



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ABSTRACT

The objective of the present study was to estimate genetic parameters for growth and reproductive traits of Morada Nova sheep reared by smallholder farmers in the semi-arid northeastern region of Brazil. Data from 11 participating flocks, between 2007 and 2011, were used for the estimation of (co)variance components and genetic parameters for birth weight (BW), weight at weaning adjusted for 112 days of age (WW), average daily weight gain from birth to weaning (ADG), days to lambing (DL), lambing interval (LI), total litter weight at birth (LWB), total litter weight at weaning (LWW) and the ratio between total litter weight at birth and weaning and metabolic weight of the dam (LWB/MW and LWW/MW, respectively). The direct heritabilities obtained by one-trait analysis were 0.19, 0.14, 0.11, 0.13, 0.0, 0.44, 0.19, 0.41, 0.15, respectively for BW, WW, ADG, DL, LI, LWB, LWW, LWB/MW and LWW/MW. The direct heritabilities for BW and WW obtained by two-trait analysis were similar to those estimated by one-trait analysis. However, the direct heritabilities for LWB, LWW and LWW/MW obtained by two-trait analysis were higher than those estimated by one-trait analysis. The genetic correlation between BW and WW were 0.75 and between LWB, LWW and LWW/MW were 0.8, 0.9 and 1.0, respectively. In conclusion, except for LI, there is genetic variability that can be explored by direct and indirect selection to obtain genetic gains in the flocks participating in the Nucleus of Participatory Breeding of Morada Nova Sheep.

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1. Introduction

In 2010, Brazil had 1.7% of the global sheep population, occupying 16th position with 17,662,200 heads (FAO, 2012). Although still far from reaching economic expressiveness in Brazil, sheep farming is of social importance for the northeastern region of the country, where more

than 50% of the national sheep flock is found. In this region, 59.1% (9.61 million) of Brazilian population are classified as “extremely poor” (IBGE, 2010). In this respect, the development of sheep production may have a direct influence on the income and quality of life of part of this population.

Most part of the northeastern sheep flocks consists of animals of nondescript and locally adapted breeds. As observed in other developing countries, a large part of locally adapted breeds in Brazil is at risk of extinction. The Morada Nova breed is one of the main locally adapted breeds in northeastern Brazil (Paiva et al., 2005, 2006). Previous studies indicate the suitability of this breed for meat

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and skin production and highlight its adaptation to the production conditions of the semiarid northeast, with these animals showing good fertility and prolificacy (Selaive-Villarreal and Fernandes, 2000; Quesada et al., 2002). These aspects make the breed an important genetic resource for rural producers in northeastern Brazil (Facó et al., 2008).

When native breed has potential to production and environment adaptation, it is possible to develop an association between conservation programs and breeding (Lauvie et al., 2011). Within this context, it is important to do genetic evaluation and selection in order to have genetic gain for traits that influence the flock profitability. The knowledge of the genetic parameters of these traits is essential to conduct this process. The objective of the present study was to estimate genetic parameters for growth and reproductive traits of locally adapted Morada Nova sheep reared by smallholder farmers in the semiarid northeastern region of Brazil.

2. Material and methods

The data used refers to Morada Nova sheep born between 2007 and 2011 and were obtained from an existing database from Nucleus of Participatory Breeding of Morada Nova Sheep. This Nucleus was formed until the end of 2006 by 11 flocks located in the municipalities of Morada Nova, Jaguaratama, Limoeiro do Norte and Sobral, all in the state of Ceará, Brazil. The region is characterized by a hot and dry climate with an average annual rainfall of 713 mm and an average temperature of 27–33 °C.

The breeding season and parentage control were implemented in the herds to create genetic connection between them. For this, four reference rams with known growth potential, selected in centralized individual performance tests, were chosen to guarantee genetic connectedness between flocks (Facó et al., 2009). In any case, the exchange of rams between breeders of the nucleus is common practice, a fact also favoring genetic connectedness.

The following growth traits were analyzed in male and female animals: birth weight (BW), weight at weaning adjusted for 112 days of age (WW), and average daily weight gain from birth to weaning (ADG). The animals were weaned between 70 and 150 days of age and weaning weight was adjusted for 112 days of age using the following formula:

$$WW = WW_i + [ADG \times (112 - AW)]$$

where WW is the adjusted weaning weight, WW_i is the weight of the animal on the weaning date, ADG is the average daily weight gain from birth to weaning, and AW is the age of the lamb at weaning. ADG was calculated as:

$$ADG = \frac{WW - BW}{AW}$$

The following reproductive traits were also analyzed: days to lambing (DL; number of days between the beginning of the breeding season and the lambing), lambing interval (LI), total litter weight at birth (LWB), total litter weight at weaning (LWW), and ratio between total litter weight at birth and weaning and metabolic weight of the

Table 1

Data structure for growth and reproductive traits.

Trait	N	Mean ± SD	CG	CV (%)
BW (kg)	2022	2.26 ± 0.59	176	26.30
WW (kg)	957	12.36 ± 3.54	99	28.36
ADG (g/day)	957	89.41 ± 34.29	99	34.29
DL (day)	1301	169.93 ± 24.12	36	14.19
LI (day)	742	283.38 ± 75.59	70	26.67
LWB (kg)	1532	3.47 ± 1.22	113	35.26
LWW (kg)	557	15.57 ± 6.30	69	40.45
LWB/MW	1468	0.27 ± 0.08	111	32.86
LWW/MW	567	1.22 ± 0.56	68	38.78

N, number of observations, SD, standard deviation, CG, number of contemporary groups, CV, coefficient of variation; BW, birth weight; WW, weaning weight; ADG, average daily weight gain from birth to weaning; DL, days to lambing; LI, lambing interval; LWB, total litter weight at birth; LWW, total litter weight at weaning; LWB/MW, ratio between total litter weight at birth and metabolic weight of the dam; LWW/MW, ratio between total litter weight at weaning and metabolic weight of the dam.

dam (LWB/MW and LWW/MW, respectively) (Lobo et al., 2012).

Classes were defined for the ewe's age at lambing: Class 1: less than 2 years of age; Class 2: 2–3 years; Class 3: 3–4 years; and Class 4: more than 4 years. The age of the dams was mainly determined based on dental evaluation since no birth data were available for many dams at the time of implementation of the nucleus. For growth traits, the contemporary groups were formed by animals of the same sex, born on the same flock and in the same year and month. For reproductive traits, the contemporary groups consisted of animals of the same flock lambing in the same year and month.

For consistency analysis of the data, records of contemporary groups with fewer than four observations and records ± 3.5 standard deviations of the mean of the contemporary groups were excluded. Table 1 shows the number of the remaining observations after consistency analysis. The relationship matrix included 3266 animals. Of these, 68 were sires and 778 were dams with progeny in the data, 1748 animals had a complete pedigree (sire and dam known) and 845 were from the basal flock; 672 animals had an unknown sire. The average number of offspring per dam was 3.11 and the number of offspring per sire was 25.7. The animal model was used in the present study.

The general model used for the analyses can be written as follows:

$$y = X\beta + Z_1a + Z_2m + Wp + e$$

where y is the vector of observations; β is the vector of fixed effects; a is the vector of direct additive genetic effects; m is the vector of maternal additive genetic effects (present only for growth traits); p is the vector of permanent environmental effects (maternal environment for growth traits and environment of the animal itself for reproductive traits); e is the vector of random residual effects; X , Z_1 , Z_2 and W are incidence matrices relating the data to the fixed, direct additive genetic, maternal additive genetic and permanent environmental effects, when present, respectively.

For BW, WW and ADG the model included contemporary group, type of birth and ewe's age class as fixed effects

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