Genetic evaluation is possible on community pastoral small ruminant flocks in the presence of multiple sires and uncertain of paternity

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ARTICLE INFO

ABSTRACT

Many sheep flocks in the world are raised collectively, in a communal way, where animals of different owners graze together. These conditions make it difficult or impossible to identify the paternity of the offspring, since several sires and dams can mate without any control. This practice inhibits the achievement of accurate genetic evaluations using the animal model procedures. Therefore, it is proposed here to evaluate the efficiency of the use of two methods, the hierarchical animal model (HM) and the average numerator relationship matrix (ANRM), in the estimation of genetic parameters and breeding values of sheep, with uncertainty of paternity in which there are mating in the presence of multiple sires. The methods were compared in two situations, one with a simulated trait with a phenotypic variance of 7.5 kg^2, an average of 14.5 kg and a heritability of 0.30, so that the true genetic parameters were known, and the other with real data, with weights at birth and weaning of animals of a flock of Santa Inês sheep breed. The results confirmed that genetic evaluation models with multiple sires, which consider paternity uncertainty, are efficient in estimating genetic parameters and ranking superior sires in sheep flocks with community pastoral characteristics. Despite the best fit of the data by HM, both models were similar for the estimates and can be considered in the genetic evaluations.

1. Introduction

The production of small ruminants in a large part of the terrestrial globe, especially in Africa, is predominantly carried out extensively, often with animals collectively managed, in a communitarian way, where animals of different owners graze together. This form of breeding, in addition to the absence of practices of animal recording, makes it difficult to identify the sires of the progenies, since several males are present and can mate with the females occasionally and indiscriminately. This reduces the efficiency of obtaining genetic evaluations using animal model procedures.

The use of the average numerator of relationship matrix (ANRM) for cases in which there are multiple sires for a group of females (Henderson, 1988) could contribute to the solution of this problem. Foulley et al. (1987) reported that as long as the a priori probabilities of paternity uncertainty are known, Bayesian procedures are potentially useful under conditions such as those of a natural mating in extensive systems, such as pastoral systems. Cardoso and Tempelman (2003) developed a hierarchical animal model (HM) using Bayesian procedures

using Markov chain Monte Carlo (MCMC) techniques to predict the genetic merit of animals with uncertainty of paternity. With the use of data simulation, this method allowed the estimation of a posteriori paternity probabilities and surpassed the use of ANRM.

Despite the great frequency of situations with uncertainty of paternity and use of pastoral systems in small ruminants, these strategies have not been evaluated in sheep. Thus, the objective of this study was to evaluate the efficiency of the use of the HM and ANRM methods in the estimation of the genetic parameters and the breeding values of sheep, in a situation of paternity uncertainty in which there are mating in the presence of multiple sires.

2. Material and methods

To evaluate the efficiency of the genetic evaluation of a flock with paternity uncertainty and multiple sires, a data set was simulated, similar to the one commonly observed for a trait such as weaning weight in sheep. A polygenic trait was simulated, with a phenotypic variance of 7.5 kg^2, an average of 14.5 kg and a heritability of 0.30. Ten

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Table 1

Number of inbred animals (NIA) and average inbreeding coefficient (AIC) for simulated data and real data of Santa Inês sheep breed, according to the model.

Parameter	MCP		MTUP		ANRM/HM	
	Simulated	Real Data	Simulated	Real Data	Simulated	Real Data
NIA	2216	245	0	0	4902	635
AIC	0.05	0.07	0.00	0.00	0.64	0.33

MCP = model with complete pedigree; MTUP = model with total uncertainty of paternity; ANRM = model with multiple sires and average numerator relationship matrix; HM = hierarchical model with multiple sires.

Table 2

Average deviance (DEV), penalty of the model – effective number of parameters (p_d), deviance information criteria (DIC), conditional predicate ordinate (CPO) and pseudo Bayes factor for the models with multiple sires and average numerator relationship matrix (ANRM) and hierarchical model with multiple sires (HM) for simulated data and real data of Santa Inês sheep breed.

Criteria	Data Type	Model	
		ANRM	MH
DEV	Simulated data	41409.99	41408.66
	Real Data	5117.78	5118.79
p_d	Simulated data	16546.09	16545.96
	Real Data	1968.49	1904.83
DIC	Simulated data	57956.08	57954.61
	Real Data	7086.27	7023.62
CPO	Simulated data	33337.89	33338.34
	Real Data	4369.90	4382.52
PBF	Simulated data	26890.61	26846.76
	Real Data	4227.33	4185.20

generations were simulated, with an average historical size of 420 animals, whose founding population consisted of 405 females and 15 males.

Throughout the generations, the animals were selected only on the basis of the phenotype, with a replacement yearly rate of 50% and 20% for males and females, respectively. The rates of twins and triplet were simulated by 30% and 2%, respectively. These data were simulated using the QMSim software (Sargolzaei and Schenkel, 2009). The result of the simulation generated a pedigree with 5880 animals, all with phenotype and breeding value known, with only the founders (420

animals) without knowledge of paternity.

The simulated trait was analysed by the software INTERGEN (Cardoso, 2008, 2010), which uses a Bayesian approach and the method for paternity uncertainty in which there are mating in the presence of multiple sires. In this software, data were analysed in four ways: Model 1) with the complete pedigree, such it was simulated; Model 2) ignoring the knowledge of the sires, that is, attributing total ignorance of paternity and only knowledge of maternity; Model 3) considering the use of multiple sires and ANRM, attributing equal probability of paternity to each sire within the group; Model 4) considering the use of multiple sires and different probabilities for each possible sire within the group, estimated a posteriori according to the information available in data (hierarchical model – HM). The criterion for grouping multiple sires was the generations.

In analyses, the chains length were 1,100,000 and the burn-in period was 400,000 with each 10th sample collected. The effective size of the chains was 70,000 samples. Analyses considered a simple animal model, with systematic effects of sex and random effects of animal (genetic) and residual.

The two models with multiple sires, considering equal (model 3) or different (model 4) probabilities among the sire candidates, were compared by the deviance information criteria (DIC; Spiegelhalter et al., 2002) and pseudo Bayes factor (PBF; Gelfand, 1996).

The losses in the genetic parameter estimates and the consequences of the paternity uncertainty for the animal ranking were verified through the correlation (Pearson and Spearman) between the breeding values estimated in each analysis based on the complete pedigree model and the real breeding values.

Subsequently, the same procedures were used to estimate genetic parameters in real field data. Information between the years 2006 and

Table 3

Estimates of variance and heritability for the simulated trait, according to the model.

Parameter	Mean ± SD	Median	Mode	HPD95%	MCE
Model with complete pedigree					
$\sigma^2\alpha$	2.0634 ± 0.1539	2.0589	2.0436	1.7746–2.3775	0.0011
$\sigma^2 e$	5.2795 ± 0.1346	5.2778	5.2698	5.0191–5.5458	0.0007
$\sigma^2 p$	7.3429 ± 0.1462	7.3416	7.3449	7.0609–7.6363	0.0007
h^2	0.2809 ± 0.0181	0.2806	0.2817	0.2462–0.3172	0.0001
Model with total uncertainty of paternity					
$\sigma^2\alpha$	8.4471 ± 0.2797	8.4448	8.4391	7.9009–9.0003	0.0030
$\sigma^2 e$	1.0712 ± 0.1548	1.0683	1.0457	0.7767–1.3835	0.0020
$\sigma^2 p$	9.5183 ± 0.1926	9.5160	9.5235	9.1477–9.9031	0.0011
h^2	0.8873 ± 0.0171	0.8877	0.8885	0.8528–0.9195	0.0002
Model with multiple sires and average numerator relationship matrix					
$\sigma^2\alpha$	1.6584 ± 0.1345	1.6552	1.6337	1.4043–1.9304	0.0011
$\sigma^2 e$	5.1767 ± 0.1508	5.1764	5.1852	4.8851–5.4762	0.0009
$\sigma^2 p$	6.8352 ± 0.1399	6.8341	6.8370	6.5641–7.1122	0.0007
h^2	0.2426 ± 0.0183	0.2423	0.2426	0.2077–0.2792	0.0001
Hierarchical model with multiple sires					
$\sigma^2\alpha$	1.6586 ± 0.1355	1.6559	1.6581	1.4026–1.9319	0.0011
$\sigma^2 e$	5.1765 ± 0.1509	5.1756	5.1800	4.8835–5.4759	0.0009
$\sigma^2 p$	6.8351 ± 0.1405	6.8339	6.8310	6.5627–7.1141	0.0007
h^2	0.2426 ± 0.0184	0.2423	0.2417	0.2075–0.2792	0.0001

$\sigma^2\alpha$ = additive genetic variance; $\sigma^2 e$ = environmental variance; $\sigma^2 p$ = phenotypic variance; h^2 = heritability; HPD95% = 95% highest density probability confidence interval; MCE = Monte Carlo error.