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Bayesian estimates of genetic parameters for bodyweights in Mecheri sheep of India

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Abstract

An understanding of genetic information and relationships among traits is required for an improvement programme to be successful. Therefore, this study aims to estimate certain (co)variance components for bodyweights Mecheri sheep collected at various ages. The data consisted of 2 768 records that were produced by the progeny of 110 sires and 748 dams maintained in the tropical climatic conditions of Tamil Nadu, India, between 2010 and 2020. Computations of the genetic parameters were made using Bayesian methods with Gibbs sampling. The direct heritability estimates for weight at birth (BWT), weaning (WWT), 6 months (6WT), 9 months (9WT) and one year old (12WT) were 0.155, 0.262, 0.069, 0.111 and 0.067, respectively. The maternal heritabilities obtained for the pre- and post-weaning traits were low, with the mean values for BWT, WWT, 6WT, 9WT and 12WT being 0.067, 0.030, 0.036, 0.040 and 0.039, respectively. The estimates of additive genetic correlations between bodyweights at the various ages were positive and of variable magnitude ranging from 0.198 (BWT–12WT) to 0.970 (6WT–9WT). The heritability of WWT was higher than the weights at other ages, and indicated the presence of significant genetic variation in this trait. There were also high correlations between WWT and post-weaning weights. Thus, WWT, recorded early in life, could be used as a selection criterion for improving the growth traits.

Keywords: Bayesian analysis, Gibbs sampling, genetic parameters, Mecheri sheep, non-genetic factors
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Introduction

Sheep farming in India is based mainly on 'zero input' management systems and the animals are reared for meat, wool and manure. They can serve as the sole source of livelihood for sheep farmers or as a subsidiary. Sheep can sustain themselves in arid, semi-arid, hilly, heavy rainfall and drought-prone areas, where they survive on sparse forage and under extreme climatic conditions more efficiently than the other species of domestic livestock. With 44 recognised breeds and a substantial number of non-descript and mixed varieties, India possesses a large repository of sheep genetic resources (Thiruvenkadan *et al*., 2017).

According to the Twentieth Livestock Census (as of 2019), the total sheep population in India was 74.26 million and Tamil Nadu state (in southern part of India) ranked fourth in India with a total estimated sheep population of 4.50 million, which constituted 6.06 per cent of the total number of sheep of the country (Livestock Census Report, 2019). Sheep rearing is a financially feasible and essential subsidiary occupation in this state. The Mecheri is a meat breed that is prized for its skin quality, dressing percentage, and ability to resist hard weather (Karunanithi *et al*., 2005).

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In general, a number of non-genetic factors influence lamb growth and make assessing lamb growth potential difficult. Furthermore, because genetic variables rely on (co)variance components, exact variance component estimations are crucial to animal breeding programmes. As a result, new statistical methods for estimating variance components are constantly being developed, and the Bayesian approach of analysis for estimating genetic parameters has recently become popular (Ghavi Hossein-Zadeh & Ardalan, 2010). As opposed to the restricted maximum likelihood approach, Bayesian methodology takes account of previous information on unknown parameters and provides a solution for small sample sizes. Furthermore, the Gibbs sampling process generates posterior parameter distributions, allowing for random sample estimates based on a specific data collection (Ghavi Hossein-Zadeh & Ardalan, 2010; Ghavi Hossein-Zadeh, 2015).

The data on genetic characteristics for several growth qualities in the Mecheri sheep breed are limited and based are on restricted maximum likelihood, with no previous studies based on the Bayesian approach. As a result, the goal of the current study was to estimate the heritability for bodyweight traits in Mecheri sheep and genetic correlations between weights at various ages using a Bayesian algorithm and Gibbs sampling. The goal of the research was to develop a suitable selection strategy for improving Mecheri sheep's growth rate at various stages of development.

Materials and Methods

This study took place at Mecheri Sheep Research Station, Pottaneri, Tamil Nadu, India, at a longitude of 77° 56'E, latitude of 11° 45'N. The data arose from animal management activities that had been approved by the Institutional Animal Ethics Committee of the Veterinary College and Research Institute. The animals grazed as a flock for seven to eight hours during the day in natural pasture at a distance of three to four kilometres from the research station. Owing to the lack of fodder in the grazing fields during the summer, the sheep were supplemented with cultivated fodder crops and neem *(Azadirachta indica)* leaves. Within 24 hours of lambing, the lambs were ear-tagged and weighed. The lambs were weaned at three months old, and the young ewes were initially introduced to the rams at 1.5 years. Ewes were kept in the flock until they were seven years old. All of the lambs were vaccinated against major diseases and drenched to manage internal and external parasites and mineral combination blocks were readily available to them.

The birth weight (BWT), weaning weight (WWT), 6-month weight (6WT), nine-months weight (9WT) and 12-month weight (12WT) data consisted of 2768 records from 110 sires and 758 dams that were collected from 2010 to 2020. The model that was used to analyse the data was:

$$y = Xb + Z_1a + Z_2m + Pc + e$$

where, y is the vector of records and b, a, m, c and e are vectors of fixed effects, and random direct additive genetic, maternal additive genetic, permanent environmental effects of the dam, and residual effects, respectively. The incidence matrices X, Z_1, Z_2 and P associate the effects that were to be estimated with the data. The fixed effects included birth year (10 levels), sex (2 levels), birth season (2 levels), type of birth (2 levels), parity (six levels) and bodyweight of the dam as a linear covariate. Expectations of the variances (Var) and covariance (Cov) for the random effects were:

$$Var(a) = A\sigma_a^2,\ Var(m) = A\sigma_m^2,\ Var(c) = I\sigma_c^2,\ Var(e) = I\sigma_e^2, \text{ and } Cov(a,m) = A\sigma_{a,m}$$

where, A was the numerator relationship matrix among animals and $\sigma_{a,m}$ was the covariance between the additive direct and maternal genetic effects.

The systematic effects listed above and the (co)variance components included in the model were assumed to have a uniform a priori Gaussian distribution, and the direct additive, maternal, permanent environmental, and residual variances were assumed to be distributed as inverse Wishart distributions (Sorensen & Gianola, 2002). Estimates of the effects were obtained using Gibbs sampling as implemented in the program GIBBS2F90 (Misztal *et al*., 2015). One chain with 1 500 000 iterations was used to obtain the marginal posterior distribution for each parameter. Burn-in was removed after the first 500 000 iterates, and the thinning interval was set at 100. For all estimations from the individual marginal posterior distributions, the remaining iterates were utilized to generate the mean, SD, and high posterior density (HPD) regions. The HPD region is a measure of reliability that encompasses a given percentage of the samples. Non-symmetric distributions can also be quantified using the HPD (Hyndman, 1996; Ghavi Hossein-Zadeh, 2015). The phenotypic variance ($\sigma_P^2 = \sigma_a^2 + \sigma_m^2 + 2\sigma_{a,m} + \sigma_c^2 + \sigma_e^2$), direct heritability ($h_a^2 = \sigma_a^2/\sigma_P^2$), maternal heritability ($h_m^2 = \sigma_m^2/\sigma_P^2$), genetic correlation between the direct and maternal effects ($r_{a,m} = \sigma_{a,m}/\sqrt{\sigma_a^2\sigma_m^2}$) and the maternal permanent environmental variance expressed as a proportion of the phenotypic variance ($C^2 = \sigma_c^2/\sigma_P^2$) were estimated from the posterior distributions. Similar bivariate analyses were conducted to estimate correlations between each pair of weights. The starting values for the bivariate analyses were derived from the single-trait analyses.

Results and Discussion

The posterior distribution of the estimates for each effect contained 10 000 Gibbs samples. Estimates of the (co)variance components derived from the posterior distributions of the effects for the bodyweight traits are presented in Table 1.

Table 1 Estimates of (co)variance components for bodyweights of Mecheri sheep from posterior distributions of Gibbs samples

Trait	Parameters	Posterior mean	Posterior SD	95% HPD regions	
				2.5%	97.5%
Birth weight	Additive genetic variance	0.017	0.007	0.008	0.033
	Covariance of direct and maternal additive effects	-0.007	0.004	-0.015	-0.001
	Maternal genetic variance	0.007	0.004	0.002	0.017
	Permanent environmental variance	0.020	0.004	0.012	0.027
	Residual variance	0.081	0.005	0.071	0.089
	Phenotypic variance	0.110	0.005	0.101	0.119
Weaning weight	Additive genetic variance	1.088	0.341	0.520	1.885
	Covariance of direct and maternal additive effects	-0.243	0.142	-0.530	-0.002
	Maternal genetic variance	0.122	0.125	0.003	0.461
	Permanent environmental variance	0.257	0.091	0.082	0.445
	Residual variance	3.184	0.220	2.729	3.591
	Phenotypic variance	4.165	0.173	3.816	4.492
6-month weight	Additive genetic variance	0.461	0.227	0.130	0.965
	Covariance of direct and maternal additive effects	-0.023	0.134	-0.331	0.184
	Maternal genetic variance	0.243	0.161	0.014	0.621
	Permanent environmental variance	0.108	0.093	0.003	0.337
	Residual variance	5.980	0.283	5.430	6.538
	Phenotypic variance	6.747	0.280	6.215	7.314
9-month weight	Additive genetic variance	1.180	0.737	0.244	2.991
	Covariance of direct and maternal additive effects	-0.268	0.386	-1.262	0.275
	Maternal genetic variance	0.422	0.310	0.065	1.276
	Permanent environmental variance	0.206	0.197	0.004	0.718
	Residual variance	9.482	0.623	8.168	10.645
	Phenotypic variance	10.753	0.547	9.656	11.820
12-month weight	Additive genetic variance	0.655	0.372	0.195	1.511
	Covariance of direct and maternal additive effects	0.160	0.215	-0.394	0.504
	Maternal genetic variance	0.376	0.288	0.055	1.074
	Permanent environmental variance	0.639	0.358	0.088	1.449
	Residual variance	7.755	0.503	6.798	8.778
	Phenotypic variance	9.745	0.518	8.769	10.799

SD: standard deviation, HPD: high posterior density

The direct heritability estimate observed for BWT (Table 2) was comparable with the reported value of 0.16 for Malpura sheep (Prince *et al*., 2010). However, the value observed was higher than many earlier reports for different breeds of sheep (Kushwaha *et al*., 2009; Javed *et al*., 2013; Jalil-Sarghale *et al*., 2014; Boujenane and Diallo, 2017; Kumar *et al*., 2017; Sallam *et al*., 2019; Ali *et al*., 2020). Higher estimates for the direct heritability of birth weight than that observed in the current study have also been reported (Prince *et al*., 2010; Prakesh *et al*., 2012; Singh *et al*., 2014; Gowane *et al*., 2015; Kumar *et al*., 2020). The direct heritability estimate for WWT (0.262 ± 0.083) of Mecheri sheep was similar to the value reported by Kumar *et* *al*. (2020) and marginally higher than those reported by Hanford *et al.* (2003) for Targhee sheep (0.22), Mandal *et al*. (2006a) in Muzaffarnagri sheep (0.21). However much higher estimates (Prince *et al*., 2010; Gowane *et al*., 2015) and much lower estimates (Kushwaha *et al*., 2009; Boujenane *et al*., 2015) can be found in the literature for various sheep breeds. The direct heritability estimates for 6WT, 9WT and 12WT were much lower than the reports for the Iran-Black (Kamjoo *et al*., 2014), Marwari (Singh *et al*., 2014) and Harnali (Banger *et al*., 2020) breeds of sheep. The heritability estimate for WWT was higher than the heritability estimates for weights obtained later in life. Thus, selection for WWT has a good chance of producing more rapid genetic improvement compared with selection based on weights at older ages.

Table 2 Estimates of genetic parameters for bodyweights of Mecheri sheep from posterior distributions of Gibbs samples for the modelled parameters

Traits	Parameters	Posterior Mean	Posterior SD	95% HPD region	
				2.5%	97.5%
Birth weight	Direct heritability	0.155	0.063	0.075	0.303
	Maternal heritability	0.067	0.039	0.020	0.158
	Genetic correlation of direct and maternal effects	-0.717	0.240	-0.999	-0.141
Weaning weight	Direct heritability	0.262	0.083	0.126	0.457
	Maternal heritability	0.030	0.032	0.001	0.117
	Genetic correlation of direct and maternal effects	-0.775	0.242	-0.997	-0.030
6-month weight	Direct heritability	0.069	0.034	0.019	0.144
	Maternal heritability	0.036	0.024	0.002	0.095
	Genetic correlation of direct and maternal effects	0.020	0.425	-0.712	0.779
9-month weight	Direct heritability	0.111	0.072	0.022	0.301
	Maternal heritability	0.040	0.031	0.006	0.125
	Genetic correlation of direct and maternal effects	-0.298	0.435	-0.894	0.719
12-month weight	Direct heritability	0.067	0.038	0.020	0.155
	Maternal heritability	0.039	0.030	0.006	0.110
	Genetic correlation of direct and maternal effects	0.461	0.416	-0.503	0.966

SD: standard deviation, HPD: high posterior density

The estimated maternal genetic effect was very low at birth. Similar low estimates were reported by Gowane *et al*. (2010a), Prakash *et al.* (2012) and Gowane *et al*. (2015). The maternal heritability estimates for weights that were measured subsequently were also low and similar in magnitude (Table 2). These estimates were far lower than published values for Turkish Merino (Ekiz et al., 2004), Marwari sheep (Singh et al., 2014) and Nellore sheep (Kumar et al., 2020). The estimates of maternal genetic effects on weights collected between birth and one year old indicated that the maternal genetic influence on growth in Mecheri sheep was minimal. Several publications, on the other hand, showed stronger maternal heritability before weaning with a significant drop in the magnitude of maternal genetic effects after weaning (Kushwaha *et al*., 2009; Prakash *et al*., 2012; Banger *et al*., 2020; Kumar *et al*., 2020). For the bodyweights observed in the present study, the estimates of direct heritability were greater than those for maternal heritability. The significant genetic variability in WWT can be used to aid in the selection process. In the current flock of Mecheri sheep, selection at WWT rather than 6WT may accelerate genetic gain per unit of time.

The estimates of the genetic correlation of direct and maternal effects for pre-weaning bodyweights were highly negative, which is in accordance with the observations of Mandal *et al*., (2006b) for Muzaffarnagri sheep and of Prince *et al*. (2010) in the Avikalin sheep of India. This conflict between the influence of the genes of an individual affecting its bodyweight and those that condition its maternal contribution to progeny might be attributable to natural selection towards an intermediate optimum (Tosh & Kemp, 1994). As a result, selection for the additive genetic effects on early growth is likely to reduce maternal qualities, making the consistent improvement of the early-in-life phenotypes difficult.

Estimates of the correlations of direct effects, maternal effects, and residual effects for bodyweight are presented in Table 3. The genetic correlations of BWT with WWT (0.683) was higher compared with the estimates of 0.56 by Hanford *et al*. (2002) in Columbia sheep, 0.45 by Gowane *et al*. (2010a, 2010b) in Bharat Merino sheep and 0.16 by Kumar *et al*. (2020) in Nellore sheep. The high genetic association between BWT and WWT suggested that the traits were controlled by the same genetic and physiological pathways. Other authors who studied growth traits have validated this conclusion (Mohammadi *et al*., 2013; Sallam *et al*., 2019).

Table 3 Estimates of additive direct, maternal genetic and residual correlations among bodyweight traits in Mecheri sheep from posterior distributions of Gibbs samples for modelled parameters

Trait pairs		Additive direct genetic correlation		Maternal genetic correlation		Residual correlation	
		Mean	SD	Mean	SD	Mean	SD
BWT	WWT	0.683	0.110	0.481	0.134	0.239	0.032
BWT	6WT	0.319	0.209	0.224	0.152	0.316	0.041
BWT	9WT	0.281	0.206	0.206	0.144	0.250	0.042
BWT	12WT	0.198	0.222	0.097	0.148	0.251	0.041
WWT	6WT	0.780	0.150	0.792	0.097	0.737	0.027
WWT	9WT	0.619	0.167	0.627	0.109	0.502	0.031
WWT	12WT	0.552	0.190	0.547	0.129	0.454	0.035
6WT	9WT	0.970	0.055	0.926	0.049	0.865	0.017
6WT	12WT	0.858	0.108	0.852	0.062	0.768	0.017
9WT	12WT	0.931	0.053	0.856	0.060	0.902	0.016

BWT: birth weight, WWT: weaning weight (90 days), 6WT: weight at six months. 9WT: weight at 9 months, 12WT, weight at 12 months

Selection for BWT may result in considerable improvements in WWT, modest improvements at 6WT and 9WT when the sheep are typically marketed, and only slight improvements in 12WT owing to a positive genetic association between these characteristics. As expected, the genetic correlations between successive traits were stronger than those between non-successive traits and the estimates in this study were higher than previous estimates in the Bharat Merino, Marwari, and Nellore sheep breeds, respectively (Gowane *et al*., 2010a; Singh *et al.,* 2014; Kumar *et al*., 2020).

Conclusion

Enhancement of bodyweight attributes in Mecheri sheep appeared to be attainable through genetic selection programmes. Because of the substantial genetic association between WWT and post-weaning weights and the relative large estimate of direct heritability for WWT, WWT could be employed as a selection criterion for increasing growth traits. These latest estimates could aid in the redesign of the breeding programme and the development of new genetic improvement programmes for Mecheri sheep.

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Conflict of Interest Declaration

The authors declare no conflict of interest.

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