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# Multi-trait Bayesian analysis and genetic parameter estimates in production characters of Mecheri sheep of India

Thiruvenkadan Aranganoor Kannan<sup>1</sup> · Muralidharan Jaganathan<sup>2</sup> · Rajendran Ramanujam<sup>3</sup> · Bandeswaran Chinnaondi<sup>4</sup> · Satish Kumar Illa<sup>5</sup> · Kadir Kizilkaya<sup>6</sup> · Sunday O. Peters<sup>7</sup>

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#### Abstract

The present study was carried out to estimate the genetic parameters for direct and maternal influences on Mecheri sheep (Ovis aries) growth traits using Bayesian multi-trait animal model. The genetic parameters were calculated using data from 2825 Mecheri lambs born between 2010 and 2020 that were kept in semi-arid tropical climate. Mecheri sheep body weight (mean  $\pm$  SE) at various stages, viz. BW, WW, and BW12, were  $2.6 \pm 0.01$ ,  $11.1 \pm 0.05$ , and  $20.7 \pm 0.13$  kg, respectively. The Mecheri sheep gained 71.5 percent of their body weight at the age of 6 months. With the exception of birth weight, the weights of the animals varied considerably (P < 0.01) by the year of birth. The fixed effect of sex significantly (P < 0.01) influenced all the growth traits examined. The direct estimates of heritability ( $\pm$  SD) for BW, WW, BW6, and BW12 was  $0.21 \pm 0.041$ ,  $0.21 \pm 0.041$ ,  $0.12 \pm 0.052$ , and  $0.13 \pm 0.053$ , respectively, and the maternal heritability for BW, WW, BW6, and BW12 was  $0.18 \pm 0.021$ ,  $0.08 \pm 0.023$ ,  $0.11 \pm 0.022$ , and  $0.13 \pm 0.033$ , respectively. Significant variance was indicated by moderately larger direct heritability estimates for BWT and WWT, indicating that there will be more opportunities for selection response during the genetic improvement programme. For the majority of the variables examined, direct heritability values were higher than maternal heritability values. The additive genetic correlation between WW and BW6, BW9, and BW12 was  $0.70 \pm 0.145$ ,  $0.57 \pm 0.171$ , and  $0.50 \pm 0.194$ , respectively. The maternal genetic correlations ranged from  $0.06 \pm 0.152$  (BW–BW12) to  $0.86 \pm 0.046$  (BW6–BW9), and the residual correlation varied from  $0.18 \pm 0.034$  (BW–WW) to  $0.85 \pm 0.013$  (BW9–BW12). The BW had a stronger genetic relationship with WW and a weaker relationship with other growth traits. The WW and BW6 showed a favourable genetic relationship, even if the tendency was decreasing in the latter stages of maturation. The BW6 and BW9 demonstrated the strongest positive genetic relationship  $(0.90 \pm 0.052)$  of all the variables analysed. After examining the heritabilities and genetic correlation between WW and BW6, it was established that selection based on at WW was beneficial, since it manifests early in life and would result in moderate genetic progress through selection.

Keywords Heritability · Gibbs sampling · Body weight · Maternal influence · Multi-trait

Thiruvenkadan Aranganoor Kannan	<sup>1</sup> Department of Animal Genetics and Breeding, Veterinary
drthirusiva@gmail.com	College and Research Institute, Salem, Tamil Nadu, India
Muralidharan Jaganathan	<sup>2</sup> Mecheri Sheep Research Station, Pottaneri, Salem,
jmvetdr@gmail.com	Tamil Nadu, India
Rajendran Ramanujam	<sup>3</sup> Department of Animal Genetics and Breeding, Veterinary
drrajjam@gmail.com	College and Research Institute, Theni, Tamil Nadu, India
Bandeswaran Chinnaondi	<sup>4</sup> Department of Animal Nutrition, Madras Veterinary College,
bandeswaran@gmail.com	Chennai, Tamil Nadu, India
Satish Kumar Illa	<sup>5</sup> Livestock Research Station, Palamner, Andhra Pradesh, India
satish.vety@gmail.com	<sup>6</sup> Faculty of Agriculture, Department of Animal Science,
Kadir Kizilkaya	Biometry and Genetics Unit, Aydın Adnan Menderes
kkizilkaya@adu.edu.tr	University, Aydın, Turkey
Sunday O. Peters	<sup>7</sup> Department of Animal Science, Berry College, Mount Berry,
speters@berry.edu	GA 30149, USA

#### Introduction

India has a great diversity of sheep breeds that are well adapted to difficult climatic conditions and have played an integral role in India's diversified agro-climatic conditions (Thiruvenkadan et al., 2017). Mecheri sheep is one of the 44 known sheep breeds of India, and some of the notable qualities of this breed is the adaptation to harsh climatic conditions as well as excellent quality of meat and skin (Karunanithi et al., 2005). Nucleus flock of Mecheri sheep was established at the Mecheri Sheep Research Station (MSRS), Pottaneri, India, and selective breeding is practiced to enhance the overall performance of flock, particularly for body weight, except distribution of elite germplasm for genetic improvement in farmers' flocks (Thiruvenkadan et al., 2011; 2017).

Lamb meat is widely consumed not only in India but also in Tamil Nadu, and as the per capita income has risen significantly, the demand for lamb is continuously increasing (Devi et al., 2014). Growth rate is an important economic index that deserve special attention in breeding programmes aimed at increasing lamb meat production (Jalil-Sarghale et al., 2014). The additive genetic, maternal, and environmental components are known to affect growth traits in sheep, and the potential choice of selection depends on their genetic parameters. Traits recorded at an early age were influenced by maternal abilities (Ahmad et al. 2021; Oyieng et al., 2022); therefore, accurate and fair assessment of the covariance parts and genetic parameters are certainly essential for designing effective breeding plans for rapid as well as sustainable genetic improvement. The exactness of the variance components is based totally on wide variety of parameters observed in addition to method being employed (Kumar et al., 2020). Consequently, advancement in statistical methodologies for estimation of variance components are continuously evolving, and currently, Bayesian methods of evaluation with GIBBS sampling are widely used to evaluate genetic parameters (Ghavi Hossein-Zadeh, 2017). When compared to REML approach, Bayesian methodology has the benefit of taking into account previous information on unknown parameters and also solved the problem of a small sample size (Ghavi Hossein-Zadeh, 2017). In addition, the Gibbs sampling technique generates posterior distributions of parameters (Ghavi Hossein-Zadeh and Ardalan, 2010; Ghavi Hossein-Zadeh, 2015).

The information on the genetic parameters of the various productive traits of Mecheri sheep in the literature is meagre and is primarily based on univariate REML method (Thiruvenkadan et al., 2011, 2022; Jeichitra et al., 2016). It is important to note that the Bayesian approach has practical advantages over the traditional (REML) approach (Pretorius and van der Merwe, 2000); the current study used the Gibbs sampler animal model to extract genetic parameters for direct and maternal impacts on Mecheri sheep growth traits with multi-trait animal model. The most recent estimations of genetic parameters in this breed could be used to develop an appropriate breeding programme for genetic improvement of growth parameters.

### **Materials and methods**

#### Location of study and flock management

This study was made with the available data collected at the MSRS, Pottaneri, India. The climate of the region is warm, semi-arid, and tropical and the total grazing area of station is 164.36 acres. The maximum and minimum temperatures recorded are 37.4 °C (in the month of May) and 18.5 °C (in the month of January) respectively. Mecheri sheep flock of four hundred breeding ewes is being maintained at the station and is reared under semi-intensive management system. They were able to graze on the farm pasture for about 7 to 8 h with supplementation in line with the season, physiological status of the animals, and age category and are housed at night. Mecheri ewes are non-seasonal, but the majority of ewes were mated during the monsoon season (June to November), with off-season mating occurring during the summer months (i.e. March and April). Each lamb was first identified by an ear tag, and information on sex, date, and type of birth, as well as weight at birth, was recorded. After weaning (90 days), they have been allowed separately to graze the pasture fields.

#### Data set and studied traits

The study included data from 2825 Mecheri sheep with pedigrees of 119 rams and 758 ewes, collected from 2010 to 2020. Animals were weighed using an electronic/mechanical platform scale. The traits considered were weight at birth (BW), weaning (WW), 6-month (BW6), 9-month (BW9), and 1-year-old (BW12). The accuracy of the collected data was checked, and the defective in addition to out of range information had been removed.

#### **Statistical analysis**

Data were examined using the GLM process of SAS 9.2 statistical software to discover the fixed variables influencing body weight at different stages (SAS, 2009). The fixed effects investigated included birth year, season, lamb sex, birth type, and parity, with dam weight at birth included a covariate. To compare the mean of fixed effects at different levels, the Tukey Kramer test was utilised. Significant variables were used as fixed effects in

the statistical model to estimate the variance components by the Bayesian approach using the GIBBS2F90 (Misztal et al., 2018) software programme. Multiple trait analysis of BW, WW, BW6, BW9, and BW12 accounting for fixed effects and direct additive genetic effect of animal was carried out using a linear model which is defined for animal i below:

$$y_i = X_i b + Z_{i1} a + Z_{i1} m + e_i$$

 $y_i = [y_{i,BW}, y_{i,WW}, y_{i,BW6}, y_{i,BW9}, y_{i,BW12}]$  is the vector of phenotypic values of BW, WW, BW6, BW9, and BW12 for animal *i*, *b* is the vector of fixed effects (ewe weight at lambing as covariate, year of birth ordered into 11 levels, season of birth classified into two levels (main and off season), parity of the ewe ordered into seven levels, lamb sex coded into two levels (female or male), and type of birth classified into two levels (single or twin)), *a* and *m* are the vectors of random additive direct and maternal genetic effects and  $e_i = [e_{i,BW}, e_{i,WW}, e_{i,BW6}, e_{i,BW9}, e_{i,BW12}]'$  is the vector of residuals for animal *i*.

A flat prior was assigned for the fixed effects (b). Direct additive (a) and maternal (m) genetic effects were assumed to be distributed as multivariate normal with null mean vector (0) and (co)variance matrix  $G_0 \otimes A$ , where A is the numerator relationship matrix,  $G_0$  is the (co)variance matrix, and  $\otimes$  denotes the Kronecker product. Residuals were assumed to follow a multivariate normal distribution with null mean and (co)variance matrix  $I \otimes R_0$ , where I is the identity matrix and

$$R_{0} = \begin{bmatrix} \sigma_{e_{\rm BW}}^{2} & \sigma_{e_{\rm BW,WW}} & \sigma_{e_{\rm BW,BW6}} & \sigma_{e_{\rm BW,BW9}} & \sigma_{e_{\rm BW,BW12}} \\ \sigma_{e_{\rm WW,BW}} & \sigma_{e_{\rm WW}}^{2} & \sigma_{e_{\rm WW,BW6}} & \sigma_{e_{\rm WW,BW9}} & \sigma_{e_{\rm WW,BW12}} \\ \sigma_{e_{\rm BW6,BW}} & \sigma_{e_{\rm BW6,WW}} & \sigma_{e_{\rm BW6}}^{2} & \sigma_{e_{\rm BW6,BW9}} & \sigma_{e_{\rm BW6,BW9}} \\ \sigma_{e_{\rm BW9,BW}} & \sigma_{e_{\rm BW9,WW}} & \sigma_{e_{\rm BW9,BW6}} & \sigma_{e_{\rm BW9}}^{2} & \sigma_{e_{\rm BW9,BW12}} \\ \sigma_{e_{\rm BW12,BW}} & \sigma_{e_{\rm BW12,WW}} & \sigma_{e_{\rm BW12,BW6}} & \sigma_{e_{\rm BW12,BW9}} & \sigma_{e_{\rm BW12}}^{2} \end{bmatrix}.$$

Flat prior distributions were assigned to  $G_0$  and  $R_0$ . Inferences on parameters of  $b,a, m, G_0$ , and  $R_0$  were made from the posterior distributions formed using Markov Chain Monte Carlo (MCMC) methods such as Gibbs sampling (Geman and Geman, 1984; Gelfand and Smith, 1990). The direct additive  $(h_{a_j}^2)$  and maternal heritability  $(h_{m_j}^2)$ , additive, maternal genetic, and residual correlation  $(r_{g_{j,k}})$  estimates were obtained from estimates of (co)variances matrices  $G_0$ and  $R_0$  according to the formula described earlier (Kizilkaya et al., 2010; Peters et al., 2014).

Bayesian inferences on the parameters b, a, m,  $G_0$ , and  $R_0$  were made using Gibbs sampling using the application



GIBBS2F90 (Misztal et al., 2018). Integration of multivariate density functions yielded the marginal posterior distribution for each parameter after 1,500,000 iterations. The chain's thinning interval was 100, and the initial discard was 500,000. Visual inspection of the sample trace plots was used to check for convergence, as proposed by Kumar et al. (2020). From the individual marginal posteriors, the Bayesian output analysis was used to generate the mean, SD, and credibility interval for all parameters (Ghavi Hossein-Zadeh, 2015).

Table 1 Data structure on growth characteristics

Trait	Total records	Number of ewes	Number of rams	Mean records per	
				Ewe	Ram
Birth	2825	758	119	3.72	23.74
Weaning	2568	743	117	3.45	21.94
6-month	1617	644	112	2.51	14.44
9-month	1299	604	108	2.15	12.02
1-year-old	1004	501	95	2.00	10.57

# Results

# Pedigree structure, descriptive statistics, and environmental factors

The pedigree file consisted of 2825 animals as presented in Table 1. A total of 1004 lambs with full records of BW, BW3, BW6, BW9, and BW12. The mean number of record per ewe (Table 1) ranged between 2.00 (BW12) to 3.72 (BW), and for rams, the values were 10.57 (BW12) and 23.74 (BW). The pedigree composition check revealed that the pedigree is extensive and has enough data to estimate genetic components. Mecheri sheep body weight (mean  $\pm$  SD) at BW, WW, and BW12 were 2.57  $\pm$  0.01,  $11.09 \pm 0.05$ , and  $20.67 \pm 0.13$  kg respectively (Table 2). At six months of age, the Mecheri sheep had gained 71.5 percent of their body weight. The coefficient of variation for the studied traits ranged between 16.95 (BW) and 23.74 (BW9). When it comes to the non-genetic elements that were investigated in this study, different influences was seen at different phases of sheep growth. The weights of the experimental animals changed significantly (P < 0.01) by year of birth in all age groups except birth weight. However, there was not much of a difference when it comes to seasons. With respect to birth type, the weight difference between singles and twins was statistically significant (P < 0.05) at BW, BW3, and BW6 alone, indicating a stage of accelerated growth in later ages, particularly after a period of poor growth up to 6 months of age. All of the growth traits studied were significantly affected (P < 0.01) by the fixed effect of sex. Birth weights (P < 0.01) and 12-month age (P < 0.05) alone showed significant variation in the dams' (ewes') parity, but no significant variation in the other stages.

#### Estimation of genetic effects and parameters

Between different stages of growth, the additive genetic variations ranged from  $0.03 \pm 0.010$  (BW) to  $1.68 \pm 0.704$  (BW12). The BW, BW6, and BW12 had maternal additive genetic variance of  $0.02 \pm 0.000$ ,  $0.81 \pm 0.193$ , and  $1.67 \pm 0.371$ , respectively, with residual variance estimates of  $0.08 \pm 0.000$ ,  $5.76 \pm 0.322$ , and  $9.67 \pm 0.653$ , respectively (Table 3). For BW, WW, and BW12, the direct estimates of heritability (SD) were  $0.21 \pm 0.041$ ,  $0.21 \pm 0.041$ , and  $0.13 \pm 0.053$ , respectively, while the maternal heritability values were  $0.18 \pm 0.021$ ,  $0.08 \pm 0.023$ , and  $0.13 \pm 0.033$ , respectively. Direct heritability values were larger than maternal heritability values for most of the variables investigated, and maternal heredity had a minimal impact during the weaning and post-weaning stages. For direct heritability, the credibility intervals for the BW and BW3 ranged from 0.14 to 0.29 and 0.13 to 0.30, respectively. The direct heritability estimates for BWT and WWT was moderate, signalling that there will be more opportunities for selection response during the genetic improvement programme.

#### **Correlation between the traits**

Table 4 shows the posterior means of correlation between growth traits. Direct additive genetic co-variances (Mean $\pm$ SD) between body weights ranged from 0.04 $\pm$ 0.051 (BW vs. BW12) to 1.57 $\pm$ 0.695 (BW9 vs. BW12), while maternal additive genetic co-variances across body weight traits followed a similar pattern, with values ranging from 0.01 $\pm$ 0.030 (BW vs. BW12) to 1.33 $\pm$ 0.329. (BW9 vs. BW12). BW and WW had the lowest residual co-variance (0.09 $\pm$ 0.020), and the values increased with age, with the largest co-variances identified between BW9 and BW12 (8.14 $\pm$ 0.576). Positive additive

Summary statistics	Birth	Weaning	6-month	9-month	1-year old
Mean	2.6	11.1	14.8	18.2	20.7
Minimum	0.80	3.10	5.60	9.50	10.30
Maximum	3.90	20.50	27.30	39.30	38.70
Standard deviation	0.44	2.54	3.20	4.31	4.04
Number of observations	2825	2568	1617	1299	1004
Standard error	0.01	0.05	0.08	0.12	0.13
Coefficient of variation (%)	16.95	22.90	21.68	23.74	19.52
Non-genetic factors					
Birth year	NS	**	**	**	**
Birth season	NS	**	NS	NS	NS
Lamb sex	*	*	**	**	**
Birth type	**	**	*	NS	NS
Dam parity	**	NS	NS	NS	**
Body weight at lambing	**	**	**	**	**

\**P*<0.05, \*\**P*<0.01; *NS*, non-significant (*P*>0.05)

Table 2 Outline statistics of

traits

non-genetic factors on growth

Table 3 Components of variances and heritability values for growth characteristics

Trait	Mean ± SD	CI		Mean $\pm$ SD	CI		Naïve SE	Time series SE	
		2.5%	97.5%		2.5%	97.5%			
	Additive direct genetic variance			Direct heritab	ability				
BW	$0.03 \pm 0.010$	0.02	0.04	$0.21 \pm 0.041$	0.14	0.29	0.00	0.00	
WW	$0.96 \pm 0.231$	0.56	1.42	$0.21 \pm 0.041$	0.13	0.30	0.00	0.00	
BW6	$0.91 \pm 0.383$	0.31	1.74	$0.12 \pm 0.052$	0.04	0.23	0.00	0.01	
BW9	$1.84 \pm 0.741$	0.75	3.45	$0.14 \pm 0.051$	0.06	0.26	0.00	0.01	
BW12	$1.68 \pm 0.704$	0.72	3.24	$0.13 \pm 0.053$	0.06	0.24	0.00	0.01	
	Maternal genetic variance	variance			tability				
BW	$0.02 \pm 0.000$	0.02	0.03	$0.18 \pm 0.021$	0.13	0.23	0.00	0.00	
WW	$0.39 \pm 0.101$	0.22	0.59	$0.08 \pm 0.023$	0.05	0.12	0.00	0.00	
BW6	$0.81 \pm 0.193$	0.49	1.22	$0.11 \pm 0.022$	0.07	0.16	0.00	0.00	
BW9	$1.62 \pm 0.362$	1.03	2.44	$0.13 \pm 0.034$	0.08	0.18	0.00	0.00	
BW12	$1.67 \pm 0.371$	1.03	2.46	$0.13 \pm 0.033$	0.08	0.18	0.00	0.00	
	Residual variance								
BW	$0.08 \pm 0.000$	0.07	0.09						
WW	$3.31 \pm 0.171$	2.97	3.63						
BW6	$5.76 \pm 0.322$	5.15	6.34						
BW9	$9.41 \pm 0.601$	8.22	10.53						
BW12	$9.67 \pm 0.653$	8.38	10.94						

BW, birth weight; WW, weaning weight; BW6, 6-month weight; BW9, 9-month weight; BW12, 1-year-old weight; CI, credibility interval

genetic correlations were found for various growth traits, with values ranging from low to high (0.17 between BW and BW12 and 0.90 between BW6 and BW9). We found that BW had a stronger genetic relationship with WW and a weaker relationship with BW6, BW9, and BW12. In addition, the WW and BW6 had a substantial positive genetic association  $(0.70 \pm 0.145)$ , although the tendency was declining in the subsequent stages of growth. The strongest positive genetic correlation was found between BW6 and BW9 (0.90±0.052) across all variables analysed. The maternal genetic correlations between live weight estimates varied from 0.06 (BW-BW12) to 0.86 (BW6-BW9) and were all favourable, and the maternal genetic correlation between WW and BW6, BW6 and BW9, BW6 and BW12, and BW9 and BW12 was positive and strong. The residual correlation between BW and different ages was low and positive, while the association between BW6 and subsequent stages, as well as BW9 and BW12, was higher in magnitude and positive. The residual correlation increased with the advancement of age in all the correlation estimates (Fig. 1).

#### Discussion

### **Effect of environmental factors**

Domestic animal growth characteristics are influenced not only by the animal genetic potential but also by long-term environmental influences. Regarding the non-genetic factors studied in this study, various impacts could well be observed at various stages of sheep growth. These elements have also been shown to be principle factors in earlier studies (Thiruvenkadan et al., 2011; Khosravi et al., 2018; Kumar et al., 2020; Ali et al., 2020; Bangar et al., 2021; Ahmad et al. 2021; Bukhari et al., 2022; Oyieng et al., 2022). The weights of the experimental animals varied considerably by birth year (P < 0.01), with some years performing better than others at certain phases. In terms of year-to-year changes, good precipitation in certain years seems to have a direct and positive influence on feed availability, and vice versa (Prakash et al., 2012; Ali et al., 2020; Ahmad et al. 2021; Bukhari et al., 2022; Oyieng et al., 2022). The weight difference between single and twins was statistically significant at BW, BW3, and BW6 alone, and the previous research has demonstrated that single kids or lambs always outperform their twin born counterparts (Ali et al., 2020; Ahmad et al. 2021; Bukhari et al., 2022; Oyieng et al., 2022) due to the competition for milk among the latter. Furthermore, most dams (ewes) may have been unable to provide sufficient milk for their twin lambs. Single-born Mecheri lambs were only marginally heavier than twin lambs at 9 and 12 months, albeit this difference was not significant (P > 0.05) and indicated a time of accelerated growth, particularly after a period of poor growth. Other studies have found that twins frequently overcome the circumstance of limited milk supply (an early disadvantage) from ewes as they mature, minimising their reliance on dam's milk (Ahmad et al. 2021; Bukhari et al., 2022; Oyieng et al., 2022). The significant

#### Table 4 Components of (co)variances and correlations between growth characteristics

Trait		$Mean \pm SD$	CI		$Mean \pm SD$	CI		Naïve SE	Time series SE	
			2.5%	97.5%		2.5%	97.5%			
Additive direct genetic covariance				Additive direct genetic correlation						
BW	WW	$0.10 \pm 0.027$	0.049	0.156	$0.63 \pm 0.112$	0.377	0.816	0.002	0.008	
BW	BW6	$0.04 \pm 0.037$	-0.022	0.122	$0.25 \pm 0.206$	-0.173	0.616	0.004	0.022	
BW	BW9	$0.06 \pm 0.050$	-0.041	0.160	$0.24 \pm 0.207$	-0.230	0.603	0.004	0.022	
BW	BW12	$0.04 \pm 0.051$	-0.053	0.145	$0.17 \pm 0.226$	-0.292	0.569	0.005	0.025	
WW	BW6	$0.65 \pm 0.265$	0.198	1.247	$0.70 \pm 0.145$	0.320	0.885	0.003	0.020	
WW	BW9	$0.76 \pm 0.345$	0.163	1.506	$0.57 \pm 0.171$	0.161	0.835	0.003	0.020	
WW	BW12	$0.64 \pm 0.344$	0.051	1.386	$0.50 \pm 0.194$	0.053	0.809	0.004	0.022	
BW6	BW9	$1.17 \pm 0.486$	0.417	2.242	$0.90 \pm 0.052$	0.767	0.973	0.001	0.005	
BW6	BW12	$0.99 \pm 0.452$	0.318	1.965	$0.79 \pm 0.112$	0.542	0.968	0.002	0.014	
BW9	BW12	$1.57 \pm 0.695$	0.571	3.094	$0.88 \pm 0.075$	0.691	0.975	0.001	0.011	
Maternal genetic covariance					Maternal geneti	c correlation	L			
BW	WW	$0.04 \pm 0.016$	0.010	0.070	$0.42 \pm 0.136$	0.133	0.651	0.003	0.011	
BW	BW6	$0.02 \pm 0.021$	-0.019	0.061	$0.15 \pm 0.149$	-0.163	0.421	0.003	0.010	
BW	BW9	$0.03 \pm 0.029$	-0.025	0.086	$0.16 \pm 0.145$	-0.146	0.429	0.003	0.010	
BW	BW12	$0.01 \pm 0.030$	-0.045	0.071	$0.06 \pm 0.152$	-0.244	0.350	0.003	0.010	
WW	BW6	$0.40 \pm 0.117$	0.192	0.649	$0.71 \pm 0.094$	0.485	0.857	0.002	0.008	
WW	BW9	$0.46 \pm 0.143$	0.197	0.767	$0.58 \pm 0.113$	0.329	0.772	0.002	0.009	
WW	BW12	$0.40 \pm 0.145$	0.137	0.699	$0.49 \pm 0.133$	0.210	0.726	0.003	0.010	
BW6	BW9	$0.99 \pm 0.232$	0.589	1.486	$0.86 \pm 0.046$	0.755	0.930	0.001	0.004	
BW6	BW12	$0.91 \pm 0.222$	0.517	1.405	$0.78 \pm 0.066$	0.631	0.887	0.001	0.005	
BW9	BW12	$1.33 \pm 0.329$	0.769	2.046	$0.81 \pm 0.057$	0.671	0.898	0.001	0.004	
Residual	covariance				Residual correlation					
BW	WW	$0.09 \pm 0.020$	0.056	0.132	$0.18 \pm 0.034$	0.112	0.246	0.001	0.002	
BW	BW6	$0.17 \pm 0.028$	0.110	0.219	$0.24 \pm 0.038$	0.164	0.315	0.001	0.003	
BW	BW9	$0.18 \pm 0.040$	0.100	0.259	$0.20 \pm 0.043$	0.120	0.289	0.001	0.003	
BW	BW12	$0.19 \pm 0.042$	0.112	0.275	$0.22 \pm 0.045$	0.131	0.306	0.001	0.003	
WW	BW6	$2.86 \pm 0.205$	2.464	3.270	$0.66 \pm 0.024$	0.606	0.701	0.000	0.002	
WW	BW9	$2.51 \pm 0.264$	1.995	3.032	$0.45 \pm 0.035$	0.379	0.517	0.001	0.003	
WW	BW12	$2.25 \pm 0.276$	1.705	2.777	$0.40 \pm 0.039$	0.320	0.467	0.001	0.003	
BW6	BW9	$5.89 \pm 0.396$	5.090	6.641	$0.80 \pm 0.014$	0.770	0.824	0.000	0.001	
BW6	BW12	$5.22 \pm 0.384$	4.457	5.958	$0.70 \pm 0.021$	0.655	0.737	0.000	0.001	
BW9	BW12	$8.14 \pm 0.576$	6.967	9.224	$0.85 \pm 0.013$	0.826	0.876	0.000	0.001	

BW, birth weight; WW, weaning weight; BW6, 6-month weight; BW9, 9-month weight; BW12, 1-year-old weight; CI, credibility interval

effect of ewe body weight regression on body weight characters could be related to the strong influence of sheep body condition scores on Mecheri lamb birth weight and is in accordance with the reports of Bukhari et al. (2022) in Bakarwal and its crossbred sheep populations as well as Oyieng et al. (2022) in Red Maasai and its crossbreds. The strong impact of maternal age on growth traits is likely connected to the ewes' bodyweight, reproductive system, level of physical development, and increased milk production as ewes mature. Due to their insufficient physical development, younger ewes spend a portion of the nutrients they get on their own physical growth, which is detrimental to the development of the foetus and the production of ewe's milk (Shahroudi et al., 2002).

#### Estimation of genetic effects and parameters

The direct heritability estimate obtained for Mecheri sheep for birth weight (i.e. 0.21) agrees with the previous reports in different sheep breeds (Prakash et al., 2012; Gowane et al., 2015; Arthy et al., 2018, Ambike et al., 2022). However, lower (Javed et al., 2013; Amarilho-Silveira et al., 2017; Kumar et al., 2017, 2020; Bangar et al., 2021; Dhakad et al., 2022) and higher (Prince et al., 2010; Singh et al., 2016; Habtegiorgis et al., 2022) than the current values were also observed in various sheep breeds. Reduced phenotypic variation might explain the medium direct heritability estimate in birth weight. According to a direct estimate of the heritability



Fig. 1 Correlation between different stages of growth

of birth weights derived from Mecheri sheep, breeding is likely to enhance birth weights.

Direct estimates of the heritability of WW (0.21) in Mecheri sheep are congruent with published values (Mandal et al., 2006; Gizaw et al., 2007; Prince et al., 2010; Prakash et al., 2012; Jawasreh et al., 2018). These findings revealed that there was enough direct additive genetic variance for weaning weight and that would yield optimal results when employed in selection programmes, if no undesirable correlation exists with other economic traits. Estimates higher than the current values were reported for different sheep breeds (Rashidi et al., 2008; Eskandarinasab et al., 2010; Ahmad et al. 2021; Dhakad et al., 2022; Habtegiorgis et al., 2022). In addition, various authors have reported lower than the current values (Javed et al., 2013; Gowane et al., 2015; Eskandarinasab et al., 2010; Tesema et al., 2020). The higher or lower heritability in different research can be attributed to the huge influence of the environment as well as higher or lower estimates of non-additive genetic effects (Jawasreh et al. 2018; Tesema et al. 2020). After analysing the heritability of numerous variables under different breed, it was discovered that selecting lambs based on their live weight at 3 months of age (weaning age) resulted in the best genetic improvement (Ghaderi-Zefrehei et al., 2021; Ahmad et al. 2021; Dhakad et al., 2022; Habtegiorgis et al., 2022; Oyieng et al., 2022).

Maternal additive genetic variation for birth weight was minimal, but weaning weights were comparatively lower, which is consistent with earlier results on several sheep breeds (Jalil-Sarghale et al., 2014; Ali et al., 2020; Kumar et al., 2020; Ghaderi-zefrehei et al., 2021). In addition to the genetic influence of the mother, maternal influences that primarily take into account the uterine environment supplied by the dam as well as nursing behaviour till weaning have been given serious consideration. The milk productivity of Mecheri sheep is insufficient to meet the needs of the fast-growing sheep, so the addition of the concentrate was implemented from 2 months of age. Under these conditions, milk production in ewes decreases rapidly and can lead to lower levels of maternal heritability at weaning. This implied that the contribution of maternal influences in phenotypic variation is anticipated to diminish with increasing lamb age due to the decrease in lamb dependency on the mother, and as a result, the ratio of permanent maternal environmental variance to phenotypic variance reduced.

The lower heritability estimates of post-weaning traits observed in Mecheri sheep is in agreement with the reports of Mokhtari et al. (2008), Shahdadi and Saghi (2016), and Ahmad et al. (2021) in Kermani, Kourdi, and Corridale sheep populations. This indicated that the post-weaning growth traits in Mecheri sheep were much affected by permanent environmental effects, and therefore, in order to enhance the performance of post-weaning characteristics in Mecheri sheep, more attention should be paid to modifying the effect of non-genetic factors such as improving environmental conditions along with managerial and nutritional needs. The higher estimates of direct heritability at post-weaning ages than those observed in Mecheri sheep were reported for Chokla (Kushwaha et al., 2009), Avikalin (Prince et al., 2010), Marwari (Singh et al., 2016), Malpura (Gowane et al., 2015), and Nellore (Kumar et al., 2020) sheep of India as well as Ghaderi-Zefrehei et al. (2021) in Lori-Bakhtiari sheep. The differences in estimates for the weights across studies might be also influenced by the model used to analyse sheep breeds, the structure and volume of information available to estimating variance components, differences in multiple herd management, and different breeding programmes (Kamjoo et al. 2014). The maternal heritability for post-weaning traits in Mecheri sheep was low and might be due to decreased maternal genetic variance at different stages and is in accordance with earlier reports on varied sheep breeds (Bahreini Behzadi et al., 2007; Singh et al., 2016; Kumar et al., 2020; Oyieng et al., 2022).

In general, the direct heritabilities decreased with the increasing age in the current study as well as in other investigations (Jawasreh et al., 2018; Tesema et al., 2020; Ghaderi-Zefrehei et al., 2021; Habtegiorgis et al., 2022). This might be attributable to greater environmental variability after weaning. After weaning, the Mecheri sheep were allowed to graze as a small flock, exposing them to a range of environmental conditions with varying fodder availability (Kumar et al., 2020). Low heritability for post-weaning traits in Mecheri lambs signified that the majority of variation in this trait are due to factors other than the lamb's additive genetic makeup. Environmental variables play a significant role in the variability in lamb post-weaning traits. As a result, phenotypic selection may not be advantageous based on these traits and the benefits arising would require several generations of rigorous selection.

#### **Correlation between the traits**

Estimate of correlation (genetic) between BW and WW in Mecheri sheep was positive and high, and the estimates were higher than the values of 0.56 for Columbia (Hanford et al., 2002), 0.43 for Corridale (Ahmad et al. 2021), and 0.54 for Red Maasai (Oyieng et al., 2022) breeds of sheep. The high genetic association between BW and WW suggested that both variables are governed by genetic and physiological mechanisms that are similar. Selection for BW can lead to considerable improvements in WW, modest improvements in weights at marketing age (BW6 and BW9), and slight improvement in BW12. However, direct selection for greater BWT may result in more difficult births and is also impacted by maternal effects that must be considered. The genetic correlation between the WW and BW6 was positive and high (0.70) and is higher than the value of 0.35 for Doyogena (Habtegiorgis et al., 2022) and 0.52 for Lori sheep (Mohammadi et al., 2015). Ahmad et al. (2021) reported a much higher value of 0.913 for Corridale sheep. Due to the substantial genetic relationship between these two variables, it would be better to record WWT and utilise it for post-weaning body weight improvement programmes. As a consequence, the time and money spent on data collection and genetic analysis will be saved, resulting in accelerated progression through the breeding programme.

As predicted, the genetic component between sequential attributes was greater than the genetic correlation between non-consecutive traits and the observed trend is in agreement with estimates from earlier studies (Mohammadi et al., 2010; Javed et al., 2013; Ahmad et al. 2021; Oyieng et al., 2022). The maternal genetic correlation estimates for different traits were positive and slightly higher than the values reported for Mehraban sheep (Gamasaee et al., 2010). The maternal correlation observed in the current study was lower than the direct additive genetic correlation in all the growth traits studied. As lamb age grows, the contribution of maternal impacts on phenotypic variation is projected to diminish, and therefore, the ratio of permanent maternal environmental variance to phenotypic variance decreases.

# Conclusion

In general, the research of the effect of environmental variables revealed that fixed factors have a considerable impact on the phenotypic occurrence of growth traits. The heritability for different body weight traits ranged between low (BW6, BW9, and BW12) and medium (BW and WW). Due to the facts that post-weaning weights are lowly heritable, more emphasis should be placed on better environmental conditions, as well as managerial and nutritional requirements. Additionally, indirect selection based on traits with high heritability and genetically correlated with post-weaning weight traits may be beneficial. A strong positive genetic correlation between WW and BW6 indicated that the improvement in WW trait will lead to improvement in other traits. Therefore, Mecheri lambs will respond better to selection if they are bred for weight at weaning age than at the current selection methods (i.e. weight at six-month of age). For optimal breeding programme design, population or breed-specific genetic and phenotypic variables are necessary. The current genetic parameter estimations for Mecheri sheep will aid in the construction of a viable breeding programme in a semi-arid environment for continued genetic improvement.

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**Data availability** The authors declare that the raw data used to elaborating this paper will not be available to the readers of this research paper. However, in case of any interest by some researcher or reader, the authors will share the raw data with them.

Code availability Not applicable.

#### Declarations

Ethics approval Not applicable.

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Competing interests The authors declare no competing interests.

#### References

- Ahmad, S.F., Khan, N.N., Ganai, N.A., Shanaz, S., Rather, M.A. and Alam, S., 2021. Multivariate quantitative genetic analysis of body weight traits in Corriedale sheep. Tropical Animal Health and Production, 6;53(2):197. https://doi.org/10.1007/ s11250-021-02632-3
- Ali, A., Javed, K., Zahoor, I. and Anjum, K.M., 2020. Analysis of non-genetic and genetic influences underlying the growth of Kajli lambs. South African Journal of Animal Sciences, <u>50</u>, 613-625, https://doi.org/10.4314/sajas.v50i4.13.
- Amarilho-Silveira, F., Dionello, N.J.L., Mendonça, G. De, Motta, J.F., Fernandes, T.A. and Silva, N.D.S., 2017. Genetic components of birth weight of Texel sheep reared in extensive system. Acta Scientiarum. Animal Sciences, https://doi.org/10.4025/ actascianimsci.v40i0.36481
- Ambike, V., Venkataramanan, R., Karthickeyan, S.M.K. and Tirumurugaan, K.G., 2022. Meta-analysis of performance and genetic parameter estimates for growth and body weight traits of sheep in the tropics. Small Ruminant Research, 206, 106597, ISSN 0921–4488, https://doi.org/10.1016/j.smallrumres.2021.106597.
- Arthy, V., Venkataramanan, R., Sivaselvam, S.N., Sreekumar, C. and Balasubramanyam, D., 2018. Genetic evaluation of growth in farmers' flocks of Madras Red sheep under long-term selection in a group breeding scheme. Tropical Animal Health and Production, https://doi.org/10.1007/s11250-018-1581-z
- Bahreini Behzadi, M.R., Shahroudi, F.E. and Van Vleck, L.D., 2007. Estimates of genetic parameters for growth traits in Kermani sheep. Journal of Animal Breeding and Genetics, 124, 296–301.
- Bangar, Y.C., Magotra, A., Malik, B.S., Malik, Z.S. 2021. Evaluation of growth curve traits and associated genetic parameters in Harnali sheep. Small Ruminant Research, 195, 106314, ISSN 0921–4488, https://doi.org/10.1016/j.smallrumres.2020.106314
- Bukhari, S., Ganai, N.A., Shanaz, S., Khan, H.M., Rather, M., Khan, N., Mir, V., Alam, S., Shah, R. and Mir, S., 2022. Effect of breed and some non-genetic factors on growth performance of sheep under temperate conditions of Kashmir. Small Ruminant Research, 215, 106728, ISSN 0921–4488, https://doi.org/10. 1016/j.smallrumres.2022.106728.
- Devi, S,M., Balachandar, V., Lee, S.I. and Kim, I.H. 2014. An Outline of Meat Consumption in the Indian Population - A Pilot Review.

Korean Journal of Food Science Animal Resources, 34(4):507-15. https://doi.org/10.5851/kosfa.2014.34.4.507

- Dhakad, G.S., Saini, S., Mallick, P.K., Misra, S.S., Gowane, G.R., Sharma, S., Prakash, V., Kumar, A., Mahala, S. and Singh, N. 2022. Elucidating genotype by environment interaction over the growth trajectory of Malpura sheep in the semi-arid region of India through Random regression model, Small Ruminant Research, 216, 2022, 106791, ISSN 0921-4488, https://doi.org/ 10.1016/j.smallrumres.2022.106791.
- Eskandarinasab, M., Ghafouri-Kesbi, F., Abbasi, M.A., 2010. Different models for evaluation of growth traits and Kleiber ration in an experimental flock of Iranian fat-tailed Afshari sheep. Journal of Animal Breeding Genetics, 127, 26–33.
- Gamasaee, V.A., Hafezian, S.H., Ahmadi, A., Baneh, H., Farhadi, A. and Mohamadi, A., 2010. Estimation of genetic parameters for body weight at different ages in Mehraban sheep. African Journal of Biotechnology, 9(32): 5218-5223.
- Gelfand, A.E. and Smith, A.F.M., 1990. Sampling-Based Approaches to Calculating Marginal Densities. Journal of American Statistics Association, 85, 398-409.
- Geman, D. and Geman, S., 1984. Stochastic relaxation, Gibbs distributions, and the Bayesian restoration of images. IEEE Trans Pattern Anal Mach Intell. 6, 721-741.
- Ghaderi–Zefrehei, M., Safari, A., Moridi, M. Khanzadeh, H. and Rashidi Dehsaraei, A.R 2021.. Bayesian estimate of genetic parameters for growth traits in Lori Bakhtiari sheep. Tropical Animal Health and Production, 53, 457 (2021). https://doi.org/ 10.1007/s11250-021-02900-2
- Ghavi Hossein-Zadeh, N., 2015. Estimation of genetic relationships between growth curve parameters in Guilan sheep. *Journal of Animal Science* and *Technology*, 57, 19. doi:https://doi.org/10. 1186/s40781-015-0052-6
- Ghavi Hossein-Zadeh, N., 2017. Estimates of genetic parameters and genetic trends for production and reproduction traits in Iranian buffaloes (Bubalus bubalis). Animal Production Science, 57, 216–222.
- Ghavi Hossein-Zadeh, N and Ardalan M., 2010. Estimation of genetic parameters for body weight traits and litter size of Moghani sheep, using a Bayesian approach via Gibbs sampling. The Journal of Agricultural Science, 148, 363–70.
- Gizaw, S., Lemma, S., Komen, H. and Johan, A.M. 2007. Estimates of genetic parameters and genetic trends for live weight and fleece traits in Menz sheep. Small Ruminant Research, 70: 145-153
- Gowane, G.R., Prince, L.L.L., Lopes, F.B., Paswan, C. and Sharma, R.C., 2015. Genetic and phenotypic parameter estimates of live weight and daily gain traits in Malpura sheep using Bayesian approach. Small Ruminant Research, 128, 10–18.
- Habtegiorgis K., Haile, A., Getachew, T., Kirmani, M.A. and Gemiyo, D. 2022. Analysis of genetic parameters and genetic trends for early growth and reproductive traits of Doyogena sheep managed under community-based breeding program. Heliyon, 18;8(6):e09749. https://doi.org/10.1016/j.heliyon.2022.e09749.
- Hanford, K.J., Van Vleck, L.D. and Snowder, G.D., 2002. Estimates of genetic parameters and genetic change for reproduction, weight, and wool characteristics of Columbia sheep. Journal of Animal Science, 80, 3086–3098.
- Jalil-Sarghale, A., Kholghi, M., Moradi Shahrebabak, M., Moradi Shahrebabak, H., Mohammadi, H. and Abdollahi-Arpanahi, R.,2014. Model comparisons and genetic parameter estimates of growth traits in Baluchi sheep. Slovak Journal of Animal Science, 47, 12-18.
- Javed, K., Iram, A., Abdullah, M., Sattar, M.A. and Akhtar, M., 2013. Genetic trends for some productive traits of Lohi sheep in Pakistan. Pakistan Journal of Science, 65, 492-495.
- Jawasreh, K., Ismail, Z.B., Iya, F., Castaneda-Bustos, V.J., Valencia-Posadas, M., 2018. Genetic parameter estimation for preweaning growth traits in Jordan Awassi sheep. Veterinary world, 11(2), 254.

- Jeichitra, V., Rajendran, R., Karunanithi, K. and Rahumathulla, P.S., 2016.Genetic analysis of growth traits in Mecheri sheep. Indian Journal of Animal Research, 50, 430-433.
- Kamjoo, B., Baneh, H., Yousefi, V., Mandal, A., Rahimi, G., 2014. Genetic parameter estimates for growth traits in Iran-Black sheep. Journal of Applied Animal Research, 42(1), 79-88.
- Karunanithi, K., Purushothaman, M.R., Thiruvenkadan, A.K., Gurmej Singh, Sadana, D. K. and Murugan, M., 2005. Breed characteristics of Mecheri sheep. Animal Genetic Resource Information, 37, 53-62.
- Khosravi, S., Asadi Fozi, M., Esmaili Koshkooyeh, A., 2018. Evaluation of Genetic Progress of Growth Traits in Kermani Sheep Breeding Station. Research On Animal Production (Scientific and Research), 8(18), 187-193.
- Kizilkaya, K., Garrick, D.J., Fernando, R.L., Mestav, B. and Yildiz, M.A.,2010. Use of linear mixed models for genetic evaluation of gestation length and birth weight allowing for heavy-tailed residual effects. Genetics Selection Evolution, 42, 26 (2010). https://doi.org/ 10.1186/1297-9686-42-26.
- Kumar, S., Kumar, V., Gangaraju, G., Nath, S. and Thiruvenkadan, A.K., 2017. Estimates of direct and maternal (co) variance components as well as genetic parameters of growth traits in Nellore sheep. Tropical Animal Health and Production, 49, 1431–1438. https://doi.org/10. 1007/s11250-017-1344-2.
- Kumar, S. I.,Gangaraju, G., Lopes, F.P., Nath, S. and Thiruvenkadan, A.K., 2020. Multi trait genetic evaluation of growth traits in Nellore sheep raised on pasture in semi-arid regions of India using Bayesian approach. Small Ruminant Research, 106224. 10.106/J. smallrumresearch.2020.106224.
- Kushwaha, B.P., Mandal, A., Arora, A.L., Kumar, R., Kumar, S. and Notter, D.R., 2009. Direct and maternal (co) variance components and heritability estimates for body weights in Chokla sheep. Journal of Animal Breeding and Genetics, 126, 278–287.
- Mandal, A., Neser, F.W.C., Rout, P.K., Roy, R. and Notter, D.R., 2006. Estimation of direct and maternal (co) variance components for pre-weaning growth traits in Muzaffarnagari sheep. Livestock Science, 99, 79–89.
- Misztal, I., Tsuruta, S., Lourenço, D., Aguilar, I., Legarra, A. and Vitezica, Z., 2018. Manual for BLUPF90 Family of Programs. http://nce. ads.uga.edu/wiki/lib/exe/fetch.php?media=blupf90\_all7.pdf
- Mohammadi, Y., Rashidi, A., Mokhtari, M.S. and Esmailizadeh, A.K., 2010. Quantitative genetic analysis of growth traits and Kleiber ratios in Sanjabi sheep. Small Ruminant Research, 93, 88-93.
- Mohammadi, K., Abdollahi-Arpanahi, R., Amraei, F., Mohamadi, E.M., Rashidi, A., 2015. Genetic parameter estimates for growth and reproductive traits in Lori sheep. Small Ruminant Research, 131, 35–42. https://doi.org/10.1016/j.smallrumres.2015.07.029.
- Mokhtari, M.S., Rashidi, A. and Mohammadi, Y., 2008. Estimation of genetic parameters for post-weaning traits of Kermani sheep. Small Ruminant Research, https://doi.org/10.1016/j.smallrumres.2008.08.002
- Oyieng, E., Mrode, R., Ojango, J.M.K., Ekine-Dzivenu, C.C., Audho, J. and Okeyo, A.M., 2022. Genetic parameters and genetic trends for growth traits of the Red Maasai sheep and its crosses to Dorper sheep under extensive production system in Kenya. Small Ruminant Research 206: 106588.
- Peters, S., Kizilkaya, K., Garrick, D., Fernando, R., Pollak, E., Enns, R., De Donato, M., Ajayi, O. and Imumorin, I., 2014. Use of robust multivariate linear mixed models for estimation of genetic parameters

for carcass traits in beef cattle. Journal of Animal Breeding Genetics, 131: 504-512. https://doi.org/10.1111/jbg.12093

- Prakash, V., Prince, L.L.L., Gowane, G.R. and Arora, A.L., 2012. The estimation of (co)variance components and genetic parameters for growth traits and Kleiber ratios in Malpura sheep of India. Small Ruminant Research, 108,54–58.
- Pretorius, A.L. and van der Merwe, A.J., 2000. A nonparametric Bayesian approach for genetic evaluation in animal breeding. South African Journal of Animal Science, 30, 138-140.
- Prince, L.L.L., Gowane, G.R., Chopra, A. and Arora, A.L., 2010. Estimates of (co) variance components and genetic parameters for growth traits of Avikalin sheep. Tropical Animal Health and Production, 42, 1093–1101.
- Rashidi, A., Mokhtari, M.S., Safi Jahanshahi, A., Mohammad Abadi, M.R., 2008. Genetic parameter estimates of pre-weaning growth traits in Kermani sheep. Small Ruminant Research, 74, 165–171.
- Shahdadi, A.R. and Saghi, D.A., 2016. Estimating genetic parameters of body weight traits in Kourdi sheep. Iranian Journal of Applied Animal Science, 6, 657–663
- Shahroudi, E., Bahrini, M., Doulk, V., Mesgaran, M.D., 2002. The factor affecting some economical traits in Kermani sheep. Iranian Journal of Agriculture Science, 33(3), 395-402.
- Singh, H., Pannu, U., Narula, H.K., Chopra, A., Naharwara, V. and Bhakar, S.K., 2016. Estimates of (co) variance components and genetic parameters of growth traits in Marwari sheep. Journal of Applied Animal Research, 44, 27–35.
- Statistical Analysis System (SAS), 2009. User's Guide. SAS Institute, Cary, NC, Version 9.2.
- Tesema, Z., Alemayehu, K., Getachew, T., Kebede, D., Deribe, B., Taye, M., Tilahun, M., Lakew, M., Kefale, A., Belayneh, N., Zegeye, A., Yizengaw, L., 2020. Estimation of genetic parameters for growth traits and Kleiber ratios in Boer x Central Highland goat. Tropical Animal Health and Production, 52, 3195–3205.
- Thiruvenkadan, A. K., Karunanithi, K., Muralidharan, J. and Narendra Babu, R., 2011.Genetic Analysis of Pre-weaning and Post-weaning Growth Traits of Mecheri Sheep under Dry Land Farming Conditions. Asian-Australasian Journal of Animal Science, 24, 1041 – 1047.
- Thiruvenkadan A. K., Muralidharan, J., Rajendran, R., Msalya, G.M. 2022. Assessment of growth and population structure revealed sufficient genetic diversity among lambs of Mecheri sheep in Tamil Nadu, India, Small Ruminant Research, 216, 106781, ISSN 0921-4488, https://doi.org/10.1016/j.smallrumres.2022.106781.
- Thiruvenkadan, A.K., Arun, L., Rajkumar, R., Misra, S.S., Prince, L.L.L. and Arun Kumar, 2017. Mecheri Sheep - A Monograph. Tamil Nadu Veterinary And Animal Sciences University Chennai – 600 051, Tamil Nadu & Indian Council Of Agricultural Research, New Delhi.

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