



Genetic evaluation of growth in farmers' flocks of Madras Red sheep under long-term selection in a group breeding scheme

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Abstract

The Network Project on Sheep Improvement (NWPSI)–Madras Red field unit is a group breeding scheme involving 198 farmers' flocks of Madras Red sheep in which selection for growth traits and rotation of rams have been practised for over two decades. Growth data collected from these flocks were used to evaluate the performance and understand the direct and expected responses to selection based on genetic parameters. The body weight at birth (BW), weaning weight (WW), 6-month weight (6W), 9-month weight (9W), 12-month weight (YW), pre-weaning average daily gain (ADG1, birth to 3 months), post-weaning ADG2 (3–6 months), ADG3 (6–9 months), ADG4 (9–12 months) and ADG5 (3–12 months) were 2.67, 10.05, 14.56, 18.36, 21.36, 80.13, 49.05, 43.00, 34.21 and 41.18 g, respectively. Univariate analyses were carried out using animal and sire models to estimate variance components. Heritability obtained from animal model for BW was 0.36 and the values for other body weight traits were almost unity. Heritability estimate for pre-weaning ADG1 was 0.31. Very high genetic variability was observed in spite of long-term selection and this sustenance of variability is one of the main advantages of a group breeding scheme, combining several flocks of smaller size. An increasing genetic and phenotypic trend was noticed for almost all the traits studied. The expected responses calculated based on genetic parameters also indicated scope for improvement.

Keywords Long-term selection · Genetic parameters · Breeding value · Genetic trend · Response to selection

Introduction

Madras Red sheep is a medium-sized hairy sheep well adapted to the hot and humid conditions of the northeastern agro-climatic region of Tamil Nadu (Acharya 1982). It is a meat-type breed mainly distributed in Thiruvallur, Kancheepuram, Chennai, Vellore and Villupuram districts of Tamil Nadu (Raman et al. 2003). This sheep serves as a source of livelihood for several small, marginal and landless livestock farmers. The only way to increase the profit is by increasing the growth rate, which is possible through genetic improvement.

The ICAR–Network Project on Sheep Improvement (NWPSI) jointly funded by the Indian Council of Agricultural

Research (ICAR) and Tamil Nadu Veterinary and Animal Sciences University (TANUVAS) has been functioning at the Postgraduate Research Institute in Animal Sciences (PGRIAS) for over two decades, with the main objective of conservation and genetic improvement of Madras Red breed of sheep in their native locality. This is a group breeding scheme involving 198 farmers' flocks of Madras Red sheep, in which selection and rotation of rams is practised. Farmers owning a flock strength of 30 to 40 breedable ewes are identified and provided with breeding rams selected for body weight. The main criteria for selection of breeding rams was 6-month body weight.

The evaluation of performance under actual conditions of rearing is important for overall improvement of the trait under any long-term breeding programme. However, lack of documented information due to difficulty in recording has resulted in paucity of studies of this nature. Data from the field flocks, even when available, usually does not fulfil all the requirements for various statistical estimation methods. In sheep, growth traits such as body weight and average daily gains are the important response indicators. The objective of this study is to evaluate the growth performance of Madras Red sheep under extensive system of management in field

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condition and to estimate genetic parameters for different growth traits.

Materials and methods

The present study on the growth performance of Madras Red sheep was based on data obtained from 198 field flocks of

Madras Red sheep, born to the elite rams supplied through the NWPSI. Data on animal identity, date of birth, sire, sex, age on day of weightment, village, farmer and weights at various ages of progenies in the beneficiary flocks of NWPSI, for the period 1993 to 2017 (25 years), was utilised. Information on 48,699 progenies born to 502 sires was available, while there was no maternal information. The mean number of progeny per sire was 52.23 (SD = 48.8).

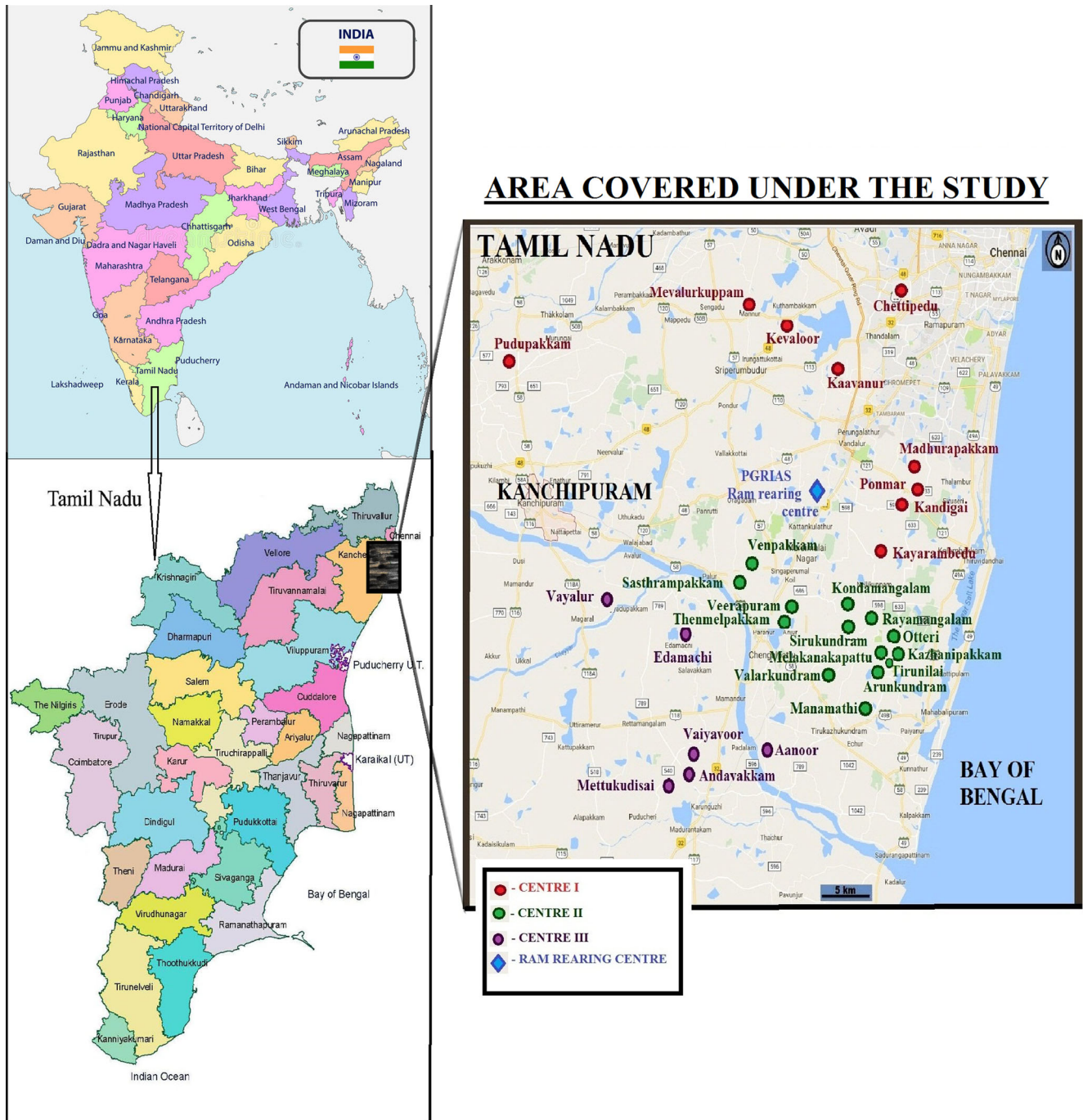


Fig. 1 Map of villages covered under the Network Project on Sheep Improvement

The NWPSI has been functioning in 29 villages (Fig. 1) of Kancheepuram district. The area of coverage was classified into three centres and one ram-rearing centre (PGRIAS).

The area of study has a hot and humid climate with a mean temperature varying from 19.69 °C in January to 37.53 °C in May. The relative humidity ranges from 51.19 to 66.65% and is found to be the highest during the month of December. The area receives rain from both the southwest and northeast monsoons, with maximum rainfall during the latter. The average annual rainfall recorded in the region was 105.23 cm (source: Regional Meteorology Centre, Chennai).

The technical programme of the scheme involves:

- i. Rearing of the rams in ram-rearing centre and distributing them to the field flocks for breeding
- ii. Performance recording of the progenies born to the breeding rams
- iii. 20% of the rams are replaced by superior rams procured from the registered field flocks selected based on 6-month body weight.
- iv. Rotation of rams is followed once in 2 years, among the beneficiary flocks to avoid inbreeding.

The body weight traits studied were weight at birth (BW), weaning (WW), 6-month (6W), 9-month (9W) and 12-month (YW) of age. The weaning age of the lambs was 3 months and 6W was the main criteria for selection. Since it is a field breeding programme, it is impractical to obtain weights of the progenies exactly at specific ages and the variation in age at measurement of weight was adjusted to obtain body weight at specific ages based on the weight gain of individual animals. The range of ages in days used for arriving at BW, WW, 6W, 9W and YW were < 7, 75 to 105, 165 to 195, 255 to 285 and 350 to 380 days. Thus, different subsets of data available for analysis of different growth traits varied in number of records. The adjusted body weights were used to derive average daily weight gain (ADG) for pre-weaning (ADG1, birth to 3 months) and post-weaning periods (ADG2, 3–6 months; ADG3, 6–9 months; ADG4, 9–12 months and ADG5, 3–12 months).

Centre, season, sex and period were the non-genetic sources of variation studied. The villages in each centre were identified based on location as shown in Fig. 1. Centre 1, located close to Chennai city, had less pasture compared to the centres 2 and 3 where the villages had natural grazing lands and irrigated cultivable lands as well. The period of 25 years was divided into six classes with 4 years each in the first five classes and 5 years in the last class. Seasons were identified based on the meteorological data collected from the Regional Meteorology Centre, Chennai. Months with uniform temperature, rainfall and humidity which were classified as one season and three classes viz. March to June, July to October and November to February were formed. Temperature was maximum during the months of March to June and minimum during the months of November to February.

Rainfall in the region begins during southwest monsoon and green pasture in natural range lands is available after June.

Statistical analysis

From the base data, 1055 records were removed as biological outliers leaving a final data set with 47,644 records. Data was screened for outliers and records over and below 3 SD from the arithmetic mean for each trait were removed. Single trait analyses for each body weight trait were carried out by fitting a general linear model (GLM) to study the effect of various non-genetic factors on each of the trait.

Estimation of variance components and genetic parameters

(Co)variance components for calculation of genetic parameters were estimated by fitting animal and sire models. The fixed effects found to be significant through GLM as described above were included in the mixed model. All the non-genetic sources of variation included in the study namely the centre, season, sex and period had a significant influence on all the traits studied and hence were included in the models for estimation of variance components using restricted maximum likelihood (REML) method of estimation. The software used was WOMBAT (Meyer 2007). The performance recording was in field flocks of sheep and information was available only on the sires. Relationship among sires were ignored as the farmers did not follow any identification system and the only relationship available for the animals was half sib.

Statistical models

$$Y = Xb + Z_a a + e \quad (\text{model 1})$$

$$Y = Xb + Z_s s + e \quad (\text{model 2})$$

where ‘Y’ is an $N \times 1$ vector of records, ‘b’ denotes the fixed effects in the model with association matrix X, ‘a’ is the vector of animal genetic effects with the association matrix Z_a , ‘s’ is the vector of sire effects with the association matrix Z_s and ‘e’ denotes the vector of residual (temporary environment) effect. The fixed effects included in the model were those found to have significant effect in the initial least squares analyses.

For the animal model, animal genetic effect, ‘a’ was assumed to be normally distributed with mean 0 and variance $A\sigma_a^2$, where A is the additive numerator relationship matrix and σ_a^2 , the additive genetic variance. For the sire model, sire effect was assumed to be normally distributed with mean 0 and variance $I_s\sigma_s^2$ where I_s an identity matrix with order equal to the number of sires and σ_s^2 is the sire variance. The residual effect was assumed to be normally distributed with mean 0 and variance $I_n\sigma_e^2$, where I_n is an identity matrix with order equal to the number individual records and σ_e^2 is the residual variance.

Starting values of variance components for the iterations were decided based on the total phenotypic variation and estimates available for the population in literature. The convergence criterion for REML iterations was based on change in log likelihood ($< 5 \times 10^{-4}$), change in vector of parameters ($< 10^{-8}$) and change in norm of gradient vectors ($< 10^{-3}$), the details of which are provided by Meyer (2007).

Heritability estimates of direct additive genetic effect (h^2) were calculated as ratio of estimates of additive genetic variance (σ^2_a) to total phenotypic variance (σ^2_p). Heritability from sire variance was estimated using the formula

$$h^2 = \frac{4\sigma^2_s}{\sigma^2_s + \sigma^2_e}$$

Bivariate analyses including all possible combinations of growth traits were done to obtain genetic and phenotypic covariances and correlations. The genetic trend and expected responses to selection for various body weight traits were estimated from the genetic parameters obtained.

Results and discussion

Among the body weight traits, coefficient of variation was highest for weaning weight (13.82) and lowest (8.41) for 9-month weight (Table 1). The least squares mean of BW, WW, 6W, 9W and YW for field flocks of Madras Red sheep were 2.67, 10.05, 14.56, 18.36 and 21.36 kg, respectively. All the non-genetic factors were included in the study as they had a very high influence on all the body weight traits studied.

The means of the efficiency traits ADG1, ADG2, ADG3, ADG4 and ADG5 were 80.13, 49.05, 43.00, 34.21 and 41.18 g, respectively. The growth performance of field flocks of Madras Red sheep was comparable with that of values

reported earlier for the breed (Balasubramanyam and Kumarasamy 2011).

The body weight of Madras Red sheep at various ages was observed to be mostly moderate when compared to the range of body weights among the Indian breeds of sheep and on the higher side when compared to other breeds of Tamil Nadu (Ganesakale and Rathnasabapathy 1973) in terms of production. The maximum overall ADG was observed from birth to 3 months (80.13 g) and the least value was noticed during the period from 9 to 12 months (34.21 g).

Nellore Brown is a breed similar to Madras Red sheep in its phenotype and distributed in parts of the neighbouring state of Andhra Pradesh. The works carried out in this breed bring to light that it has a similar birth weight like that of the Madras Red sheep, while other body weight traits like WW, 6W, 9W and YW were found to be slightly more for Nellore compared to Madras Red breed of sheep (Ekambaram et al. 2013; Reddy et al. 2017).

All the non-genetic sources of variation included in the study namely the centre, season, sex and period had a significant influence on all the traits studied including the average daily weight gains and hence were included in the models. In general, animals born in centres 2 and 3 were found to have better body weights and this could be due to their location away from the urban areas, while poor growth performance in centre 1 could be attributed to urbanisation leading to lesser availability of grazing area than that in centre 2 and centre 3. Madras Red sheep are reared exclusively on grazing, and reduction in grazing area due to urbanisation can lead to poor growth performance. The season July to October was found to have a better influence on the BW and WW, followed by November to February for 6W and 9W and finally March to June for YW. This shows that the animals born in good season will have better body weights at the later ages also. The period from 2013 to 2017 had a better 6W, which is an important

Table 1 Descriptive statistics of growth parameters in field flocks of Madras Red sheep (1993–2017)

	<i>n</i>	Minimum (kg)	Maximum (kg)	Mean (kg)	SD (kg)	Variance (kg ²)	CV (%)
BW	33,208	0.51	4.00	2.74 ± 0.002	0.315	0.099	11.496
WW	36,193	5.28	18.00	10.12 ± 0.007	1.399	1.957	13.824
6W	32,959	8.54	25.00	14.60 ± 0.008	1.541	2.376	10.555
9W	20,900	11.16	29.40	18.26 ± 0.011	1.536	2.360	8.412
YW	16,508	15.15	38.96	20.97 ± 0.014	1.768	3.127	8.431
Average daily gain							
	<i>n</i>	Minimum (g)	Maximum (g)	Mean (g)	SD (g)	Variance (g ²)	CV (%)
ADG1	31,258	26.67	168.89	81.98 ± 0.070	12.450	154.993	15.187
ADG2	29,643	0.89	156.11	49.27 ± 0.063	10.887	118.517	22.097
ADG3	19,955	0.33	128.89	41.61 ± 0.068	9.641	92.943	23.170
ADG4	14,851	0.67	151.11	31.76 ± 0.089	10.818	117.023	34.062
ADG5	14,857	11.52	82.96	41.05 ± 0.039	4.714	22.220	11.484

Table 2 Estimates of (co)variance components and genetic parameters obtained from univariate analysis for body weight traits in field flock of Madras Red Sheep

Model	σ^2_a	σ^2_s	σ^2_e	σ^2_p	$h^2_a \pm \text{S.E.}$	$h^2_s \pm \text{S.E.}$
Birth weight						
Animal	0.030	–	0.054	0.085	0.36 ± 0.029	–
Sire	–	0.0106	0.0779	0.0885	–	0.48 ± 0.040
Weaning weight						
Animal	1.748	–	0.00000046	1.748	1.00 ± 0.039	–
Sire	–	0.343	1.248	1.591	–	0.86 ± 0.048
6-month weight						
Animal	2.336	–	0.0000082	2.336	1.00 ± 0.036	–
Sire	–	0.891	1.528	2.419	–	1.47 ± 0.064
9-month weight						
Animal	2.061	–	0.0000036	2.061	1.00 ± 0.042	–
Sire	–	1.656	1.459	3.115	–	2.13 ± 0.072
12-month weight						
Animal	2.694	–	0.0000055	2.694	1.00 ± 0.044	–
Sire	–	1.832	1.539	3.370	–	2.18 ± 0.072

σ^2_a , additive genetic variance; σ^2_s , sire variance; σ^2_e , error variance; σ^2_p , phenotypic variance; h^2_a , heritability, animal model; h^2_s , heritability, sire model

criteria on which majority of the selection programmes are based upon. The increase in weight in the later years in comparison to the earlier years in a long-term selection programme can be a result of the continuous selection which is being practised over the years (Balasubramanyam et al. 2012).

The (co)variance components and heritability estimates obtained by animal and sire models are presented in Tables 2 and 3.

The large data set utilised in the study has resulted in precise estimates of variance components with very low standard error. Heritability obtained from animal model for BW was 0.36 and the values for other body weight traits were almost unity. Heritability estimate for pre-weaning ADG1 was 0.31. The larger values of genetic variance obtained through animal model could be due to lack of maternal information and incomplete pedigree in a field recording system (not accounting for all relationships).

Table 3 Estimates of (co)variance components and genetic parameters obtained from univariate analysis for ADG in field flock of Madras Red Sheep

Model	σ^2_a	σ^2_s	σ^2_e	σ^2_p	$h^2_a \pm \text{S.E.}$	$h^2_s \pm \text{S.E.}$
ADG1						
Animal	30.510	–	69.585	100.10	0.31 ± 0.022	–
Sire	–	14.572	99.559	114.13	–	0.51 ± 0.040
ADG2						
Animal	51.936	–	42.040	93.976	0.55 ± 0.028	–
Sire	–	46.960	89.806	136.77	–	1.37 ± 0.068
ADG3						
Animal	46.124	–	44.482	90.606	0.51 ± 0.037	–
Sire	–	24.840	81.791	106.63	–	0.93 ± 0.064
ADG4						
Animal	72.869	–	0.00012	72.869	1.00 ± 0.054	–
Sire	–	20.459	53.768	74.227	–	1.10 ± 0.068
ADG5						
Animal	20.139	–	0.00019	20.139	1.00 ± 0.052	–
Sire	–	9.683	15.377	25.061	–	1.54 ± 0.080

σ^2_a , additive genetic variance; σ^2_s , sire variance; σ^2_e , error variance; σ^2_p , phenotypic variance; h^2_a , heritability, animal model; h^2_s , heritability, sire model

The values of sire variance obtained in the present study were high compared to those in earlier studies (Ahmad et al. 2005; Balasubramanyam et al. 2012; Ganesan et al. 2013; Devendran et al. 2014; Reddy et al. 2017). Though the estimates obtained through REML for sire variances were within the parameter space, heritability estimates are obtained as four times of sire variance and thus the traits like 9W, YW, ADG4 and ADG5 had values more than 1 (Weller 2009).

Heritability estimates obtained from the sire model for BW, WW, 6W, 9W, YW, ADG1 and ADG5 were 0.48, 0.47, 0.84, 1.03, 1.27, 0.51 and 1.54, respectively. Other studies in Indian breeds of sheep where half sib correlation was used as method of estimation also were indicative of higher heritability values for growth (Balasubramanyam et al. 2012; Rani 2012; Ganesan et al. 2013; Joshi et al. 2014; Reddy et al. 2017). However, our study showed values even larger than those obtained in these reports. Most of these studies were done under farm conditions, where the sample size was less in comparison to the present study. The present study covered 198 flocks and the period of study was also longer. Moreover, field recording system had the lacunae of incomplete pedigree information and thus complete relationship among the sires could not be utilised. The high variability available in large population of Madras Red sheep covered under the group breeding scheme (Network Project on Sheep Improvement), and variation in number of progeny per sire as indicated by high SD and ignoring relationships due to incomplete pedigree, could be some of the reasons for the large value of heritability. Higher estimate from sire model using paternal half sib method may also be due to the common environmental effect among the half sibs (Burfening and Kress 1993). The main advantage of a group breeding scheme is to sustain genetic variability by maintaining a higher base population, and large values of heritability obtained through this study are a testimony to this fact. The variation is being maintained in spite of continuous selection over a considerable period of time.

The low heritability of birth weight obtained in both the models indicates that additive genetic variance was lower with larger influence of non-genetic factors. Heritability estimates for body weights at various ages tended to increase from birth to adult which is attributed to a certain gene being turned on and off as an animal ages (Meyer 1998). Similar findings were observed in earlier studies on growth in sheep (Cloete et al. 2001; Jeichitra 2009; Farokhad et al. 2010; Balasubramanyam et al. 2012).

Genetic and phenotypic correlations among the body weight traits are presented in Table 4. The values were positive and high except for phenotypic correlation of BW with body weights at later ages. The genetic correlation was found to be positive and high among the weights

Table 4 Genetic and phenotypic correlations (\pm S.E.) among body weights and ADG at different ages from multivariate analyses

Trait	BW	WW	6W	9W	YW	ADG1	ADG2	ADG3	ADG4	ADG5
BW	–									
WW	0.73 \pm 0.030	–								
6W	0.47 \pm 0.049	0.52 \pm 0.008	–							
9W	0.54 \pm 0.045	0.76 \pm 0.022	0.32 \pm 0.012	–						
YW	0.51 \pm 0.049	0.80 \pm 0.021	0.74 \pm 0.006	0.26 \pm 0.015	–					
ADG1	0.59 \pm 0.044	0.67 \pm 0.031	0.85 \pm 0.016	0.81 \pm 0.007	0.23 \pm 0.016	–				
ADG2	–0.08 \pm 0.064	0.99 \pm 0.001	0.77 \pm 0.022	–	0.60 \pm 0.011	0.22 \pm 0.010	–			
ADG3	0.40 \pm 0.060	0.34 \pm 0.050	0.91 \pm 0.010	0.91 \pm 0.011	0.75 \pm 0.010	0.98 \pm 0.000	–0.11 \pm 0.014	–		
ADG4	–0.04 \pm 0.068	–0.14 \pm 0.065	0.59 \pm 0.042	0.83 \pm 0.019	0.66 \pm 0.035	0.75 \pm 0.005	–0.10 \pm 0.017	0.04 \pm 0.014	–0.02 \pm 0.014	–0.02 \pm 0.017
ADG5	0.39 \pm 0.058	0.51 \pm 0.047	–0.01 \pm 0.064	0.08 \pm 0.063	0.48 \pm 0.047	–0.10 \pm 0.061	0.54 \pm 0.046	–0.13 \pm 0.064	–0.08 \pm 0.018	–0.14 \pm 0.021
			0.74 \pm 0.028	0.86 \pm 0.016	0.96 \pm 0.005	0.49 \pm 0.047	0.81 \pm 0.021	0.72 \pm 0.031	–0.08 \pm 0.022	–0.08 \pm 0.022
									–0.07 \pm 0.025	0.44 \pm 0.017
									0.48 \pm 0.019	0.69 \pm 0.012
									–0.06 \pm 0.014	0.86 \pm 0.006
									0.002 \pm 0.021	–0.12 \pm 0.018
									–0.12 \pm 0.018	0.67 \pm 0.011
									–	0.57 \pm 0.013
									–	0.54 \pm 0.014
									0.59 \pm 0.040	–

Genetic correlations are below diagonal and phenotypic correlations are above diagonal

at later ages. The phenotypic correlations were found to be lower than the values for genetic correlation. In general, most of the traits studied had a high positive genetic correlation among them, which indicates the possibility of correlated responses through multiple trait selection. Similar results have been reported in earlier studies (Ganesan et al. 2013; Reddy et al. 2017). As expected, very high phenotypic correlation of WW with ADG1 (0.98) and YW with ADG5 (0.86) was observed.

There was an increasing genetic (Fig. 2) and phenotypic (Fig. 3) trends observed for almost all the traits. The genetic trend values for BW, WW, 6W, 9W, YW, ADG1

and ADG5 were 0.0015 ± 0.000 kg, 0.0261 ± 0.002 kg, 0.0368 ± 0.005 kg, 0.0429 ± 0.006 kg, 0.017 ± 0.007 kg, 0.6314 ± 0.041 g and 0.139 ± 0.024 g, respectively. The phenotypic trend for BW, WW, 6W, 9W, YW, ADG1 and ADG5 were 0.0165 ± 0.000 kg, 0.0985 ± 0.001 kg, 0.041 ± 0.002 kg, 0.039 ± 0.002 kg, 0.0081 ± 0.003 kg, 1.0537 ± 0.014 g and -0.092 ± 0.009 g, respectively. Similar results of positive trend for growth have been reported earlier (Mokhtari and Rashidi 2010; Arora et al. 2010; Balasubramanyam et al. 2012). The expected responses estimated also indicate good scope for selection in these traits. The direct response was found to increase

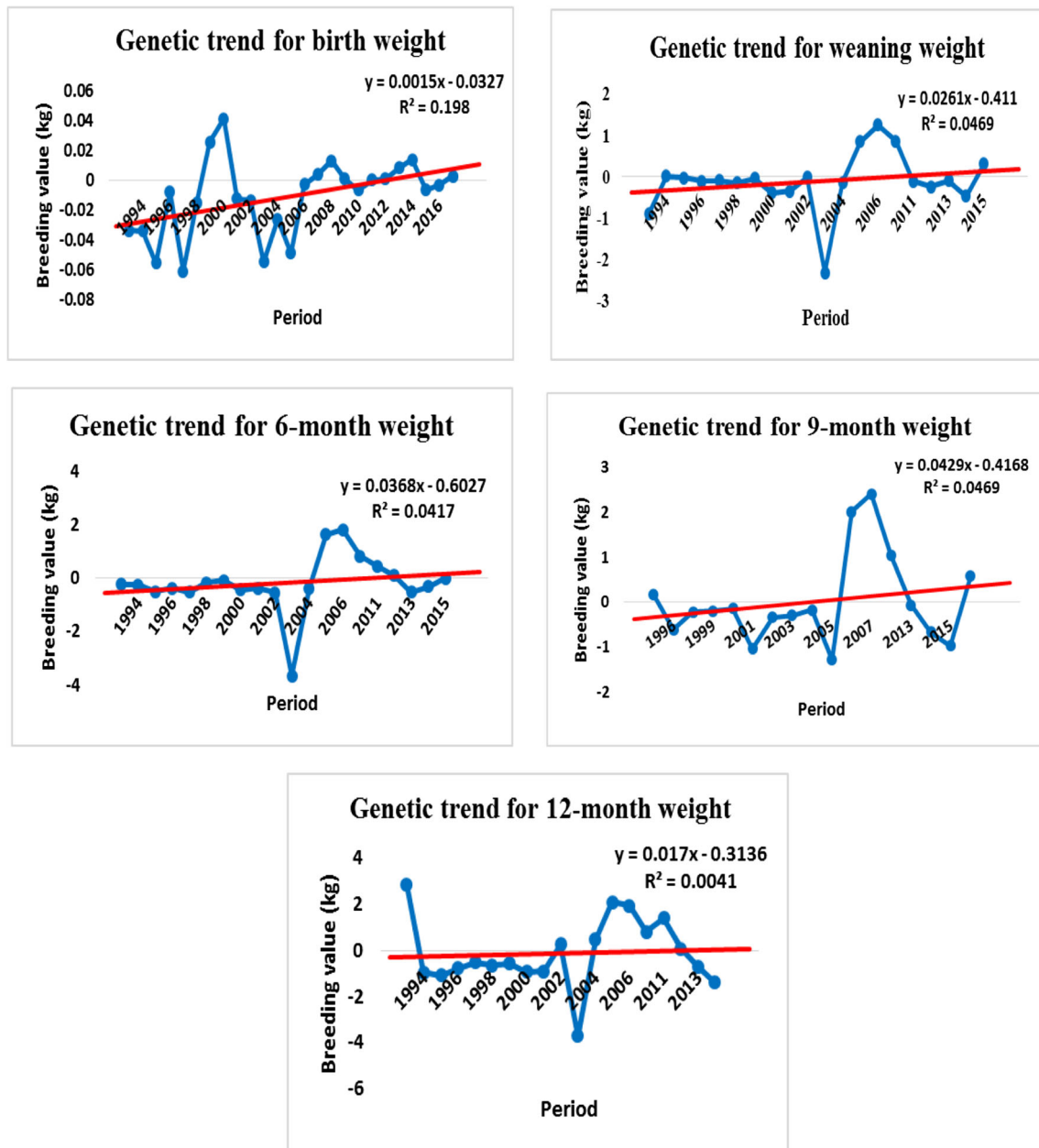


Fig. 2 Genetic trends for body weight at different ages

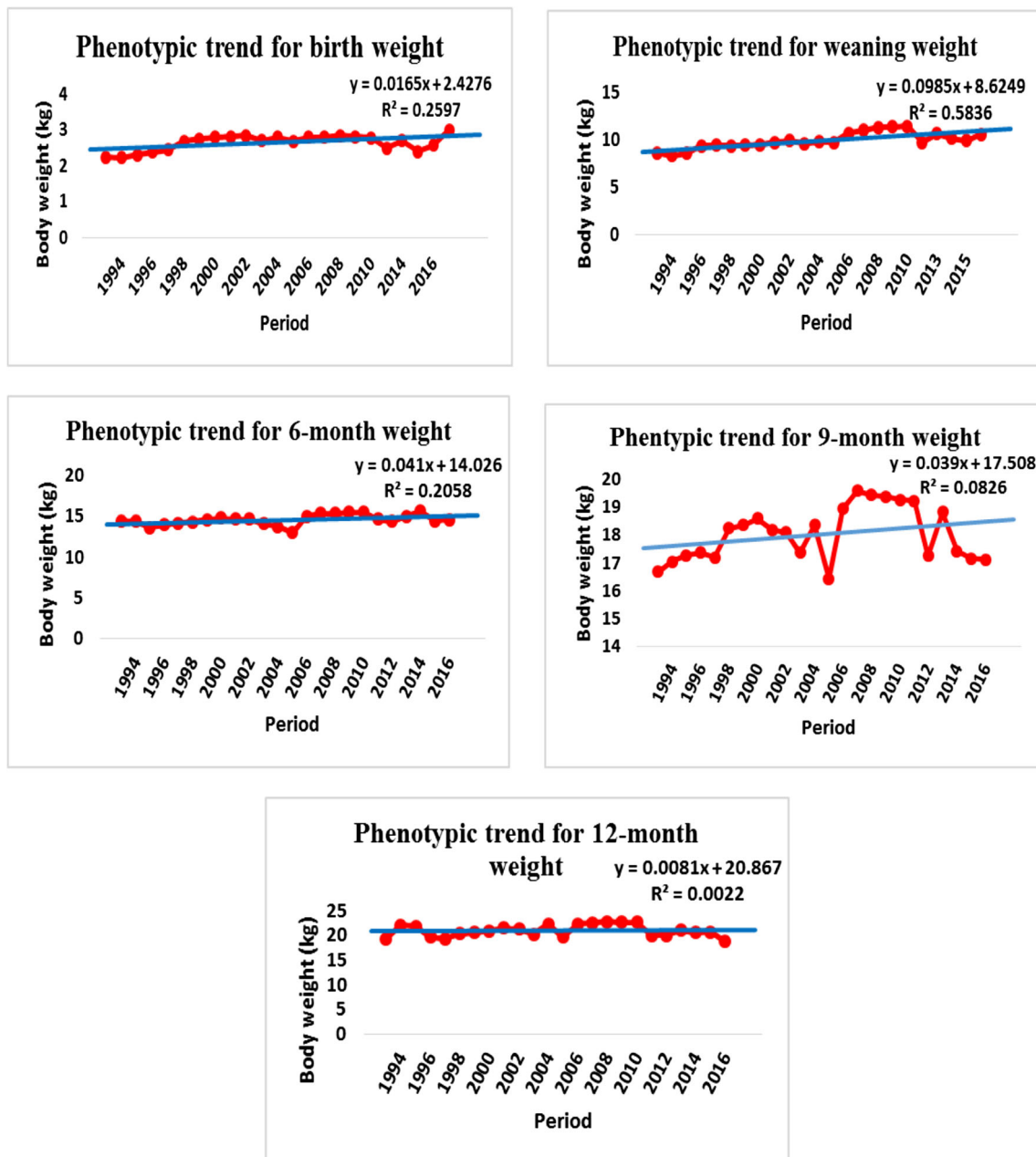


Fig. 3 Phenotypic trends for body weight at different ages

with age and the YW had the maximum response (2.741 kg/generation) among the body weight traits, and for pre- and post-weaning ADGs the values were 7.850 and 11.112 g/generation, respectively.

The highest expected correlated response was for YW (2.131 kg/generation), when selection is made on 9W followed by 6W (1.713 kg/generation). The first measurable trait, BW, when chosen as a trait for selection, maximum expected response was observed in YW of 0.733 kg/generation. The indirect response in YW when selection was on pre-weaning ADG was higher (1.396 kg/generation). All the values obtained for expected response were positive.

The advantage of an open nucleus breeding scheme involving several smallholder flocks in terms of sustenance of genetic variability is evident from this study in spite of long duration of selection. The high values of heritability, correlation and expected responses observed provide good scope for improvement in these animals through selection for growth.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

References

- Acharya, R.M., 1982. Sheep and Goat Breeds of India. FAO Animal Production and Health Paper, No: 30, FAO, Rome, Italy.
- Ahmad, M., Singh, C.V., Sharma, R.K., Sushil Kumar and Arora, A.L., 2005, Comparison of different methods of heritability estimates for body weights and wool yield traits in Avikalin sheep. *Indian Journal of Small Ruminants*, 11(2) : 121–126.
- Arora, A.L., Gowane, G.R., Prince L.L.L. and Prakash, V., 2010. Genetic trends for performance traits of Malpura sheep. *Indian Journal of Animal Sciences*, 80, 937–939.
- Balasubramanyam, D. and Kumarasamy, P., 2011. Performance of Madras Red sheep in Kancheepuram District. *Indian Journal of Fundamental and Applied Life Science*, 1, 133–137.
- Balasubramanyam, D., Raja, T.V., Kumarasamy, P. and Sivaselvam, S.N., 2012. Estimation of genetic parameters and trends for body weight traits in Madras Red sheep. *Indian Journal of Small Ruminants*, 18: 173–179.
- Burfening, P.J. and Kress, D.D., 1993. Direct and maternal effects on birth and weaning weight in sheep. *Small Ruminants Research*, 10 (2), 153–163.
- Cloete, S.W.P., Schoeman, S.J., Coetzee, J. and Morris, J.D., 2001. Genetic variances for live weight and fleece traits in Merino, Dohne Merino and South African Meat Merino sheep. *Australian Journal of Experimental Agriculture*, 41: 145–153.
- Devendran P., Cauveri, D., Murali, N. and Kumarasamy, P., 2014. Growth profile of Madras Red sheep in farmer's flocks. *Indian Journal of Small Ruminants*, 20(1), 20–23.
- Ekambaram, B., Alexander, G. and Chakravarthi, M.K., 2013. Performance of Nellore sheep (Jodipi) under farm conditions. *Indian Veterinary Journal*, 90(12), 35–37.
- Farokhad, M. L., Beigi Nassiri, M.T., Roshanfekar, H., Fayazi, J. and Mamouei, M., 2010. Genetic parameters for direct and maternal effects on growth traits of Arman lambs, *Research Journal of Biological Sciences*, 5 (1), 71–74.
- Ganesakale, D. and Rathnasabapathy, V., 1973. Sheep breeds of Tamil Nadu. *Cheiron*, 2, 146–155.
- Ganesan, R., Dhanavanthan, P., Balasubramanyam, D., Kumarasamy, P. and Kiruthika, D., 2013. Estimation of genetic parameters of growth traits in Madras Red sheep. *IOSR Journal of Agricultural and Veterinary Science*, 3(5), 69–73.
- Jeichitra, V., 2009. Genetic Analysis of Growth Traits in Mecheri Sheep. Ph.D. Thesis submitted to the Tamil Nadu Veterinary and Animal Sciences University, Chennai.
- Joshi, R.K., Narula, H.K., Singh, H. and Chopra, A., 2014. Heritability estimates of growth traits in Magra sheep. *Indian Journal of Small Ruminants*, 20: 109–111.
- Meyer, K., 1998. Estimating covariance functions for longitudinal data using random regression model. *Genetic Selection and Evolution*, 30, 221–240.
- Meyer, K., 2007. WOMBAT—A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *Journal of Zhejiang University Science*, 8, 815–821.
- Mokhtari, M.S. and Rashidi, A., 2010. Genetic trends estimation for body weights of Kermani sheep at different ages using multivariate animal models. *Small Ruminant Research*, 88, 23–26.
- Raman, K.S., Sundararaman, M.N., Haribhaskar, S. and Ganesakale, D., 2003. Biometrics and breed characteristics of Madras Red sheep. *Indian Journal of Small Ruminants*, 9, 6–9.
- Rani, 2012. Genetic studies on the performance on Nellore sheep. M.V.Sc thesis submitted to Sri Venkateswara Veterinary University, Tirupati.
- Reddy VV, D., Sreenivas, D., Gnanaprakash, M. and Harikrishna, Ch., 2017. Genetic analysis of growth performance of Nellore Brown sheep. *International Journal of Science*, 6(1), 774–778.
- Weller J. I., 2009. *Quantitative Trait Loci Analysis in Animals*, 2nd edition. Published by CABI Publishing, United Kingdom.