Bayesian estimates of genetic parameters and genetic trends for morphometric traits and their relationship with yearling weight in Moghani sheep

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ABSTRACT
This study was conducted to estimate variance components, genetic parameters and genetic trends for morphometric traits and their relationship with yearling weight in Moghani sheep. The data set and pedigree information of Moghani sheep were obtained from the breeding station of Moghani sheep (in Ardebil province, Iran) and comprised 2387 lamb records for morphometric traits during 1994 to 2012. Traits considered were height at withers (HW), height at rump (HR), body length (BL), heart girth (HG), leg circumference (LC) and yearling weight (YW). Four different animal models were fitted, differentiated by including or excluding maternal effects, with covariance between maternal and direct genetic effects were implemented by Gibbs sampling methodology. Selection of the best model of analysis for each trait was based on Akaike’s information criterion (AIC). Posterior mean estimates of direct heritabilities for BL, HW, HR, LC, HG and YW were 0.34, 0.037, 0.47, 0.073, 0.065 and 0.17, respectively. Estimates of direct genetic correlation between morphometric traits varied from 0.21 (between BL–LC) to 0.67 (between LC–HG). Estimates of direct genetic correlation between morphometric traits and YW were positive and varied from 0.08 (between HW–YW) to 0.52 (between HG–YW). Estimates of direct genetic trends for BL, HW, HR, LC and HG were significant (p < .0001), and their corresponding values were 0.054 ± 0.009, 0.005 ± 0.001, 0.032 ± 0.006, −0.009 ± 0.002 and −0.014 ± 0.003, respectively. The results implied that applicable genetic variations observed for under study traits could be applied in designing future genetic selection plans for Moghani sheep.

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Introduction
Meat production is a complex polygenic character that is greatly influenced by genetic and environmental factors. Linear measurements or morphometric traits which would be controlled by genetic mechanisms would be applied as indirect selection criteria in many livestock species to aid amendment of meat production. Body measurements depict more perfectly an individual animal or breed characteristics than the routine ways of grading or weighing (Salako 2006). Body measurements could be used to predict live body weight and considered as functional measures in animal breeding. Also, they are major criteria for the evaluation and selection of meat producing animals (Atta and El khidir 2004; Salako 2006; Mandal et al. 2008). However, effective relationship between body size of animal with carcass quality characters must be determined. Therefore, it can still be declared that a smaller or larger size of animal does not indicate greater productivity (Figueiredo Filho et al. 2012).

The phenotype of body measurements or biometric traits is the outcome of the direct and maternal genetic merits and the environmental effects. Evaluating body measurements may be occurred at a relatively early age; therefore, effect of maternal factors on these characters requires to be measured in order to propose optimal programmes of animal breeding (Mandal et al. 2008). In many farm animals, genetic evaluation procedures and selection programmes conducted to provide breeding values of animals for biometric traits. Biometric traits have been applied for evaluating the characteristics of the animals which may differ because of the influence of environment, evolution of breed, and feeding. Applying morphometric measurement...
criteria, animal breeders are able to distinguish early and late maturing animals with distinct body sizes (Brown et al. 1973). It would be useful to recognise proper animals at an earlier phase of growth for selection purposes and predict mature size of animals.

The Moghani sheep breed is one of the most important fat-tailed meat breeds among Iranian sheep. A breeding station was founded in Ardebil province of Iran in order to genetically improve the performance of Moghani sheep, through identifying the best rams and distributing them to the commercial flocks. Although breeding animals were initially selected based on their general appearance and coat colour earlier in the breeding station of Moghani sheep (Jafaroghli et al. 2010), but the results of recent studies (Ghavi Hossein-Zadeh and Ardalan 2010a; Ghavi Hossein-Zadeh 2017a) showed that animals were currently selected based on growth traits such as 3-month weight, 6-month weight or average daily gain from three to six months of age. Moghani sheep raise under a traditional migratory system, summer in the mountainous areas and winter in the flat areas and pastures. There was a controlled mating system so that the identity of the sire and dam of each lamb were known. Ewe lambs and ram lambs were bred at 18 months of age. Rams were used for only one year and ewes were used for up to 6 years. Male and female lambs were maintained in separate flocks from 6 months of age onwards (Ghavi Hossein-Zadeh and Ardalan 2010a).

Restricted Maximum Likelihood (REML) and Bayesian methods of analysis have been used widely in animal breeding to estimate genetic parameters and (co)variance components (Malhado et al. 2012; Ghavi Hossein-Zadeh 2017b). The benefit of Bayesian methodology is to regard the prior information on the unknown parameters when compared with REML. Bayesian method provided a solution for the problem of limited sample size because each small or large data set from which inferences can then be drawn is supported by an exact a posteriori distribution (Ghavi Hossein-Zadeh 2017b). Carneiro Júnior et al. (2007) found that the Bayesian methodology is well justifiable for analysing small populations or data set when great historical information is attainable. The Gibbs Sampling algorithm produces posterior distributions of parameters to permit random sample estimation of parameter estimates based on a specific data set (Magnabosco et al. 2000; Ghavi Hossein-Zadeh 2015; Ghavi Hossein-Zadeh 2017b). The aims of current study were to estimate variance components, heritabilities and genetic trends for morphometric traits and to estimate genetic correlations between these traits and yearling weight in Moghani sheep using Bayesian algorithm via Gibbs sampling.

Materials and methods

Data set

The data set and pedigree information of Moghani sheep were obtained from the breeding station of Moghani sheep (in Ardebil province, Iran) and comprised 2387 lamb records for biometric traits during 1994 to 2012. Number of records for each morphometric trait varied from 30 to 258 over the years. The number of animals (in total), sires, dams, founders and non-founders in the pedigree of Moghani sheep were 35,076, 1085, 9954, 16,344 and 18,732, respectively.

Traits considered were height at withers (HW), height at rump (HR), body length (BL), heart girth (HG), leg circumference (LC) and yearling weight (YW). HW measures the distance from a platform on which the animal stands to the withers. The measurement is best made with a special measuring stick on two arms, one held vertically, and the other at right angles, so that it slides firmly up and down to record the height. HR is the distance from the surface of a platform to the rump using a measuring stick as described for height at withers. BL refers to the distance from the first cervical vertebra to the base of the tail where it joins the body. HG is a circumferential measure taken around the chest just behind the front legs and withers with a tape measure. LC refers to the circumference of the rear legs. The midpoint between the hock and pin bone on the right rear leg is used to measure leg circumference, using a tape measure (Bakhshalizadeh et al. 2016). Age of animals at recording morphometric traits was 414.79 ± 75.43 days. The data were screened several times and defective, doubtful and out of range data were deleted. Therefore, lambs with no records of morphometric traits were removed. Also, lambs with incomplete records of parentage and or animal registration numbers lower than the numbers of their parents were left out. The characteristics of data used in this study are presented in Table 1.

Statistical and genetic analysis

The selection of fixed variables to be included in the final model of analysis was made after examining the statistical significance of the effects using the GLM procedure of SAS (SAS Institute Inc., Cary, NC). Significance level for the inclusion of variables into the statistical model of analysis was considered at p < .05. The model of analysis for HW and LC included the
fixed class effects of lambing year and month, lamb sex, litter size, dam age and covariate effect of lamb age at recording. The model of analysis for HG was similar to the model used for HW and LC, but lambing month excluded from the model. The model of analysis for YW included the fixed class effects of lambing year and month and lamb sex. The model of analysis for BL included the fixed class effects of lambing year, lamb sex, litter size and dam age. Also, the model of analysis for HR included the fixed class effects of lambing year and month and lamb sex. The model of analysis for YW included the fixed class effects of lambing year and month, lamb sex and litter size. The univariate animal models considered for the genetic analysis of morphometric traits were as follows:

- **Model 1**: \( y = Xb + Za + e \)
- **Model 2**: \( y = Xb + Za + Zc + e \)
- **Model 3**: \( y = Xb + Za + Zm + e \)
  - with \( \text{Cov}(a,m) = A \sigma_{am} \)
- **Model 4**: \( y = Xb + Za + Zm + Zc + e \)
  - with \( \text{Cov}(a,m) = A \sigma_{am} \)

where, \( y \) is a \( N \times 1 \) vector of records, \( b \) denotes the fixed effects in the model with association matrix \( X \), \( a \) is the vector of direct genetic effects with the incidence matrix \( Za \), \( m \) is the vector of maternal genetic effects with the incidence matrix \( Zm \), \( c \) is the vector of maternal permanent environmental effects with the incidence matrix \( Zc \) and \( e \) denotes the vector of residual (temporary environmental) effects. From a Bayesian perspective, it was assumed that prior distributions for additive direct and maternal effects were multivariate normal distribution with mean 0 and variance \( A \sigma^2_a \) and \( A \sigma^2_m \), respectively, where \( A \) is the additive numerator relationship matrix, \( \sigma_{am} \) is the covariance between direct and maternal genetic effects, and \( \sigma^2_a \) and \( \sigma^2_m \) are additive direct and maternal variances, respectively. Residual effects were assumed to be multivariate normally distributed with mean 0 and variance \( \mathbf{I}_n \sigma^2_e \), where \( \mathbf{I}_n \) is identity matrix with order equal to the number of individual records and \( \sigma^2_e \) is residual variance. Permanent environmental effects of the dam were assumed to be multivariate normally distributed with mean 0 and variance \( \mathbf{I}_d \sigma^2_{pe} \), where \( \mathbf{I}_d \) is identity matrix with order equal to the number of dams and \( \sigma^2_{pe} \) is maternal permanent environmental variance. Selection of the best model of analysis for each morphometric trait was based on Akaike’s information criterion (AIC) (Akaike 1983):

\[
AIC = n \cdot \ln \left( \frac{RSS}{n} \right) + 2p
\]

RSS is residual sum of squares, \( n \) is the number of observations and \( p \) is the number of parameters in the model. AIC is a good statistic for comparison of models with different complexity because it corrects the RSS for number of parameters in the model. A smaller numerical value of AIC shows a better fit when comparing models. Pair-wise or bivariate analyses were conducted for every pair of the traits. The models used in bivariate analyses were the best fitted univariate models for the studied traits.

Marginal posterior distributions of parameters and variance components were estimated, using TM programme (Legarra et al. 2011). The prior distribution for the genetic and residual (co)variance matrices is assumed to be an inverted Wishart distribution. Flat priors are used for fixed effects and variance components. The Gibbs sampler was run 500,000 rounds, and the first 100,000 rounds were discarded as a warming-up period (Legarra et al. 2011). A thinning interval of 100 rounds was used to retain sampled values that reduced lag correlation among thinned samples. In the TM programme it is assumed a priori that the direct and maternal effects are correlated. The Bayesian Output Analysis (BOA version 1.1.5; Smith 2005) package was used to calculate the mean, SD, and 95% high posterior density (HPD) interval for all parameters from the individual marginal posteriors and to control and verify the convergence of genetic analyses, under the free software R (http://www.rproject.org/). The Geweke and Heidelberger and Welch tests were used to check the convergence of genetic analyses. The HPD region provides the interval that includes 95% of samples and is a measure of reliability. Also, the HPD can be applied to non-symmetric distributions (Hyndman 1996). Genetic and phenotypic trends were obtained by regressing yearly mean estimates of breeding values and phenotypic values on birth year, respectively.

### Results and discussion

Averages of BL, HW, HR, LC, HG and YW were 49.36 cm, 68.46 cm, 69.81 cm, 29.42 cm, 86.06 cm and 39.08 Kg in Moghani sheep, respectively (Table 1). Jafari and Hashemi (2014) reported the means of BL, HW, HR, LC and HG were 49.5, 62.6, 64.1, 32.7 and

| Trait | Number of observations | Mean  | SD   | CV (%) |
|-------|------------------------|-------|------|--------|
| BL, cm| 2387                   | 49.36 | 11.97| 24.25  |
| HW, cm| 2387                   | 68.46 | 7.75 | 11.32  |
| HR, cm| 2387                   | 69.81 | 12.92| 18.51  |
| LC, cm| 2387                   | 29.42 | 5.45 | 18.52  |
| HG, cm| 2387                   | 86.06 | 8.42 | 9.78   |
| YW, kg| 2854                   | 39.08 | 5.88 | 15.05  |

Table 1. Summary statistics for morphometric traits and yearling weight in Moghani sheep.
81.5 cm in Makuie sheep, respectively. Janssens and Vandepitte (2004) reported greater values of BL and HG in Belgian Bleu du Maine, Suffolk and Texel sheep than the values in the current study. Mandal et al. (2008) reported the least-squares means for BL, HW and HG of animals were 33.65, 37.54 and 34.61 cm, respectively, at birth and the corresponding values were 56.93, 58.02 and 57.40 cm, respectively, at weaning in Muzaffarnagari sheep of India.

Comparison of different models used for genetic analysis of morphometric traits and yearling weight of Moghani sheep is shown in Table 2. The results indicated that model 1 was selected as the best model for genetic analysis of all morphometric traits and yearling weight due to the lowest AIC values compared with other models. This result implied the absolute importance of direct genetic effects for genetic analysis of morphometric traits and live body weight at yearling in Moghani sheep.

The posterior means, medians and modes of variance components and genetic parameters and their HPDs for BL, HW, HR, LC, HG and YW are presented in Table 3. Posterior mean estimates of direct heritabilities were 0.10, 0.11, 0.16, 0.11 and 0.23 for BL, HW, HR, LG and HG in Moghani sheep, respectively. Mandal et al. (2008) estimated greater direct heritabilities for HG (0.25), HW (0.47), HR (0.12) in Muzaffarnagari sheep at weaning. Horstick (2001) obtained high estimates of direct heritability for BL, HW and HG of adult sheep in Blue du Maine (0.30, 0.43 and 0.45, respectively), Suffolk (0.35, 0.57 and 0.39, respectively) and Texel sheep (0.28, 0.40 and 0.40, respectively). Horstick (2001) obtained high estimates of heritability for BL (0.72), HW (0.70) and HG (0.56) in East Friesian and Black-Brown milk sheep compared with our estimates. Figueiredo Filho et al. (2016) estimated lower direct heritability estimates for BL (0.005) and HR (0.15) in Santa Inês sheep compared with this study. Bakhshalizadeh et al. (2016) used restricted maximum likelihood method (REML) and reported direct heritabilities were 0.10, 0.11, 0.16, 0.11 and 0.23 for HW, HR, BL, HG and LC in Moghani sheep, respectively. Compared with the current study, Oliveira et al. (2014) estimated greater direct heritabilities for HG (0.25), HW (0.48) and lower heritability estimate for BL (0.24) in Santa Inês sheep. Generally consistent with the results of this study, Abbasi and Ghafoori-keshbi (2011) obtained low to medium direct heritability estimates for biometric traits in Makuie sheep. Abbasi and Ghafoori-keshbi (2011), and Jafari and Hashemi (2014) reported greater direct heritability estimates for YW in Makuie sheep (0.22 and 0.36, respectively). Similar to the results of current study, Jafaroghli et al. (2010) and Ghavi Hossein-Zadeh and Ardalan (2010b) reported the direct heritability estimate for YW was 0.17 in Moghani sheep. Gad (2014) obtained lower direct heritability estimate (0.10) for YW in Barki lambs.

Estimates of variance components for morphometric traits and yearling weight showed slight differences between means, medians and modes (Table 3) and it would be possible to consider normal distribution for these components. The variation ranges of HPDs for the direct heritabilities were located at the region greater than zero. Therefore, there was a probability equal to zero for obtaining zero estimates for these genetic parameters. Direct heritabilities for the traits

| Model | Trait | Value Mean | Value Median | Value Mode | Value HPD |
|-------|-------|------------|--------------|------------|-----------|
| 1     | BL    | 46.67      | 46.93        | 48.23      | 27.99–68.00 |
| 2     | HW    | 90.71      | 90.28        | 80.45      | 75.01–107.88 |
| 3     | HR    | 137.38     | 137.13       | 136.04     | 129.04–146.54 |
| 4     | HG    | 0.34       | 0.34         | 0.35       | 0.21–0.48   |
| 5     | LC    | 2.06       | 1.91         | 1.62       | 2.01–3.94   |
| 6     | YW    | 55.34      | 55.26        | 54.60      | 52.03–58.37 |

Table 2. Comparison of different models used for genetic analysis of morphometric traits and yearling weight in Moghani sheep based on Akaike’s Information Criterion (AIC) values.

| Trait | Item | Value Mean | Value HPD |
|-------|------|------------|-----------|
| BL    | a,2  | 32.54      | 32.54–32.54 |
| HW    | a,2  | 11.41      | 11.41–11.41 |
| HR    | a,2  | 0.30       | 0.30–0.30   |
| HG    | a,2  | 0.16       | 0.16–0.16   |
| YW    | a,2  | 0.20       | 0.20–0.20   |

Table 3. The posterior mean, median and mode of direct genetic, residual and phenotypic variance components and direct heritability for morphometric traits and yearling weight of Moghani sheep [standard deviations (PSD) of marginal posterior distribution of mean estimates are in brackets].
under study showed a normal posterior density with no or slight differences between mode, median and mean (Table 3). This result indicated the existence of no or slight differences between mode, median and under study showed a normal posterior density with no or slight differences between mode, median and mean (Table 3). This result indicated the existence of normal distribution for direct heritabilities. Estimation of genetic parameters is necessary for designing an appropriate breeding programme and proposing an effective system for genetic evaluation (Jurado et al. 1994). Several variables would have affected on the distinctions between parameter estimates which included existence of genetic variation within population, breed and type of the animal, environmental and management conditions, the model and or method of estimating a parameter, etc. (Ghavi Hossein-Zadeh 2014).

The posterior means of direct genetic correlations between morphometric traits are shown in Table 4. Estimates of direct genetic correlation between morphometric traits varied from −0.21 (between BL–LC) to 0.67 (between LC–HG). Estimates of direct genetic correlation between morphometric traits and YW were positive and varied from 0.08 (between HW–YW) to 0.52 (between HG–YW) (Table 4). In spite of direct genetic correlations between BL with HR, LC and HG, all other direct correlations were positive. Therefore, selection on BL may result in a negative indirect effect on HR, LC and HG. Jafari and Hashemi (2014) obtained positive direct genetic correlations between biometric traits in Makuei sheep which varied from 0.25 (LC–HG) to 0.99 (HW–HR). Similar to the current results, Abbasi and Ghafouri-kesbi (2011), Jafari and Hashemi (2014) reported positive direct genetic correlations between morphometric traits and YW in Makuei sheep. Gad (2014) reported positive and high direct genetic correlations between BL–HW (0.81), BL–HG (0.82) and HW–HG (0.46) in Barki sheep. Also, Oliveira et al. (2014) estimated positive and high direct genetic correlations between body measurement traits in Santa Ines sheep. Bakhshalizadeh et al. (2016) reported direct genetic correlation estimates varied from −0.55 (between BL–LC) to 0.99 (between HW–HR) in Moghani sheep using REML method. The positive genetic correlation between most morphometric traits reported in this study, especially between LC–HG, indicated that genes that positively influence one biometric trait would result in greater values of other trait. Also, positive genetic correlation between YW and morphometric traits showed that selection for yearling weight resulted in possible increase of morphometric traits in Moghani sheep and vice versa. The positive genetic correlations between traits under study are evidence for common genetic and physiological mechanism controlling these traits. Also, positive genetic correlation suggesting that selection of sheep based on a morphometric trait would also improve other morphometric character. Although there was no possible reason for negative genetic correlation between some of the morphometric traits in this study, but the negative genetic correlation estimates showed that breeders should be aware of the undesirable effects of selection based on only one group of traits (Jafari et al. 2014). The greatest genetic correlation between morphometric traits and YW was for HG–YW (0.52). Similar finding was reported by other studies (Salako 2006; Abbasi and Ghafouri-kesbi 2011; Gad 2014; Jafari and Hashemi 2014). Heart girth is a part of tissue measurements (Blackmore et al. 1958), while other measurements are related to skeletal measurements (Salako 2006). This can explain, to some extent, the greater correlation between YW and HG. The HG is the most credible trait for the prediction of YW among the morphometric traits. In a genetic selection programme based on biometric characters, HG would be considered as an appropriate selection criterion because it has high genetic relationship with body weight at yearling (Jafari and Hashemi 2014).

Estimates of phenotypic correlations between morphometric traits were positive and ranged from 0.04 (between BL–HR) to 0.27 (between LC–HG) (Table 4). Also, estimates of phenotypic correlations between morphometric traits with YW varied from 0.10 (BL–YW and HR–YW) to 0.35 (HG–YW) (Table 4). Therefore, phenotypic selection for one morphometric trait would increase the other morphometric trait and or YW from phenotypic perspective. Also, estimates of residual correlations between morphometric traits were positive

### Table 4. The posterior mean of genetic, residual and phenotypic correlations between morphometric traits and yearling weight in Moghani sheep (posterior standard deviation (PSD) of estimates are within the brackets).

| Traits          | \( r_{g,1} \) | \( r_{e,1} \) | \( r_{p,1} \) |
|-----------------|---------------|---------------|---------------|
| BL–HW           | 0.13 (0.27)   | 0.08 (0.02)   | 0.09 (0.04)   |
| BL–HR           | −0.09 (0.15)  | 0.04 (0.02)   | 0.12 (0.08)   |
| BL–LC           | −0.21 (0.26)  | 0.05 (0.02)   | 0.11 (0.04)   |
| BL–HG           | −0.07 (0.28)  | 0.10 (0.02)   | 0.14 (0.05)   |
| HW–HR           | 0.25 (0.26)   | 0.14 (0.02)   | 0.16 (0.04)   |
| HW–LC           | 0.23 (0.34)   | 0.14 (0.02)   | 0.13 (0.02)   |
| HW–HG           | 0.06 (0.38)   | 0.17 (0.02)   | 0.17 (0.02)   |
| HR–LC           | 0.004 (0.23)  | 0.09 (0.02)   | 0.12 (0.05)   |
| HR–HG           | 0.38 (0.22)   | 0.11 (0.02)   | 0.05 (0.05)   |
| LC–HG           | 0.67 (0.20)   | 0.27 (0.02)   | 0.24 (0.03)   |
| BL–YW           | 0.09 (0.25)   | 0.10 (0.02)   | 0.10 (0.07)   |
| HW–YW           | 0.08 (0.38)   | 0.16 (0.02)   | 0.17 (0.04)   |
| HR–YW           | 0.13 (0.09)   | 0.10 (0.02)   | 0.70 (0.36)   |
| LC–YW           | 0.41 (0.27)   | 0.17 (0.02)   | 0.14 (0.04)   |
| HG–YW           | 0.52 (0.22)   | 0.35 (0.02)   | 0.31 (0.04)   |

\( r_{g,1} \): posterior mean of direct genetic correlation between traits; \( r_{e,1} \): posterior mean of residual correlation between traits; \( r_{p,1} \): posterior mean of phenotypic correlation between traits; BL: body length; HW: height at withers; HR: height at rump; LC: leg circumference; HG: heart girth; YW: yearling weight.
and varied from 0.05 (between HR–HG) to 0.24 (between LC–HG) (Table 4). In addition, residual correlation estimates between morphometric traits and YW ranged from 0.10 (between BL–YW) to 0.70 (between HR–YW) (Table 4). Positive residual correlation between the traits under study indicated the environmental dependency of these traits and by changing the environmental factors affecting one character it is possible to modify the other trait in similar direction. Consistent with the results of this study, positive phenotypic and residual correlations were reported between morphometric traits in different studies (Abbasi and Ghafouri-kesbi 2011; Gad 2014; Jafari and Hashemi 2014; Bakhshalizadeh et al. 2016).

The values of average annual phenotypic trends obtained from fitting linear regression of annual mean morphometric traits were $-0.02 \pm 0.15 \text{cm}$ ($p > 0.05$), $0.07 \pm 0.09 \text{cm}$ ($p > 0.05$), $0.03 \pm 0.12 \text{cm}$ ($p > 0.05$), $0.56 \pm 0.18 \text{cm}$ ($p < 0.01$) and $0.26 \pm 0.30 \text{cm}$ ($p > 0.05$) for BL, HW, HR, LC and HG, respectively. Therefore, LC increased over the years. Estimates of direct genetic trends for BL, HW, HR, LC and HG were significant ($p < 0.0001$), and their corresponding values were $-0.054 \pm 0.009 \text{cm}$, $-0.005 \pm 0.001 \text{cm}$, $0.032 \pm 0.006 \text{cm}$, $-0.009 \pm 0.002 \text{cm}$ and $-0.014 \pm 0.003 \text{cm}$, respectively. Because there was positive direct genetic trend for HR, it appears that genetic merit for this trait was increased in Moghani sheep over the years. Positive genetic trend estimate for HR in the current study may be due to the greater heritability of this trait compared with other morphometric traits. The significant and positive phenotypic trend of LC despite the negative genetic trend showed the positive influence of environmental factors on the phenotypic expression of LC over the years. Bakhshalizadeh et al. (2016) obtained irregular genetic changes for biometric traits over the years in Moghani sheep using the REML method. One of the best approaches accessible for reaching to maximum selection response in a breeding programme is accurate prediction of breeding values for animals. The success of a breeding programme can be evaluated by assessing the actual fluctuation in breeding value indicated as a part of expected theoretical change in the mean of breeding value for a given trait (Jurado et al. 1994).

Conclusions

Current estimates of genetic parameters for morphometric traits could be used in designing selection plans and constructing selection indices for Moghani sheep. Therefore, improvement of these traits in sheep seems possible in selection programmes. Regarding the low to high direct heritabilities for morphometric traits along with positive genetic correlations between most of them make it clear that genetic changes in body size of this sheep breed can be accomplished. The positive genetic correlation between yearling weight and morphometric traits showed that selection for body measurements would possibly result in improvement of body weight and vice versa. Regarding to the high heritability estimate of HR, positive genetic trend for this trait and positive genetic correlations with most morphometric traits, it would be possible to consider HR as selection criterion in the current breed of sheep. Therefore, in designing future selection programme for Moghani sheep, genetic improvement in morphometric traits, especially HR, would be one of the main components of selection goals.

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Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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