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Structural equation modeling for genetic analysis of body weight traits in Moghani sheep

*Morteza Jafaroghli[1], Mohammad Soflaee Shahrbabak[2], Farhad Ghafouri-Kesbi[3], Morteza Mokhtari[4] **

[1]Department of Animal Science, Faculty of Agricultural Science, Payame Noor University (PNU), Tehran, Iran
[2]Kerman Agricultural and Natural Resources Research and Education Center, AREEO, Kerman, Iran
[3]Department of Animal Science, Faculty of Agriculture, Bu-Ali Sina University, Hamedan, Iran
[4]Department of Animal Science, Faculty of Agriculture, University of Jiroft, P.O. Box 364, Jiroft, Iran

*Corresponding author,
E-mail address:
msmokhtari@ujiroft.ac.ir
Tel:
+983443347066

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ORCID
Morteza Jafaroghli
0000-0002-2191-3074
Farhad Ghafouri-Kesbi
0000-0002-2219-055X
Morteza Mokhtari
0000-0002-3971-628X

Abstract The aim of the present study was to investigate the advantages of structural equation modeling for genetic evaluation of body weight traits in Moghani sheep, using data collected on 6,320 Moghani lambs during a 23-year period (1988 to 2011) in Jafarabad Breeding Station of Moghani Sheep. Traits investigated were the body weight at birth (BW), weaning (WW), six-month (6MW), nine-month (9MW) and yearling weight (YW). Three multivariate animal models including the standard (SMM), fully recursive (FRM) and temporal recursive (TRM) models were compared in terms of deviance information criterion (DIC) and predictive ability measures including mean square of error (MSE) and Pearson's correlation coefficient between the observed and predicted values ($r(y,\hat{y})$) of records. Spearman's rank correlation coefficients between posterior means of direct genetic effects for the studied traits were also calculated across all, 50% top-ranked, 10% top-ranked and 1% top-ranked animals. In general, TRM performed better than SMM and FRM in terms of DIC, MSE and $r(y,\hat{y})$: resulting in the lowest DIC and MSE and the highest $r(y,\hat{y})$. All structural coefficients estimated by TRM were statistically significant. Comparisons of Spearman's rank correlations between posterior means of direct genetic effects of lambs for the studied body weight traits under SMM and TRM showed that considering the causal relationships among the studied growth traits resulted in considerable re-ranking of the animals based on the estimated breeding values, especially for the top-ranked animals; implying that TRM had more plausibility over SMM for genetic evaluation of these traits in Moghani sheep.

Keywords: causal relationship, genetic evaluation, growth, lambs, predictive ability

Introduction

In livestock species such as sheep and goat, body weights at different ages are important traits which affect the profitability of the production systems. As pointed out by Boujenane and Kansari (2002), selection of the genetically superior animals for growth potential is a practicable method for enhancing meat production. Therefore, growth traits should be considered when designing breeding programs in sheep (Tosh and Kemp 1994). The erosion of animal genetic resources and, at the same time, the need to provide sustainable livelihoods to small holders, as the integral part of animal husbandry systems in the tropical areas, are challenging issues and require implementation of appropriate breeding strategies for enhancement of production efficiency (Cardellino, 2009). Accurate estimates of breeding values by multivariate animal models are necessary for setting up an

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appropriate selective procedure. Structural equation model (SEM) (Wright, 1921) is an extension of multivariate model which allows studying and testing cause-and-effect relationships between phenotypes. Gianola and Sorensen (2004) developed statistical genetic models for addressing conditions in which causal relationships exist among the traits in a multivariate framework. Rosa et al. (2011) stated that in any multiple traits genetic evaluation breeding program, studying potential causal relationships among the traits is necessary. By considering computational demands, fitting SEM is more parsimonious than standard multivariate models (SMM), which didn't enable to consider causal relationships, as uncorrelated residual effects were assumed for fitting SEM (Rosa et al., 2011).

The potential existence of causal relationships among growth traits has been studied in sheep (Amou Posht-e Masari et al., 2019, Mohammadi et al., 2020; Mokhtari et al., 2020) and goat (Mokhtari et al., 2018; Razmkabir et al., 2020) breeds by applying SEM. These studies have shown the superiority of multi-trait models with causal relationships over the SMM in terms of the predictive ability of models and ranking of animals based on the estimated breeding values.

Moghani is one of the most important Iranian native sheep, well known for large body size, tolerance to harsh environmental conditions and capability of producing heavy lambs. The breed is polled in both sexes, fat-tailed, predominantly white with brown face, legs and feet (Jafaroghli et al., 2010). Genetic parameters for growth traits of Moghani sheep by applying standard multivariate animal models, without considering causal relationships among the traits, are available (Jafaroghli et al., 2010). Therefore, the objective of the present study was to analyze the growth traits of Moghani sheep by two types of SEM-based multivariate models and comparing results with standard multivariate animal model. The effect of considering causal effects in the model on the ranking of the animals based on their predicted breeding values was also investigated.

Materials and methods

Data and flock management

Pedigree information used in the present study was collected during 1988 to 2011 at the Jafarabad Breeding Station of Moghani sheep, located in north-west of Iran. Data included the birth year, sex, birth type, dam age and the identification number of newborn lambs and their parents.

The flock was kept on the summer range from May to October, and on the winter range from November to April. Breeding season started from August and lasted to October, using a controlled mating system so that the identity of sire and dam of each lamb was known. Under the controlled mating system, ewes were organized into groups of 10-15 heads and each group was allocated to a fertile ram. Approximately 30-35 fertile rams were used annually for mating. To avoid inbreeding, in different breeding seasons, each group of ewes was mated to different rams. In other words, rams were used rotationally among ewe groups. Ewe lambs and ram lambs were bred for first time at approximately 18 months of age. Rams were used only for 1 breeding year, while the ewes were used for up to 8 years. Lambing commenced in January and lasted to February. Lambs were weaned at approximately 3 months of age. Male and female lambs were kept in separate flocks after 6 months of age. Breeding animals were selected in July, primarily based on the general appearance and coat color. Health care and veterinary treatments including vaccination and antiparasitic drug administration were practiced according to the station's routine protocols.

Evaluated traits

The investigated traits were birth weight (BW), weaning weight (WW), six-month weight (6MW), nine-month weight (9MW) and yearling weight (YW). Data and pedigree were monitored and edited several times and lambs with erroneous information were excluded from the data set. In addition, animals with body weights outside of the range of mean ±3×S.D. were excluded from the data set. The structure and summary of the data set used is presented in Table 1.

Table 1. Descriptive statistics for the weight traits in Moghani sheep

Item	Traits (kg) ¥				
	BW	WW	6MW	9MW	YW
Mean	4.51	24.31	35.22	34.43	38.88
S.D.	0.69	4.40	5.09	5.27	6.60
Min.	1.70	11.20	18.90	20.20	23.50
Max.	7.30	43.20	53.20	60.90	69.00
C.V. (%)	15.30	18.10	14.45	15.30	16.97

¥ BW: Birth weight; WW: Weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight

Statistical analyses

In mammalian species growth traits especially those measured early in life, are determined not only by the animal's own additive genetic merit but also by maternal effects. Previous studies confirmed the importance of including maternal effects in genetic evaluation models for growth traits in sheep (Amou Posht-e Masari et al., 2019; Mohammadi et al., 2020). Therefore, for studying the importance of maternal effects six animal models including different combinations of direct additive genetic, maternal additive genetic and maternal permanent environmental, were tested fitting a restricted maximum likelihood (REML) procedure by Wombat program of Meyer (2013). The models (in matrix notation) were as below:

$y = Xb + Z_1a + e$ Model 1

$y = Xb + Z_1a + Z_3pe + e$ Model 2

$y = Xb + Z_1a + Z_2m + e$ $\mathrm{Cov}(a,m) = 0$ Model 3

$y = Xb + Z_1a + Z_2m + e$	$Cov(a,m) = A\sigma_{am}$	Model 4
$y = Xb + Z_1a + Z_2m + Z_3pe + e$	$Cov(a,m) = 0$	Model 5
$y = Xb + Z_1a + Z_2m + Z_3pe + e$	$Cov(a,m) = A\sigma_{am}$	Model 6

where, **y** is a vector of records for the studied traits; **b, a, m**, **pe** and **e** are vectors of fixed, direct genetic, maternal genetic, maternal permanent environmental and the residual effects, respectively. The matrices of **X**, $\mathbf{Z_a}$, $\mathbf{Z_m}$, and $\mathbf{Z_{pe}}$ are design matrices associating corresponding effects to vector **y**. Also, **A** is the numerator relationship matrix and σ_{am} denotes covariance between additive and maternal effects. Common fixed effects included in the models for the studied traits were sex of lambs in 2 classes (male and female), dam age at lambing in 7 classes (2-8 years old), birth year in 23 classes (1988-2010) and birth type in 3 classes (single, twin and triplet). Interactions among fixed effects were also fitted. Age of lambs at weaning, six months, nine months and yearling body weight recordings (in days) was considered as a linear covariate for WW, 6MW, 9MW and YW, respectively. Analysis of fixed effects was carried out using the general linear model (GLM) procedure of SAS software (SAS, 2004). The interactions between fixed effects were not significant and omitted from the final model.

The Bayesian Information Criterion (BIC) (Schwarz, 1978) was applied for determining the most appropriate model among the tested models. In each case, the model with the lowest BIC was considered as the best model.

After selection of the most appropriate animal model for each trait, Bayesian Markov Chain Monte Carlo (MCMC) implementation was carried out applying the GIBBS2F90 program of Mizstal et al. (2002), which implements Gibbs sampling to evaluate the posterior density of the parameter estimates. The length of the chain and the burn-in period were examined by visual inspection of the trace plots of posterior samples of the parameters. For each multivariate model, 100,000 iterations were run and posterior samples from each chain were thinned considering thinning intervals of 10 iterations after discarding the first 20,000 iterations as burn-in. Hence, 8,000 samples were considered for computing features of the posterior distribution. Posterior analyses for calculating posterior means and posterior standard deviations were carried out applying the POSTGIBBSF90 program of Mizstal et al. (2002).

It was assumed that the direct additive and maternal additive genetic effects followed a multivariate normal distributions, a priori, with a null mean vector and a (co)variance matrix $\mathbf{G} \otimes \mathbf{A}$, where **G** and **A** are the genetic (co)variance matrix and numerator relationship matrix among animals, respectively. Furthermore, it was assumed that the vector of residual effects followed a multivariate normal distribution with a null mean vector and (co)variance matrix $\mathbf{R} \otimes \mathbf{I_n}$, where $\mathbf{I_n}$ is an identity matrix and **R** is the residual (co)variance matrix; $\otimes$ shows the Kronecker product. The SEMs are not identifiable at the likelihood level because of the presence of extra parameters including the structural coefficients. For achieving identification, it was assumed that residual correlations in system were uncorrelated. In other words in SEMs, **R** was assumed to be a diagonal matrix for the identification purposes.

Recursive models were handled by fitting parent trait as a covariate for other trait(s) while genetic correlations between traits were considered in multivariate analyses (Lopez de Maturana et al., 2007). In this case, trait(s) measured as parent causally influences other trait(s). Therefore, this methodology was applied in the present study.

Statistical measures for model comparisons

Schematic presentations of temporal recursive multivariate (TRM) and fully recursive multivariate (FRM) models are presented in Figures 1 and 2, respectively. The SMM, TRM and FRM were compared using deviance information criterion (DIC), predictive ability measures and Spearman's rank correlations between posterior means of genetic effects under the models. The DIC takes into account the trade-off between model goodness-of-fit and corresponding complexity of model. Model with smaller DIC values are better supported by the data.

For assessing the predictive ability of the models (SMM, TRM and FRM), the dataset was randomly partitioned five times into two sets including the training (50% of data set) and testing (retained 50% data set) sets. Then, solutions for all fixed and random effects of the training set were estimated and used to predict body weight records in the testing set. The model predictive ability was assessed by PREDICTF90 program of Mizstal et al. (2002) and compared applying two measures; first measure was mean square of error (MSE) as follow:

$$\mathrm{MSE} = \frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{n}$$

Where, y_i and $\hat{y}_i$ denote i^{th} observed and predicted record for each trait in testing data set and n is the number of records in testing data set. The second measure was the Pearson's correlation coefficient between the observed and predicted values ($r(y,\hat{y})$) in the testing set. The MSE and $r(y,\hat{y})$ values were calculated five times and averaged finally: lower MSE and higher $r(y,\hat{y})$ values indicated higher model superiority.

The models were also compared using Spearman's rank correlations between the posterior means of genetic effects for all, 50% top-ranked, 10% top-ranked and 1% top-ranked animals. For this purpose, breeding values (equivalent to standard multivariate model) were estimated following Konig et al. (2008):

$$\mathbf{BV}^{*} = \mathbf{\Lambda}^{-1}\,\mathbf{BV}$$

Where, **BV** is vector of breeding values estimated under SEM. The matrix **Λ** is the structural coefficients matrix, in which diagonal elements are filled with 1 and the off-diagonal elements are determined based on the causal relationships between the traits. Structural coefficients are in fact a type of regression coefficient, which are estimated by fitting SEMs (Gianola and Sorensen, 2004). The matrix of structural coefficients with five traits under a FRM, was as below:

$$\boldsymbol{\Lambda}_{5\times5}=\begin{bmatrix}1&0&0&0&0\\-\boldsymbol{\lambda}_{21}&1&0&0&0\\-\boldsymbol{\lambda}_{31}&-\boldsymbol{\lambda}_{32}&1&0&0\\-\boldsymbol{\lambda}_{41}&-\boldsymbol{\lambda}_{42}&-\boldsymbol{\lambda}_{43}&1&0\\-\boldsymbol{\lambda}_{51}&-\boldsymbol{\lambda}_{52}&-\boldsymbol{\lambda}_{53}&-\boldsymbol{\lambda}_{54}&1\end{bmatrix}$$

Where, the first trait affects second, third, fourth and fifth traits, the second trait affects third, fourth and fifth traits, the third trait affects fourth and fifth traits, and eventually the fourth trait has a causal effect on the fifth trait.

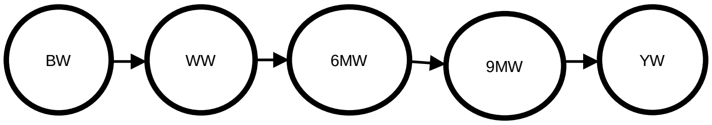

Figure 1. Temporal recursive model considered among weight traits in Moghani sheep (BW: Birth weight; WW: Weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight). Arrows represent the direction of causal effects.

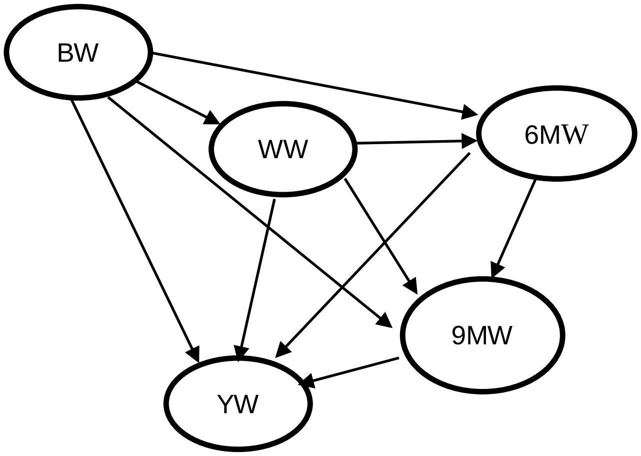

Figure 2. Multivariate fully recursive model considered among weight traits in Moghani sheep (BW: birth weight; WW: weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight). Arrows represent the direction of causal effects.

The matrix of structural coefficients with five traits under a TRM study was:

$$\boldsymbol{\Lambda}_{5\times5}=\begin{bmatrix}1&0&0&0&0\\-\boldsymbol{\lambda}_{21}&1&0&0&0\\0&-\boldsymbol{\lambda}_{32}&1&0&0\\0&0&-\boldsymbol{\lambda}_{43}&1&0\\0&0&0&-\boldsymbol{\lambda}_{54}&1\end{bmatrix}$$

Where, the first trait affects the second, the second one affects the third, the third trait affects the fourth one, and eventually the fourth trait has a causal effect on the fifth trait.

Results and discussion

General considerations

The BIC values of the six animal models for each trait are given in Table 2. According to BIC values, Model 3 which included direct additive genetic and maternal additive genetic effects, without considering covariance between them was the most appropriate model for BW and WW for other traits studied, Model 1, in which direct additive, genetic effects was the only random effect, selected as the best model. The necessity of considering maternal effects for genetic evaluation of the growth-related traits in sheep has been documented in the literature (Amou Posht-e Masari et al., 2019; Mokhtari et al., 2020; Mohammadi et al., 2020).

Statistical comparisons among the investigated multivariate models

The DIC values obtained under SMM, TRM and FRM were 89929.79, 88959.11 and 89896.21, respectively. Generally, fitting two types of structural equation-based models, TRM and FRM, resulted in lower DIC compared with SMM, indicating the importance of considering causal effects in multivariate genetic analyses of body weight traits in Moghani sheep. TRM had the lowest DIC among the tested multivariate models which was in agreement with findings of Amou Posht-e Masari et al. (2019) in Lori-Bakhtiari sheep and Mokhtari et al. (2020) in Kermani sheep breeds.

The SMM, TRM and FRM were also compared in terms of the predictive ability measured by average mean square of error (MSE) and average Pearson's correlation coefficient between observed and predicted records ($r(y,\hat{y})$) of traits (Table 3). Generally, for all the studied traits, FRM and TRM had lower MSE values compared to SMM, more pronouncing for 6MW, 9MW and YW. Comparing TRM and FRM, it was TRM which provide lower MSE and so ranked first. Similar trend was observed for the average Pearson's correlation coefficient between observed and predicted records. For all the studied traits, the highest values for $r(y,\hat{y})$ were obtained under TRM. In general, by considering the comparative measures, TRM was performed better than SMM and FRM. Therefore, TRM was selected for inferring causal relationships among the studied traits.

Amou Posht-e Masari et al. (2019) compared three multivariate models including standard multivariate, temporal recursive multivariate and fully recursive multivariate models for genetic evaluation of growth traits in Lori-Bakhtiari sheep and found the superiority of TRM over SMM and FRM in terms of predictive ability measures. They concluded that considering causal relationships among the studied growth traits in Lori-Bakhtiari sheep may provide a better explanation for biological relationships among the traits.

Mohammadi et al. (2020) compared predictive abilities of standard multivariate and two types of structural equation-based multivariate models (FRM and ICM) in terms of predictive ability for growth traits of Kurdi sheep and reported that models included causal relationships performed better than standard multivariate model as they resulted in lower mean square error and higher Pearson correlation coefficients.

Table 2. The BIC values for weight traits of Moghani sheep under different animal models

Model	Traits [¥]				
	BWT	WWT	6MW	9MW	12YW
Model 1	1081.511	-17909.6	**-15941.843**	**-14153.509**	**-13360.325**
Model 2	1082.819	-17913.3	-15916.408	-14143.377	-13354.492
Model 3	**1077.692**	**-17943.4**	-15915.464	-14143.389	-13356.354
Model 4	1080.649	-17914.1	-15917.974	-14142.488	-13356.732
Model 5	1091.826	-17909.2	-15915.433	-14145.360	-13358.023
Model 6	1094.485	-17913.8	-15917.639	-14144.792	-13358.743

[¥] BW: Birth weight; WW: Weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight
The best model is shown in bold face.

Table 3. Predictive ability for the weight traits under the different multivariate studied models

Traits [a]	Model [¥]					
	SMM		FRM		TRM	
	[b] MSE	[b] $r(y,\hat{y})$	[b] MSE	[b] $r(y,\hat{y})$	[b] MSE	[b] $r(y,\hat{y})$
BW	0.18	0.80	0.18	0.81	0.16	0.83
WW	6.91	0.81	6.81	0.81	5.35	0.86
6MW	10.28	0.79	7.55	0.84	6.27	0.87
9MW	11.22	0.79	6.70	0.87	6.47	0.89
YW	13.27	0.84	7.68	0.91	6.29	0.93

[a] BW: Birth weight; WW: Weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight
[b] MSE: mean square error, $r(y,\hat{y})$: Pearson correlation between observed and predicted values
[¥] SMM: Standard multivariate model, FRM: Fully recursive multivariate model, TRM: Temporal recursive multivariate model

Structural coefficients

Features of the posterior means and posterior standard deviations (PSD) for structural coefficients among the studied body weight traits obtained by applying TRM are presented in Table 4. All the estimated structural coefficients were positive and highly significant. Under TRM, BW had a direct causal effect of 1.19 on WW (Figure 1). Thus, it can be concluded that about 1.19 kg increase in WW will be expected following one kg increase in BW. Direct causal effects of WW on 6MW (0.67), 6MW on 9MW (0.72) and 9MW on YW (0.71) were positive and statistically significant (99% highest posterior density intervals did not include zero). In other words, 0.67 kg increase in 6MW, 0.72 kg increase in 9MW and 0.71 kg increase in YW will be expected by one kg increase in WW, 6MW and 9MW, respectively. In general, any improvement in BW (as a parent trait) had positive causal effects on the other body weight traits in Moghani sheep. Mokhtari et al. (2020) studied causal relationships among body weight traits of Kermani sheep using TRM and estimated causal effects of BW on WW and of WW on 6MW as 1.10 and 0.70 kg, respectively. Mohammadi et al. (2020) reported the causal effects of BW on WW, WW on 6MW, 6MW on 9MW and 9MW on YW of Kurdi sheep as 1.478, 0.737, 0.776 and 0.929 kg, respectively.

Table 4. Posterior means ± posterior standard deviation (PSD) for the structural coefficients under TRM in Moghani sheep

Traits [¥]	Mean ± PSD [¥¥]	99% HPD interval [¥¥]
BW-WW	1.19 ± 0.13	0.856-1.524
WW-6MW	0.67± 0.02	0.619-0.721
6MW-9MW	0.72 ± 0.02	0.669-0.771
9MW-YW	0.71 ± 0.02	0.659-0.761

[¥] BW: Birth weight; WW: Weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight.
[¥¥] PSD: Posterior Standard Deviation, 99% HPD intervals did not include zero.

Valente et al. (2013) pointed out that the genetic effects from SMM and SEM have different meanings, while the SMM represents overall genetic effects that included direct and indirect effects (which mediating by - other traits) on each trait, SEM measures only direct effects (which not mediating by other traits in the causal network). In the present study, as shown in Figure 1, BW had indirect causal effect on 6MW (mediated via WW), -

on 9MW (mediated via WW and 6MW) and on YW (mediated via WW, 6MW and 9MW). Causal effect of BW on 6MW, mediated via WW, was calculated as the product of direct causal effects of BW on WW (1.19) and WW on 6MW (0.67) which equals to 0.797. Mokhtari et al. (2020) reported indirect causal effect of WW on 6MW (mediated via WW) of Kermani lambs as 0.77 which was in agreement with the findings of the present study. A value of 1.312 was reported for causal effect of BW on 6MW (mediated through WW) by Mohammadi et al. (2020) in Kurdi sheep which was higher than the estimated value in the present study.

Considering the same manner, causal effects of BW on 9MW (mediated through WW and 6MW) and on YW (mediated through WW, 6MW and 9MW) were 0.574 and 0.407, respectively. Mohammadi et al. (2020) who applied TRM for analyzing growth traits of Kurdi sheep, reported values of 0.845 and 0.785 for indirect causal effects of BW on 9MW and indirect causal effects of BW on YW, respectively which were higher than current results.

Causal effects of WW on 9MW (mediated through 6MW) and for WW on YW (mediated through 6MW and 9MW) were calculated as 0.482 and 0.342, respectively (Table 4). As a result, any increase in WW of Moghani lambs significantly increases 6MW, 9MW and YW. Causal effect of 6MW on YW (mediated through 9MW) was calculated as 0.511. In Kurdi sheep, Mohammadi et al. (2020) reported values of 0.572 and 0.531 for indirect causal effects of WW on 9MW and indirect causal effects of WW on YW, respectively.

In the present study, indirect causal effect of 6MW on YW (which mediated via 9MW) was 0.511. This estimate was smaller than the value 0.721 as reported by Mohammadi et al. (2020) in Kurdi sheep.

Ranking of animals under SMM and TRM

Spearman's rank correlations between posterior means of direct genetic effects within the studied traits applying SMM and TRM for the total animals and 50%, 10% and 1% of top-ranked animals are shown in Table 5. In general, a descending trend was observed for Spearman's rank correlations between breeding values of animals obtained by SMM and TRM across all categories of animals selected, from all to 1% top-ranked animals. Therefore, causal relationships among the traits should be considered in genetic evaluation of growth traits in Moghani sheep because ignoring the causal relationships between traits may lead to inaccurate ranking of animals especially superior ones.

The highest Spearman's rank correlation between posterior means of direct genetic effects was obtained for BW. In other words, considering causal relationships among the studied growth traits of Moghani sheep had relatively very low impact on the posterior means of direct genetic effects of BW. When TRM was applied on growth traits of Moghani sheep (Figure 1) the parent trait was BW, which influenced all other traits but not influenced by the others. The obtained Spearman's rank correlation between posterior means of direct genetic effects of BW may be explained partly by such causal structure.

When 50% and 10% of top-ranked animals were considered, the lowest Spearman's rank correlation was obtained for YW (Table 5). There were substantial changes for rank correlations between posterior means of genetic effects under SMM and TRM for 1% top-ranked animals, except for BW; implied substantial re-ranking of animals for WW, 6MW, 9MW and YW under SMM and TRM especially for top-ranked animals. Latter result showed the importance of model choice in breeding value estimation. As a result, accounting for causal relationships among growth traits in Moghani sheep may has beneficial effects on accurate prediction of breeding values and consequently accurate ranking of animals. Similar pattern on re-ranking of animals under SEM-based models were also reported by Amou Posht-e Masari et al. (2019) in Lori-Bakhtiari sheep. Razmkabir et al. (2020) studied the effect of including the causal effects on genetic evaluation of growth traits in Markhoz goats and concluded that considering the causal relationships among the growth traits in kids could result in considerable re-ranking of animals based on their breeding values, especially for the top-ranked animals.

Table 5. Spearman's rank correlations of posterior means of the direct genetic effects for weight traits in Moghani sheep under SMM and TRM

Traits ¥	All animals	50% top-ranked	10% top-ranked	1% top-ranked
BW	0.95 **	0.97 **	0.97 **	0.96 **
WW	0.96 **	0.89 **	0.75 **	0.62 **
6MW	0.95 **	0.87 **	0.76 **	0.54 **
9MW	0.97 **	0.91 **	0.78 **	0.56 **
YW	0.96 **	0.89 **	0.70 **	0.51 **

¥ BW: Birth weight; WW: Weaning weight; 6MW: Six-month weight; 9MW: Nine-month weight; YW: Yearling weight.
**: P-value <0.01.

Conclusions

Inferring relationships among the studied body weight traits in Moghani sheep could help to identify development of the growth process from birth to yearling age. In the current study, three multivariate animal models including standard (SMM), fully recursive (FRM) and temporal recursive (TRM) models were used for genetic evaluation of Moghani lamb. Regarding the predictive ability, TRM was superior to SMM and FRM -

as it provided predictions with lower MSE and higher Pearson's correlation coefficients between observed and predicted records. Comparisons of rank correlations between posterior means of direct genetic effects for the growth traits under SMM and TRM revealed that including the causal relationships among growth traits of Moghani sheep in the model of genetic evaluation could cause considerable re-ranking for the animals, especially top-ranked ones, in terms of the estimated breeding values.

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