

## MODEL COMPARISONS AND GENETIC PARAMETER ESTIMATES OF GROWTH TRAITS IN BALUCHI SHEEP

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### ABSTRACT

Genetic and non-genetic parameters were estimated for growth traits and average daily weight gains of Iranian Baluchi lambs using univariate and multivariate models. Data on body weight collected for a period of 25 years (1984-2009) were used to model the growth trajectory and estimate genetic parameters. Studied traits were birth weight (BW), 3-month weight (3MW), 6-month weight (6MW), 9-month weight (9MW), yearling weight (YW), pre-weaning average daily gain (ADG1) and post-weaning average daily gain (ADG2). Genetic parameters were estimated using the restricted maximum likelihood (REML) procedure under univariate and multivariate animal models. Random effects were explored by fitting additive direct genetic effects, maternal additive genetic effects, maternal permanent environmental effects, the covariance between direct and maternal genetic effects and common litter effects in twelve different models for analysis of each trait. The heritability, estimated from the most appropriate model for BW, 3MW, 6MW, 9MW, YW, ADG1 and ADG2 trait, were  $0.062 \pm 0.02$ ,  $0.12 \pm 0.02$ ,  $0.16 \pm 0.03$ ,  $0.21 \pm 0.03$ ,  $0.17 \pm 0.03$ ,  $0.08 \pm 0.02$  and  $0.1 \pm 0.02$ , respectively. The maternal heritabilities of these traits were  $0.09 \pm 0.02$ ,  $0.04 \pm 0.01$ ,  $0.045 \pm 0.017$ ,  $0.015 \pm 0.02$ ,  $0.02 \pm 0.012$ ,  $0.03 \pm 0.01$  and  $0.05 \pm 0.02$ , respectively. The present study shows the importance of inclusion of maternal effects in designing appropriate breeding programs for genetic improvement in Baluchi lambs for growth traits.

**Key words:** growth traits; average daily weight gain; variance components; heritability; Baluchi sheep

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### INTRODUCTION

The sheep population in Iran in 2011 was about 54 million heads, including 27 breeds and ecotypes (the Iranian ministry of agriculture, 2011). Among them Baluchi sheep is one of the most widely occurred breed, which represents approximately 30 % (near to 15 million head) of total sheep population (Madad and Ghazanfari, 1999). The body colour is generally white with black spots at the end of the muzzle, ears, eyes, and metacarpus and metatarsus area. This breed is widely distributed from north-east to south-east of the country and is reared mainly for meat purposes.

Growth rate of animals is influenced not only by direct additive genetic effects but also affected by

maternal genetic and maternal permanent environment. Results of several studies showed that including of the maternal effects into models caused more accurate estimation of (co)variance and genetic parameter of production and reproductive traits (Miraei-Ashtiani *et al.*, 2007; Zamani and Mohammadi, 2008; Mohammadi *et al.*, 2013ab).

Thus, accurate estimation of (co)variance components is outcome for designing any breeding program and genetic evaluation system. Because of lack of such comprehensive estimates for growth traits of Baluchi sheep in Iran this study has been performed with the objective of accurate estimation of (co)variance components and corresponding genetic parameters for growth traits of Baluchi sheep.

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## MATERIAL AND METHODS

### Flock management and data sources

Data used in the present study were collected from Breeding Sheep Center, located in North East of Iran in Mashhad, Khorasan Razavi province. During the spring and summer, the flock was kept on pastures and in the autumn it was grazed on wheat and barley stubbles. During the winter, the lambs were kept indoors and hand-fed. Supplementary feed, offered to all animals during winter and to ewes late in pregnancy, consisted of wheat and barley straw, alfalfa hay, sugar beet pulp and concentrate. The investigated traits in this study were: birth weight (BW), 3-month weight (3MW), 6-month weight (6MW), 9-month weight (9MW), yearling weight (YW), pre-weaning average daily gain (ADG1) and post-weaning average daily gain (ADG2) with using records of 45,656 lambs of 1,380 sires and 13,988 dams born between 1984 to 2009. The structure of the data used in the analysis is shown in Table 1.

### Statistical analysis

Data were analyzed by a least squares analysis of variance using the general linear model (GLM) procedure of the SAS software package (SAS, 2004). The fixed effects considered were: sex of lambs in two classes (male-female), type of birth in three classes (single, twins, triplets), age of the dam at lambing in seven classes (2 to 8 years old), year of birth in 26 classes (1984 to 2009) and number of flocks in eight classes (1 to 8), respectively. The interactions between fixed factors were not significant and, therefore, these factors were excluded from the final model. Moreover, the age of lambs was placed in the model as a covariate factor. (Co)variance components and corresponding genetic parameters for the studied traits were estimated with the help of twelve univariate animal models. Tested models (in matrix notation) were as follows:

$$\begin{array}{ll}
 y = Xb + Z_a a + e & \text{Model (1)} \\
 y = Xb + Z_a a + Z_c c + e & \text{Model (2)} \\
 y = Xb + Z_a a + Z_m m + e & \text{Cov(a,m)=0 Model (3)} \\
 y = Xb + Z_a a + Z_m m + e & \text{Cov(a,m)=A}\sigma_{am} \text{ Model (4)} \\
 y = Xb + Z_a a + Z_m m + Z_c c + e & \text{Cov(a,m)=0 Model (5)} \\
 y = Xb + Z_a a + Z_m m + Z_c c + e & \text{Cov(a,m)=A}\sigma_{am} \text{ Model (6)} \\
 y = Xb + Z_a a + Z_4 l + e & \text{Model (7)} \\
 y = Xb + Z_a a + Z_c c + Z_1 l + e & \text{Model (8)} \\
 y = Xb + Z_a a + Z_m m + Z_1 l + e & \text{Cov(a,m)=0 Model (9)} \\
 y = Xb + Z_a a + Z_m m + Z_1 l + e & \text{Cov(a,m)=A}\sigma_{am} \text{ Model (10)} \\
 y = Xb + Z_a a + Z_m m + Z_c c + Z_1 l + e & \text{Cov(a,m)=0 Model (11)} \\
 y = Xb + Z_a a + Z_m m + Z_c c + Z_1 l + e & \text{Cov(a,m)=A}\sigma_{am} \text{ Model (12)}
 \end{array}$$

Where  $y$  is a vector of records for the different traits;  $a$ ,  $b$ ,  $c$ ,  $m$ ,  $l$  and  $e$  are vectors of direct additive genetic effects, fixed effects, maternal permanent

environmental effects, maternal additive genetic, common environmental and residual effects, respectively;  $X$ ,  $Z_a$ ,  $Z_m$ ,  $Z_c$  and  $Z_l$  are design matrices associating the fixed effects, direct additive genetic effects, maternal permanent environmental effects, maternal additive genetic effects and common environmental effects to vector of  $y$ , respectively. All the means of random effects are equal to zero. In the matrix notation, the (co)variance structure was as follows:

$$v \begin{bmatrix} a \\ m \\ c \\ l \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & A\sigma_{am} & \circ & \circ & \circ \\ A\sigma_{am} & A\sigma_m^2 & \circ & \circ & \circ \\ \circ & \circ & Id\sigma_c^2 & \circ & \circ \\ \circ & \circ & \circ & ll\sigma_l^2 & \circ \\ \circ & \circ & \circ & \circ & In\sigma_e^2 \end{bmatrix},$$

where  $A$  is the additive numerator relationship matrix,  $\sigma_a^2$ , is the direct additive genetic variance,  $\sigma_m^2$  is the maternal additive genetic variance,  $\sigma_{am}$  is the direct-maternal additive genetic covariance,  $\sigma_c^2$  is the maternal permanent environmental variance,  $\sigma_l^2$  is the common environmental variance,  $\sigma_e^2$  is the residual variance and  $I_d$ ,  $I_c$  and  $I_n$  are identity matrixes with orders equal to number of dams, litters and records, respectively. Also, in these models  $\sigma_{am}$  is the (co)variance of direct and maternal additive genetic effects. All traits were analyzed with WOMBAT software package by AI-REML algorithm (Meyer, 2006). The most appropriate model for each trait was selected based on Akaike's information criterion (AIC) (Akaike, 1974):

$$AIC_i = -2 \log L_i + 2 p_i$$

where  $\log L_i$  represents the maximized log likelihood, and  $p_i$  is the number of parameters obtained for each model. The model that has the lowest AIC, is the appropriate model for that trait. Total heritability was estimated according to the following equation:

$$h_t^2 = \frac{\sigma_a^2 + 0.5 \sigma_m^2 + 1.5 \sigma_{a,m}}{\sigma_p^2}$$

Genetic and phenotypic correlations were estimated using bivariate analyses applying the best model determined in univariate analyses. If the values of  $-2 \log$  likelihood variance in the Simplex function were below  $10^{-8}$ , it was assumed convergence had been achieved (Mohammadi *et al.*, 2013b).

**Table 1: Descriptive statistics for traits studied**

Traits <sup>a</sup>	No. of records	Mean (kg)	SD <sup>b</sup> (kg)	CV (%)	No. of dams	No. of sires
BW	13682	3.9	0.8	20	3648	371
3MW	10015	22.9	5.27	23	2842	267
6MW	8150	29.8	5.56	18	2624	249
9MW	7194	33.1	5.4	16	2480	247
YW	6615	38.8	6.83	17	2394	246
ADG1	10015	0.20	0.061	30	2842	267
ADG2	8119	0.034	0.022	64	2624	249

Traits: BW: birth weight, 3MW: 3 month weight, 6MW: 6 month weight, 9MW: 9 month weight, YW: yearling weight, pre-weaning average daily gain: ADG1 and post-weaning average daily gain: ADG2

**Table 2: Least square means  $\pm$  SE of pre- and post-weaning growth traits of Baluchi lambs**

Fixed effects	Traits <sup>a</sup>						
	BW(kg)	3MW(kg)	6MW(kg)	9MW(kg)	YW(kg)	ADG1(kg)	ADG2
Overall mean	3.9 $\pm$ 0.80	22.9 $\pm$ 5.27	29.8 $\pm$ 5.56	33.1 $\pm$ 5.40	38.8 $\pm$ 6.83	0.2 $\pm$ 0.061	0.03 $\pm$ 0.022
Sex	**	**	**	**	**	**	**
Male	4.06 <sup>a</sup> $\pm$ 0.81	23.9 <sup>a</sup> $\pm$ 4.87	31.29 <sup>a</sup> $\pm$ 4.73	34.61 <sup>a</sup> $\pm$ 5.55	41.23 <sup>a</sup> $\pm$ 6.96	0.214 <sup>a</sup> $\pm$ 0.062	0.037 <sup>a</sup> $\pm$ 0.020
Female	3.81 <sup>b</sup> $\pm$ 0.87	21.87 <sup>b</sup> $\pm$ 5.44	28.41 <sup>b</sup> $\pm$ 5.91	31.55 <sup>b</sup> $\pm$ 4.77	36.4 <sup>b</sup> $\pm$ 5.70	0.19 <sup>b</sup> $\pm$ 0.058	0.030 <sup>b</sup> $\pm$ 0.012
Type of birth	**	**	**	**	**	**	**
Single	4.30 <sup>a</sup> $\pm$ 0.74	25.24 <sup>a</sup> $\pm$ 4.9	31.83 <sup>a</sup> $\pm$ 5.30	34.57 <sup>a</sup> $\pm$ 5.39	40.06 <sup>a</sup> $\pm$ 6.9	0.22 <sup>a</sup> $\pm$ 0.06	0.033 <sup>a</sup> $\pm$ 0.02
Twin	3.66 <sup>b</sup> $\pm$ 0.66	21.04 <sup>b</sup> $\pm$ 4.6	28.25 <sup>a</sup> $\pm$ 5.05	31.80 <sup>ab</sup> $\pm$ 4.90	37.7 <sup>a</sup> $\pm$ 6.5	0.18 <sup>b</sup> $\pm$ 0.05	0.035 <sup>a</sup> $\pm$ 0.03
Triplet	3.02 <sup>c</sup> $\pm$ 0.70	19.43 <sup>b</sup> $\pm$ 4.8	26.67 <sup>a</sup> $\pm$ 5.23	30.50 <sup>a</sup> $\pm$ 5.40	36.50 <sup>a</sup> $\pm$ 6.7	0.17 <sup>b</sup> $\pm$ 0.05	0.034 <sup>a</sup> $\pm$ 0.03
Age of dam (Year)	**	**	*	*	**	**	*
2	3.81 <sup>a</sup> $\pm$ 0.78	22.65 <sup>ab</sup> $\pm$ 5.10	29.87 <sup>ab</sup> $\pm$ 5.52	32.87 <sup>a</sup> $\pm$ 5.42	38.18 <sup>a</sup> $\pm$ 6.87	0.20 <sup>ab</sup> $\pm$ 0.050	0.035 <sup>ab</sup> $\pm$ 0.02
3	3.98 <sup>b</sup> $\pm$ 0.80	23.13 <sup>ab</sup> $\pm$ 5.21	30.07 <sup>a</sup> $\pm$ 5.61	33.22 <sup>b</sup> $\pm$ 5.44	38.94 <sup>b</sup> $\pm$ 6.94	0.20 <sup>a</sup> $\pm$ 0.059	0.033 <sup>ab</sup> $\pm$ 0.02
4	3.97 <sup>b</sup> $\pm$ 0.81	22.86 <sup>ab</sup> $\pm$ 5.30	29.68 <sup>b</sup> $\pm$ 5.44	33.23 <sup>b</sup> $\pm$ 5.45	39.15 <sup>b</sup> $\pm$ 6.80	0.20 <sup>b</sup> $\pm$ 0.060	0.033 <sup>a</sup> $\pm$ 0.02
5	3.99 <sup>bc</sup> $\pm$ 0.79	22.94 <sup>ab</sup> $\pm$ 5.20	29.95 <sup>ab</sup> $\pm$ 5.63	33.05 <sup>ab</sup> $\pm$ 5.21	38.63 <sup>ab</sup> $\pm$ 6.65	0.20 <sup>a</sup> $\pm$ 0.061	0.035 <sup>ab</sup> $\pm$ 0.02
6	3.98 <sup>bc</sup> $\pm$ 0.83	22.84 <sup>ab</sup> $\pm$ 5.40	29.86 <sup>ab</sup> $\pm$ 5.69	33.00 <sup>ab</sup> $\pm$ 5.50	39.2 <sup>b</sup> $\pm$ 6.90	0.20 <sup>ab</sup> $\pm$ 0.060	0.034 <sup>ab</sup> $\pm$ 0.02
7	4.04 <sup>bc</sup> $\pm$ 0.80	22.92 <sup>ab</sup> $\pm$ 5.10	29.97 <sup>ab</sup> $\pm$ 5.49	33.4 <sup>ab</sup> $\pm$ 4.94	39.5 <sup>b</sup> $\pm$ 6.30	0.20 <sup>ab</sup> $\pm$ 0.070	0.037 <sup>b</sup> $\pm$ 0.02
8	4.18 <sup>c</sup> $\pm$ 0.85	23.21 <sup>ab</sup> $\pm$ 5.60	30.39 <sup>ab</sup> $\pm$ 5.69	33.4 <sup>ab</sup> $\pm$ 5.20	40.2 <sup>b</sup> $\pm$ 6.50	0.18 <sup>ab</sup> $\pm$ 0.070	0.039 <sup>b</sup> $\pm$ 0.02
Year of birth	**	**	**	**	**	**	**

<sup>a</sup>for trait abbreviations see footnote of Table 1. \*P < 0.05; \*\*P < 0.01; and ns: non-significant (P > 0.05)

## RESULTS AND DISCUSSION

### Fixed Factors

Least square means for studied traits are shown in Table 2. The result of variance analysis showed that the year of birth had significant effects on all studied

traits (p < 0.01). Sex of lamb had significant effect on all traits (p < 0.01). The significant effect of fixed factors in these characters could be assigned partly to the differences in the endocrine system of female and male lambs. Also, age of dam had significant effect on BW, 3MW, 6MW, 9MW, YM, ADG1, and ADG2 (p < 0.05).

Type of birth had a significant effect on weight changes in all traits ( $p < 0.01$ ). Single born lambs had higher body weights and pre-weaning growth rate than twins and triplets.

### Heritability estimates

Estimates of phenotypic variance using different models were generally similar for all considered traits. Residual variance was also similar in models 1 to 6, but was reduced when models 7 to 12 were fitted. The estimations of (co)variance components and corresponding genetic parameters are presented in Table 4. Also, determination of the most appropriate model of each trait is shown in bold in Table 3.

The most appropriate models for BW, ADG1, and 3MW were Model 12, 11 and 5 respectively. The most appropriate models for ADG2, 6MW, 9MW and YW were Model 9, 5, 9 and 10 respectively.

Maternal permanent environmental effects had a considerable impact on variation for BW, 3MW, 6MW, 9MW and ADG1. Maternal permanent environmental estimates of 0.13 were obtained for both ADG and 3MW. Estimated correlations between direct and maternal genetic effects for various traits are presented in Table 4. Estimates of the genetic correlation between direct and maternal genetic effects varied between traits and ranged from 0.47 for BW to 0.96 for YW, and 0.84 for ADG2, respectively.

### Correlation estimates

Estimates of correlations between growth traits are presented in Table 5. There was no contrast

relationship between these traits in terms of phenotypic, genetic and environmental correlations accordingly, selection for any of these body weights will bring out positive response to selection for others. Estimates of additive genetic correlations between body weights were positive and high; varied from 0.60 for BW and YW to 0.97 for 9MW and YW. Phenotypic correlation estimates ranged from 0.30 for BW and YW to 0.79 for 9MW and YW and estimates of environmental correlation from 0.18 for BW and YW to 0.71 for 9MW and YW.

In general, the values observed in this study are in agreement with the estimates reported by the other researchers (Zamani and Mohammadi, 2008; Mohammadi *et al.*, 2013a). Maternal additive genetic correlation estimates between body weights were positive and ranged from 0.67 (between BW and 3MW) to 0.98 (between 9MW and YW).

Differences in managing practice, feed availability, climatic conditions and breeding systems through years, are possible reasons for significant effects of year on the considered traits (Mohammadi *et al.*, 2013a). According to the previous reports, the growth rate of female lambs was slower than in male lambs, and thus their weight was less, respectively (Mohammadi *et al.*, 2013b). Also, competition for milk consumption can be effective between twins and triplets particularly in pre-weaning period, which was consistent with other reports (Ozcan *et al.*, 2005). Including of birth age as a correlated variable into the statistical model (covariate) had a significant effect on all traits ( $p < 0.01$ ).

The estimate of direct heritability for BW in

**Table 3: AIC values <sup>a</sup> under different models for the body weight traits<sup>b</sup>**

Model	Traits						
	BW	3MW	6MW	9MW	YW	ADG1	ADG2
Model 1	-747.83	38393.30	32585.600	28200.62	27692.470	85775.160	55535.36
Model 2	-1290.25	38281.20	32524.440	28148.97	27673.068	85670.260	55535.36
Model 3	-1276.83	38304.90	32528.880	28152.35	27673.068	85702.006	55517.68
Model 4	-1275.82	104259	43013.640	28152.35	27670.480	85702.006	55517.68
Model 5	-1336.49	<b>38275.6</b>	<b>32519.040</b>	28150.53	27675.032	85666.060	55533.70
Model 6	-1337.63	38275.60	32519.060	28141.84	27667.900	85667.950	55519.10
Model 7	5182.90	38372.61	32549.740	28183.18	27677.130	85748.030	55509.18
Model 8	-1561.26	38281.14	32519.272	28144.00	27666.192	85667.740	55511.18
Model 9	-1579.16	38299.86	32528.890	<b>28137.43</b>	27668.078	85691.580	<b>55495.32</b>
Model 10	-1581.24	105059.50	69195.322	28138.45	<b>27660.470</b>	85691.580	55495.32
Model 11	-1608.06	38282.23	32526.774	28147.44	27668.000	<b>85663.300</b>	55510.64
Model 12	<b>-1612.29</b>	38283.06	32526.924	28138.45	27660.550	85665.230	55497.32

<sup>a</sup> as deviations from the model with the lowest AIC value

<sup>b</sup> for trait abbreviations see footnote of Table 1

**Table 4: Estimates of (co) variance components and genetic parameters for the body weight traits with the best model**

Traits <sup>a</sup>	Model	$\sigma_a^2$	$\sigma_m^2$	$\sigma_{pe}^2$	$\sigma_l^2$	$\sigma_{a,m}$	$\sigma_e^2$	$\sigma_p^2$	$h_a^2 \pm S.E$	$m^2 \pm S.E$	$c^2 \pm S.E$	$l^2 \pm S.E$	$r_{a,m} \pm S.E$	$h_t^2$
BW	12	0.023	0.034	0.03	0.87	0.013	0.18	0.37	0.062 ± 0.02	0.09 ± 0.02	0.09 ± 0.02	0.23 ± 0.01	0.47 ± 0.02	0.15
3MW	5	2.28	0.70	1.46	-	-	13.13	17.75	0.12 ± 0.02	0.04 ± 0.01	0.08 ± 0.01	-	-	0.15
6MW	5	3.56	0.95	1.29	-	-	15.32	21.11	0.16 ± 0.03	0.045 ± 0.10	0.06 ± 0.016	-	-	0.19
9MW	9	4.11	0.28	1.43	1.17	-	12.62	19.63	0.21 ± 0.03	0.015 ± 0.20	0.07 ± 0.02	0.06 ± 0.03	-	0.21
YW	10	4.41	0.50	-	2.43	1.44	16.90	25.79	0.17 ± 0.03	0.02 ± 0.02	-	0.09 ± 0.03	0.96 ± 0.37	0.25
ADG1	11	174	57.80	152	85.69	-	1542.6	2013	0.08 ± 0.02	0.03 ± 0.01	0.07 ± 0.01	0.13 ± 0.03	-	0.01
ADG2	9	35.26	16.54	-	45.007	-	273.4	349.9	0.10 ± 0.02	0.05 ± 0.02	-	0.13 ± 0.02	0.84 ± 0.08	0.24

$\sigma_a^2$ : direct additive genetic variance;  $\sigma_m^2$ : maternal additive genetic variance;  $\sigma_{pe}^2$ : maternal permanent environmental variance;  $\sigma_l^2$ : common litter variance;  $\sigma_{a,m}$ : covariance between direct and maternal additive genetic effects;  $\sigma_e^2$ : residual variance;  $\sigma_p^2$ : phenotypic variance;  $h_a^2$ : direct heritability;  $m^2$ : maternal heritability;  $c^2$ : ratio of maternal permanent environmental variance to phenotypic variance;  $l^2$ : ratio of common litter variance to phenotypic variance;  $r_{a,m}$ : direct - maternal genetic correlation; *S.E*: standard error;  $h_t^2$ : total heritability

<sup>a</sup> for trait abbreviations see footnote of Table 1

**Table 5: Correlation estimates among studied traits under bivariate animal models**

Trait 1	Trait 2	$r_{a12}^b$	$r_{p12}$	$r_{m12}$	$r_{e12}$
BW	3MW	0.72 ± 0.08	0.40 ± 0.010	0.67 ± 0.04	0.29 ± 0.01
	6MW	0.65 ± 0.09	0.36 ± 0.010	0.69 ± 0.05	0.25 ± 0.02
	9MW	0.71 ± 0.08	0.35 ± 0.010	0.71 ± 0.06	0.21 ± 0.02
	YW	0.60 ± 0.10	0.30 ± 0.010	0.75 ± 0.08	0.18 ± 0.02
	ADG1	0.52 ± 0.12	0.25 ± 0.010	0.54 ± 0.05	0.17 ± 0.01
	ADG2	-0.11 ± 0.14	0.034 ± 0.010	0.40 ± 0.14	0.025 ± 0.02
3MW	6MW	0.89 ± 0.03	0.72 ± 0.010	0.97 ± 0.02	0.65 ± 0.01
	9MW	0.82 ± 0.05	0.63 ± 0.010	0.94 ± 0.03	0.55 ± 0.01
	YW	0.85 ± 0.04	0.58 ± 0.090	0.88 ± 0.05	0.49 ± 0.01
	ADG1	0.85 ± 0.03	0.88 ± 0.010	0.87 ± 0.02	0.89 ± 0.01
	ADG2	0.13 ± 0.14	-0.22 ± 0.010	0.18 ± 0.21	-0.30 ± 0.02
6MW	9MW	0.96 ± 0.02	0.78 ± 0.050	0.97 ± 0.02	0.70 ± 0.01
	YW	0.95 ± 0.02	0.71 ± 0.010	0.93 ± 0.03	0.63 ± 0.01
	ADG1	0.82 ± 0.05	0.58 ± 0.010	0.73 ± 0.05	0.51 ± 0.01
	ADG2	0.52 ± 0.10	0.55 ± 0.010	0.51 ± 0.17	0.58 ± 0.01
9MW	YW	0.97 ± 0.01	0.79 ± 0.050	0.98 ± 0.03	0.71 ± 0.03
	ADG1	0.70 ± 0.07	0.49 ± 0.010	0.78 ± 0.06	0.12 ± 0.02
	ADG2	0.66 ± 0.09	0.32 ± 0.010	0.52 ± 0.09	0.27 ± 0.02
YW	ADG1	0.82 ± 0.05	0.46 ± 0.010	0.63 ± 0.09	0.37 ± 0.02
	ADG2	0.60 ± 0.10	0.27 ± 0.012	0.26 ± 0.26	0.23 ± 0.02
ADG1	ADG2	0.31 ± 0.05	-0.21 ± 0.040	-0.12 ± 0.21	-0.27 ± 0.05

<sup>a</sup> the symbols are the same as Table 1

$r_{a12}^b$ : direct genetic correlation between trait 1 and trait 2;  $r_{p12}$ : phenotypic correlations between trait 1 and 2;  $r_{m12}$ : maternal additive genetic correlation between trait 1 and 2;  $r_{e12}$ : residual correlations between trait 1 and 2

the current study (0.062) is lower than in the report of Mohammadi *et al.* (2013b) (0.15). Lower heritability of birth weight compared to the other weights is related to the following reasons. Fetal growth is influenced by genetic and environmental factors such as the placenta and the fetal nutrition by a dam. Therefore, environmental factors affecting dam growth, especially the quality and quantity of food and the storage of food for dam can influence the growth of the embryo. The obtained direct heritability estimate of 0.08 for ADG1 agrees with those reported by Ozcan *et al.* (2005) and Ghafouri-Kesbi *et al.* (2008). There is higher estimate reported for direct heritability of ADG1 (Mohammadi *et al.*, 2013b; Abegaz *et al.*, 2007). In the present research the estimate of direct heritability for 3MW (0.12) corresponds to the data of Jafaroghli *et al.* (2010). Higher estimate (Mohammadi *et al.* 2013a; 0.16; Mohammadi *et al.* 2013b; 0.19) have also been reported. The reason for low heritability is that the lambs are more affected by breast milk during infancy. Estimated  $m^2$  for birth weight, which is the ratio of maternal additive variance to phenotypic variance, is 0.09. Estimated maternal heritability of 0.03 for ADG1 agrees with that reported by Ghafouri-Kesbi *et al.* (2008). Thus, maternal effects and maternal power led to the increase in error variance and thus decrease in the heritability. The estimated  $m^2$  for 3MW was 0.04, whilst Maria *et al.* (1993) stated it to be 0.34. Also, total heritability estimate for BW and 3MW (0.15) corresponds to those reported by Mohammadi *et al.* (2013a).

Low estimate of direct heritability obtained for ADG2 in the present study (0.1) is similar to the estimate reported by Ghafouri-Kesbi *et al.* (2008) -0.09. In contrast to present estimate, Abegaz *et al.* (2007) obtained lower values. The estimate of direct heritability for 6MW in this study (0.16) is higher than the estimate by Mohammadi *et al.* (2013b; 0.21) and is lower than by Ghafouri-Kesbi *et al.* (2008).

Also, the estimate of direct heritability for 9MW in this study (0.21) is approximately compatible with previous results in the Shal breed by Mohammadi *et al.* (2013a; 0.18). Moreover, the obtained direct heritability value for YW (0.17) was in accordance with the estimate of Mohammadi *et al.* (2013a; 0.19). As it is explicit, direct heritability has had upward trend, which has been proved by different researchers. The estimated value for maternal heritability of ADG2 (0.05) was in concordance with estimates of Mohammadi *et al.* (2013a) in Shal sheep. Also, maternal heritability for 6MW was estimated to be 0.07 (Abegaz *et al.*, 2007), whilst in our study this parameter was estimated to be 0.045. The estimate of maternal heritability for 9MW in the present study (0.015) is higher than the estimate published by (Ghafouri-Kesbi *et al.*, 2008) -0.05. The obtained maternal heritability value for YW (0.02) was

in accordance with the estimate of Notter *et al.* (1997; 0.05).

In addition,  $c^2$  for 6MW was estimated to be 0.06, that was lower than the results reported by others researches (Mohammadi *et al.* (2013b; 0.06). The rate of  $c^2$  for 9MW was estimated to be 0.07, which is in accordance with results of others researches (Ghafouri-Kesbi *et al.*, 2008; 0.02).

The results indicate that maternal additive genetic effects, which regard to the growth of fetus, could have some beneficial effect on the post-natal growth traits too. In the other words, body weight from birth to 6MW of age is partly influenced by similar genes of the dam in terms of maternal genetic effects.

Maternal genetic correlation for BW-3MW was 0.67, which is in agreement with the estimates of Abegaz *et al.* (2007) and Mohammadi *et al.* (2013b).

The estimates of correlations between growth rate and body weights are presented in Table 5. Phenotypic and direct genetic correlation estimates between post-weaning and pre-weaning growth rate was negative implying that different mechanisms are responsible for the expression of respective pre-weaning and post-weaning traits. Negative phenotypic and genetic correlation estimates were obtained for ADG1-ADG2.

It appears that lambs with higher gain in the pre-weaning period have less gain and are also less efficient during the post-weaning period at the phenotypic and genetic level. Similar to our estimate, a negative correlation between ADG1 and ADG2 has been reported by several authors (Abegaz *et al.*, 2007, Mohammadi *et al.*, 2010).

Direct genetic correlation estimates of post-weaning growth rate with BW was negative, whilst pre-weaning growth rate with BW was positive. Several authors have been reported results similar to our estimates (Abegaz *et al.*, 2007; Mohammadi *et al.*, 2013b). They stated that 3MW and ADG1 are genetically the same traits, and the selection can be performed based on one of them. Because Iranian farmers generally sell their lambs at 3MW, if selection is performed on 3MW, an improvement in 3MW and all correlated traits would be expected. Phenotypic correlations were varied from -0.22 between 3MW and ADG2 to 0.88 between ADG1 and 3MW. In general, these values were consistent with the published estimates of other researches (Abegaz *et al.*, 2007; Mohammadi *et al.*, 2013b).

## CONCLUSION

The present research contributes to the model comparison and estimation of genetic parameters in fat-tailed sheep. It was observed that models containing both maternal genetic effects and direct genetic effects could better explain the genetic variation observed in

early growth traits. The genetic correlation between ADG1 and 3MW was positive, indicating that 3MW and ADG1 are genetically the same traits, and thus selection can be performed based on one of them. Because Iranian farmers generally sell their lambs at 3MW, if the selection is performed on 3MW, an improvement in 3MW and all correlated traits would be expected.

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