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Original Article

Relative growth rate in sheep: heritability and relationship with absolute growth rate and body weight

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Abstract

Data and pedigree information collected between 1990 and 2005 at the Zandi Sheep Breeding Station were used to estimate heritability for relative growth rate (RGR) in five growth phases, namely birth to weaning (RGR1), weaning to 6-month (RGR2), weaning to 9-month (RGR3), weaning to yearling (RGR4), and 6 months to yearling (RGR5) and to estimate genetic and phenotypic correlations with corresponding absolute growth rates (AGR1, AGR2, AGR3, AGR4, and AGR5) and body weight at different ages (birth weight, BW; weaning weight, WW; 6-month weight, W6; 9-month weight, W9 and yearling weight, YW). A derivative-free algorithm combined with a series of six univariate linear animal models was used to estimate heritability coefficients. Best model for each trait was determined with Akaike's Information Criterion (AIC). (Co)variance components between relative growth rate, absolute growth rate and body weights were estimated using a multivariate analysis. Estimates of direct heritability were 0.13, 0.12, 0.15, 0.10, and 0.04 for RGR1, RGR2, RGR3, RGR4, and RGR5, respectively. Estimates of additive coefficient of variations (CV_A) ranged from 2.53% (RGR1) to 12.74% (RGR5). Genetic correlations ranged from -0.73 (RGR1-AGR5) to 0.99 (RGR1-AGR2) and the phenotypic correlations ranged from -0.75 (RGR1-AGR5) to 0.94 (RGR2-AGR2). In sum, results indicated that genes with additive effects contributed little in the phenotypic variation of RGR in the body weight of Zandi lambs and for this reason the magnitude of possible genetic change through selection would be low. Selection for pre-weaning RGR was recommended for changing the growth curve of Zandi sheep, as it negatively correlated with BW but positively with AGR1, AGR2, WW, and W6.

Keywords: sheep, relative growth rate, absolute growth rate, animal model, genetic parameters

1. Introduction

Traits related to growth are complex traits. They reflect the effects of a complex net of gene actions under the influence of the environment. Therefore, to improve the growth performance of animals, improvement in both their genetic structure and the environment they are surrounded by is needed. In small ruminant such as sheep, pre-weaning growth rate and weaning weight are the targets of selection programs because of their impact on overall efficiency. They are measured early in life, their heritability is large enough for selection to be effective and their correlation with other economic traits is generally positive. However, heavier weaning weight is associated with some undesirable side effects, such as increased dystocia caused by heavier birth weight as well as increased maintenance requirements caused by heavier mature weight of females (Schoeman and Jordaan, 1999). For this reason, increased growth rate up to market weight with relatively little increase in birth and mature weight seems to be desirable especially in sheep industry of Iran because sheep

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production is shifting from migratory and semi-intensive systems to intensive systems in which feed intake of the ewe can comprise most of the total feed costs. Therefore, any effort for decreasing mature weight could help reduce production costs. One of the approaches that has been proposed for temperate breeds to minimize the increase in mature size is selection on the basis of ratio of growth of an organism to its initial size which is termed relative growth rate (RGR) (FAO, 1982). Fitzhough and Taylor (1971) suggested the concept of relative growth rate as a criterion for altering the shape of the growth curve and thereby to prevent above-mentioned undesirable correlated responses. According to Fitzhough and Taylor (1971) selection for RGR would tend to increase growth rate but not mature size.

In order to make genetic improvements in RGR through selection programs, information such as its heritability and its relationships with other economically important traits are needed. Although RGR has been studied in other ruminant species such as beef cattle (Winder *et al.*, 1990; Bullock *et al.*, 1993; Schoeman and Jordaan, 1999; Crowley *et al.*, 2010) and goat (Singh *et al.*, 2002), this trait has not been studied in sheep. Therefore, the aims of this study were to estimate genetic, environmental and phenotypic parameters for RGR and to study its relationship with body weight and absolute growth rate in the Zandi sheep breed.

2. Materials and Methods

2.1 Data and management

Data and pedigree information collected between 1990 and 2005 were obtained from the Zandi Sheep Breeding Station in the Khojir National Park between Tehran and Abali. The pedigree file included 5,930 pedigreed animals distributed over eight generations, of which 5,147, 4,218, 2,703, 1,981, and 1,515 animals were recorded for body weight at birth, weaning, 6-month, 9-month, and yearling age, respectively.

In general, the flock is reared by following conventional industrial procedures. The mating season commences in August. Ewes in heat undergo artificial insemination (AI), with the restriction that the maximum number of ewes allocated to each AI ram is no more than 25 per breeding year. Lambing commences in December. At birth, lambs are weighed, tagged, sexed, and identified to their parents. Birth date is also recorded. Animals are weighed at birth, then at weaning, 6-month, 9-month, and yearling, but hardly ever at higher ages.

Data included the following traits: birth weight (BW) and body weights at weaning (WW), 6 months (W6), 9 months (W9) and yearling age (YW). In order to account for the differences among animals with different ages, weaning weight, 6-month weight, 9-month weight and yearling weight were adjusted to 90, 180, 270, and 365 days of age, respectively. The increases in weight for the different growth phases, namely birth to weaning (AGR1), weaning to 6-month (AGR2), weaning to 9-month (AGR3), weaning to yearling age (AGR4) and 6-month to yearling age (AGR5) were used in calculations of absolute growth rates, as total gain divided by the number of days in the period. Body weights were used to calculate relative growth rate from birth to weaning (RGR1), weaning to 6-month (RGR2), weaning to 9-month (RGR3), weaning to yearling age (RGR4) and for the growth period between 6-month and yearling age (RGR5) as the difference in natural logarithms of beginning and ending weights divided by the number of days between the weights:

$$\text{RGR} = \text{Log}_e(\text{Weight2}) - \text{Log}_e(\text{Weight1})/\text{Days between two weightings} \quad (1)$$

The number of records for traits studied together with their mean values, standard deviations, coefficients of variation, and pedigree information are presented in Table 1.

Table 1. Characteristics of the data set[a].

Item	Trait				
	RGR1	RGR2	RGR3	RGR4	RGR5
Number of records	3530	2186	1541	1211	1032
Number of sires with progeny	162	150	148	141	137
Number of grandsires with progeny	132	112	108	92	89
Number of dams with progeny	1265	1107	950	830	824
Number of granddams with progeny	674	490	455	386	378
Mean	1.720	0.496	0.375	0.203	0.157
S.D.	0.176	0.203	0.096	0.089	0.049
CV (%)	10.23	40.09	25.60	43.84	31.21

[a] RGR1: relative growth rate at weaning, RGR2: relative growth rate at 6 months of age, RGR3: relative growth rate at 9 months of age, RGR4: relative growth rate at yearling age (weaning-yearling), RGR5: relative growth rate at yearling age (6 month-yearling).

2.2 Statistical analysis

To identify fixed effects to be included in the models, least square analyses were conducted using the GLM procedure (SAS, —2004) with a model including fixed effects of year of birth (1990 to 2005) age of dam at lambing (2 to 8 years old), sex of lambs (male and female) and type of birth (single, twin, and triplet). All these fixed effects were significant (p<0.05) for all traits and were included in the animal models. A series of six univariate linear animal models were considered that differed in the (co)variance components fitted to assess the importance of maternal effects (Table 2). The models expanded from a simple animal model (Model 1) to a comprehensive maternal effects model (Model 6). The general representation of the most complete model (Model 6) used in the analyses was:

$$y = X\beta + Z_1a + Z_2c + Z_3m + e, \mathrm{Cov}(a, m) = A\sigma_{a,m} \quad (2)$$

where y is the vector of phenotypic observations for each trait and β is the vector of fixed effects to be fitted with association matrix X. The vector a contains the direct additive genetic effects for each individual (a_i) having mean of zero with the variance-covariance matrix of additive genetic effects (G) which is equal to $A\sigma_a^2$, where A is the additive numerator relationship matrix. Estimates of additive genetic variances were used to estimate the additive coefficient of variations (CV_A) as: $CV_A = 100\times\sqrt{\sigma_a^2}/\bar{x}$, where σ_a^2 is the estimated additive genetic variance and $\bar{x}$ is the sample mean. Maternal genetic variance (σ_m^2) and maternal permanent environment variance (σ_c^2) were estimated by including m and c, the vectors of maternal genetic and maternal permanent environment effects, respectively. The variance-covariance matrix of maternal genetic effects uses the relationship matrix in the same way as additive genetic effect. $\sigma_{a,m}$ denotes the covariance between direct and maternal genetic effects. In all models, e was fitted as the vector of residual errors (corresponding to temporary environment effects) with variance of σ_e^2. Maternal permanent environmental effects and residual errors were assumed to be normally distributed with means of zero and variance-covariance matrices of $I_{nd}\sigma_c^2$ and $I_n\sigma_e^2$, where I_{nd} and I_n are identity matrices of order equal to the number of dams and number of records, respectively. The direct additive genetic effects, maternal permanent environmental effects and maternal genetic effects were related to individual records with the corresponding incidence matrices Z_1, Z_2, and Z_3, respectively.

Estimation of (co)variance components was carried out using the WOMBAT program (Meyer, 2006). Akaike's information criterion (AIC; Akaike, 1974) was computed to rank the models. Using AIC, one could compare models with the same number of parameters (Models 2 and 3) which is not feasible by log-likelihood ratio tests (LRT). Let p denote the number of random (co)variance parameters to be estimated and $Log\ L$ is the maximum likelihood, then the information criterion is defined as: AIC = $-2\ Log\ L + 2p$. The model yielding the smallest AIC fits the data best.

Table 2. (Co)variance components used in the six models.

Model	(Co)variance components[a]				
	σ_a^2	σ_c^2	σ_m^2	$\sigma_{a,m}$	σ_e^2
1	✓				✓
2	✓	✓			✓
3	✓		✓		✓
4	✓		✓	✓	✓
5	✓	✓	✓		✓
6	✓	✓	✓	✓	✓

[a] σ_a^2 : direct additive genetic variance, σ_c^2 : maternal permanent environmental variance; σ_m^2 : maternal genetic variance, $\sigma_{a,m}$: direct-maternal additive genetic covariance, σ_e^2 : residual variance.

(Co)variance components between traits were estimated from a multivariate analysis. The models applied in multivariate analysis were those fitted for each of the underlying traits in the univariate analyses.

3. Results

Least square means (±SE) for the traits studied are presented in Table 3. The year of birth, sex of lambs, and birth type contributed significantly to the variation of RGR in all growth phases (p<0.01). The effect of age of dam was significant only for RGR1 (p<0.01). Table 4 presents the results of the univariate analyses based on the best fitting models. Estimates of direct heritability (h^2) were 0.13, 0.12, 0.15, 0.10 and 0.04 for RGR1, RGR2, RGR3, RGR4, and RGR5, respectively. Only RGR1 was influenced by maternal effects. Maternal heritability (m^2) for RGR1 was estimated to be 0.07. Estimates of different correlations between traits are shown in Tables 5 to 7. The genetic correlations between RGRs at different growth phases ranged from -0.53 (RGR1-RGR5) to 0.79 (RGR4 and RGR5) and the phenotypic correlations ranged from -0.79 (RGR1-RGR4) to 0.87 (RGR3-RGR4). Genetic correlations between RGRs and body weight ranged from -0.68 (RGR5-WW) to 0.75 (RGR1-WW) and the phenotypic correlations ranged from -0.69 (RGR5-WW) to 0.83 (RGR1-WW). Moreover, genetic correlations between RGRs and absolute growth rate ranged between -0.73 (RGR1-AGR5) to 0.99 (RGR2 and AGR2) and the phenotypic correlations ranged from -0.75 (RGR5- AGR5) to 0.94 (RGR2-AGR2).

4. Discussion

4.1 Environmental effects

In most studies on growth-related traits in sheep, the year of birth has been reported as a significant environmental effect. The effect of year on RGR is caused by differences in agro-climatic conditions and differences in nutrition and

Table 3. Least squares means ± S.E of pre- and post-weaning RGR[a]

Factors	Traits				
	RGR1	RGR2	RGR3	RGR4	RGR5
Sex	**	**	**	**	**
Male	$1.743^{a}\pm0.016$	$0.509^{a}\pm0.013$	$0.396^{a}\pm0.009$	$0.215^{a}\pm0.006$	$0.166^{a}\pm0.008$
Female	$1.729^{b}\pm0.016$	$0.481^{b}\pm0.013$	$0.372^{b}\pm0.008$	$0.183^{b}\pm0.005$	$0.142^{b}\pm0.006$
Birth type	**	**	**	**	**
Single	$1.746^{a}\pm0.015$	$0.469^{a}\pm0.010$	$0.353^{a}\pm0.007$	$0.188^{a}\pm0.005$	$0.144^{a}\pm0.019$
Twin	$1.706^{b}\pm0.017$	$0.539^{b}\pm0.008$	$0.389^{b}\pm0.008$	$0.210^{b}\pm0.007$	$0.169^{b}\pm0.024$
Triplet	$1.700^{c}\pm0.015$	$0.576^{c}\pm0.011$	$0.421^{c}\pm0.011$	$0.235^{c}\pm0.006$	$0.183^{c}\pm0.031$
Dam age	**	ns	ns	ns	ns
2	$1.769^{a}\pm0.006$	$0.506^{a}\pm0.008$	$0.365^{a}\pm0.007$	$0.207^{a}\pm0.006$	$0.161^{a}\pm0.019$
3	$1.757^{a}\pm0.007$	$0.510^{a}\pm0.009$	$0.360^{a}\pm0.007$	$0.203^{a}\pm0.006$	$0.152^{a}\pm0.021$
4	$1.742^{a}\pm0.009$	$0.487^{a}\pm0.010$	$0.364^{a}\pm0.007$	$0.201^{a}\pm0.006$	$0.162^{a}\pm0.019$
5	$1.709^{b}\pm0.014$	$0.489^{a}\pm0.009$	$0.370^{a}\pm0.008$	$0.192^{a}\pm0.007$	$0.168^{a}\pm0.022$
6	$1.742^{a}\pm0.026$	$0.501^{a}\pm0.010$	$0.377^{a}\pm0.009$	$0.198^{a}\pm0.007$	$0.171^{a}\pm0.020$
7	$1.700^{b}\pm0.085$	$0.504^{a}\pm0.015$	$0.366^{a}\pm0.008$	$0.189^{a}\pm0.009$	$0.169^{a}\pm0.018$
8	$1.650^{c}\pm0.092$	$0.493^{a}\pm0.021$	$0.352^{a}\pm0.011$	$0.203^{a}\pm0.011$	$0.161^{a}\pm0.018$
Year	**	**	**	**	**

[a] Means within a column that do not have a common superscript are significantly different ($P<0.05$), **: $P< 0.01$, ns: non-significant effects, RGR1: relative growth rate at weaning, RGR2: relative growth rate at 6 months of age, RGR3: relative growth rate at 9 months of age, RGR4: relative growth rate at yearling age (weaning–yearling), RGR5: relative growth rate at yearling age (6 month–yearling)

Table 4. Variance components and heritability estimates (standard errors in parentheses)[a].

Trait	Item							
	Model	σ_a^2	σ_m^2	σ_e^2	σ_p^2	h^2	m^2	CV_A (%)
RGR1	3	0.0019	0.0011	0.0118	0.0148	0.13 (0.03)	0.07	2.53
RGR2	1	0.0036	–	0.0252	0.0288	0.12 (0.04)	–	12.10
RGR3	1	0.0011	–	0.0063	0.0074	0.15 (0.03)	–	8.84
RGR4	1	0.0004	–	0.0036	0.0040	0.10 (0.05)	–	9.85
RGR5	1	0.0004	–	0.0089	0.0093	0.04 (0.04)	–	12.74

[a] σ_a^2: direct additive genetic variance, σ_m^2: maternal genetic variance, σ_e^2: residual variance, σ_p^2: phenotypic variance; h^2: direct heritability, m^2: maternal heritability, CV_A: additive genetic coefficient of variation, RGR1: relative growth rate at weaning, RGR2: relative growth rate at 6 months of age, RGR3: relative growth rate at 9 months of age, RGR4: relative growth rate at yearling age (weaning–yearling), RGR5: relative growth rate at yearling age (6 month –yearling).

management conditions in different years (Dass *et al.*, 2004; Kuchtik and Dobes, 2006; Yilmaz *et al.*, 2007; Al-Bial *et al.*, 2012).

The significant effect of sex on traits related to growth which has been frequently reported in literatures (Dass *et al.*, 2004; Yilmaz *et al.*, 2007; Al-Bial *et al.*, 2012) may be because of secretion of different sexual hormones in males and females. Estrogen hormone produced in females limits the growth of long bones (Baneh and Hafezian, 2009). In addition, regulatory mechanisms of growth hormone secretion are sexually dimorphic in such a way that although there are no sex-related effects on total growth hormone secretion, there are clear differences in the pattern in which males and females secret the hormone. This dimorphism is partly responsible for male-female differences in growth rate (Jaffe *et al.*, 1998).

Many reports indicate a significant effect of dam age on traits related to growth in small ruminants (Kuchtik and

Table 5. Estimates of genetic (above the diagonal) and phenotypic correlations (below the diagonal) between relative growth rate in different growth phases (standard errors in parentheses)[a].

Trait	RGR1	RGR2	RGR3	RGR4	RGR5
RGR1	–	0.02 (0.03)	-0.11 (0.06)	-0.19 (0.09)	-0.53 (0.11)
RGR2	-0.21 (0.03)	–	0.62 (0.17)	0.60 (0.21)	0.43 (0.17)
RGR3	-0.36 (0.02)	0.76 (0.08)	–	0.69 (0.18)	0.41 (0.13)
RGR4	-0.79 (0.06)	0.59 (0.06)	0.87 (0.06)	–	0.79 (0.18)
RGR5	-0.75 (0.05)	0.34 (0.06)	0.42 (0.04)	0.37 (0.04)	–

[a] RGR1: relative growth rate at weaning, RGR2: relative growth rate at 6 months of age, RGR3: relative growth rate at 9 months of age, RGR4: relative growth rate at yearling age (weaning–yearling), RGR5: relative growth rate at yearling age (6 month–yearling).

Table 6. Estimates of genetic and phenotypic correlations between relative growth rate and body weights (standard errors in parentheses)[a].

Trait	BW		WW		W6		W9		YW	
	r_a	r_p	r_a	r_p	r_a	r_p	r_a	r_p	r_a	r_p
RGR1	-0.10 (0.01)	-0.05 (0.01)	0.75 (0.13)	0.83 (0.05)	0.40 (0.16)	0.61 (0.04)	0.11 (0.13)	0.13 (0.04)	0.07 (0.11)	0.09 (0.04)
RGR2	0.49 (0.11)	0.21 (0.03)	0.02 (0.02)	-0.47 (0.03)	0.62 (0.17)	0.45 (0.03)	0.42 (0.10)	0.26 (0.02)	0.58 (0.21)	0.32 (0.01)
RGR3	0.50 (0.13)	0.27 (0.03)	-0.38 (0.08)	-0.37 (0.01)	0.30 (0.11)	0.09 (0.01)	0.43 (0.08)	0.22 (0.01)	0.59 (0.19)	0.45 (0.02)
RGR4	0.13 (0.03)	-0.30 (0.04)	-0.41 (0.15)	-0.50 (0.02)	-0.23 (0.10)	-0.55 (0.01)	0.61 (0.15)	0.64 (0.03)	0.53 (0.13)	0.41 (0.04)
RGR5	0.03 (0.02)	-0.53 (0.05)	-0.68 (0.14)	-0.69 (0.03)	-0.42 (0.13)	-0.57 (0.02)	0.32 (0.11)	0.12 (0.01)	0.36 (0.09)	0.29 (0.01)

[a] RGR1: relative growth rate at weaning, RGR2: relative growth rate at 6 months of age, RGR3: relative growth rate at 9 months of age, RGR4: relative growth rate at yearling age (weaning–yearling), RGR5: relative growth rate at yearling age (6 month–yearling), BW: birth weight, WW: weaning weight, W6: 6-month weight, W9: 9-month weight, YW: yearling weight, r_a: genetic correlation, r_p: phenotypic correlation.

Table 7. Estimates of genetic and phenotypic correlations between relative growth rate and absolute growth rate (standard errors in parentheses)[a].

Trait	AGR1		AGR2		AGR3		AGR4		AGR5	
	r_a	r_p	r_a	r_p	r_a	r_p	r_a	r_p	r_a	r_p
RGR1	0.63 (0.07)	0.70 (0.01)	0.19 (0.10)	0.06 (0.01)	-0.44 (0.07)	-0.35 (0.01)	-0.43 (0.13)	-0.59 (0.01)	-0.73 (0.16)	-0.75 (0.05)
RGR2	0.01 (0.01)	-0.11 (0.01)	0.99 (0.23)	0.94 (0.01)	0.74 (0.15)	0.60 (0.01)	0.25 (0.09)	0.48 (0.01)	0.45 (0.16)	0.43 (0.03)
RGR3	-0.17 (0.08)	-0.29 (0.01)	0.82 (0.19)	0.85 (0.01)	0.97 (0.24)	0.93 (0.01)	0.42 (0.14)	0.55 (0.01)	0.29 (0.08)	0.37 (0.03)
RGR4	-0.60 (0.18)	-0.54 (0.01)	0.71 (0.16)	0.87 (0.01)	0.81 (0.23)	0.78 (0.01)	0.89 (0.17)	0.76 (0.01)	0.74 (0.14)	0.84 (0.09)
RGR5	-0.63 (0.20)	-0.72 (0.01)	0.31 (0.09)	0.39 (0.01)	0.55 (0.11)	0.64 (0.01)	0.67 (0.17)	0.58 (0.01)	0.40 (0.13)	0.55 (0.14)

[a] RGR1: relative growth rate at weaning, RGR2: relative growth rate at 6 months of age, RGR3: relative growth rate at 9 months of age, RGR4: relative growth rate at yearling age (weaning–yearling), RGR5: relative growth rate at yearling age (6 month–yearling), AGR1: absolute growth rate from birth to weaning, AGR2: absolute growth rate from weaning to 6 months of age, AGR3: absolute growth rate from weaning to 9 months of age, AGR4: absolute growth rate from weaning to yearling age, AGR5: absolute growth rate from 6 months to yearling age, r_a: genetic correlation, r_p: phenotypic correlation.

Dobes, 2006; Baneh and Hafezian, 2009; Eskandarinasab *et al.*, 2010; Al-Bial *et al.*, 2012), because very young or old ewes are generally produce less milk to feed their lambs and for this reason lambs from 2nd-5th lambing are usually heavier than lambs from ewes with first lambing or above 5th lambing (Gani and Pandey, 2000). As shown in Table 3, after weaning there is variation among mothers of different ages regarding RGR in body weight of their progenies, but the differences are not big enough to be statistically significant.

For traits, such as body weight or growth rate, it has been frequently reported that usually single lambs are heavier than twins and triplets at different stages of growth and have higher growth rate in different growth phases (Kuchtik and Dobes, 2006; Baneh and Hafezian, 2009; Eskandarinasab *et al.*, 2010). But during other growth phases, except for RGR1 for which single lambs had significantly higher RGR, triplet lambs were superior to single and twin lambs. A potential explanation could be compensatory growth phenomena (Wilson *et al.*, 2006): individuals that grow fast during pre-weaning period (single lambs) being characterized by slow late growth and *vice versa.* Accordingly, poorly-nursed lambs which have lower weaning weight, gained more weight during post-weaning period and achieved heavier body weight at higher ages which reflects in the higher RGR in triplets.

4.2 Genetic parameters

Estimates of direct heritability (h^2) for body weight at birth, weaning, nine months and yearling age and for pre- and post-weaning absolute growth rate using the same data for this population of Zandi sheep have been reported by Ghafouri-Kesbi and Eskandarinasab (2008) and Ghafouri-Kesbi *et al.* (2011) as 0.11, 0.15, 0.22, 0.26, 0.15, and 0.10, respectively. In sheep, there is a general scarcity of literature about estimates of heritability for relative growth rate. Higher estimates of h^2 for RGR have been reported in beef cattle. For example Winder *et al.* (1990) who worked on Angus cattle, reported estimates of 0.33 and 0.33 for pre- and post-weaning RGR, respectively. In addition, Bullock *et al.* (1993) worked on Polled Hereford cattle and reported heritability for pre- and post-weaning RGR as 0.24 and 0.15, respectively. Moreover, in African Bovelder cattle, Scheoman and Jordaan (1999) estimated h^2 for pre- and post-weaning RGR as 0.71 and 0.16. Estimates of CV_A were 2.53%, 12.10%, 8.84%, 9.85% and 12.74% for RGR1, RGR2, RGR3, RGR4, and RGR5, respectively. The CV_A scales the component of additive genetic variance by the trait mean instead of being scaled by the total variance and so is not confounded by the magnitude of other variance components (Houle, 1992). Therefore, CV_As can be high in traits with low heritability if there is a high residual error variance in trait development and *vice versa* (RGR1 vs. RGR5). Estimates of CV_A indicate the possible magnitude of change resulting from selection. Current estimates of CV_A indicate that pre- and post-weaning RGR displays small degrees of genetic variation relative to the means. However, a common result which comes from estimates of both h^2 and CV_A is that there is little additive variation in RGR in body weight of Zandi sheep and therefore little genetic improvement in RGR would be expected through selection programs. For traits of low heritability, improvement in management and environmental conditions may be more important than selection programs (Singh *et al.*, 2002).

Maternal heritability (m^2) for RGR1 was 0.07 which is in the range of other reports for different growth traits (Mandal *et al.*, 2006; Szwaczkowski *et al.*, 2006; Ghafouri-Kesbi and Eskandarinasab, 2008; Gowane *et al.*, 2011). Significant maternal effects show that these effects should be considered when animals are evaluated for pre-weaning RGR. Where maternal effects are significant, ignoring them can result in overestimation of breeding values of lambs. After weaning because lambs become independent of their mother and rely on their genetic potential for growth, maternal effects decrease and become non-significant (Dobek *et al.*, 2004; Mandal *et al.*, 2006; Ghafouri-Kesbi and Eskandarinasab, 2008).

Genetic and phenotypic correlations between traits studied were in a wide range. Similar to our results, in beef cattle, Winder *et al.* (1990) and Scheoman and Jordan (1999) reported negative correlations between pre-weaning RGR and post-weaning RGRs. It means that superior animals regarding RGR1, loss their superiority after weaning and that selection for pre-weaning RGR results in decreased post-weaning RGR. The compensatory growth of lambs during post-weaning period could be the reason for this phenomenon. Except for BW for which the genetic and phenotypic correlations with pre-weaning RGR were slightly negative, correlations between RGR1 and WW, W6, W9 and YW were positive. Later findings show that selection for RGR1 can result in moderate positive correlated response in WW and W6 as well as a slightly increase in W9 and YW, while decreases birth weight. In general, correlations between RGRs with body weights measured early in life were more negative, whereas the correlations with body weights measured later in life were more positive. Winder *et al.* (1990) in Angus cattle, Scheoman and Jordan (1999) in South African Bovelder cattle and Crowley *et al.* (2010) in Irish cattle reported correlations similar to current results. Complicated patterns of correlations between RGR and body weight and absolute growth rate show the importance of considering the correlations between RGR and other traits while planning selection programs. In general, the genetic correlations suggest that pre-weaning RGR would be an effective criterion for changing the shape of the growth curve.

Results obtained here show that RGR in body weight of Zandi sheep belongs to the low-heritable traits category. Selection for pre-weaning RGR seems to be effective for changing the growth curve, as it negatively correlated with BW but positively with AGR1, AGR2, WW, and W6. However, the effectiveness of such a selection strategy should be evaluated practically.

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