

GENETIC EVALUATION OF GROWTH TRAITS IN IRANIAN KORDI SHEEP USING RANDOM REGRESSION MODEL WITH HOMOGENEOUS AND HETEROGENEOUS RESIDUAL VARIANCES

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The purpose of this study was estimation of genetic parameter using random regression model (*RRM*) with various error variance in Iranian Kordi sheep. The data (consisting of 7875 weight records from birth to 360 days of age) were collected during the period 2000 to 2013 from the rearing and breeding station of Kordi sheep in Shirvan, Iran. The independent variables were Legendre polynomials (*LP*) of age at weighing and orders of fit from 2 to 5 were considered. Analyses were carried out fitting sets of random regression coefficients due to direct additive genetic, direct and maternal permanent environmental effects, with heterogeneous and homogeneous error variances. To compare the model were used different criteria such as *LogL*, *AIC*, *BIC* and *LRT*. The best fitting *RRM* among homogeneous error variance was the model with a *LP* of fourth order for fixed effect, fourth order for direct additive genetic and fifth order for direct and maternal permanent environmental effects (model 4455). Among the models with heterogeneous error variances different, model 7 (Heterogeneous error variances of 72 various classes), was selected as the best model. The variances increased along the trajectory from 3.75 to 12.81, 4.43 to 30.28 and 1.49 to 8.49; 0.25 to 27.94, 0.03 to 12.32 and 0.15 to 22.66 for direct additive genetic, direct and maternal permanent environmental effect by homogeneous and heterogeneous error variances, respectively. The direct heritability ranged from 0.15 to 0.41 and 0.11 to 0.56 by homogeneous and heterogeneous error variances, respectively. Genetic correlation between adjacent test days was more than between distant test days. This research has demonstrated the possibility of application of *RRM* with heterogeneous error variance for genetic evaluation of Iranian Kordi Sheep.

Keywords: body weight, genetic parameters, random regression model, sheep

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INTRODUCTION

Growth in sheep is generally described as a series of traits each representing weight within some predefined range in age. Lamb and mutton are the best sources of protein in Iran. The sheep population in Iran is mainly composed of fat-tailed carpet-wool native breeds. They are adapted to the poor range conditions of the country. A high percentage of the sheep population is managed under a migratory system, utilizing the range as the major source of feed (GHAFOURI KESBI *et al.*, 2008). The Kordi sheep is a native breed of Iran which adapted to cold and highland environments. They are fat-tailed sheep with a medium-sized body, brown in color. They are kept in the provinces North Khorasan and their main products are meat, wool and milk (ESMAILZADEH *et al.*, 2011). The rearing system is mostly extensive-migratory from April to September (on natural pastures in spring and summer), and semi-intensive from October to March (on stations and fed in barns during autumn and winter).

Estimation of genetic parameters using different models is one of the important breeding programme processes. There are two important recommendation method for genetic evaluation of growth in sheep: fitting nonlinear regression (e.g. logistic, exponential, Gompertz or Richards models) to the data and estimating genetic parameters for growth curves (LAMBE *et al.*, 2006) or using random regression model (*RRM*) (LEWIS and BROTHERSTONE, 2002; FISCHER *et al.*, 2004; MOLINA *et al.*, 2007). Currently *RRM* is being applied for genetic evaluation in growth trait such cattle (KREJCOVA *et al.*, 2007; NESER *et al.*, 2012; BOHLOULI *et al.*, 2013), sheep (LEWIS and BROTHERSTON, 2002; GHAFOURI KESBI *et al.*, 2008; ABEGAZ *et al.*, 2010; KARIUKI *et al.*, 2010; WOLC *et al.*, 2011) and pig (HUISMAN *et al.*, 2002) data. These models use polynomials in time to describe mean profiles with random coefficients to generate a correlation among the repeated observations on each individual (ROBERT GRANIE *et al.*, 2002). Random regression models are better than multi-trait models, because they allow appropriate modeling of the genetic parameters by avoiding age pre-adjustment, feasibility of taking into account of specific environmental effects on the time of recording, decreasing of the generation interval, increasing of accuracy of breeding values, feasibility of calculating variance for every age and covariance among any pair of ages (MEYER, 2005; SCHAEFFER, 2004).

Moreover, in literature several approaches were used univariate and bivariate analyses of data on birth, weaning, 6-month, 9-month and yearling weights in Zandi Sheep have been done (MOHAMMADI *et al.*, 2011). Also, different *RRM* were applied in the analysis of weight data in Zandi Sheep with the objective of identifying the appropriate model (BOHLOULI *et al.*, 2013). In this study different orders of (Legendre polynomial) *LP* by homogeneous error variance were applied in the analysis of body weight records taken from birth to 360 days of age with the objective of identifying the appropriate model and also select the best model among homogeneous *RRM* for analyzing in heterogeneous *RRM* to obtaining more accurate estimates and estimates of genetic changes.

MATERIALS AND METHODS

Data and management

The data set and pedigree information include 7875 live body weight records from birth day to 360 days of age of 2948 Kordi sheep. These records were collected between 2000 and 2013 from Kordi center sheep located in Shirvan, Iran. Lambs with record were progeny of 217 sires and 2293 dams. The descriptive statistics are summarized in Table 1.

Table 1. Descriptive statistics of data set

Number of records	7875
Means (kg)	27.19
SD (kg)	5.45
No. of base animal	4231
No. of animal with records	3563
No. of animal with 6 records	1256
No. of animal with 7-10 records	1512
No. of animal with 11-12 records	880
No. of animals with offspring	2510
No. of animals with unknown sire	2391
No. of animals with unknown dam	2167
No. of animals with both parents unknown	2023
Average No. of generations	3487
No. of sires	217
No. of dams	2293
Year	21
Month	8

Selection of parents for the next generation was based on weight of the animals and their physical conformity to breed type. All animals are routinely weighed at birth, month three, six, nine and twelve. Animals that had six or more records within the specified age range were included in the analysis. Number of records and average weights for different ages are shown in Figure. 1.

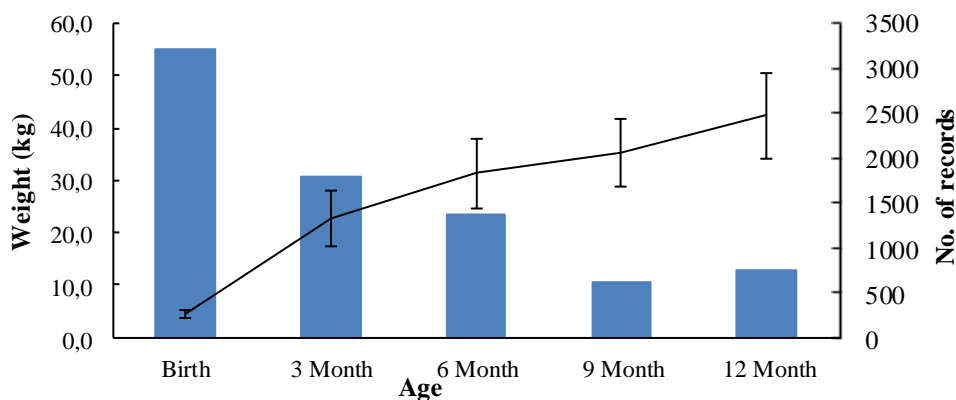


Figure 1. Number of records and mean weights among age intervals

Statistical analysis

The choice of fixed effects to be considered was made after testing whether the effects were statistically significant with a linear fixed effects model analyzed with GLM procedure of SAS (SAS, 2009). The statistical model included age of dam (2 to 6 and ≥ 7), sex of kid (male and

female), type of birth (single, twin and triples), year of birth (2000-2013), and month of birth (1, 2, 3, 4, 9, 10, 11, 12). Weight as a function of age in days at weighing was included as a fixed regression of orthogonal polynomial. This fixed regression describes the average growth curve of all animals with records. Three sets of random regression coefficients included direct genetic effect and direct and maternal permanent environmental effects, were fitted to the data. *RRM* fitted LP of age at recording (in days) as independent variables. The *RRM* fitted for the genetic analysis were used as following:

$$y_{ij} = W_{ij} + \sum_{m=0}^{m_{\alpha}-1} \beta_m \phi_m(g_{ij}^*) + \sum_{m=0}^{m_{\alpha}-1} \alpha_{im} \phi_m(g_{ij}^*) + \sum_{m=0}^{m_{\delta}-1} \delta_{im} \phi_m(g_{ij}^*) + \sum_{m=0}^{m_{\rho}-1} \rho_m \phi_m(g_{ij}^*) + e_{ij}$$

where y_{ij} , is the j^{th} record from i^{th} animal at age g_{ij}^* that g_{ij}^* , is the standardized age of recording for y_{ij} , $-1 \leq t \leq 1$ for which Legendre polynomials are defined and $\phi_k(g_{ij}^*)$ is the corresponding m^{th} LP; W_{ij} is fixed effects relating to y_{ij} (age of dam, sex of lamb, type of birth and year of birth). β_m , is the fixed regression on orthogonal polynomials of age; α_{im} , δ_{im} and ρ_m are the m^{th} order random regression coefficients for the direct genetic, maternal and direct permanent environmental effects, respectively and $m_{\alpha}-1$, $m_{\delta}-1$ and $m_{\rho}-1$ are the corresponding order of fit for each effect. e_{ij} , random residual effect associated with y_{ij} . Residual effects investigated as homogenous and heterogeneous measurement error variances. In the heterogeneous measurement, residual effects were considered independently distributed changes in measurement error variance in seven separate models. In each of the models, different classes of residual effects were considered based on age in 3 (1-120; 121-240; 241-360), 6 (1-60;...;301-360), 12 (1-30;...;331-360), 18 (1-20;...;341-360), 24 (1-15;...;346-360), 36 (1-10;...;351-360) and 72 (1-5;...;356-360) different classes.

Covariance functions calculations

Random regression analyses produce \mathbf{K} matrices containing (co)variance between random regression coefficients, especially for each random effect (direct genetic, maternal and direct permanent environmental effects). Following the proposal of KARIUKI *et al.* (2010), the (co)variance functions ($\hat{\mathbf{G}}_0$) are estimated by pre and post multiplying \mathbf{K} using a matrix containing Legendre polynomials (Φ) pertaining to a set of specific ages shown in matrix notation as:

$$\hat{\mathbf{G}}_0 = \Phi \mathbf{K} \Phi$$

Covariances between random regression coefficients pertaining to different random effects were assumed to be zero. Estimation of genetic parameters with REML methodology was done using WOMBAT software (MEYER, 2007). Additive genetic correlation for 305-days production between LP were calculated as:

$$r_{\mathbf{g}}(i,j) = \frac{\text{Cov}_{\mathbf{g}}(i,j)}{\sqrt{\text{Var}_{\mathbf{g}}(i,i) \times \text{Var}_{\mathbf{g}}(j,j)}}$$

Where $\text{Cov}_{\mathbf{g}}(i,j)$, is genetic covariance between i and j day, $\text{Var}_{\mathbf{g}}(i,i)$ and $\text{Var}_{\mathbf{g}}(j,j)$ are additive genetic variance i and j day, respectively.

Model comparison beside Likelihood criteria

Goodness of fit for the models was examined using likelihood based criteria as Logl, Akaike's Information Criterion (AIC), Bayesian information criterion (BIC) and log-likelihood ratio test (LRT). AIC and BIC criteria are:

$$AIC = -2\text{Log}l + 2 \times k; BIC = -2\text{log}L + k \times \text{log}(N - r(x))$$

Where, k is the number of parameters estimated, N is the sample size and $r(x)$ is the rank of the coefficient matrices for fixed effects in the model. Calculation of LRT for models i and j was obtained with formula:

$$LRT_{ij} = 2 \times (\text{Log}L_i - \text{Log}L_j)$$

A model with significantly the highest ($P < 0.05$) LRT and with the lowest LogL, AIC and BIC was considered to be the most appropriate model. In this research, firstly we analysis data as homogenous error variance, after selection the best model using the above criteria, the best model analyzed using heterogeneous error variance with different type of variance. In heterogeneous RRM, the whole time recording divided to 3, 6, 12, 18, 24, 36 and 72 sections. Finally the best model was select among the seven heterogeneous models.

RESULTS

Comparison of the models

The values of comparison criteria (LogL, AIC, BIC, LRT) for the various models fitted on the data were given in Table 2 and 3. Selection of a better function depends partly on the criteria that were used. Also, by heterogeneous residual variance was included in the model, significant improvement in the level of fit with increasing measurement residual classes 72 (1-5, 6-10, 11-15, ..., 356-360).

Table 2. Order of fit for the polynomial used in the different models by homogeneous residual variance and information criterion (best model in bold)

Model	K	P	No. of error measures	LogL	AIC	BIC	LRT
14	2442	24	1	-47299.859	94647.718	94846.202	10968.39
15	2444	31	1	-46895.662	93853.324	94109.702	11372.59
26	3353	28	1	-46976.803	94009.606	94241.172	11291.45
27	3354	32	1	-47954.408	94679.958	94635.995	10313.84
28	3355	37	1	-47882.913	95839.826	96145.822	10385.34
34	3555	46	1	-47990.607	96073.241	96453.642	10277.64
35	4444	31	1	-48390.154	96842.308	97098.682	9878.097
36	4445	36	1	-48272.641	96617.282	96915.008	9995.61
38	4455	41	1	-46032.496	92146.992	92486.068	12235.76
39	4544	36	1	-47991.574	96055.148	96352.872	10276.68
41	4555	46	1	-47990.009	96072.018	96452.444	10278.24
42	5555	46	1	-47792.759	95677.518	96057.942	10475.49

K: matrices containing (co)variance between random regression coefficients, for each random effect (Orders of fit for fixed, direct genetic, direct and maternal permanent environmental effects, respectively); P: Number of parameters; AIC: Akaike's Information Criterion; BIC: Bayesian information criterion; LRT: likelihood ratio test.

Therefore, among 42 models (Homogeneous residual variance), The best fitting RRM among homogeneous error variance was the model with a Legendre polynomial of fourth order for fixed effect, fourth order for direct additive genetic and fifth order for direct and maternal permanent environmental effects (model 4455). For heterogeneous error variances of various classes for different models depending on age, model 7 (Heterogeneous error variances of 72 various classes, 1-5, 6-10, ..., 356-360), was selected as the best model.

Table 3. Order of fit for the polynomial used in the different models by heterogeneous error variances, number of parameters (p), and information criterion (best model in bold)

Model	No. of error measures	p	LogL	AIC	BIC	LRT
1	3	43	-47922.290	95930.581	96286.196	-
2	6	46	-47872.907	95837.814	96218.241	98.766
3	12	52	-47397.440	94898.880	95328.928	1049.7
4	18	58	-47047.159	94210.318	94689.986	1750.262
5	24	64	-46426.293	92980.586	93509.876	2991.994
6	36	76	-46279.764	92711.528	93340.058	3285.052
7	72	112	-44794.861	89813.722	90739.976	6254.858

Random regression coefficients

Estimates of (co)variance matrices between random regression coefficients, the corresponding correlations and their eigenvalues from the best model (4455 by 1 measurement error classes and 72 measurement error classes) are shown in Table 4 and 5. For all random effect, intercept of the polynomial regression explained the highest proportion of variation. In all cases, the first eigenvalue of K matrix was the largest throughout, indicating that 56-68% of total variation can be explained by the first eigenfunction by homogeneous residual variance of each covariance function and that 81-95% by heterogeneous residual variance with 72 measurement error classes.

Table 4. Estimates of covariance (lower triangle) and correlations (upper triangle) between random regression coefficient together with the eigenvalues of the covariance matrices fitting Legendre polynomial with model 4455 and 1 measurement error classes

No. of error measures	1 ^a	2 ^b	3 ^c	4 ^d	5 ^e	Eigen values	%
<i>Direct additive genetic</i>							
1	7.5838	0.1280	-0.9303	0.5539		9.01	63.55
2	0.75925	4.6387	0.1524	-0.1090		4.67	32.97
3	-2.9540	0.37850	1.3296	-0.3678		0.49	3.48
4	1.2091	-0.18606	-0.33612	0.62816		0.00	0.00
<i>Direct permanent environmental</i>							
1	1.4400	0.2685	-0.5135	-0.1810	-0.3642	3.93	67.75
2	0.62182	3.7237	0.3414	-0.2957	-0.0221	1.54	26.60
3	-0.43119	0.46099	0.48971	0.0095	-0.3609	0.23	4.01
4	-0.068627	-0.18033	0.0021039	0.099851	0.3632	0.10	1.64
5	-0.090657	-0.0088537	-0.052381	0.023805	0.04301	0.00	0.00
<i>Maternal permanent environmental</i>							
1	8.3949	-0.3518	-0.8777	0.0443	0.0102	10.94	55.65
2	-0.95066	0.86975	-0.0822	-0.3674	0.1638	6.05	30.75
3	-4.3793	-0.13197	2.9655	-0.0992	-0.1959	1.80	9.18
4	0.16908	-0.45189	-0.22526	1.7389	0.3546	0.87	4.43
5	0.070752	0.36438	-0.80477	1.1157	5.6927	0.00	0.00

a, intercept; b, linear; c, quadratic; d, cubic; e, quartic.

Table 5. Estimates of covariance (lower triangle) and correlations (upper triangle) between random regression coefficient together with the eigenvalues of the covariance matrices fitting Legendre polynomial with model 4455 and 72 measurement error classes

No. of error measures	1 ^a	2 ^b	3 ^c	4 ^d	5 ^e	Eigenvalues	%
<i>Direct additive genetic</i>							
1	20.137	0.5480	-0.6546	0.5329		22.42	83.58
2	5.2603	4.5753	0.1065	-0.1309		3.72	13.86
3	-3.4567	0.26813	1.3848	-0.2832		0.68	2.55
4	2.0313	-0.23776	-0.28308	0.72155		0.00	0.00
<i>Direct permanent environmental</i>							
1	6.9103	0.9339	0.3891	-0.0352	-0.4570	10.93	94.74
2	5.0634	4.2540	0.6191	0.0178	-0.1314	0.49	4.27
3	0.49076	0.61265	0.23022	0.6457	0.2561	0.11	0.97
4	-0.021782	-0.002863	0.072996	0.055505	-0.0907	0.00	0.02
5	-0.20105	-0.045347	0.020563	-0.003575	0.028015	0.00	0.00
<i>Maternal permanent environmental</i>							
1	8.6235	-0.2045	-0.8607	0.0709	0.0879	10.85	80.66
2	-0.5853	0.94988	0.0774	-0.9249	0.1086	1.39	10.36
3	-4.1681	0.12443	2.7187	-0.1440	-0.5812	1.21	8.96
4	0.14618	-0.6331	-0.16679	0.49324	0.2373	0.00	0.01
5	0.21001	0.08617	-0.77989	0.13565	0.66240	0.00	0.00

For direct additive genetic effect, the intercept and the linear coefficients accounted for most of the variance (63.55 and 32.97%; 83.58 and 13.86% by homogeneous and heterogeneous residual variances, respectively). Also, For Maternal permanent environmental and direct permanent environmental effects, the intercept and the linear coefficients accounted for most of the variance by homogeneous and heterogeneous residual variances. The direct additive genetic effects had the highest covariance value between intercept and cubic coefficients at 1.21 by homogeneous residual variance and between intercept and linear coefficients at 5.26 by heterogeneous residual variance, while in direct permanent environmental effects between intercept and linear coefficients at 0.62 by homogeneous residual variances and between intercept and linear coefficients at 5.06 by heterogeneous residual variance and the maternal permanent environmental effects had the highest value between cubic and quartic coefficients at 1.12 and between intercept and quartic coefficients at 0.21 by heterogeneous residual variance. The correlation coefficients of direct additive genetic ranged from -0.93 (the lowest) between the intercept and quadratic to 0.15 (the highest) between linear and quadratic and from -0.65 (the lowest) between the intercept and quadratic to 0.55 between the intercept and linear by homogeneous and heterogeneous residual variances, respectively.

Estimates of (co)variance components and genetic parameters

The estimates of direct additive genetic, direct and maternal permanent environmental variances are shown in Figure. 2 and 3. The estimates direct additive genetic variance ranged from 3.75 (Age at 30 day) to 12.81 (Age at 360 day) for homogeneous residual variance and 0.25 to

27.94 for heterogeneous residual variance. Direct permanent environmental variance increased along the trajectory from 4.43 to 30.28 and 0.03 to 12.32, by homogeneous and heterogeneous residual variances, respectively. The pattern estimated for maternal permanent environmental variance for homogeneous residual variance was erratic and heterogeneous residual variance increased steadily throughout the trajectory.

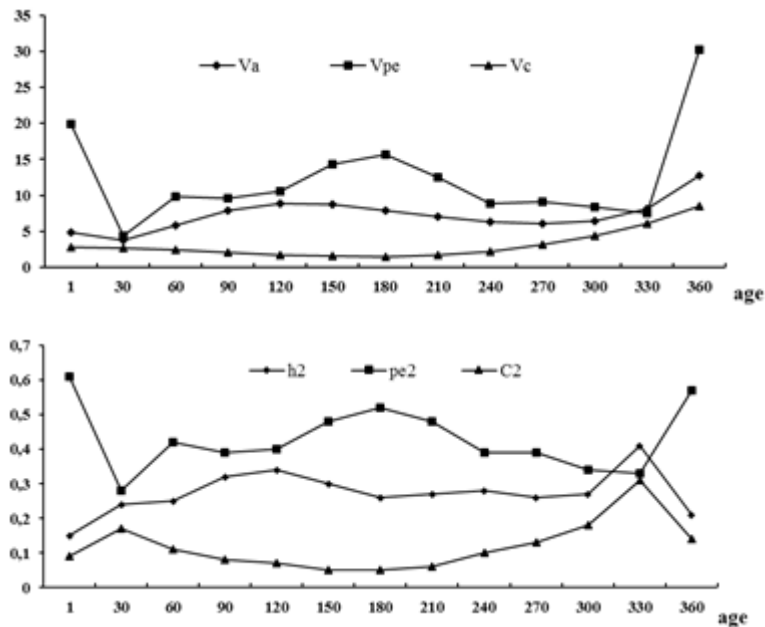


Figure 2. Estimates of direct additive genetic (V_a), direct permanent (V_{pe}) and maternal (V_c) environmental variances and direct heritability (h^2), direct (pe^2) and maternal (c^2) permanent environmental effects as a proportion of phenotypic variance for weight at selected ages, by homogeneous residual variance,,,,,

The estimates of direct heritabilities, maternal and direct permanent environmental variances as proportions of phenotypic variance for selected ages are given in Figure. 2 and 3. The increasing pattern of direct heritability observed up to 120 days and then reduced until 330 days, and increased thereafter (by homogeneous residual variance). The estimate direct heritability by heterogeneous residual variance was increasing pattern in during trajectory. The estimates direct permanent environmental variance ranged from 0.28 to 0.61 (by homogeneous residual variance) and 0.04 to 0.37 (by heterogeneous residual variance). Maternal permanent environmental variance by homogeneous residual variance, as proportions of phenotypic variance increased until 30 days of age and then reduced and end age increased and by heterogeneous residual variance was higher at the beginning and the end ages.

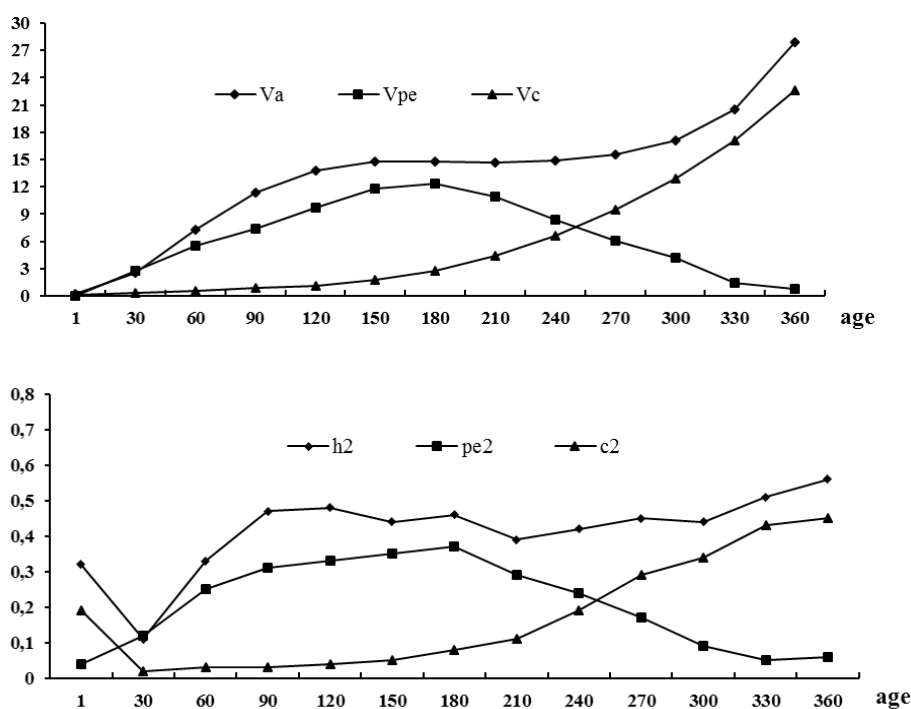
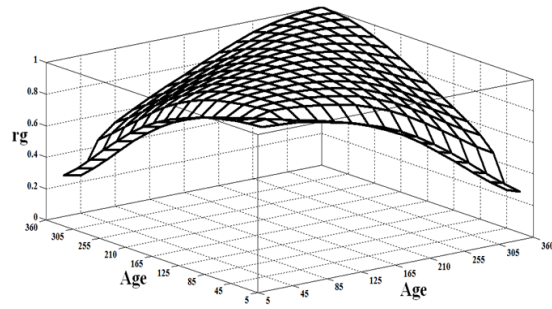


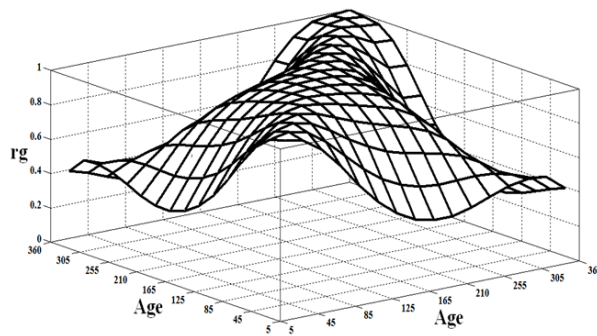
Figure. 3. Estimates of direct additive genetic (V_a), direct permanent (V_{pe}) and maternal (V_c) environmental variances and direct heritability (h^2), direct (pe^2) and maternal (c^2) permanent environmental effects as a proportion of phenotypic variance for weight at selected ages, by heterogeneous residual variance

Estimates of additive genetic correlation among weights at ages estimated in *RRM* are shown in Figure. 4. As can be seen, the (co)variance structure of data during trajectory was considering *RRM*, therefore, with this method separate (co)variance components for different weights at ages are estimating that by using them genetic correlation between different days can be calculated. Generally, the additive genetic correlations between weights at ages increased with decreasing interval between weighting; and also correlations between weight at earlier ages and at other ages were low.

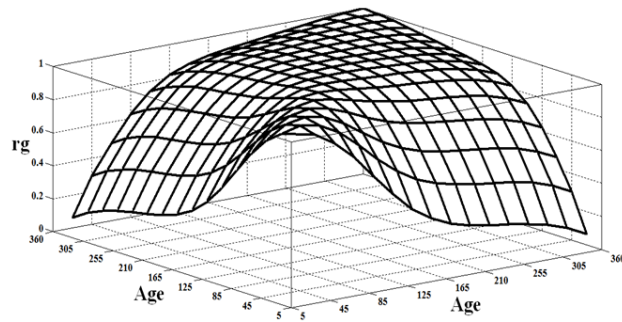
Direct additive genetic, maternal and direct permanent environmental correlations between weights at selected ages are given in Figure. 4. Direct additive genetic correlations among various days were positive and ranged from 0.25 between 45 and 360 days of age to 0.99 between 110 and 135 days of age. Maternal permanent environmental correlations among various days were positive and ranged from 0.07 between 5 and 360 days of age to 1 between 250 and 225 days of age. Also, direct permanent environmental correlations varied from 0.25 (135-360 days of age) to 0.99 (155-180 days of age).



Direct additive genetic



Direct permanent environmental



Maternal permanent environmental

Figure 4. Correlations among weights at ages

DISCUSSION

The values of comparison criteria

In this study, LP with different orders by distribution of the residual variance, were compared for better fitting performance of weights at ages. The results showed that the criteria of values decreased when the order of fit increased in the models, agreeing with the results presented by MOHAMMADI *et al.* (2014a, b); LOPEZ-ROMERO and CARABANO (2003); BIGNARDI *et al.* (2009); EL FARO *et al.* (2008) and ALBUQUERQUE and MEYER (2005); BOHLOULI *et al.* (2013). Therefore, the results showed a significant improvement in the level of fit when the heterogeneous residual variance was included in the model, in comparison to homogeneous residual variance (ABEGAZ *et al.*, 2010; BOHLOULI *et al.*, 2013) and model fit improved with increasing polynomial regression order.

Regression coefficients and variance component

The results demonstrated in this studies that a large proportion of the total variance (56-68% and 80-94%, by homogeneous and heterogeneous residual variances, Table 4 and 5) explained by the first eigenfunction of each covariance function for each random effect. These results was in accordance with other reports (BARAZANDEH *et al.*, 2012; BOHLOULI *et al.*, 2013; MOLINA *et al.*, 2007; ABEGAZ *et al.*, 2010; KARIUKI *et al.*, 2010). This implies that changes in the growth curve would be more likely achieved by selection based on this constant term (BOHLOULI *et al.*, 2013; KARIUKI *et al.*, 2010).

The direct additive genetic variance was highest at the later ages in the growth trajectory especially in the estimates with heterogeneous residual variance (Table 4 and 5). These results are similar to those estimated in Zandi sheep (BOHLOULI *et al.*, 2013), Kenya sheep (FISCHER *et al.*, 2004) and Suffolk lambs (LEWIS and BROTHERSTON, 2002). The direct permanent environmental variances were considerably lower in the early and later ages. In the models by heterogeneous residual variance increasing trend observed for maternal permanent environmental variance up to 360days, which was correspond to the results reported by BARAZANDEH *et al.* (2012) and SAFAEI *et al.* (2010) and was different from the results of FISCHER *et al.* (2004) and KARIUKI *et al.* (2010).

Genetic parameters

Direct genetic heritabilities estimated in this study were lower for earlier ages and increased with age. These trends are similar to those observed by LEWIS and BROTHERSTON, (2002); FISCHER *et al.* (2004); BARAZANDEH *et al.* (2012). The maximum direct genetic heritabilities by both residual variances were observed at the 360day weights at ages.

Direct permanent environmental variances were higher for the earlier ages by homogeneous residual variance Compared with heterogeneous residual variance in this study. Direct permanent environmental variances decreased with age (Figure. 2), which indicated environmental effects are important for earlier parts of age in Kordi sheep. These results are according to the study of KARIUKI *et al.* (2010) in Dorper sheep and FISCHER *et al.* (2004) in Poll Dorset sheep and disagreement with the results of GHAFOURI KESBI *et al.* (2008) in Mehrabani sheep. However, for heterogeneous residual variance direct permanent environmental variances were higher (12.32) for among ages (180day). The maternal permanent environmental effect was very important during the earlier ages and higher at late ages in both model (homogeneous and heterogeneous residual variances) (FISCHER *et al.*, 2004; SAFAEI *et al.*, 2010; BARAZANDEH *et al.*, 2012). This implies that

there is strong relationship among lamb, milk and maternal ability of dams for pre-weaning ages and high was in the early and end weights at ages (BOHLOULI *et al.*, 2013).

The general paucity of literature estimates for maternal effects in sheep over a range of ages make comparison difficult, however, most studies report that maternal permanent environmental effect decrease as time lapses post-weaning (FISCHER *et al.*, 2004; WOLC *et al.*, 2011). This implies that the dam's influence on the performance of their progeny was mostly affected by the environment provided to the dam. For better growth performance, it is therefore important that dams are provided with an optimum environment (BOHLOULI *et al.*, 2013; KARIUKI *et al.*, 2010). The decrease in direct genetic correlations between weights (Figure. 4) with increasing time lag between measures is evidence that different weights along the growth curve of an individual are affected by different genes and should therefore be considered as different correlated traits (KARIUKI *et al.*, 2010). The pattern of maternal permanent environmental correlations between different ages is similar in that the correlations decreased as the age distance between weights increased and higher than direct permanent environmental correlations in earlier ages. The low direct permanent environmental correlations between earlier and later ages are an indication that the performance of individuals is highly dependent on the ability of the individual to withstand the production circumstances, i.e., to produce under the harsh environment.

In conclusion, among the different models in this study, it seems that the *RRM* by heterogeneous residual variance flexible and reliable procedure for estimation of genetic parameters of growth traits in Iranian Kordi sheep.

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**GENETIČKA EVALUACIJA PARAMETARA RASTA KOD IRANSKE KORDI OVCE
UPOTREBOM RANDOM REGRESIONOG MODELA SA HOMOGENIM
I HETEROGENIM REZIDUALNIM VARIJANSAMA**

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Izvod

Svrha ovog rada bila je ocena genetičkih parametara korišćenjem slučajnog regresionog modela (RRM) sa različitim varijansama greške kod iranske ovce Kordi. Podaci (koji se sastoje od 7875 zapisa težine od rođenja do starosti od 360 dana) sakupljeni su u periodu od 2000. do 2013. godine u Stanici za uzgoj i oplemenjivanje Kordi ovaca u Shirvanu u Iranu. Analize su sprovedene sa pogodnim setovima slučajnih regresionih koeficijenata usled direktnih aditivnih genetskih, direktnih i materinskih trajnih efekata spoljašnje sredine, sa heterogenim i homogenim varijansama greške. Za poređenje modela korišćeni su različiti kriterijumi, kao što su LogL, AIC, BIC i LRT. Najpogodniji model među homogenim varijansama greške, bio je model sa LP na četvrtom mestu za fiksni efekat, četvrtom mestu za direktan aditivni efekat i na petom mestu za direktan i materinski stalni efekat sredine (model 4455). Među modelima sa heterogenom varijansom greške, model 7 je odabran kao najbolji. Varijanse su rasle od 3.75 do 12.81, 4.43 do 30.28 i 1.49 do 8.49; 0.25 do 27.94, 0.03 do 12.32 i 0.15 do 22.66 za direktan aditivni efekat, direktan i materinski stalni efekat sredine. Heritabilnost je bila u opsegu od 0.15 do 0.41, odnosno od 0.11 do 0.56 za homogene i heterogene varijanse greške. Genetičke korelacije između susednih dana testiranja, bile su veće u odnosu na udaljene dane testiranja. Ovo istraživanje je pokazalo moguću primenu RRM sa heterogenim varijansama greške za genetičku evaluaciju iranske Kordi ovce.

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