

Genetic appraisal of growth traits in Iranian native Ghezel sheep using random regression models

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Abstract: This research was carried out to estimate the genetic parameters of the body weight traits of the Ghezel sheep using three different random regression models. The used data were 39,288 test-day records collected from 13,378 animals at Ghezel Sheep Breeding Station in Miandoab, West Azerbaijan Province, Iran from 1994 to 2012. Fixed effects in models included type of birth (single, twin) and year of birth (1994–2012). The weight as a function of age in the days of weighting was considered as the fixed regression of orthogonal polynomial. The random effects of the basic model were direct genetic and direct permanent environment. Maternal genetic and maternal permanent environment effects were added to it respectively. In the basic model, increasing the order of fit for the fixed regression, direct genetic and direct permanent environment effects, increased the accuracy of the model. Adding the maternal permanent environmental effect to the model and increasing the order of fit increased the accuracy of the model. However, adding the maternal additive genetic effect to the model and increasing the order of fit for this effect, decreased the model accuracy. Direct heritability for birth weight and weight at 90, 180, 270, and 360 days of age were: 0.30, 0.22, 0.39, 0.38, and 0.55, respectively. These heritability estimates reduced after birth and reached the lowest amount for body weight at 20 days of age; however, after that, they increased as the age increased (this increase was not uniform and had some fluctuations). The direct additive genetic correlations between the traits of weight at 90 days of age and the weight at 180 days of age was the highest (0.955) and between the birth weight and 180 days of age was the lowest (0.072). These correlations between adjacent age groups were closer than the remote age groups. The value of the direct genetic, direct permanent environment, maternal permanent environment, and the phenotypic variances for birth weight was the lowest and increased by increasing of the age (maximum was for weight of 360th day of age).

Key words: Random effect, order of fit, fixed regression, likelihood ratio test, test-day records

1. Introduction

The population of Ghezel sheep in Iran is around 2 million which is bred in the northwest of this country. This native breed is fatty-tailed and large sized (the mean of one-year-old body weight was 38.2 kg for females and 41.7 kg for males) and it also has adapted to the life in cold and mountain climates (-22.8 °C to 38.3 °C). This breed is firstly bred for meat and then for milk and wool (1). The color of this sheep usually varies from light brown to dark brown. The feet are suitable for long walk in meadows and pastures and they are dark brown. Beside the feet, the tail and the udder are darker than the other parts of the body. The shape of the tail (unique characteristic of this breed) is absolutely round and has pear-shaped tailbone and a sidewise look at the tail displays S-shaped tailbones. The popularity of the sheep decreases as the tail is less S-shaped. Most of them have knobs in the front part of their necks. Some of the herdsmen believe that the most

original ewes are red, fawn, without horn and have white spots on their forehead (2). Furthermore, a traditional and delicious kind of cheese called Lighvan cheese is basically made from Ghezel sheep milk in the area of Sahand mountainside, located in the northwest of Iran. It is the most popular traditional and expensive cheese made from raw sheep's milk in East Azerbaijan Province. The Lighvan cheese is characterized by its unique hardness (semihard), saltiness, and spiciness (3). Thus, improving this native sheep breed for these traits can increase products in which milk, meat, wool, and skin; and consequently, more dairy products and meat will economically be obtained.

The goal of animal breeding is to modify the genetic potential of livestock in order to improve the production efficiency. Successes in animal breeding and enhancement of the production highly depend on the identification of animals with desirable genes and selection of them as the parents of the next generation. The most important

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part of this is to determine the appropriate criteria for determining the superior animals and their selection. Nowadays, the selection index is being used for animal ranking. For determination of selection index, accurate estimation of genetic parameters is essential. These estimates are usually calculated by distinct models such as univariate, multivariate, repeatability, fixed regression and random regression (RR). Recently, the RR models have been proposed as an appropriate alternative method for analyzing the repeatedly occurring traits during the life of animals (4–8). The RR model is widely used to estimate the genetic parameters and to predict the breeding values since it has advantages over animal models in that it does not need record correction to obtain the weight for a specific age, it can also exert the environmental effect for daily recording in statistical analysis. In addition, it can predict the livestock breeding value at an early age and let decide the deleting or selection of the animal on time. This can result in the reduction of generation interval and fostering the accuracy of genetic parameters and prediction of breeding values due to increasing the number of records per animal (9,6).

In the usual univariate and bivariate models and also in fixed regression (simple repeatability), due to the failure in the forming of (co)variance structure, variations in variance components were considered independent from time and the phenotypic values of the traits in different ages were considered different traits. Thus, in these models the estimates were calculated for specific ages (birth, 3 months, 6 months, 9 months, and 12 months of age) and no estimate for their intervals was done, while in RR models because of forming of (co)variance functions for every random effect, variations in the variance components were considered a function of time and the value of any component for all of the days within the range of the recorded ages can be estimated. We can also estimate the variance component values for the days for which there is no record, using the (co)variance components provided that they are in the recording range.

Meyer (10), by using the simulated data, indicated that the use of the RR models can increase the accuracy of the genetic evaluation of the animals. This conclusion can be true if there are more records per animal and they have a uniform distribution in the growth period (8). However, if there are fewer records per animal and the records do not have a uniform distribution, RR models evaluations will be affected by the structure of the data. Under these conditions, wherever of the growth path the number of records decreases, the sampling variance increases; and consequently, these models are not good models for showing the variance components. Thus, the resulting curve will break and overestimate the variance components (11). In these models, a fixed regression is

used to show the mean of the growth curve and a random regression is used for every animal to show the deviation from the mean. This will result in that the measured records on each animal would be used in the genetic evaluations (12,8). Fixed regression estimates an average curve for the observations of each group and evaluates the difference between each group. Random regression shows the estimates of the genetic variation between animals using deviation from the fixed curve. Thus, the genetic differences between animals can be shown as a deviation from the fixed regression using random parametric curves or orthogonal polynomials like Legendre polynomial or even non-parametric curves such as cubic splines in the model. Legendre polynomial is often used in the studies since it does not have any assumption for the curve status and is easy to use (13).

The aim of this study was to estimate the genetic parameters of the body weight traits in Ghezel sheep using different RR models.

2. Material and methods

2.1. Data and management

The Ghezel sheep breeding center was established in 1985 with the overall area of 27 ha (5446 m² roofed space and 5223 m² nonroofed space) located in Miandoab, West Azerbaijan, Iran. The goal of this station is to identify the production capacity, sustain the breed, improve the performance of the productive traits, and transfer the progress made to the herd owners. The sheep nurturing system in this station is moderately semiextensive; in the warm seasons the animals are grazed during the day and fed with forage and mineral supplements at nights. However, in cold seasons they are fed with alfalfa, grain, and corn. Recording of the animals was initiated from their birth and regarding the examined trait based on the instruction of the sheep breeding center of the country continued. The data used in this research included 39,288 weight records of Ghezel sheep collected from 1994 to 2012 within the range of 1-day to 365-day in the Ghezel sheep breeding center of Miandoab. These records belong to 13,378 animals that are comprised of birth, 90-day, 180-day, 270-day, and 360-day weights. The whole numbers of the animals in the data file was 22,278, of which 13,378 were recorded and 8900 were not. The number of the pedigreed animals was 43,313 from 1986 to 2012. The descriptive statistics of the data are listed in Table 1. The distribution of the records in different ages is also presented in Figure 1.

2.2. Statistical analysis

The selection of fixed effects to be regarded in the model was made after testing whether the effects were statistically significant ($P < 0.01$) with GLM procedure of SAS 9.1 (14). The obtained results showed that the statistical model should include the birth type (single and twins) and year

Table 1. The descriptive statistics for different ages of weighting.

Age (day)	No. of records	Mean of weight (kg)±SE	Range of weight	Mean of age (day) ±SE	Range of age (day)
Birth	13,378	4.04 ± 0.007	1.9-6.7	1	-
90	12,424	21.92 ± 0.035	6.8 –36.1	97.78 ± 0.159	12–149
180	10,053	31.49 ± 0.060	17.5–50	189.65 ± 0.189	150–240
270	2826	39.91 ± 0.157	21–62	271.5 ± 0.315	241–327
360	607	43.19 ± 0.258	26.5–62.5	347.47 ± 0.456	328–365

SE: Standard error

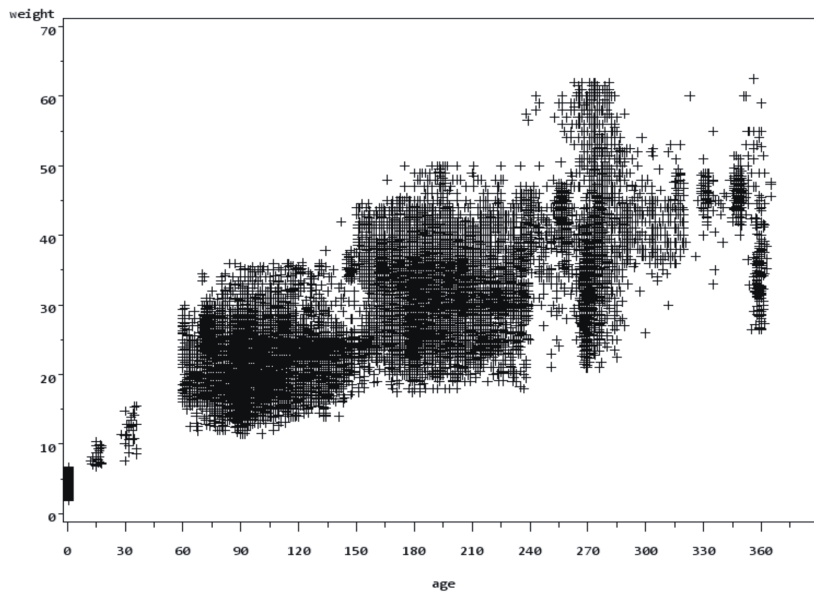


Figure 1. Distribution of the records at different ages.

of birth (1994–2012) as classic fixed effects. The weight as a function of age in the days of weighting was considered as the fixed regression of orthogonal polynomial. This fixed regression explains the average growth curve of all animals with records (4). Three sets of random regression coefficients were fitted to the data. These comprised of direct and maternal additive genetic effects and direct and maternal permanent environmental effects. The RR model fitted Legendre polynomials of age at recording (in days) as independent variables. The general models for the analysis were:

$$1. y_{ij} = F_{ij} + \sum_{m=1}^f \beta_m \varphi_m(a_{ij}) + \sum_{m=0}^{ka-1} \alpha_{im} \varphi_m(a_{ij}) + \sum_{m=0}^{kc-1} \delta_{im} \varphi_m(a_{ij}) + \varepsilon_{ij}$$

$$2. y_{ij} = F_{ij} + \sum_{m=1}^f \beta_m \varphi_m(a_{ij}) + \sum_{m=0}^{ka-1} \alpha_{im} \varphi_m(a_{ij}) + \sum_{m=0}^{km-1} \gamma_{im} \varphi_m(a_{ij}) + \sum_{m=0}^{kc-1} \delta_{im} \varphi_m(a_{ij}) + \varepsilon_{ij}$$

$$3. y_{ij} = F_{ij} + \sum_{m=1}^f \beta_m \varphi_m(a_{ij}) + \sum_{m=0}^{ka-1} \alpha_{im} \varphi_m(a_{ij}) + \sum_{m=0}^{kc-1} \delta_{im} \varphi_m(a_{ij}) + \sum_{m=0}^{kq-1} \rho_{im} \varphi_m(a_{ij}) + \varepsilon_{ij}$$

where y_{ij} is the j^{th} record from i^{th} animal at age a_{ij} , that a_{ij} is the standardized age of recording for y_{ij} , $-1 \leq a \leq 1$ for which Legendre polynomials are defined and $\varphi_m(a_{ij})$ is the corresponding m^{th} Legendre polynomial; F_{ij} is fixed effects relating to y_{ij} (type of birth and year of birth). β_m is the fixed regression on orthogonal polynomials of age; α_{im} , γ_{im} , δ_{im} , and ρ_{im} are the m^{th} order RR coefficients for the direct additive genetic, maternal additive genetic, direct and maternal permanent environmental effects, respectively and $ka - 1$, $km - 1$, $kc - 1$, and $kq - 1$ are the corresponding order of fit for each effect and ε_{ij} denotes the residual effect.

2.3. (Co) variance functions

Random regression analyses produce \mathbf{K} matrices containing (co)variance between random regression

coefficients, particularly for each random effect (direct and maternal additive genetic, direct and maternal permanent environmental effects). The (co)variance functions (G_0) were estimated by pre- and post-multiplying K using a matrix containing Legendre polynomials (Φ) pertaining to a set of specific ages shown in matrix notation as:

$$G_0 = \Phi k \Phi'$$

(Co)variances between RR coefficients relating to different random effects were assumed to be zero. The genetic analyses were performed using Remlf90 1.74 (15). Software with residual maximum likelihood (REML) method for estimation of (co) variance components. Convergence criterion was 10^{-11} .

2.4. Model selection

The first model was considered as the basic model and after determining the best orders of fit for fixed regression, direct additive genetic and direct permanent environmental effects, other random effects were added to the model and the best order of fit was selected. Finally, the best model was selected, and the genetic parameters were estimated using this model.

Models with different orders and number of parameters for different effects were compared based on Akaike's information criterion (AIC) (16) and Schwarz's Bayesian information criterion (BIC) (17). Models with different orders of fitting were compared by AIC, BIC, and log-likelihood ratio test (LRT). A model with significantly the highest ($P < 0.01$) LRT and with the lowest AIC and BIC was considered to be the most appropriate model. Calculation of LRT for models i and j was obtained with this formula:

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

The information criteria are indicated below:

$$AIC = -2 \log L + 2p$$

$$BIC = -2 \log L + p \log(N-r),$$

where:

p: number of parameters estimated,

N: number of records,

r: rank of incidence matrix for the fixed effects,

Log L: REML maximum log likelihood.

3. Results

3.1. Determination of the best model

The estimates of the comparative criteria by the best order of fit in each model are indicated in Table 2 and for all orders of fit of each model are represented in the appendix.

In the first model, the fifth order of fit for fixed regression and the direct permanent environment effect and the third order of fit for direct additive genetic effect were chosen as the most appropriate order of fit, since it had the lowest AIC, BIC, and $-2\text{Log}l$. However, the (3, 5, 1) model had the lowest and the (3, 3, 1) model had the highest RV, respectively.

In the second model, none of the orders of fit was significant ($P < 0.01$) in the LRT. The insignificance of the model by increasing the order of fit for maternal direct genetic effect indicates that by increasing the order of fit, the accuracy of the model decreased. This decrease was evident in all of the orders of fit of maternal genetic except the fourth one.

In the third model, the fifth order of fit for fixed regression and direct permanent environment effect, third order of fit for direct additive genetic and the second for maternal permanent environment effects was selected as the best model and was utilized to estimate the genetic parameters of the body weight traits. In this model, the (5, 3, 5, 3) model and the (5, 5, 2, 1) model had the lowest and the highest RV value, respectively.

3.2. Estimates of (co)variance components and genetic parameters

In Table 3, a number of (co)variance components by the third model are indicated. The variance of the direct additive genetic effect for birth weight was the lowest and with the increase in age it increased such that it was the maximum at one year of age. This increase from birth to one year of age was gradual and steady. The variance of the direct permanent environment for the birth was the least; thereafter, increased as the age increased. However, this increase was not steady, and it had sudden oscillations at some ages. The variance of the maternal permanent

Table 2. The most appropriate order of fit for each of the models.

Model	LP ¹ _(i, j, k, l)	No. of parameters	RV ²	AIC ³	BIC ⁴	-2Logl	LRT ⁵	
1		5, 3, 5	22	0.1851	180351.23	180408.30	180307.23	-
2		5, 3, 5, 1	26	0.0669	186410.42	186477.86	186358.42	-12102.38
3		5, 3, 5, 2	25	0.176	180322.77	180387.62	180272.77	68.92**

Legendre's polynomials (i, j, k, l) i order of fit for fixed regression, j direct additive genetic, k direct permanent environment, l maternal direct genetic for the third model and maternal permanent environment for the fourth model, 2. Residual variance,

3. Akaike's information criterion, 4. Bayesian information criterion, 5. Likelihood ratio test

** Significance variations ($P < 0.01$)

Table 3. Variance (diagonal), (co)variance (above diagonal), and correlations between different ages (below diagonal) for the third model.

Age(days)	Birth	90	180	270	360
Direct additive genetic					
Birth	0.09581	0.06155	0.05677	0.0820	0.1374
90	0.1242	2.56408	3.92238	4.0994	3.0964
180	0.0715	0.9552	6.57651	7.9636	8.0891
270	0.0777	0.7510	0.9110	11.6205	15.0823
360	0.0904	0.3939	0.9426	0.9013	24.0976
Direct permanent environment					
Birth	0.0271	0.25864	0.14515	0.5268	0.0491
90	0.54859	8.20216	1.36211	3.5502	8.3525
180	0.29492	0.15909	8.93805	1.9165	1.4192
270	0.78731	0.30498	0.15722	16.52	-3.9624
360	0.07534	0.73728	0.12001	-0.24645	15.675
Maternal permanent environment					
Birth	0.011171	0.01412	0.01711	0.02009	0.02308
90	0.2769	0.23286	0.45415	0.67507	0.89637
180	0.170985	0.99409	0.8963	1.33771	1.77986
270	0.13444	0.9894	0.99932	1.99926	2.66189
360	0.11596	0.98652	0.99845	0.99982	3.54539

environment effect for the birth was the minimum and with the increase in age, it showed a gradual and steady increase.

The direct genetic correlation between the birth and the 180 days was the least and between the 90 days and 180 days was the highest (Figure 2) and in most of the cases by increasing the age interval it decreased. The direct permanent correlation between 270 days and the 360 days was the lowest and between the birth and the 270 days was the highest (Figure 2) and apparently, there is no relation between the age intervals and the value of the correlation. The maternal permanent environment correlation between birth and the 360 days was the lowest and between the 270 days and the 360 days was the highest. In this diagram, with the increase in age intervals, the value of the correlation decreased.

The values of direct heritability, repeatability, ratio of direct permanent environment to the phenotypic variance (p^2) and ratio of maternal permanent environment to the phenotypic variance (c^2) are represented in Figure 3. The direct heritability from birth to the 20 days decreased and then by increasing of age till 350 days increased that was not uniform (showed some fluctuations). However, the variations of the p^2 had inverted relations with the direct heritability. The c^2 showed a slight increase with the

increase in age. The repeatability increased from birth to 20 days and after that remained almost at a fixed value.

4. Discussion

4.1. Determination of the best model

In most of the cases of the base model, increasing the orders of fit in fixed regression, direct genetic effect and direct permanent environment effect led to a decrease in 2Logl, AIC, BIC, and RV, which shows increase in accuracy by this increase. This is probably due to the increasing flexibility of Legendre's polynomials coefficient resulted from increasing the order of fit. It can also calculate a more precise estimation of residual variance; therefore, estimates of the other (co)variances will be more accurate. Other researchers (6,8,18,19) reported an increase in accuracy with the increase in the order of fit.

By adding the maternal direct genetic effect into the model; the AIC, BIC, and -2Logl increased. This may show that the accuracy of the model has decreased. Hence, the first model in which the maternal genetic effect has not been added is more accurate than the second model. It can be inferred that there is no need to add this effect into the model and the first model can have a more precise estimation of genetic parameters than the second one. By adding the maternal direct genetic effect into the model,

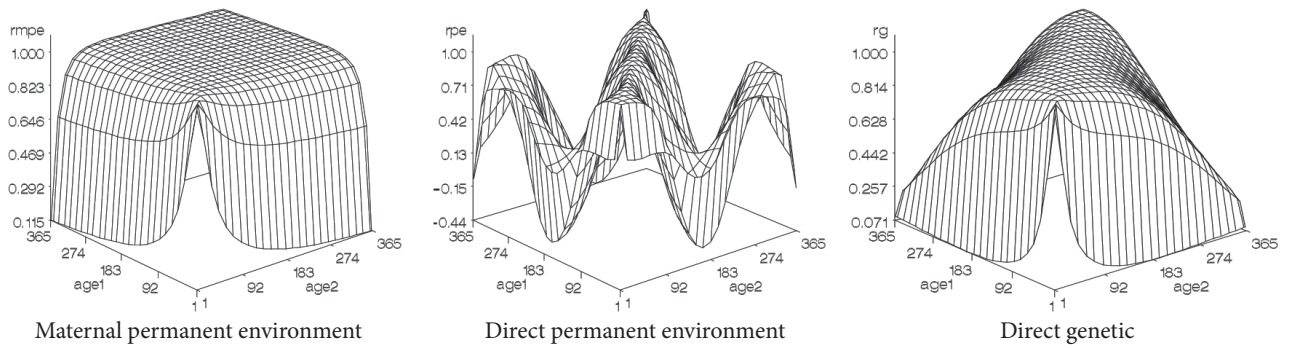


Figure 2. Correlation diagrams.

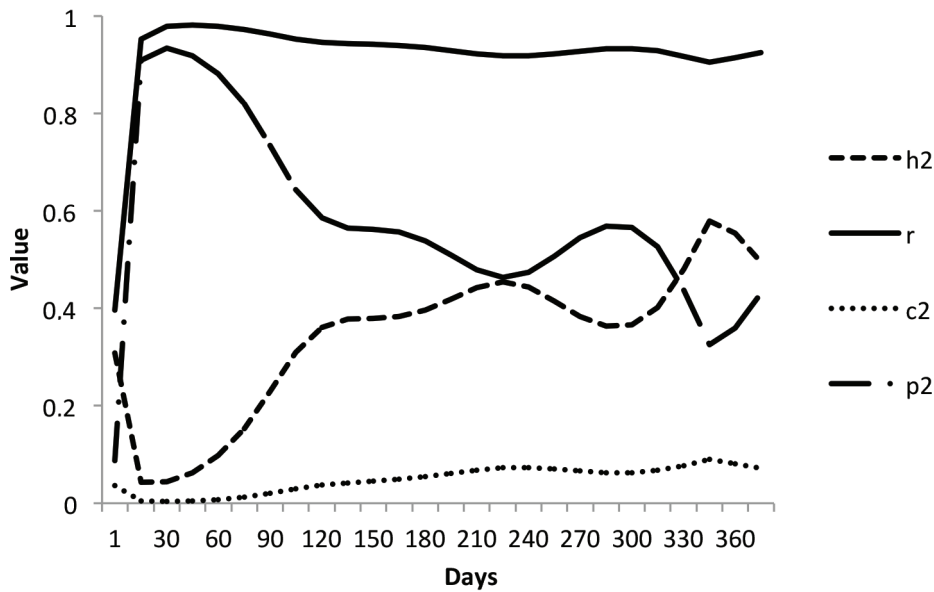


Figure 3. Diagram of heritability (h^2), repeatability (r), maternal (c^2) and direct permanent (p^2) environment effects for weight at selected ages.

RV value decreased and by increasing the order of fit it kept on. This is probably due to the expelling of the part of the residual variance as maternal direct genetic variance.

By adding maternal permanent environment effect into the model and increasing of order of fit, the $-2\log l$, AIC, and BIC values decreased. This decline shows the rise of the model precision as a result of increasing of this effect into the model. In most of the cases, by increasing the order of fit of maternal permanent environment, the RV value decreased. This most likely indicates a better dissociation of variance components in higher order of fits to its ingredients and subsequently the decreasing of the RV. Even though this decrease for some orders is little, it is notable on the whole. Comparison criterion values of the third model were lower than the first one, which shows the escalation of the model accuracy subsequent to

the adding of maternal permanent environment into the model. Hence, it can be concluded that the third model with fifth order of fit for the fixed regression and the direct permanent environment, third order of fit for direct genetic and second order of fit for maternal permanent environment (5, 3, 5, 2) was the most accurate model and was utilized to estimate the genetic parameters of the body weight traits.

Although the (5, 3, 5, 5) model had the greatest LRT, its difference from (5, 3, 5, 2) was not significant ($P > 0.01$) from the Chi-square test perspective; thus, the model with lower number of parameters was selected as the optimum model.

4.2. Variance component and genetic parameters

The direct genetic variance was minimum for birth and with the increase in age it increased such that it reached

its highest amount in one year. This increase from birth till one year was uniform and happened gradually, which is in accordance with the results of Ghafouri Kesbi et al. (6). The variance of direct permanent environment was the least for birth and then with the increase in age it increased. This increase was not uniform and sometimes it showed some sudden fluctuations; however, it happened gradually. This shows that the variation of the direct permanent environment effect was abundant that consequently resulted in the increase in the variance. The permanent maternal environment for birth was the least and with the increase in age showed a uniform and gradual increase. Since the variations of the direct genetic and maternal permanent environment were uniform, the phenotypic variance diagram has imitated the direct permanent environment diagram.

The direct genetic correlation between the birth and 180-day weight was the lowest, and between 90-day and 180-day weights it was the highest. In most cases, with the increase in age interval, its value decreased. The direct permanent environment correlation between 270-day and 360-day weights was minimum, and between the birth and 270-day weights it was the highest. Actually, there's no specific relation between age interval and the correlation value. The permanent maternal environment correlation between the birth and 360-day weights was the lowest and between 270-day and 360-day weights it was the highest. With the increase in the age intervals, this correlation decreased, which is in accordance with the results of others (6,18).

The direct heritability from birth till 20 days declined and then with the increase in age till 350 days, its value increased with some fluctuations. The increase in the direct heritability as with the increase in age can be due to the increase in genes expression of animals that had additive effect on the body weight.

The variations of the p^2 showed the converse relation with the heritability variations. This difference can be traced to their relationship with direct permanent environment variance such that its variations on the direct heritability are vice versa and on the p^2 is direct. Bahreini et al. (20), in their study on Balouchi sheep, indicated a similar trend for the h^2 and p^2 .

The repeatability estimate showed increase from birth to 20 days and then was almost constant.

Difference between the heritability and the repeatability is due to direct permanent environment so that the repeatability is comprised of not only direct genetic, but also direct permanent environment. Therefore, the repeatability indicates the genetic similarity of the records beside similarity resulted from permanent environment. Having fixed and high repeatability estimate shows the

high reliability of genetic parameter estimations.

The c^2 value indicated a slight rise by increasing of age. Other researchers (6,21) showed decrease in c^2 with the increase in age, which is not in accordance with the results of this study.

The increase in c^2 with the increase in age represents continuous effect of maternal permanent effect on animal till end of one year of age. In herds where animals are weaned at a later time, dependency of the lamb on the ewe increases such that it results in the long effect of the maternal effect on the animal which in turn rises the c^2 .

The enigmatic part of the all diagrams was their fluctuation from birth to about the one month that is probably due to the fewer number of records.

Meyer (10) showed, as mentioned previously, that if there are fewer records without uniform distribution, the RR model evaluations will be affected by the data structure that will consequently increase the sampling variance which will finally overestimate the variance components. This problem is called the end effect of polynomials or Rangas phenomenon which can result from sensitivity of Legendre polynomials to data structure. On the other side, Meyer (22) showed that while using the Legendre polynomials in RR models, the effect of each observation is general. On the other hand, having fewer number of observations in specific age not only influences the sampling variance of intended age but it also affects the variance component estimate of the other ages.

This clarifies the importance of the number of records and their uniform distribution in the estimation of the random regression models (Figure 1).

This study showed that the RR model including fifth order of fit for fixed regression, third order of fit for the direct genetic, fifth order of fit for permanent direct environment and second order of fit for permanent maternal environment is the most appropriate for the genetic parameter evaluation. Also, adding maternal direct effect to the model decreases the model accuracy. The trend of genetic parameter variations from birth to 360-day weights represented that between birth and 90 days, in which the number of records is low, the genetic parameter estimation indicated some disorders and has led to sudden increase or decrease of the trend. This needs an ordered and systematic increase of weight recording numbers at different ages in order to estimate more accurate parameters.

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Table A1. The values of -2Logl, AIC, BIC and RV to compare the orders of fit in model 1

LP _(i,j,k) ¹	No. of parameters	RV	AIC	BIC	-2Logl	LRT
3, 3, 1	8	5.229	215172.97	215193.72	215156.97	-
3, 3, 3	13	2.642	209136.80	209170.52	209110.80	12092.34
3, 3, 5	22	3.1798	186140.34	186197.41	186096.34	58121.26
3, 4, 1	12	0.5985	201513.89	201545.02	201489.89	27334.16
3, 4, 5	26	0.1824	192076.02	192143.46	192024.02	46265.90
3, 5, 1	17	0.1780	199305.06	199349.16	199271.06	31771.82
3, 5, 2	19	0.1957	198700.15	198749.44	198662.15	32989.64
3, 5, 3	22	0.1944	198392.92	198449.99	198348.92	33616.10
3, 5, 4	26	0.1928	198218.27	198285.71	198166.27	33981.40
3, 5, 5	31	0.1919	198194.96	198275.37	198132.96	34048.02
4, 3, 1	8	2.059	202596.28	202617.03	202580.28	25153.38
4, 3, 2	10	3.810	206573.89	206599.83	206553.89	17206.16
4, 3, 3	13	1.907	203038.25	203071.97	203012.25	24289.44
4, 3, 5	22	0.1863	183191.17	183248.24	183147.17	64019.60
4, 4, 1	12	0.6003	199063.46	199094.59	199039.46	32235.02
4, 4, 5	26	0.1896	189373.34	189440.78	189321.34	51671.26
4, 5, 1	17	0.1879	196946.69	196990.79	196912.69	36488.56
4, 5, 3	22	0.1998	195996.11	196053.18	195952.11	38409.72
4, 5, 4	26	0.1954	195731.48	195798.92	195679.48	38954.98
4, 5, 5	31	0.1957	195631.49	195711.90	195569.49	39174.96
5, 3, 1	8	1.881	198378.59	198399.34	198362.59	33588.76
5, 3, 2	10	1.884	198032.78	198058.72	198012.78	34288.38
5, 3, 3	13	1.756	198492.51	198526.23	198466.51	33380.92
5, 3, 5	22	0.1851	180351.23	180408.30	180307.23	69699.48**
5, 4, 1	12	1.212	206688.68	206719.81	206664.68	16984.58
5, 4, 5	26	0.1855	186640.81	186708.25	186588.81	57136.32
5, 5, 1	17	0.1891	194516.74	194560.84	194482.74	41348.46
5, 5, 2	19	1.898	208767.54	208816.83	208729.54	12854.86
5, 5, 4	26	0.1955	193150.38	193217.82	193098.38	44117.18
5, 5, 5	31	0.1942	193006.52	193086.93	192944.52	44424.90

1. Legend's polynomials (i, j, k) by the order of fit for fixed regression, direct genetic and direct permanent environment (those orders of fit that do not have the convergence are not shown in the table) ** Significance variations (p< 0.01)

Table A2. The values of -2Logl, AIC, BIC and RV to compare the orders of fit in model2

$LP_{(i,j,k,l)}^1$	No. of parameters	RV	AIC	BIC	-2Logl	LRT
5, 3, 5	22	0.18510	180351.23	180408.30	180307.23	-
5, 3, 5, 1	26	0.06691	186410.42	186477.86	186358.42	-12102.38
5, 3, 5, 2	31	0.05402	192562.18	192642.59	192500.18	-24385.90
5, 3, 5, 3	37	0.05038	198874.66	198970.64	198800.66	-36986.86
5, 3, 5, 4	53	0.05098	205330.91	205468.39	205224.91	-49835.36
5, 3, 5, 5	52	0.04972	211769.47	211904.36	211665.47	-62716.48
5, 4, 5, 1	31	0.06847	192701.48	192781.89	192639.48	-24664.50
5, 4, 5, 2	37	0.05773	198792.24	198888.22	198718.24	-36822.02
5, 4, 5, 3	44	0.05301	205085.80	205199.94	204997.80	-49381.14
5, 4, 5, 4	52	0.05481	211376.22	211511.11	211272.22	-61929.98
5, 4, 5, 5	61	0.05306	217822.36	217980.59	217700.36	-74786.26
5, 5, 5, 1	37	0.07965	199047.24	199143.22	198973.24	-37322.02
5, 5, 5, 2	44	0.07134	205148.62	205262.76	205060.62	-49506.78
5, 5, 5, 3	52	0.06292	211422.36	211557.47	211318.58	-62022.70
5, 5, 5, 4	61	0.06431	217698.28	217856.51	217576.28	-74538.10
5, 5, 5, 5	71	0.06255	224038.43	224222.60	223896.43	-87178.40

1. Legendre's polynomials (i, j, k, l) by the order of fit for fixed regression, direct genetic, direct permanent environment and maternal direct genetic (those orders of fit that do not have the convergence are not shown in the table)

Table A3. The values of -2Logl, AIC, BIC and R.V. to compare the orders of fit in model 3

LP _(i,j,k,l) ¹	No. of parameters	RV	AIC	BIC	-2Logl	LRT
5, 3, 5	22	0.185	180351.23	180408.30	180307.23	-
5, 3, 2, 1	11	1.818	197899.24	197927.77	197877.24	-35140.02
5, 3, 2, 2	13	1.817	197873.26	197906.98	197847.26	-35080.06
5, 3, 2, 3	16	1.816	197899.53	197941.03	197867.53	-35120.60
5, 3, 3, 1	14	1.763	197668.37	197704.69	197640.37	-34666.28
5, 3, 3, 2	16	1.761	197631.97	197673.47	197599.97	-34585.48
5, 3, 3, 3	19	1.760	197640.69	197689.98	197602.69	-34590.92
5, 3, 3, 4	23	1.201	194962.98	195022.64	194916.98	-29219.50
5, 3, 4, 1	18	0.4916	192386.66	192433.35	192350.66	-24086.86
5, 3, 4, 3	23	0.4260	185327.51	185387.17	185281.51	-9948.56
5, 3, 4, 4	27	0.4255	185348.21	185418.25	185294.21	-9973.96
5, 3, 4, 5	32	0.2674	182217.21	182300.22	182153.21	-3691.96
5, 3, 5, 1	23	0.1780	180347.13	180406.79	180301.13	12.20
5, 3, 5, 2	25	0.1760	180322.77	180387.62	180272.77	68.92**
5, 3, 5, 3	28	0.1772	180326.71	180399.34	180270.71	73.04
5, 3, 5, 4	32	0.1777	180335.94	180418.95	180271.94	70.58
5, 3, 5, 5	37	0.1777	180334.23	180430.21	180260.23	94
5, 4, 2, 1	15	0.4286	192469.02	192507.93	192439.02	-24263.58
5, 4, 2, 3	20	0.4275	192386.19	192438.07	192346.19	-24077.92
5, 4, 2, 4	24	0.4230	192446.48	192508.74	192398.48	-24182.50
5, 4, 2, 5	29	0.2733	189320.56	189395.79	189262.56	-17910.66
5, 4, 3, 1	18	0.4290	192008.80	192055.49	191972.80	-23331.14
5, 4, 3, 4	27	0.4219	192074.54	192144.58	192020.54	-23426.62
5, 4, 3, 5	32	0.2700	188920.71	189003.72	188856.71	-17098.96
5, 4, 4, 1	22	0.4269	191700.62	191757.69	191656.62	-22698.78
5, 4, 4, 4	31	0.4264	191684.01	191764.42	191622.01	-22629.56
5, 4, 4, 5	36	0.2674	188561.67	188655.05	188489.67	-16364.88
5, 4, 5, 1	27	0.1789	186636.22	186706.26	186582.22	-12549.98
5, 4, 5, 2	29	0.1799	186607.10	186682.33	186549.10	-12483.74
5, 4, 5, 3	32	0.1799	186612.78	186695.79	186548.78	-12483.10
5, 4, 5, 4	36	0.1801	186624.65	186717.65	186552.27	-12490.08
5, 4, 5, 5	41	0.1785	186626.65	186733.00	186544.65	-12474.84
5, 5, 2, 1	20	1.884	208229.24	208281.12	208189.24	-55764.02
5, 5, 2, 2	22	0.1922	193802.70	193859.77	193758.70	-26902.94
5, 5, 2, 3	25	0.1921	193767.46	193832.31	193717.46	-26820.46
5, 5, 2, 4	29	0.1908	193743.80	193819.03	193685.80	-26757.14
5, 5, 2, 5	34	0.1903	193756.91	193845.11	193688.91	-26763.36
5, 5, 3, 1	23	0.1925	193482.02	193541.68	193436.02	-26257.58
5, 5, 3, 2	25	0.1928	193447.71	193512.56	193397.71	-26180.96
5, 5, 3, 3	28	0.1943	193455.43	193528.06	193399.43	-26184.40
5, 5, 3, 4	32	0.1937	193438.29	193521.30	193374.29	-26134.12

Table A3. (Continued).

5, 5, 3, 5	37	0.1929	193447.76	193543.74	193373.76	-26133.06
5, 5, 4, 2	29	0.1893	193110.33	193185.56	193052.33	25490.20
5, 5, 4, 3	32	0.1893	193116.68	193199.69	193052.68	-25490.90
5, 5, 4, 4	36	0.1891	193128.81	193222.19	193056.81	-25499.16
5, 5, 4, 5	41	0.1887	193133.53	193239.88	193051.53	-25488.60
5, 5, 5, 1	22	0.1874	193002.29	193039.36	192938.29	-25262.12
5, 5, 5, 2	36	0.1862	192971.83	193068.91	192903.53	-25192.60
5, 5, 5, 3	37	0.1853	192978.32	193074.30	192904.32	-25194.18
5, 5, 5, 4	41	0.1857	192989.48	193095.84	192907.49	-25200.52
5, 5, 5, 5	46	0.1852	192993.25	193112.67	192901.35	-25188.24

1. Legendre's polynomials (i, j, k, l) by the order of fit for fixed regression, direct genetic and direct permanent environment and maternal permanent environment** Significance variations ($p < 0.01$)