

Random regression models for estimation of covariance functions of growth in Iranian Kurdi sheep

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Abstract Body weight (BW) records ($n=11,659$) of 4961 Kurdi sheep from 215 sires and 2085 dams were used to estimate the additive genetic, direct and maternal permanent environmental effects on growth from 1 to 300 days of age. The data were collected from 1993 to 2015 at a breeding station in North Khorasan province; Iran. Genetic parameters for growth traits were estimated using random regression test-day models. The residual variances were modeled by a step function with various classes. The model 16 with a polynomial of 3 order for fixed effect, 6 order for direct genetic effect, 6 order for direct permanent environmental and 6 order for maternal permanent environmental effects with the lowest Bayesian information criterion (BIC) was considered to be the best model. The direct heritability ranged from 0.01 at day 1 of age to 0.36 at 300 days of age. Genetic correlations ranged from 0.03 to 0.98 for body weight between different days of age. The small value of genetic correlation (0.03) among early (day 1) and late (300 days) weights showed that early weights were not under the same genetic control as weights at older ages. Genetic progress was realized and the estimated genetic parameters obtained could be used for further improvement of sheep and small ruminants.

Keywords: Kurdi sheep, growth traits, genetic parameters, Legendre polynomials

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Introduction

Lamb and mutton are common sources of protein in Iran and the consumption levels are high in comparison with cattle and goat meat. (Yazdi et al., 1997). The sheep population in Iran is mainly composed of fat-tailed carpet-wool native breeds. They are mostly adapted to the poor range conditions of the country. A high percentage of the sheep population is man-aged under a migratory system, utilizing the range as the major source of feed (Ghafouri-Kesbi et al., 2008). Kurdi sheep is a meat type sheep breed in North Khorasan province (Nassiry et al., 2007). According to formal statistics of the Ministry of Agriculture, the average lambing rate in Khorasan province is 0.7 lambs per ewe/year (Fallah and Farzaneh, 2007). A high proportion of the sheep population in Iran is managed under the migratory system, depending on the ranges as the major source of feed (Ghafouri-Kesbi et al., 2008). Estimates of (co)variance components and genetic parameters are very important in making informative genetic evaluation, predicting the direct and correlated responses to selection and for development of multi-trait selection indices. Random regression (RR) models have been used increasingly to estimate the genetic parameters and predict breeding values, due to

their relative advantages as compared to conventional animal models (Schaeffer, 2004). Random regression models (RRM) have been proposed as the most satisfactory models to describe the changes in the (co)variances of repeated measures obtained throughout the life of an animal, such as milk yield, which is measured monthly (Jamrozik and Schaeffer, 1997). These models assume all production records of the same animal to be the same trait (Kirkpatrick et al., 1994), but consider environmental differences between measures, an approach that permits estimation of the trajectory of the trait over time for each animal as a deviation of the fixed curve estimated for the population. Therefore, the random regression models allow estimates of covariance between coefficients of random functions or, equivalently, estimates of covariance functions. In general, orthogonal Legendre polynomials have been employed in RRM to model the random trajectories for the additive and permanent environmental effects, as well as the fixed trajectory and generate better convergence properties than models using other functions (Pool et al, 2000). Studies on the use of RR indicated higher accuracy of prediction and estimation to analyze sheep growth. This is due to units

serving as their own control and due to the possibility of estimating (co)variance components at any point on the trajectory of time (Fischer et al., 2004; Lewis and Brotherton, 2002; Molina et al., 2007). The random regression models allow obtaining the breeding values at any day of test in a continuous manner or for functions of the growth curve, instead of finite dimensional models that only give punctual predictions of the breeding values. Also, the random regression models allow estimates of covariances between coefficients of random functions or, equivalently, estimates of covariance functions (Jamrozik et al., 2000; Schaeffer et al., 2000). To determine the optimal breeding strategies for increasing the efficiency of sheep production, knowledge of genetic parameters for weight at various ages and also the genetic relationships between the traits are needed (Boujenane et al., 1991). Therefore, the aim of this study was to estimate genetic covariance function for growth traits of Iranian Kurdi sheep in various ages using RRM.

Materials and methods

Geographical location and herd management

The data used in this research were collected from the flock of Kurdi sheep during the period 1993–2015 at the rearing and breeding station of Kurdi sheep located in North Khorasan province that is located in 37°46'N and 57°33'E, Iran. Alfalfa, barley, corn silage, concentrates, and grass are used to feed the animal during the semi-intensive rearing period. The aim of the project was to establish a nucleus source to improve other flocks in the region. The starting animals were purchased from different sheep farms in the region. The flock is generally reared by following conventional industry practices (Nassiry et al., 2007).

The data included of weight records from 1 to 300 days of age. A total of 11, 659 records of 4961 animals that had at least 2 records per lamb with an average weight of 20.61 kg were finally available. Animals with records were progeny of 215 sires and 2085 dams and the pedigree included 5935 animals. The description of data set is shown in Table 1.

Number of records and mean weights for different ages are given in Figure 1. Body weights increased evenly linear with increasing in age from 1 to 270 days of age. Therefore, the coefficient of variation remained at the relatively constant across ages.

Statistical analysis

A preliminary analysis for determination of the fixed effects affecting the body weight records was performed

Table1. Descriptive statistics of the data set from 1 to 300 days of age in Kurdi sheep.

Number of records	11659
Body weight	
Mean (kg)	20.61
Standard deviation (kg)	16.33
No. of animal with records	4961
No. of animals in the analysis	5935
No. of sires	215
No. of dams	2085
No. of sires with records and progeny	43
No. of dams with records and progeny	1232

by general linear model analysis using the GLM procedure (SAS, 2004). The statistical model included age of the dam (2 -7), sex of kid (male and female), type of birth (single, twin and triples), and year of birth (1993 to 2013). All of the fixed effects were significant (P<0.01) and included in the final models. Weight, 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 (Abegaz et al., 2010). Three sets of random regression coefficients were fitted to the data. These included direct genetic, and direct and maternal permanent environmental effects. The random regression (RR) model fitted Legendre polynomials of age at recording (in days) as independent variables. Additive genetic effects (**a**), maternal permanent (**pm**) and direct permanent environmental effects (**pe**) were modeled via quadratic, cubic, quadric, quintic and sixth degree polynomial functions, comprising $K_a= 2, 3, 4, 5$ and 6 , $K_{pm}=3, 4, 5$ and 6 and $K_{pe}= 3, 4, 5,$ and 6 random regression coefficients, respectively. Orders of fit for fixed effects cubic were considered. The model in matrix notation was:

$$Y = Xb + Z_1a + Z_2pm + Z_3pe + e \tag{1}$$

where, **y** is the vector of observations, **b** is the vector of fixed effects (including fixed effects and fixed regression), **a** is the vector of random coefficients for additive direct effects, **pm** is the vector of random coefficients for maternal permanent environment effects, **pe** is the vector of random coefficients for animal permanent environment effects, **e** is the vector of residual effects and **X**, **Z**₁, **Z**₂ and **Z**₃ are related to incidence matrices. The model was based on the following hypothesis:

$$Var \begin{bmatrix} a \\ m \\ p_e \\ e \end{bmatrix} = \begin{bmatrix} K_a \otimes A & 0 & 0 & 0 \\ 0 & K_m \otimes I & 0 & 0 \\ 0 & 0 & K_{p_e} \otimes I & 0 \\ 0 & 0 & 0 & R \end{bmatrix} \tag{2}$$

where, K_a , K_{pm} and K_{pe} are (co)variance matrices between

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random regression coefficients for direct additive, maternal and animal permanent environmental effects, respectively. **A** is the relationship matrix, **I** is an identity matrix, \otimes is the Kronecker product between matrices and **R** is a block diagonal matrix containing residual variances. Correlations between random regression coefficients for different effects were set to zero.

Residual variances were modelled via a step function with 1 (Homogenous), 9 (1-35, 36-65, ..., 246 - 300), 12 (1-26, ..., 287-300), 17 (1-20, 21-36, ..., 281-300) and 30 (1-12, 13-20, ..., 291-300) classes (Madad et al., 2016).

Random regression analyses produce **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{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:

$$\hat{G}_0 = \Phi K \Phi \quad (3)$$

Covariances between RR coefficients, pertaining to different random effects, were assumed to be zero. Genetic analyses were performed using WOMBAT software (Meyer, 2007) with residual maximum likelihood (REML) method for estimation of (co)variance components. Solutions for the random regression coefficients for each animal can be used to estimate the breeding value (BV) for any point in the age curve between 1 and 300 d. For example, BV for the animal *i* at 300 d of age

will be:

$$BV_{i,300} = q_{300} \times \alpha_i \quad (4)$$

where, α_i represents solution for animal *i*, and q_{300} is the vector of coefficients of the Legendre polynomial corresponding to 300 d of age.

Let *p* denote the number of parameters estimated, *N* the sample size, *r(X)* the rank of the coefficient matrix of fixed effect in the model of analysis and log *L* is the REML maximum log likelihood. The information criteria are then given as:

$$AIC = -2 \log L + 2 p \quad (5)$$

and

$$BIC = -2 \log L + p \log (N-r(x)) \quad (6)$$

Calculation of LRT for models *i* and *j* was obtained with formula:

$$LRT_{ij} = 2 \times (\log L_i - \log L_j) \quad (7)$$

Results from different models of analyses were compared by the Restricted Maximum Likelihood (REML) criterion (BIC) (Schwarz, 1978), and by inspecting the variance component and genetic parameter estimates. A model with the highest significant ($P < 0.05$) log-likelihood ratio test (LRT) and with the lowest BIC was conform of the Akaike information criterion (AIC) (Akaike, 1974), the Schwarz' Bayesian information sidered to be the most appropriate model.

Results

A summary of the random regression model fit for the

Table 2. Order of fit of additive genetic (k_a), maternal permanent (k_{pm}) and direct permanent environmental (k_{pe}) effects, residual (e) with heterogeneous classes (HET), or homogeneous classes (HOM), number of parameters (P), log likelihood value, Akaike information criterion (AIC), Bayesian information criterion (BIC) and Likelihood ratio test (LRT)

Model	k_{pm}	k_{pe}	K_a	e	Parameter	Log L	AIC	BIC	LRT
1	3	3	3	Hom	19	-9673.18	19384.36	19423.63	
2	3	3	3	Het1	27	-6137.20	12328.40	12527.14	(2-1) 7071.96*
3	3	3	3	Het2	30	-4678.79	9417.58	9638.40	(3-2) 2916.82*
4	3	3	3	Het3	34	-4619.78	9307.56	9557.84	(4-3) 118.02*
5	3	3	3	Het4	49	-4743.00	9584.00	9944.68	(5-4) 246.44*
6	3	3	2	Het3	31	-4776.77	9615.54	9843.72	
7	4	3	2	Het3	35	-5112.87	10259.74	10553.38	(7-6) 672.2*
8	5	3	2	Het3	40	-4747.98	9575.96	9870.40	(8-7) 729.78*
9	6	3	2	Het3	46	-4686.31	9464.62	9803.22	(9-8) 123.34*
10	4	4	3	Het3	42	-4585.25	9254.50	9563.66	(10-9) 202.12*
11	5	4	3	Het3	47	-4613.25	9320.50	9666.48	(11-10) 56*
12	6	4	3	Het3	53	-4548.26	9202.52	9592.64	(12-11) 129.98*
13	4	5	4	Het3	51	-4691.64	9485.28	9590.68	(13-12) 286.76*
14	5	5	4	Het3	56	-4826.74	9764.94	10177.16	(14-13) 270.20*
15	6	5	5	Het3	67	-4593.43	9320.86	9459.32	(16-15)1862.20*
16	6	6	6	Het3	79	-3662.33	7482.66	8064.18	

* $P < 0.05$

studied traits is shown in Table 2. The order of fit for the additive genetic and maternal and permanent environmental effects was kept constant to define the best variance structure in modeling the residual variances. The values for log L, AIC and BIC indicated a significant improvement in the level of fit when the residual variance was considered heterogeneous. These indicated that residual variances showed different behavior during the growth curve; therefore, it is necessary to consider a heterogeneous variance structure for the residuals.

The AIC values indicated that a step function with 17 classes was the most adequate to model the residual variances. However, the LRT and BIC values that penalized more highly parameterized models showed the same results. After having chosen the most adequate structure to model the residual variances, several models were compared varying in the order of covariance functions for additive genetic (k_a), maternal (k_{pm}) and animal permanent environmental effects (k_{pe}). The BIC criteria indicated that the best fitting RRM was the model with a polynomial of 3 order for fixed effect, 6 order for direct genetic effect, 6 order for direct permanent environmental and 6 order for maternal permanent environmental effects (6.6.6. het3).

Direct additive genetic, maternal and direct permanent environmental variance estimates are presented in table 3. Direct additive genetic variance decreased up to 180 days of age and then increased until 300 days of age. Maternal permanent environmental variance decreased from 8.89 at birth day to 0.23 at 150 and then increased until 270 days of age and after that decreased with age. The pattern estimated for permanent environmental variance and phenotypic variance were erratic. The estimates of direct heritabilities, maternal and direct permanent environmental variances as proportions of phenotypic variance for selected ages are given in Table 3. Direct heritability (h^2) increased along the trajectory from 0.01 at birth day to 0.36 at 300 days of age. Maternal permanent environmental variance (c^2) as proportions of phenotypic variance increased to 60 days and

then declined erratically until 300 days of age. Direct permanent environmental variance (pe^2) as a proportion of the phenotypic variance decreased fairly along the trajectory.

Analyses using random regression models yield estimates of covariance functions which can be evaluated to provide estimates of genetic and environmental (co)variance components for every age on test. To simplify presentation, results are given for selected days only (Figure 2). Generally, the genetic and phenotypic correlations between weights increased with decreasing interval between weights. Genetic correlations among various traits were positive, low to high and ranged from 0.03 between 1 and 300 days of age to 0.98 between 270–300 days of age. Maternal and direct permanent environmental correlations between weights at selected ages are given in Table 4. Maternal permanent environmental correlations among various days were positive and ranged from 0.16 between 120 and 300 days of age to 0.94 between 1 and 60 days of age. The estimate of permanent environmental correlations was in ranges of 0.17 to 0.93. Generally, permanent environmental correlations decreased in higher age intervals.

The genetic trends of birth weight, 150-d weight and 300-d weight are given in Figure 3. For birth weight, the genetic changes increased from 1993 to 1997 and then from 1997 to 2003 genetic trend decreased along the trajectory. Generally, the genetic trend for birth weights was different than those of the other selected body weight traits. The genetic changes of the other selected body weight traits increased from 1997 to 2003 and plots of the mean predicted breeding values on year of birth indicated an increase over time.

Discussion

The order of fit for the random effects was kept constant to define the best variance structure to model the residual variances. The results of LRT indicated a significant ($P<0.05$) improvement in the level of fit when the heterogeneous residual variance was included in the model,

Table 3. Estimates of phenotypic (σ^2_p), direct additive genetic (σ^2_a), maternal (σ^2_c) and direct permanent (σ^2_{pe}) environmental variances and direct heritability (h^2), maternal (c^2) and direct (pe^2) permanent environmental effects as a proportion of phenotypic variance for weight at selected ages.

Age (days)	1	30	60	90	120	150	180	210	240	270	300
σ^2_p	75.05	12.54	6.11	9.85	7.02	2.13	4.66	11.66	19.24	22.86	24.65
σ^2_a	1.14	0.13	0.12	0.23	0.23	0.09	0.30	1.19	2.84	5.73	8.99
σ^2_c	8.89	5.43	2.73	1.00	0.24	0.23	0.49	0.51	1.18	2.29	0.68
σ^2_{pe}	63.49	5.45	3.13	7.58	5.51	1.60	2.85	9.09	14.35	12.99	10.21
h^2	0.01	0.01	0.02	0.02	0.03	0.04	0.06	0.10	0.14	0.25	0.36
c^2	0.11	0.43	0.44	0.10	0.03	0.10	0.10	0.04	0.06	0.10	0.02
pe^2	0.84	0.43	0.51	0.76	0.78	0.75	0.61	0.78	0.74	0.56	0.41

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Table 4. Maternal (above diagonal) and direct permanent environmental correlations (below diagonal) among weights at selected ages.

Age	1	60	120	180	240	300
1		0.94	0.91	0.64	0.45	0.23
60	0.84		0.87	0.79	0.58	0.31
120	0.75	0.93		0.50	0.44	0.16
180	0.67	0.65	0.75		0.91	0.81
240	0.65	0.32	0.39	0.89		0.74
300	0.58	0.17	0.37	0.87	0.85	

in comparison to homogeneous residual variance (Abegaz et al., 2010) and model fit improved with increasing polynomial regression order. These indicated that residual variances had different behavior along the age. The BIC and LRT results indicated that a step function with 17 classes was the most adequate to model the residual variances. The BIC results showed 6.6.6 het3 model was the most adequate one to describe the covariance structure of data. One of the main objectives of the present study was to determine the change patterns in the mean and variance components of ewe body weight at different ages in Kurdi sheep. Direct additive genetic variance decreased up to 180 days of age and then increased until 300 days of age and was highest at the later ages in the growth trajectory (Table 3). Despite of the effect of selection on additive genetic variance (Bulmer effect), the increasing trend of additive genetic variance in older ewes shows that it is likely that several genes with additive effects were activated in older ewes. This pattern of changes in additive genetic variance indicated that body weight of Kurdi ewes are different traits at early, mid and older ages. This increasing pattern of additive genetic variance is in agreement with Nephawe (2004). Other studies modeling growth in sheep using random regression models have reported direct genetic variances that increased with time (Lewis and Brotherston, 2002; Fischer et al., 2004; Kariuki et al., 2010). A decreasing trend was observed for maternal permanent environmental variance up to around 150 days that increased with age thereafter (except 300 days), which was correspond to the result reported by Kariuki et al. (2010) and was different from the result of Ghafouri-Kesbi et al. (2008). Except for day 1 of age, direct permanent environmental variances were considerably higher at later ages and were inconsistent with the report of Fischer et al. (2004). Since the permanent environmental variance is related to both non-additive genetic and non-genetic permanent environmental effects and due to the pattern changes in permanent environmental variance component, it can be concluded that there may be genes with non-additive genetic effect and (or) non-genetic permanent effects that can be activated in the

later ages. This observation denotes an important effect of the permanent environmental effects on body weight in the older ages for the studied population. The decreasing trend was observed for phenotypic variance up to around 150 days and increased with age thereafter, which is directly related to a temporary decline in measurement error variance (Fischer et al., 2004). Generally, there were similar trends for the direct additive genetic and the permanent environmental variances estimations. As indicated in Table 3, increasing pattern for direct heritability was observed up to 300 days. Fogarty (1995) and Safari et al. (2005) reported that the value of heritability was increased along with the growth curve of the animal. General trend of direct heritability in current study is inconsistent with the result of Kariuki et al. (2010). However, there are some researchers who found lower estimated direct genetic heritabilities for earlier ages (Lewis and Brotherston, 2002; Fischer et al., 2004; Barazandeh et al., 2012); the lower direct genetic heritabilities could be attributed to higher residual variance ratios in earlier ages and due to culling surplus kids and lower number of records compared with other ages. However, direct heritability was larger for post-weaning weight than pre-weaning weight. These findings were in accordance with other studies (Mugambi et al., 2007; Safari et al., 2005; Zhang et al., 2009). Maternal permanent environmental variance (c^2) as proportions of phenotypic effect had high estimates between 30 and 60 days of age and subsequently decreased along the trajectory, which was in agreement with the reports of Albuquerque and Meyer (2001). In contrast, low estimates for maternal permanent environmental variance (c^2) were observed in the present study which is in agreement with Kariuki et al. (2010). However, estimates of c^2 were different from the reports of Fischer et al. (2004) and Ghafouri-Kesbi et al. (2008) who showed that moderate values in early ages are followed by a continuous decline with age. This difference could be attributed to many factors including different populations, environments and models used for analysis. The general paucity of literature estimates for maternal effects in sheep over a range of ages make the comparison more difficult;

however, most studies reported that c^2 decreased as time lapses post-weaning (Fischer et al., 2004). 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 (Kariuki et al., 2010). Direct permanent environmental variances as proportions of phenotypic variances (pe^2) were higher for the birth day, when direct heritability had the least importance for this population. According to the study of Kariuki et al. (2010) in Dorper sheep and in disagreement with the results of Fischer et al. (2004) in Poll Dorset sheep and Ghafouri-Kesbi et al. (2008) in Mehraban sheep, direct permanent environmental variance (pe^2) increased with age (Table 3), indicating that the environmental effects are important for later age in Kurdi sheep. Kids were housed before weaning they had access to pasture after weaning. The post-weaning environmental variance would therefore be more suited as an indication of the individual's response to stress (Kariuki et al., 2010). Based on the estimated values of various parameters in the present study, it could be concluded that most of the phenotypic variation of body weight in Kurdi sheep from birth to 300 day of age are due to direct genetic and permanent environmental effects, while the maternal effect has a low contribution. The decrease in genetic correlations between weights (Figure 2) 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). Also, The values of genetic correlations among ewe body weight at different ages obtained in this study implied that if animals are selected for weight, it is possible for an animal to be below the average weight at younger ages and above average weight at older ages; however, this has implications for potential to select on the shape of the growth curve. The pattern of maternal permanent environmental correlations between different ages (Table 4) is similar in that the correlations decreased as the age distance between weights increased. 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.

Generally, the genetic trends for birth weights were very different from those of other body weight traits. Based on Figure 3, the genetic change increased from 1993 to 1997 but decreased from 1997 to 2003 that was

probably due to the genetic trend provided by the use of negative and lowly predicted transmitting ability (PTA). This trend was almost in agreement with the reports of Mokhtari and Rashidi (2010) in Kerman sheep and Bohlouli et al. (2013) in Zandi sheep. Selection based on birth weight was minimal in comparison to other body weight traits (Bohlouli et al., 2013). For all selected ages, there were abrupt decreases in the yearly mean predicted breeding values of animals especially in 2007. Generally, genetic trends showed a yearly gain and were consistently positive but small. Although the average yearly gain is a trait of economic importance for beef production systems, it is not so much important for milk production systems because selection for average yearly gain would result in increased nutritional requirements early in life, with higher costs for maintenance of dairy ewes (Lobo et al., 2000).

Conclusions

According to the results of this study, random regression model seemed to be a flexible and reliable procedure for the genetic evaluation of growth traits in Kurdi sheep. BIC criteria indicated that the best fitting RRM was the model with a polynomial of 3 order for fixed effect, 6 order for direct genetic effect, 6 order for direct permanent environmental and 6 order for maternal permanent environmental effects. However, data collection needs to be improved to enhance the accuracy of parameter estimates and allow more comprehensive evaluations. The results of the present study indicated that most of the phenotypic variation of body weight in Kurdi sheep from 1 to 300 days of age were due to the direct genetic and permanent environmental effects. The decrease in genetic correlations between weights with increasing time lag between measures showed that different weights along the growth curve of an individual were affected by different genes and should be considered as different correlated traits. Estimates of genetic trends indicated that there was positive genetic improvement in all studied traits and selection would be effective for the improvement of body weight traits in this breed.

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مدل های تابعیت تصادفی برای برآورد توابع کوواریانس از رشد در گوسفندان کردی ایران

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چکیده در این پژوهش، از ۱۱۶۵۹ رکورد وزن بدن ۴۹۶۱ مربوط به گوسفند کردی و متعلق به ۲۱۵ پدر و ۲۰۸۵ مادر برای پیش بینی اثرهای ژنتیک افزایشی، ژنتیک مادری، محیطی مادری و محیطی دائمی در روزهای ۱ تا ۳۰۰ از سن حیوان استفاده شد. داده های پژوهش به وسیله مرکز اصلاح نژاد در استان خراسان شمالی ایران بین سال های ۱۳۷۱ تا ۱۳۹۳ جمع آوری شده بود. پارامترهای ژنتیکی مربوط به صفات رشد با استفاده از مدل تابعیت تصادفی برآورد شدند. واریانس باقی مانده به وسیله تابعی با کلاس های مختلف مدل سازی شد. معیار BIC برای انتخاب بهترین مدل RRM به کار برده شد به شیوه ای که مدل ۱۶ با چند جمله ای درجه ۳ برای اثر ثابت، ۶ برای اثر ژنتیکی افزایشی، ۶ برای اثر محیطی دائمی و ۶ برای اثر محیطی مادری در نظر گرفته شد. دامنه وراثت پذیری از ۰/۰۱ برای روز یکم تا ۰/۳۶ برای روز ۳۰۰ ام از سن حیوان برآورد شد. دامنه همبستگی ژنتیکی وزن بدن از ۰/۰۳ تا ۰/۹۸ بین روزهای مختلف برآورد شد. مقدار پایین همبستگی ژنتیکی (۰/۰۳) بین روزهای ابتدایی (روز یکم) و پایانی (۳۰۰ ام) نشان داد که وزن بدن در روزهای آغازین در کنترل ژن های مشابه با وزن در روزهای پایانی نیست. از دیگر سو، روند ژنتیکی مثبت شناسایی شده صفات رشد و برآوردهای روند ژنتیکی مربوط به بازدهی رشد نشان دادند که تصمیم گیری های گزینشی در خلال برنامه های بهنژادی، به شیوه شایان توجه ای موجب بهبود صفات وزن بدن شدند.