ESTIMATION OF GENETIC PARAMETERS FOR BODY WEIGHT TRAITS IN MAZANDARAN NATIVE BREEDER HENS BY RANDOM REGRESSION MODELS

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The primary concern of this study is to investigate appropriate random regression model for estimate genetic parameters body weight at hatch (BW1), eight (BW8), twelve (BW12) and thirty two (BW32) weeks of ages by the restricted maximum likelihood method. The body weight records set included 39872 during 16 generations of hens kept at the Mazandaran Breeding Center of Iran. Random regression were modelled using generation-hatch as a fixed effect and additive genetic and permanent environmental effects as random effects Residual variances were modeled through a step function with 1 and 3 classes. The model was considered to be the most appropriate with the highest significant log likelihood ratio test (LRT) and the lowest Akaike information criterion (AIC) and Bayesian information criterion (BIC). Heritability values increased from 0.21 for BW1, to 0.40 for BW32. Genetic correlations of body weight at different record keeping were often higher than permanent environmental correlations. Genetic correlations between pairs of body weight measures were moderate to high with a range from 0.25 to 0.97. The largest genetic correlation, as well as permanent environmental correlation, was observed between BW12and BW32. High and moderate broad sense heritability values for all studied traits shows that these traits are less influenced by residual effects which make them effectively transmitted to the progeny. Findings show that genetic improvement for body weight can be achieved by selection. The Heritability of body weight at thirty two weeks of ages and its relatively

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high genetic correlation with all other ages showed that it could be the most appropriate period for selection. Also, the genetic trend estimates for body weight traits showed that selection decisions made during the breeding program effectively improved the growth performance.

Keywords: Akaike information criterion (AIC), Bayesian information criterion (BIC), Mazandaran Native Breeder Hens, Random Regression Model

INTRODUCTION

National flocks in Africa and Asia were used for genetic progress and variation to produce breeds adjusted to local conditions (HOFFMANN, 2005). Consumer concerns are very important, so meat hens producers have been required to meet animal welfare standards (VANHONACKER and VERBEKE, 2009; SMITH *et al.,* 2012). There are clear evidences that 50 percent of chicken breeds have been classified as being at risk. Despite their low growth rates and egg production, indigenous hens can survive under harsh nutritional and environmental conditions and they have more resistant to various diseases (MINGA *et al.*, 2004).Iranian native hens are meat-egg type or multipurpose but they have generally poor producers of eggs and meat in comparison with commercial breeds. The conservation of genetic resources of each country has paramount importance So that during the past several decades importing non‐native breeds have increased risk of elimination Iranian native hens (GHAZIKHANI-SHAD *et al.*, 2007). In order to meet the growing request for animal protein particularly poultry egg and meat, commercial poultry farms developed in early 1950's in Iran. Iranian poultry production has made great progress in the industry in the last few decades (ENAYATI and RAHIMI, 2009). The first attempt for breeding and extension of Iranian indigenous hens done in 1984 with creating six breeding stations in different regions of Iran (Mazandaran, Fars, Esfahan, West Azarbaijan, Yazd, and Khorasan) (ENAYATI and RAHIMI, 2009). Indigenous chicken genetic resources in Iran are very worthwhile, but they Exposed under risk of extinction therefore should be protected in order to make genetic progress of the indigenous hens and to increase their population (KIANIMANESH *et al.*, 2001). One of the most popular provinces in Iran is Mazandaran that located on the southern coast of the Caspian Sea with an average temperature of 25°C in summer and about 8°C in winter. Winters are cool and rainy while summers are hot and humid (SHADPARVAR and ENAYATI, 2012). Although there is much evidence that local chicken production plays an important role in the lives of rural households, a very few work has been done in terms of improving the productivity of local hens. Improvement in the productivity of indigenous breeds requires attention to nutritional, breeding, health, and management aspects (NORRIS and NGAMBI, 2006). The literature is scarce in relation to animal breeding studies involving Mazandaran Native Breeder Hens for body weight traits via random regression model. Therefore, it is very important to study different models that accurately describe variance components of Iranian indigenous hens for body weight traits. The body weight can be considered as a longitudinal trait and can be analyzed during life of a chicken by using univariate or bivariate, repeatability and recently random regression model. However, Random regression models (RRM) have been proposed as a main methodology for the analysis of genetic traits or repeated measures records. So, RRM were recommended for analyses of repeated measures animal breeding (SCHAEFFER and JAMROZIK, 2008). Random regression analyses mainly fitted polynomials of time or age as basic functions at recording. Even though no information between points was available the covariance functions which are applied in RRM allow the prediction of variances and

covariances in points during the growth curve or the studied path (EL FARO and ALBUQUERQUE, 2003). Especially, Legendre polynomials (LPs) have been widely used to estimate covariance functions for growth traits in the livestock. Legendre polynomials a parametric function gets more robust estimates of covariance matrices than other parametric functions across different datasets (SCHAEFFER, 2004; BOHMANOVA *et al.*, 2008). Estimates of genetic parameters can differ with the order therefore the order of LPs in RRM is necessary and has to be considered (MISZTAL *et al.*, 2000). In addition, RRMs consider either homogeneous or heterogeneous variance structures. When first studies assumed a homogeneous structure for the residual variance in random regression models problems were observed of fitting the permanent environment effect, additive genetic variances were overestimated (JAMROZIK *et al.*, 1997). However, when heterogeneous residual variances are applied, it is possible to develop the partition of the total variance into the variances attributed to the random effects comprised in the model (KIRKPATRICK *et al.*, 1990).

Therefore, the objective of this research was to renew those estimates using broader information and estimate genetic parameters for BW at ages one (hatching) to body weight at thirty two weeks of ages in Mazandaran Native Breeder Hens by use of random regression models adjusted by Legendre polynomial functions of different orders.

MATERIALS AND METHODS

Animals and Data

A total of 39872 weekly records of body weight (g) inclusive body weight at hatch (BW1), eight (BW8), twelve (BW12) and thirty two (BW32) weeks of ages with 16 generations of hens that were gathered between (1993 to 2011) in Mazandaran breeding center were applied. In 1986, Mazandaran native hens breeding center Started when around 5,000 males and females were gathered from rural areas across the province and shifted to an isolation farm for one year. Then almost 2,500 birds of both sexes were kept to generate hatching eggs after acting isolation procedures, and chickens produced from these eggs were relocated to the station in 1988 (NIKNAFS *et al.*, 2012). The number of hens with records, number of sires, and number of dams were 9968, 431, and 2608, respectively. The GLM (General Linear Model) method was applied to examination the fixed effects. The fixed effects used after testing when the effects were statistically significant with R Software (VENABLES and RIPLEY, 2002). All of the fixed effects were significant (p<0.05) and were considered in the final model of analysis. Only observations of hens with at least three tests were kept. The structure of records has shown in table 1.

Table1. Summary of data structure used in this study

Characters	amount
No of records	39872
No of hens with records	9968
No of sires	431
No of dams	2608
hens with 3 records	4685
hens with 4 records	3788
Hens with 5 records	1495

Residual variances were modeled via a step function with the following classes: 1, 3 (1-8, 9-12 and 13–32 weeks) (SESANA *et al.*, 2010).

Statistical Analysis

The following random regression model was applied for the analysis:

$$y_{ikl} = GH_i \; x \sum_{m=0}^{k} \beta_m z_{klm} + \sum_{m=0}^{k_a-1} \alpha_{km} z_{klm} + \sum_{m=0}^{k_p-1} \gamma_{km} z_{klm} + e_{ikj}$$

Where y_{ikj} is the record of hen *k* in period *l* with generation−hatch *i* (*i* = 1 … 31*)*; GH_i illustrate the fixed effect of generation−hatch *i*; β_m is the fixed regression coefficient for the *m*th order of the polynomial of the period; α_{km} and γ_{km} are the *m*th random regression coefficients for direct additive genetic and direct permanent environmental effects of animal *k*, respectively; k_α-1 and k_ρ-1 are the corresponding order of fit for each effect; z_{klm} is the Covariate coefficient of Legendre polynomial for period *l* of animal *k*; and e_{ikj} is the random residual effect. Also, we used same order of Legendre polynomial for fixed effect (4, for all of them) in this study.

Covariance Functions and Breeding Value Calculations

Random regression models create K matrices inclosing (co)variance between random regression coefficients, specifically for each random effect (direct genetic and permanent environmental effects). Following the proposal of KARIUKI *et al.* (2010), the (co)variance functions ($\hat{G}_0$) are expected by pre and post multiplying K by use of a matrix inclosing Legendre polynomials (ϕ) related to a set of particular ages shown in matrix notation as:

$$\hat{G}_0 = \phi K \hat{\phi}$$

Covariances between RR coefficients related to different random effects were supposed to be zero. The genetic analyses were done by use of 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 applied to estimate breeding values (BV) for any point in the age curve between 1 and 32 weeks. For example, BV for the animal i at 32 weeks of age will be:

$$BV_{i,32} = q_{32} \times \alpha_i'$$

Where α_i displays solution for animal i, and q_{32} is the vector of coefficients of the Legendre polynomial related to 32weeks of ages.

Model selection

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:

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

and

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

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

$$LRT_{ij} = 2 \times \left(logL_i - logL_j \right)$$

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

RESULTS

Log Likelihoods and Information Criteria

The information about testing the goodness of fit of regression models are described on Table 2.After comparing a number of different regressions based on AIC, BIC and LRT, the best suitable RRM was the model with a polynomial of fourth order for fixed effect, third order for direct genetic effect and third order for direct permanent environmental effects (3.3.het3 model). It is generally acknowledged, that there are certain conditions in which LRT offers an appropriate basis for model comparison.

Table 2. Models, numbers of parameters, and model selection criteria with different orders of adjustment in the random regression models [1] (best model in bold).

model	Polynomial order K_a	K_b	e	p	2 Log L	AIC	BIC	LRT
1	3	3	Hom	13	-149390	149416	149528	
2	3	4	Hom	17	-149340	149374	149520	
3	3	5	Hom	22	-149333	149384	149572	
4	3	6	Hom	28	-149310	149396	149636	
5	3	7	Hom	35	-149362	149432	149732	
6	4	4	Hom	21	-279590	279632	279812	
7	5	5	Hom	31	-149330	149392	149658	
8	6	6	Hom	43	-149348	149434	149804	
9	**3**	**3**	Het3	15	-149340	149370	149498	(9-10)73,894[**]
10	3	4	Het3	19	-223234	223272	223436	(10-11)71,898[**]
11	3	5	Het3	24	-151336	149388	149594	(11-12)24,270[**]
12	3	6	Het3	30	-175606	175666	175924	(12-13)26,266[**]
13	3	7	Het3	37	-149340	149414	149730	
14	4	4	Het3	23	-228120	228166	228364	
15	5	5	Het3	33	-149334	149400	149682	
16	6	6	Het3	45	-149334	149424	149810	

[1] ka, order of fit of additive genetic effect; kp, order of fit of permanent environmental effect; e, residual effect with heterogeneous (het) or homogeneous (hom) classes; P, number of parameters; Log L, log likelihood value; AIC, Akaike information criterion; BIC, Bayesian information criterion; and LRT, likelihood ratio test. [**]Significant at 1% probability. [ns]Nonsignificant.

Variance Component and Genetic Parameters

Number of records and average body weights for different ages are given in Figure 1.

Body weights increased evenly linear with increasing in age from hatch to 32 weeks of age, so that the mean hatch weight (BW1) of Mazandaran native hens was about 36.8 grams, which increased to 1726.7 grams at 32 weeks of age. Ranges for direct additive genetic

variances, for animal permanent environmental variances, and for phenotypic variances for native hens studied are given in Figure 2.Direct additive genetic variance decreased to 12weeks of age and then increased until 32weeks of age. Residual variance was constant from BW1 to BW8but then decreased with age. The pattern estimated for permanent environmental variance and phenotypic variance were similar.
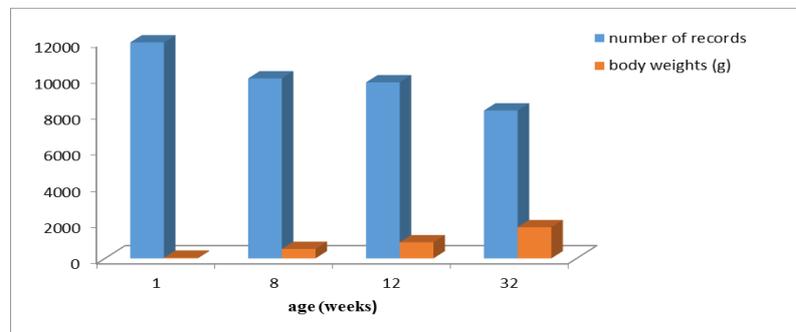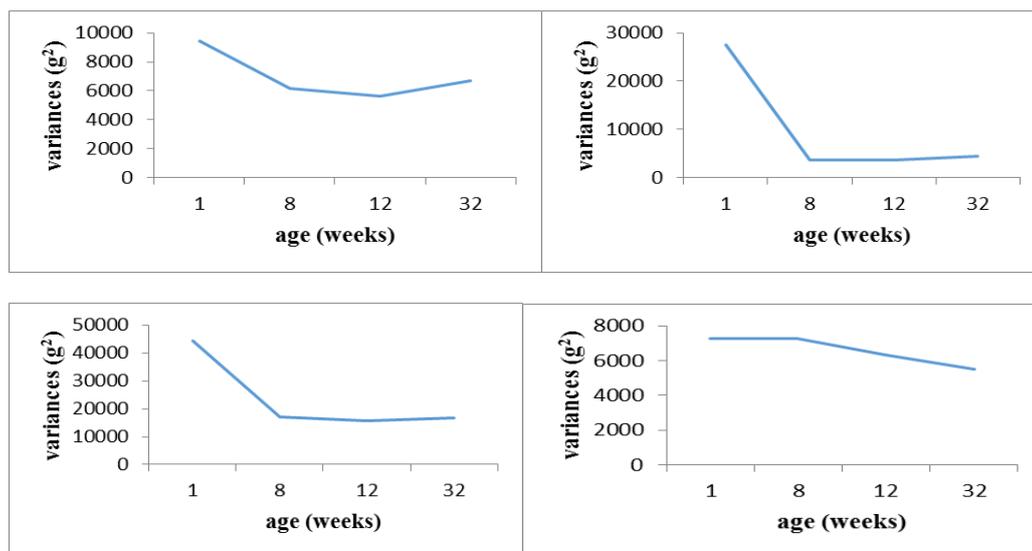

Figure 1. Number of records and body weights (g) for each week of age.

Figure 2. Additive genetic (A), permanent environmental (B), phenotypic (C), and residual (D) variance estimates to body weight traits for weeks of ages of Mazandaran Native Breeder Hens, obtained with a model with three classes of heterogeneous residual effect and orders of fit for direct additive and permanent environmental effects equal to 3.
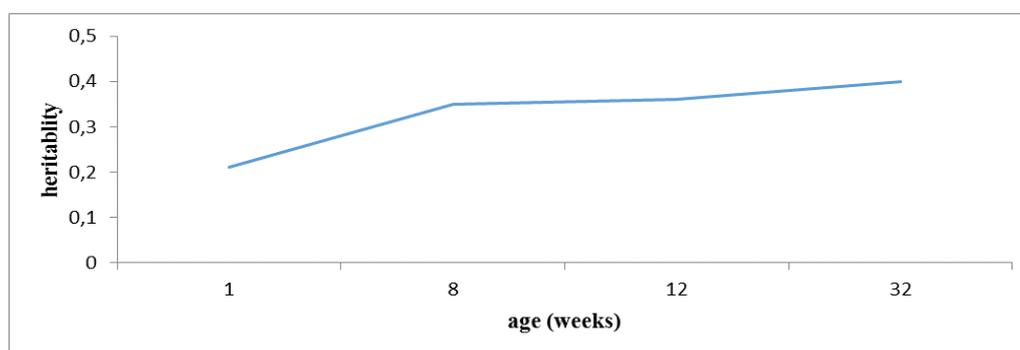
Figure 3. Heritability estimates to body weight traits for weeks of ages for Mazandaran Native Breeder Hens, obtained with a model with three classes of heterogeneous residual effect and orders of fit for direct additive and permanent environmental effects equal to 3.

In summary, results are given for selected weeks in table 3.Generally, the genetic and permanent environmental correlations between weights increased with decreasing interval between weights. Genetic correlations among various traits were positive, moderate to high and ranged from 0.25 between BW1 and BW32 to 0.97 between 12–32 weeks of age. The estimate of permanent environmental correlations was in ranges of 0.07 to 0.76. Generally, permanent environmental correlations decreased in higher age intervals. Also, Genetic correlations of body weight at different record keeping were often higher than permanent environmental correlations.

Table 3. Estimated genetic correlations (above diagonal) and permanent environmental correlations (below diagonal) among different weeks of ages for body weight traits in Mazandaran Native Breeder Hens.

week	week			
	1	8	12	32
1		0.58	0.37	0.25
8	0.25		0.75	0.86
12	0.19	0.68		0.97
32	0.07	0.27	0.76	

Genetic Trend

The genetic trends of body weight at hatch, BW8, BW12 and BW32 weeks of ages are given in Figure 4. For BW1, the genetic changes decreased from 7 to 11 generation and then increased until 15 generation. Generally, the genetic trend for BW1 was different than those of the other selected body weight traits. The genetic changes of body weight at hatch declined from 7 to 11 generation; but for the other selected weights, plots of the mean predicted breeding values on generation indicated an increase over time.
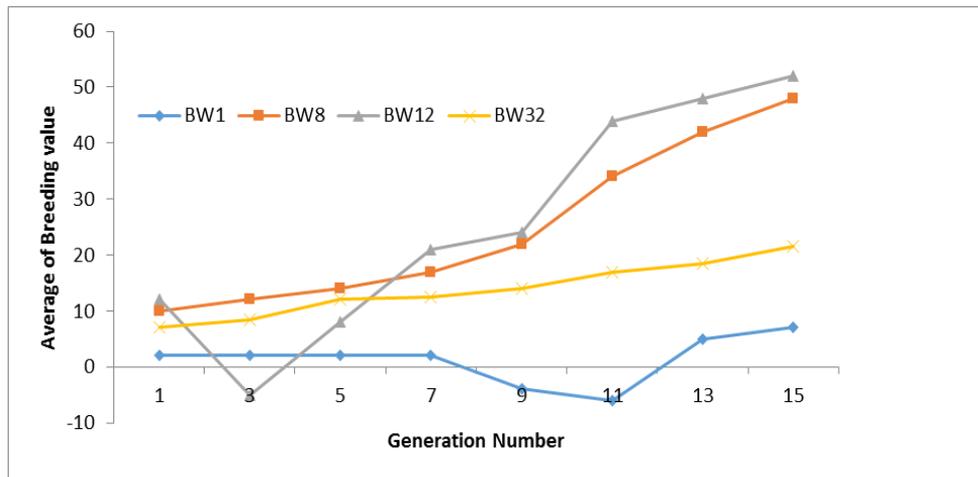
Figure 4. Mean of predicted breeding value to body weight traits for weeks of ages for Mazandaran native breeder hens on generation with genetic trend.

DISCUSSIONS

Log Likelihoods and Information Criteria

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 log L, AIC, BIC and LRT indicated 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) and model fit improved with increasing polynomial regression order to 3.3.het3 model and then worsened to 6.6.het3 model. These indicated that residual variances had different behavior along the age. The AIC, BIC and LRT results indicated that a step function with 3 classes was the most adequate to model the residual variances. The AIC and BIC results showed 3.3.het3 model was the most adequate one to describe the covariance structure of data.

Variance Component and Genetic Parameters

Body weights increased evenly linear with increasing in age from 1 to 32 weeks of age, so that the mean hatch weight (BW1) of Mazandaran native hens was about 36.8 grams, which increased to 1726.7 grams at 32 weeks of age (Figure 1). Mean hatch weight of Esfahan native chickens offered approximately 37.75 grams, which increased to 1461.37 grams at12 weeks of age (YOUSEFI-ZONUZ *et al*., 2013). Also, SHADPARVAR and ENAYATI (2012) reported estimates for body weights of Mazandaran native breeder hens in different ages from 37.09 to 1714.79 grams for body weights at one day of age to body weight at sexual maturity, respectively. Ranges for direct additive genetic, permanent environmental, phenotypic and residual variances all considered ages are showed on Figure 2. Generally, direct additive genetic variance decreased up to 12 weeks of age and then increased until 32 weeks of age and was highest at the later ages in the growth trajectory. The decreasing trend was observed for permanent environmental

variance up to 8weeksand then consistently increased with age. The pattern estimated for permanent environmental variance and phenotypic variance were similar. Residual variance was constant from first week to eight weeks but then decreased with age. However, these differences between the variance components (direct additive genetic, permanent environment, phenotypic and residual) did significantly effect on the heritability estimates, which were dissimilar in different ages.

Ranges BW heritabilities estimated by 3.3.het3 model were from 0.21 to 0.40 for the period of one to 32 weeks of age (Figure 3), with lower value for BW1 (0.21) which shows that finding of genetic variability for body weight at 1 week of age is more hard than 8, 12 and 32 weeks of age. LEDUR et al. (1992) estimated heritabilities for hatching weight of 0.20 studying a different line. ROVADOSCKI et al. (2016) reported estimated heritability for BW at 84 days which were ranged from 0.15 to 0.36 using random regression analysis. However, other authors Calculated higher values than this study; LWELAMIRA et al. (2009) estimated a heritability of 0.45.Heritability estimates for body weights of Mazandaran native breeder hens by use of multiple-trait animal model reported by SHADPARVAR and ENAYATI (2012) which were ranged from 0.134 to 0.29, and was lower than the reported value in present study. Estimated higher heritability by using RRM Can is described by overestimation of variances at the extremes of the growth curve by Legendre polynomials' lack of asymptotes (LOPEZ-ROMERO et al., 2004; BOHMANOVA et al., 2008).Estimated heritability for BW8 was dissimilar to the value described by KIANIMANESH et al. (2001) and also was higher than described value by GHAZIKHANI et al. (2007) for Mazandaran fowls and NIGUSSIE et al. (2011) for Horro chickens of Ethiopia. However, there are some different reports that estimated heritabilities in their studies were higher for BW12 (KAMALI et al., 2007; GHAZIKHANI et al., 2007). AKBAS et al. (2002), estimated heritability for BW32 with value 0.43 which was higher than reported value in present study. Genetic and permanent environmental correlations among BW records were positives and ranged from moderate to high for Mazandaran Native Breeder Hens. The corresponding estimates of genetic correlations were generally higher than the permanent environmental correlations. Many researchers reported Similar results in which the genetic and permanent environmental correlations were high and positive among different BW in broilers (MIGNON-GRASTEAU et al., 1999; KUHLERS and MC DANIEL, 1996; ZEREHDARAN et al., 2004; LWELAMIRA et al., 2009; GAYA et al., 2006). Genetic and permanent environmental correlations were shown lower among the BW1 with other ages which was consistent with results found by MIGNON-GRASTEAU et al. (1999) and LEDUR et al. (1992), who showed slight genetic correlations between BW at hatching and BW at older ages. These findings indicated that the hatching weight has a slight effect on the weight at selection (6weeks of age) and slaughter weight (12weeks of age), for example. Also, the largest genetic correlation, as well as permanent environmental correlation, was observed between BW12 and BW32. This suggests that Selection for higher BW12 will result in higher body weight at 32 weeks. These results were similar to those reported by SHADPARVAR and ENAYATI (2012) by use of multiple-trait animal model.

Genetic Trend

Generally, the genetic trends for body weight at hatch were very different than those of the other body weight traits. Based on Figure 4, the genetic changes of BW1 from generation 1 to 7 appear to be flat, which was in agreement with the reports of NIKNAFS et al. (2013) in Mazandaran Indigenous Chicken. Selection based on birth weight was minimal in comparison to

other body weight traits (NIKNAFS *et al*., 2013). Generally, for the other weight traits (8 week, 12 weeks and 32 weeks weights), plots of the mean predicted breeding values on generation of birth followed similar patterns. For all selected ages, there were quick increases in mean predicted breeding values of hens especially from generation 7 to 15.

CONCLUSIONS

According to results of the present study, random regression model seems to be a flexible and reliable procedure for estimation of variance components of body weight in Mazandaran Native Breeder Hens. However, there is the need to improve data collection to enhance accuracy of parameter estimates and allow more comprehensive evaluations. The pattern of moderate to high estimates of heritability (0.21-0.40) obtained for all traits in the current study. This finding indicated that the traits of BW seem to be able to provide good response to selection. The results of the present study indicates that most of the phenotypic variation of body weight of Mazandaran Native Hens during one to 32weeks of age are due to direct genetic and permanent environmental effects, while residual effect have low to moderate contributions. Moreover, ranges of genetic correlations among BW records were positives and from moderate to high which indicated the direct selection in slaughter body weight at 12 weeks of age would have great effect on BW in several ages, especially in body weight at sexual maturity at 32 weeks of age. Estimates of genetic trends indicated that there was positive genetic improvement in all studied traits exception of body weight at hatch and indicated that selection would be effective for the improvement of body weight traits of Mazandaran Native Hens.

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PROCENA GENETIČKIH PARAMETARA ZA OSOBINE TEŽINE TELA KOD MAZANDARSKE DOMAĆE KOKOŠKE MODELIMA SLUČAJNE REGRESIJE

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Izvod

Primarni cilj ovog rada je da istraži odgovarajući model slučajne regresije za procenu genetskih parametara telesne težine na rođenju (BV1), osam (BV8), dvanaest (BV12) i trideset dve (BV32) nedelje starim pilićima metodom ograničene maksimalne verovatnoće. Beleženje težine obuhvatalo je 39872 kokoške tokom 16 generacija, uzgajanih u Mazandaran Oplemenjivačkom centru u Iranu. Randomska regresija je modelirana korišćenjem generacije-pilića kao fiksnog efekta i aditivnih genetičkih i trajnih efekata okoline kao slučajnih efekata. Preostala odstupanja su modelirana kroz stepenu funkciju sa 1 i 3 klase. Najprikladnijim modelom smatrao se onaj koji je imao najveću vrednost LRT testa i najniži Akaike informacioni kriterijum (AIC) i Baiesov informacioni kriterijem (BIC). Vrednosti heritabilnosti bile su od 0.21 za BW1, do 0.40 za BW32. Genetičke korelacije telesne težine kod različitih merenja su često bile veće od korelacija spoljašnje sredine. Genetičke korelacije između parova merenja telesne težine bile su umerene do visoke sa rasponom od 0,25 do 0,97. Najveća genetička korelacija, kao i trajna korelacija spoljašnje sredine, uočena je između BV12 i BV32. Visoke i umerene vrednosti heritabilnosti u širem smislu za sve ispitivane osobine pokazuju da na ove osobine manje utiču rezidualni efekti, što omogućava efikasno prenošenje na potomstvo. Rezultati pokazuju da se genetsko poboljšanje telesne težine može postići selekcijom. Heritabilnost telesne težine kod trideset dve nedelje starih kokoši i njena relativno visoka genetička korelacija sa svim ostalim uzrastima pokazala je da bi to mogao biti najprikladniji period za selekciju. Takođe, procene genetičkog trenda za osobine telesne težine pokazale su da odluke o selekciji donete tokom oplemenjivanja poboljšavaju performanse rasta.