Original Article

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GENETIC PARAMETERS PREDICTION FOR KHUZESTANI BUFFALOES MILK CHARACTERISTICS BY RANDOM REGRESSION METHOD

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ABSTRACT

In this research, Data of milk yield, fat and protein percentage of Khuzestani buffalo were used. The daily records of milk yield were collected in the south-west of Iran where buffalo experienced a hot climate. The data set was constructed with 8,123 records of 1,430 first lactation buffalo. A univariate random regression model (RR/CF) was applied to data. Regression of additive genetic effect based on Legendre polynomials from the day of lactation was considered in the model. The results showed that maximum residual variance for the milk and fat production was estimated at the beginning of the lactation period. The minimum amount of additive genetic variation of milk and fat traits was seen in the early lactation period and the maximum amount of the component was estimated at the end of the lactation period. The lowest heritability of the mentioned traits was at the beginning of the lactation period. The level of this parameter increased to mid-lactation and was at its maximum during the late months of lactation, then decreased to the end of lactation. The estimated additive genetic correlations between close test-days were higher than faraway test-day records for each milk yield and milk fat content. Based on the results of this study, a random regression model with fitting orders 3 and 4, seems to be suitable for additive covariance functions in order to analyze the milk test-day records of buffaloes.

Keywords: *Bubalus bubalis*, buffaloes, random regression model, covariance functions, milk and fat production, buffalo of Khuzestan

INTRODUCTION

Native buffaloes of Iran are one of the most important genetic resources in the country and plays an important role in rural economy. Khuzestan Province is one of the main provinces of buffalo breeding in Iran, which has about 1495 buffaloes. Quality and value of the products and the remarkable population of buffaloes have made this animal the most important native cattle in Khuzestan province, and it attracted attentions to products improvement and bovine breeding development. Most buffaloes are breeding in North, Northwest, South and Southwest of Khuzestan province that is Dezful, Shoshtar, Shoosh, Ahvaz and Dasht-Azadegan (Management and Planning Organization of Khuzestan, 2003). In Khuzestan province, the buffaloes are primarily intended for milk production. Buffalo milk has a special feature

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due to its high fat content (7 to 6%) and its high economic value. Increasing production capacity and using all genetic potential of this cattle, is not only effective in providing a significant portion of protein resource, but also a contribution to economic development of bovine breeding (Farhond, 2002). In this regard, it is needed to recognize products potential and reproductive potential of this cattle, and to estimate genetic parameters of products, reproductive feature, and genetic correlations between estimation of corrective values (Kordnejad, 1999). Accuracy of estimation in variance components is essential in stock breading improvement, since, as the variance increases, error of difference prediction increases between predicted values and real values. One of the most important parameters obtained via variance components is heredity. Heredity shows the way to executive plans of breading improvement. Generally, unbiased estimation of heredity is vital in achieving reliable results and rapid progress in breading improvement plans (Rashedi *et al*., 2016). Among the models that use test day records to estimate genetic parameters, random regression model showed a significant accuracy in correction value estimation, and today, in many countries, this model is used for genetic evaluations (Cobuci *et al*., 2005). In fact, in random regression model, incremental genetic effect of the animal is replaced by a number of random regression coefficients (Jamrozik *et al*., 1997). Investigations have shown that a random regression model in which random regression coefficients are fitted based on Legendre multipliers is the same as covariance function model. A new method for estimating covariance functions using a random regression model was proposed by proving the equivalence of random regression models and covariance function. In this method, variance-covariance components of random regression coefficients determine covariance function required to estimate covariance between each pair of recording time (Swalve, 2000). Using random regression model for test day records allows estimation of parameters related to shape and curve of lactation, including lactation continuity based on the level of production. Calculating continuity of production feature in breeding plans of dairy cows is considered as an important economic trait (Moradi Shahrbabak, 2001). Therefore, in order to carry out breeding activities for development and improvement of buffaloes in Khuzestan province, acute attention was paid to factors such as improving nutrition status, improving management practices, increasing the accuracy of milk recording, artificial insemination, recording pedigree and using new statistical methods to obtain more accurate breeding estimates (heritability, breeding value). The aim of this study was to investigate the potential of buffalo production in Khuzestan along with the estimation of genetic parameters by random regression, so that based on the results, it would be possible to carry out more basic measures in breeding activities and choose superior parents which in turn result in development and improvement of buffalo breeding in Khuzestan province.

In this research, in order to estimate genetic and phenotypic parameters traits of buffaloes in Khuzestan (first calving), data collected by Livestock Breeding Center of Iran in 1990 to 2013 was used. Among different traits, amount of milk, fat percentage and protein percentage were investigated. The information used was related to 21,293 livestock belonging to 482 fathers and 2,548 mothers. Visual FoxPro 9.0, Excel, and Pedigree (Sargolzaei, 2001) software were used to prepare data file and pedigree file. Buffaloes which produced less than a kilogram and more than 27.5 kg in a 24 h period were excluded from the recording of that day. In the fat percentage data file, there were only daily test records ranged from 2% to 13/50%, and other data beyond this range was deleted. Protein percentage data file included daily test records in the range of 1 to 50.9% which were analyzed, and the remaining data was excluded. In order to increase the accuracy of estimates in data file, only the buffaloes were used that had more than 3 records in the daily test. Also, to increase the accuracy of estimates, flock-years were selected which had more than 4 female buffaloes. In this study, male bulls were included that had more progeny in the herds. In this regard, bulls with more than 5 progenies were selected. Buffaloes that milked 2 or 3 times the day were kept in the data. Finally, the number of test day records for amount of milk, fat percentage and protein percentage were 8,123, 7,572 and 5,536, respectively. Significance test of invariant effects was analyzed in SAS 9.1 software using GLM procedure. The animal model of random regression test day for the traits was as follows:

$$\mathrm{y}_{\mathrm{tijmn}} = HTD_i + \mathrm{MF}_{\mathrm{j}} + \sum_{\mathrm{n}=0}^{4} \mathrm{a}_{\mathrm{mn}} \Phi_{\mathrm{n}} + \sum_{\mathrm{n}=0}^{4} \mathrm{pe}_{\mathrm{mn}} \Phi_{\mathrm{n}} + \mathrm{e}_{\mathrm{tijmn}}$$

In which: $\mathrm{y}_{\mathrm{tijmn}}$ denote the tth test-day record in ith subgroup of herd-year-month test-day record, which is shown as HTDi, MFj stands for the jth milking (j=1,2 and 3) of mth animal, a_{mn} and $\mathrm{pe}_{\mathrm{mn}}$ are nth random regression coefficient of additive genetic effect and permanent environmental effect of mth buffalo, respectively, Φ_{n} is nth Legendre polynomial for the intended test-day (5th to 270th day of milking), stands for residual random effects. The model in matrix notation can be represented as:

$$y = Xb+Qa+Zpe+e$$

Where y stands for the vector of observations (test-day of the studied traits), b is the vector of fixed effects in the model, a and pe are the vector of additive genetic effect and permanent environmental effect of buffalo, respectively, e stands for the vector of residual effects, X,Q and Z are the matrixes corresponding to the random and fixed regression coefficients. The covariance structure is defined as follows:

$$var\begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & I \otimes \sigma_P^2 & 0 \\ 0 & 0 & R \end{bmatrix}$$

Where G is the genetic covariance matrix of the random regression coefficients, $\otimes$ is Kronecker product symbol, A coefficient matrix of relationship between animals, denote the variance of permanent environmental effects, I is unit matrix and R is diagonal matrix of residual variance. To calculate standardized lactation day ($\mathrm{d}^*_{\mathrm{t}}$), the following equation was used:

$$\mathrm{d}^*_{\mathrm{t}} = -1 + 2\left(\frac{\mathrm{d}_{\mathrm{t}} - \mathrm{d}_{\mathrm{min}}}{\mathrm{d}_{\mathrm{max}} - \mathrm{d}_{\mathrm{min}}}\right)$$

Where $\mathrm{d}_{\mathrm{min}}$ (5) and $\mathrm{d}_{\mathrm{max}}$ (305) are minimum and maximum days of lactation, respectively, and d_{t} is tth day of lactation. For tth standardized day of lactation (d*t), nth Legendre polynomial $\Phi_{(\mathrm{di}^*)\mathrm{i}}$ is defined as the follows:

$$\Phi_{\left(\mathrm{D}_{\mathrm{i}}^*\right)_{\mathrm{i}}} = \frac{1}{2^{\mathrm{i}}}\sqrt{\frac{2\mathrm{i}+1}{2}} \sum_{\mathrm{m}=0}^{\mathrm{i}/2} (-1)^{\mathrm{m}} \binom{\mathrm{i}}{\mathrm{m}} \binom{2\mathrm{i}-2\mathrm{m}}{\mathrm{i}} \left(\mathrm{D}_{\mathrm{i}}^*\right)^{\mathrm{i}-2\mathrm{m}}$$

i is the Legendre polynomial and m is the number of indices needed to determine the i-th Legendre polynomial. (Co) variance matrix of random regression coefficients was estimated using

WOMBAT software and AIREML algorithm. Legendre polynomials were used to characterize (Co) variance matrix in a random regression model. Following equation (Table 1) was used to obtain these polynomials. The following formula was used to calculate heritability of different lactation days:

$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

Where σ^2_a = qGq', σ^2_{pe} = qPq, σ^2_a, σ^2_{pe} and σ^2_e are additive genetic variance, permanent environmental variance, and residual variance, respectively. G and P are covariance matrix obtained for the random regression coefficients of additive genetic and permanent environmental effects of animals, respectively, and Q is polynomials vector of the intended day. To calculate genetic correlation between lactation days, additive genetic variance-covariance matrix of different lactation days (a 266 by 266 matrix) was used:

$$r_g = \frac{Cov_{g(i,j)}}{\sqrt{Var_{g(i,i)} \times Var_{g(j,j)}}}$$

Where $Cov_{g(i,j)}$ denote the genetic covariance among the ith and the jth days, $Var_{g(i,i)}$ and $Var_{g(j,j)}$ are additive genetic variance of the ith day and the jth day, respectively.

RESULTS AND DISCUSSIONS

Incremental and phenotypic genetic variances for production of milk, fat percentage and protein percentage are shown in Figure 1. The range of variations in incremental genetic variance was 0.14 to 1.32 kg for milk production, 0.06 to 0.89 for fat percentage and 0.44 to 0.50 for protein percentage. A high incremental genetic variance increase observed in the beginning lactation period and then it declined about 25 days after lactation period. Thereafter, the upward trend was revealed, and at the end of the period, a high variance was observed. In general, genetic variation tends to increase at the beginning and end of lactation (Veerkamp and Thompson, 1999). The maximum amount of genetic variation in another study (Olori *et al*., 1999) was also related to the second half of lactation period (towards the end of lactation period). Bignardi *et al*. (2009) reported a similar trend in dairy cattle for an incremental genetic variance component. A low Incremental genetic variability was observed in milk fat percentage at about 120 days of lactation and then it increased until the end of lactation, so that the maximum incremental genetic variance was observed at the end of the period that shows a greater share of genetic variation regarding phenotypic variation of fat percentage in that period. Phenotypic variance was not the same at different stages of lactation. Therefore, the records of early and late stages of lactation, like incremental genetic variance, were more uneven than the records of mid-lactation period. Changes in daily test records of milk production were evident at the beginning (about first 65 days of lactation period) and end of lactation period, and the trend was almost invariant in the middle of lactation period. Therefore, maximum phenotypic variance was observed at the beginning and end of lactation. The trend of phenotypic variance changes for fat and protein percentages during lactation period was the same at the beginning and end of lactation. The findings of this study are in line with Zullo *et al.* (2007); Kettunen *et al.* (2000); El Faro *et al.* (2008);

Bignardi *et al.* (2009), that found the maximum phenotypic variance at the beginning and end of lactation.

The heritability value for traits of milk, fat percentage and protein percentage in a function of lactation days is shown in Figure 2. Changes in heredity estimated by various functions during lactation period were very similar. The lowest and highest heritability values for daily milk production were estimated 0.10 and 0.37 respectively. The heritability level of milk production at the beginning of lactation period was high (0.30) which was followed by a slight drop after about 20 days of lactation, and then a rising trend was observed again. This increase in heritability was not only due to an increase in the amounts of genetic variance component, but also because of the decrease in permanent environment components among the models (Biassus *et al*., 2011). Maximum heritability was observed at about 90 days of lactation and showed a rising trend at the end of lactation period. The estimated heritability was higher at the beginning of lactation, which could be due to high genetic variance and low error variance. Hurtado-Lugo *et al.* (2006) also reported a similar trend by analysis of test day records of milk production in buffaloes. Schaeffer *et al.* (2000); Mäntysaari *et al.* (1999); Silvestre *et al.* (2005) reported similar results in dairy cattle and suggested to select the buffaloes for milk production in fourth and fifth month of lactation. Heritability percentage of fat percentage at the beginning of lactation was low (0.66) and then, until about first 100 days of lactation period, the same trend was observed, and after this stage, an increasing trend was observed until the end of lactation period. The estimated heritability for milk production was higher than fat percentage. Swalve *et al.* (1998) reported that when the test day records are used, the estimated heritability for fat and protein traits is lower than milk production. The trend of heritability changes in protein percentages was observed at the beginning and end of lactation period. Estimated heritability changes ranged from 0.07 to 0.38. The remaining variance was homogeneous during lactation period for the studied traits (Figure 2).

As random regression model considers the variance-covariance structure of repeated data over time or animal lifetime, this model estimates variance-covariance components for different lactation days, by which, genetic correlation can be estimated between different days. According to figures (3, 4 and 5), it is clear that maximum incremental genetic correlation is adjacent in amount of milk production during lactation days

Table 1. Legendre polynomials (grades 1 to 6), (W: standardized lactation days).

Degree	**Equation**	**If: W= -0.2**
0	$W^{0}{}_{*}0.7071$	0.7071
1	$W^{1}{}_{*}1.2447$	-0.2449
2	$W^{2}{}_{*}2.2317+W^{0}{}_{*}-0.7906$	-0.6957
3	$W^{3}{}_{*}4.6771+W^{1}{}_{*}-2.8062$	0.5238
4	$W^{4}9.2808+{}_{*}W79550-W^{0}{}_{*}0.7955$	0.4921
5	$W^{5}{}_{*}18.4685+{}_{*}W^{3}20.5206-W^{1}{}_{*}4.3973$	-0.7212

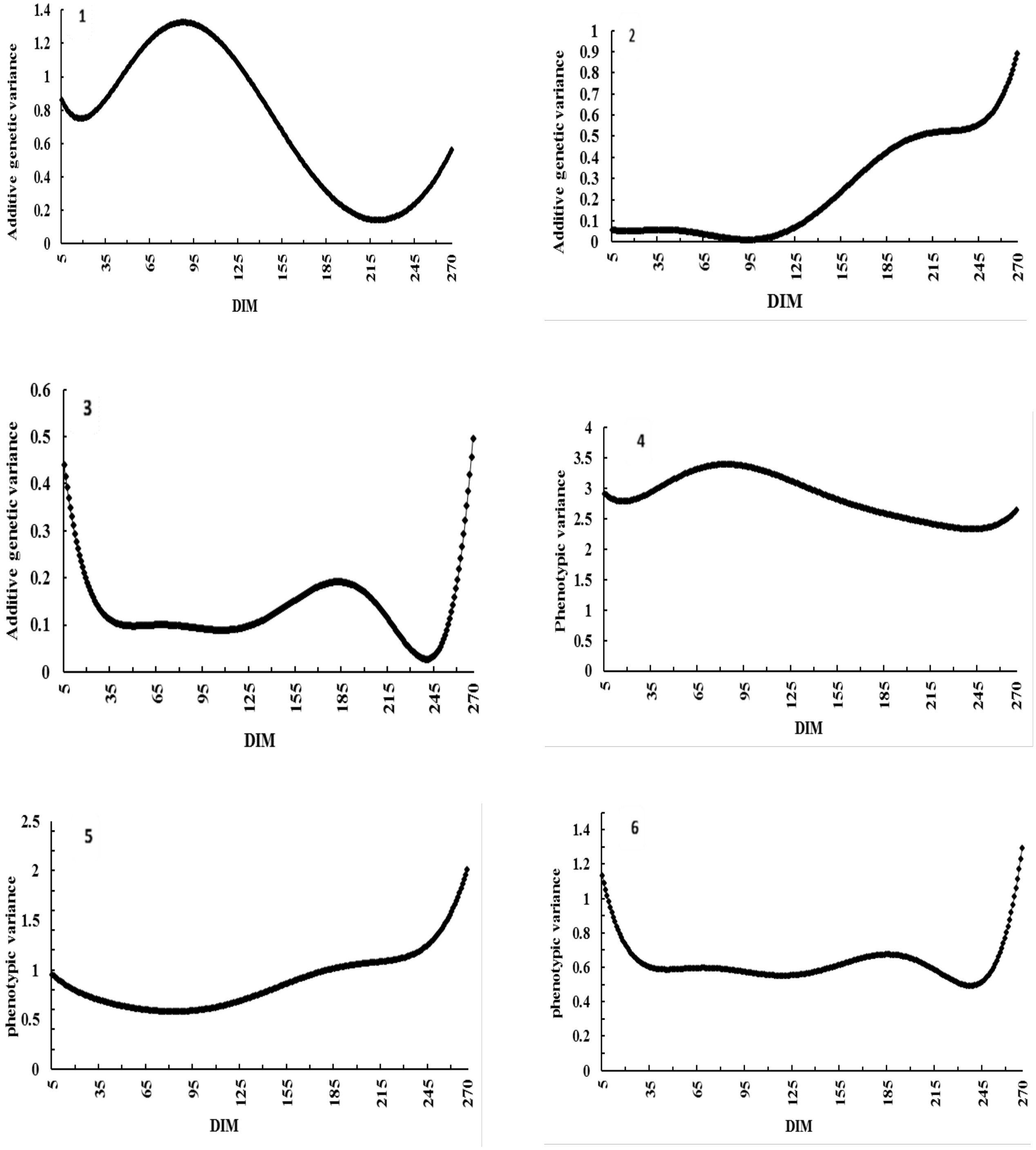

Figure 1. 1 = Additive genetic variance of milk production; 2 = Additive genetic variance of fat percentage; 3 = Additive genetic variance of protein percentage; 4 = Phenotypic variance of milk production; 5 = Phenotypic variance of fat percentage and 6 = Phenotypic variance of protein percentage regressed on lactation days (DIM).

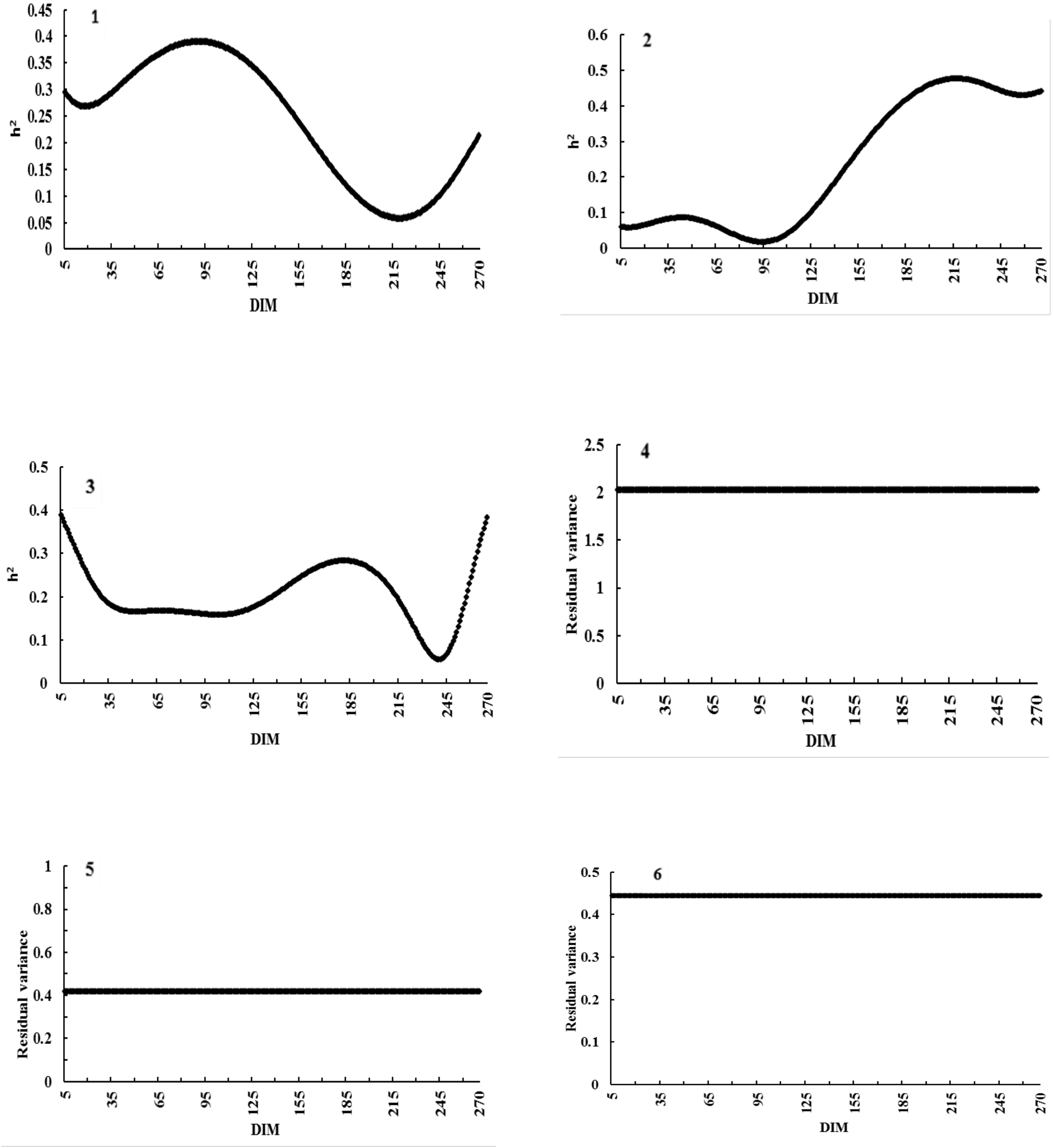

Figure 2. 1 = Heritability of milk production; 2 = Heritability of fat percentage; 3 = Heritability of protein percentage ; 4 = Residual variance of milk production 5 = Residual variance of fat percentage and 6 = Residual variance of protein percentage regressed on lactation days (DIM).

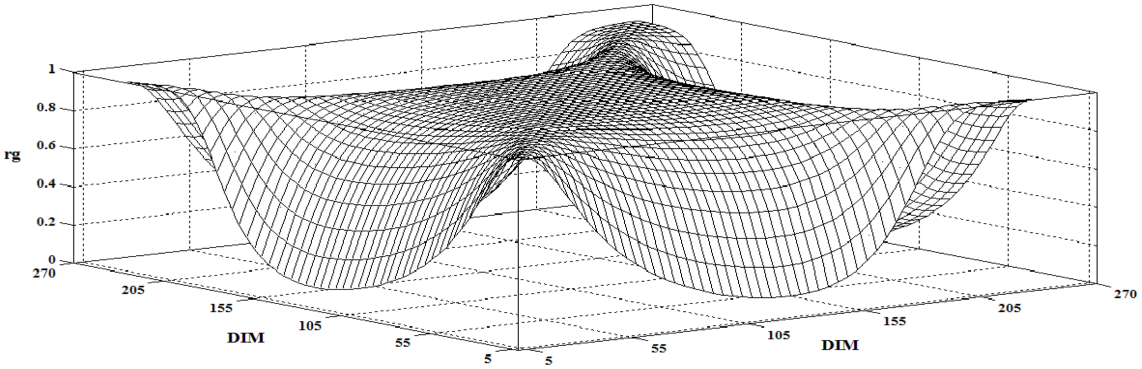

Figure 3. Additive genetic correlation (rg) of milk production between lactation days (DIM).

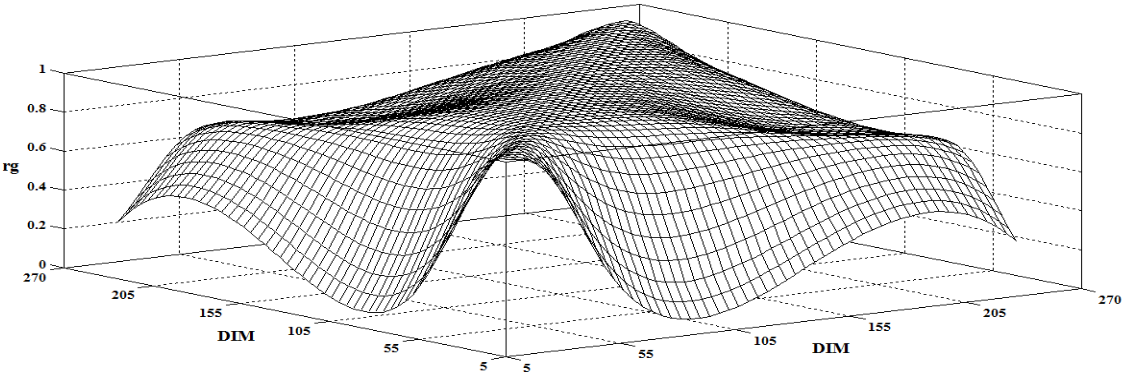

Figure 4. Additive genetic correlation (rg) of fat percentage between lactation days (DIM).

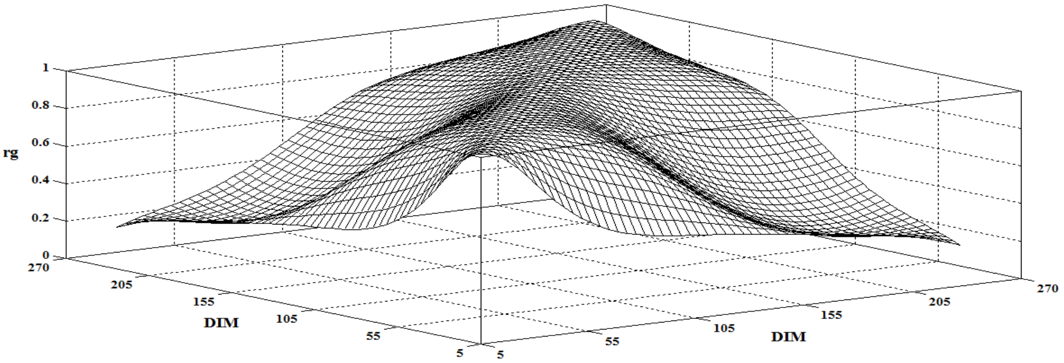

Figure 5. Additive genetic correlation (rg) of protein percentage between lactation days (DIM).

and then it decreases as the interval between lactation days increases. So that, minimum genetic correlation between the 5th and 305th day of lactation period was estimated. Milk production gained the highest genetic correlation during lactation days. These results are the same as findings reported in other studies in the field of genetic correlation estimation in a random regression model. Rekaya *et al*. (1999); Cobuci *et al*. (2005) reported a high genetic correlation durind daily test in dairy cattle. Negative genetic correlation was reported at the beginning and end of lactation period of cows using random regression model by Rekaya *et al*. (1999); Bignardi *et al*. (2009); (2000) Kettunen *et al*. Post-breeding tensions during the first days of lactation may have an impact on the results, as cows generally have a negative energy balance during early breastfeeding (Sawalha *et al*., 2005).

CONCLUSION

According to the results, heritability of test day records in milk production was estimated to be average during lactation period, which indicates that this trait can be used as a selection criterion for dairy buffaloes. Genetic correlations during lactation days are nearly high and correlation reduces with an increase in the interval during lactation days. Phenotypic variance of different traits showed that the highest changes test day records at the beginning and end of lactation period.

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