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Estimation of Genetic Trends for Test-Day Milk Yield by the Logarithmic Form of Wood Function Using a Random Regression Model

Research Article

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ABSTRACT

Estimation of genetic trends is necessary to monitor and evaluate selection programs. The objective of this study was to estimate the genetic trends for milk yield in Iranian Holsteins cows using random regression test day model. Data set was consisted of 743205 test-day records from 1991 to 2008, which were collected by the Animal Breeding Centre of Iran. Breeding, environmental and phenotypic values were estimated using a random regression test-day model. The logarithmic form of Wood function was chosen to fit the additive genetic and permanent environmental effects of milk yield. Genetic, environmental, phenotypic trends were estimated by regressing the mean of breeding values, environmental values and phenotypic values on birth year. The genetic and phenotypic trends were positive and significant, whereas environmental trends were not significant. Genetic trends of sires and dams were estimated separately and it was positive and significant for dams, but it was not significant for sires. The phenotypic, environmental and genetic correlation between each days in milk and total 305 days were estimated. The correlations related to breeding values were weak and it showed that with the logarithmic transformation of milk yield, persistency can be improved independently from milk production.

KEY WORDS genetic trend, Holstein, milk yield, random regression model, Wood function.

INTRODUCTION

In animal populations, production and efficiency can be improved by enhancing the environmental conditions and genetic structure of the herd. Selection is an effective way to alter the genetic structure of the herd and consequently to change the mean of the herd. In a population that selection have been done and mating among animals have planned considering their genetic characteristics, it is necessary to investigate the changes of the average of phenotypic and breeding value for ascertaining the efficiency or inefficiency of breeding programs (Lasslo *et al.* 1985). Accurate prediction of breeding values has a great importance in predicting the genetic trends. Genetic trend evaluates genetic variations over time and explains the variations of breeding values over consecutive years. Genetic trends of a trait could be estimated by regression mean of breeding values on birth year (Sahebhonar, 2007). Estimation of genetic parameters of traits is necessary for prediction of breeding value. Several models were proposed for estimation of breeding values of milk yield. The random regression model (RRM) assumed standard shapes to the lactation curve for all cows and the estimated additive genetic effect of animals reflects differences in the height of these curves (Jamrozik and Schaeffer, 1997). Several mathematical models have been used to describe lactation curves. Incomplete gamma function that was proposed by Wood (1967) is one of the most common functions for describing lactation curve. Parameters of the incomplete gamma function can be estimated by nonlinear techniques. However, if the incomplete gamma function be used for large numbers of animals, speed of computation could be a limiting factor. Fitting incomplete gamma function by linear regression after a logarithmic transformation has the advantage of requiring a minimum of computer time. On the other hand, because nonlinear regression does not guarantee convergence, equations related to incomplete gamma function is linearized by transforming the yield to logarithmic units (Ruiz *et al.* 2000).

Several investigations have been carried out in Iranian Holstein cows on the genetic trend of milk yield. Khorshidie *et al.* (2012) estimated genetic parameters and genetic trends for milk yield persistency and 305-day milk yield in Holstein dairy cows of Iran using a random regression model based on the Legendre polynomial functions.

Chegini *et al.* (2013) estimated genetic trends for lactation milk yield, persistency of milk yield, somatic cell count and interval between first and second calving with a multi-trait animal model in Holstein dairy cows of Iran. Khanzadeh *et al.* (2013) estimated the genetic parameters and trends for fat and protein percentages of milk in Iranian Holsteins using a random regression test day model based on the Legendre polynomial functions.

Although the genetic trends of milk yield of Iran Holsteins have been previously investigated, but genetic trends of linear form of milk yield based on Wood function has not yet been evaluated. The aim of this study was to estimate the genetic, environmental and phenotypic trends of linear form of milk yield, genetic trends of sire and dam for linear form of milk yield and the correlation between breeding, environmental and phenotypic values of linear form of milk yield of each day and 305 days in Iranian Holsteins.

MATERIALS AND METHODS

Data

Data was consisted of 743205 test-day records in first lactation of 81192 Holstein cows from 46 herds in Iran, which had been collected during 1991 to 2008. The data were restricted into cows with registered father. Only records corresponding to 3 times a day milking were used. The number of records belonging to each animal was at least 8 and maximum 12 test-days. Days in milk ranged from 5 to 305. Age at first calving was between 20 and 36 month. Milk yields ranged from 2 to 48 kg. Also, records from herds with less than 150 heads of cattle were removed from the data set. Summary of the pedigree information is presented in Table 1.

Table 1 Summary of pedigree information

Variable	Total
Number of animals	90369
Number of animals with record	81192
Number of sires	1011
Number of dams	37566
Number of inbred animals	63
Average inbreeding coefficient	0.0165

Model

The Wood function was used to describe the lactation curve as below:

$$Y_t = at^b e^{-ct}$$

Where:

Y_t: milk yield on day *t*.

a: scaling factor to represent yield at the beginning of lactation.

b and c: factors associated with the inclining and declining slopes of the lactation curve.

Using RRM to fit wood function could be a limiting factor because of its nonlinear and exponential form. For solving this problem the linear form of wood function after a logarithmic transformation was used:

$$\ln(y_t) = \ln(\alpha) + b\ln(t) - ct$$

The following RRM for fitting the logarithm of test day (TD) records was used:

$$Ln(y_{ijkl}) = G_i + Y\_S_j + HTD_k + \sum_{n=1}^{2} b_n \left(BP_{ijkl}\right)^n + \sum_{n=1}^{2} b_n \left(age\right)^n + \sum_{n=0}^{2} \beta_n \mathrm{f}\left(dim\right)_n + \sum_{n=0}^{2} \alpha_n \mathrm{f}\left(dim\right)_n + \sum_{n=0}^{2} \gamma_n \mathrm{f}\left(dim\right)_n + \varepsilon_{ijkl}$$

Where:

$Ln(y_{ijkl})$: logarithm of TD records of milk yield.

G: fixed effect of sire's sperm producing country (inside or outside proved sperm).

Y_S: fixed effect of year-season of calving.

HTD: herd TD effect.

b_n: fixed regression coefficient specific to age at calving (age) or blood percent (BP).

β_n: fixed regression coefficient.

$f(dim)_n$: corresponding to polynomial of linear wood function of the animal n.

α_n: additive genetic random regression coefficient of the animal n.

γ_n: permanent environmental random regression coefficient of the animal n.

ε_{ijkl}: residual effect for each test day yield.

Analyses were conducted under an animal model using computer software WOMBAT 1.0 (Meyer, 2007) and AI-algorithm in Linux.

The breeding value of animal i in days in milk t was estimated using the following equation (Jakobsen *et al.* 2002):

$$EBV_{it} = \sum_{j=1}^{K_a} \alpha_{ij} F_j \left(dim_t \right)$$

Where:

α_{ij}: additive genetic random regression coefficient of animal *i*.

The breeding value of animal *i* was predicted by the sum of breeding values of each days in milk. After predicting the breeding values of animals, genetic, environmental, phenotypic trends were estimated by regressing mean of breeding values, environmental values and phenotypic values on birth year. Analyses of trends were performed with the regression procedure of the SAS 9.2 software package (SAS, 2007).

The mean of breeding value of sires were estimated by following equation:

$$\sum_i n_{ip} \hat{s}_i / n_{.p}$$

Where:

n_{ip}: number of daughters of sire i in the pth birth year.

$\hat{S}_i$: breeding value of the ith sire.

Genetic trends in cow population were estimated from regression of yearly average breeding value on year. For the pth year, the average cow merit was:

$$\sum_i \hat{C}_j / m_p$$

Where:

m_p: number of cows in the pth year.

$\hat{C}_j$: predicted breeding value.

Values of linear form of milk yield of each day and 305 day were estimated with correlation procedure of SAS 9.2 software.

RESULTS AND DISCUSSION

Genetic, environmental and phenotypic trends

Estimates of genetic, environmental and phenotypic trends for milk yield in Holstein dairy cows based on the logarithmic form of Wood function are presented in Table 2. Genetic and phenotypic trends were significant and positive, but the environmental trend was not significant. The value related to genetic trends in Table 2 means that the breeding value of the logarithmic form of milk yield increases 0.62222 each year. Also, the average of phenotypic value of logarithmic form of milk yield increase 0.61094 each year. However, there is not a significant trend in the average of the environmental value of the logarithmic form of milk yield each year.

Changes in the mean of estimated phenotypic values of the logarithmic form of milk yield are shown in Figure 1.

There was a moderate increasing trend in the mean of phenotypic values up to 1990. Then decreasing phenotypic trend was observed. Phenotypic trends of the logarithmic form of milk yield had a large variation, but there was an increasing trend from 1997 onwards. Changes in the mean of estimated environmental values of the logarithmic form of milk yield are shown in Figure 2. There was no obvious variation in the mean environmental values so environmental trend was not significant. As well changes in the mean of estimated breeding values of the logarithmic form of milk yield are shown in Figure 3. It was similar to the mean of estimated phenotypic values. There was an increasing trend up to 1990. After a decreasing trend up to 1991, the average of breeding values of the logarithmic form of milk yield had a large variation, but there was an increasing trend from 1997 onwards.

Similar to the current results, Ghavi Hossein-Zadeh *et al.* (2011) reported positive genetic and phenotypic trends in adjusted milk yield of Iranian Holstein dairy cows by a linear sire model. Abdullahpour *et al.* (2013) reported positive genetic trend of milk yield in Iranian Holstein cows using Legendre polynomials in a random regression model. Chegini *et al.* (2013) reported that genetic trends for milk yield calculated by ICAR's method and Wood's gamma function were positive for Holstein dairy cows of Iran. Khorshidie *et al.* (2012) reported that there was a significant and positive genetic trend for 305 DIM in Iranian Holstein. Katok and Yanar (2012) reported positive genetic and negative phenotypic and environmental trends of 305-days milk yield by restricted maximum likelihood methodology in Turkish Holstein Friesian cows. Katkasame *et al.* (1996) reported positive genetic and phenotypic trends for adjusted milk yields.

Elahi Torshizi *et al.* (2013) estimated genetic trend of Iranian Holstein cows for milk yield by different random regression models using different functions including unequal orders of Legendre polynomial and parametric function of Ali and Schaeffer. Their study showed that the mean of milk yield from birth year 1996 to 2006 increased but the rate of increase in EBV was low. They concluded that improvement in environmental effects like changes in management; feeding regime and other environmental factors are responsible for increasing milk yield in different birth years.

Table 2 Estimation of genetic, environmental and phenotypic trends of milk yield based on logarithmic form of Wood function

Description	Intercept±SE	b^1±SE
Genetic	-1241.25096*±285.91698	0.62222*±0.14317
Environmental	22.55308±32.75882	-0.01126±0.01640
Phenotypic	-1218.67098*±304.31269	0.61094*±0.15238

[1] Linear regression coefficients (genetic trends).

* (P<0.05).

SE: standard error.

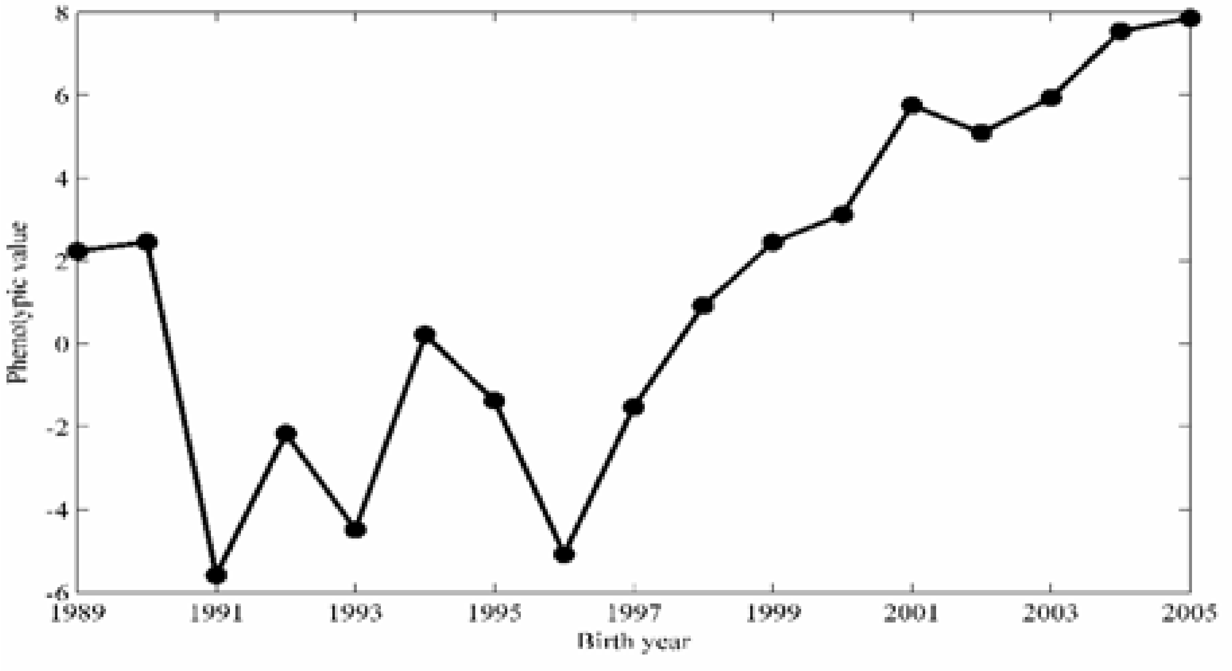

Figure 1 The changes of mean of phenotypic value

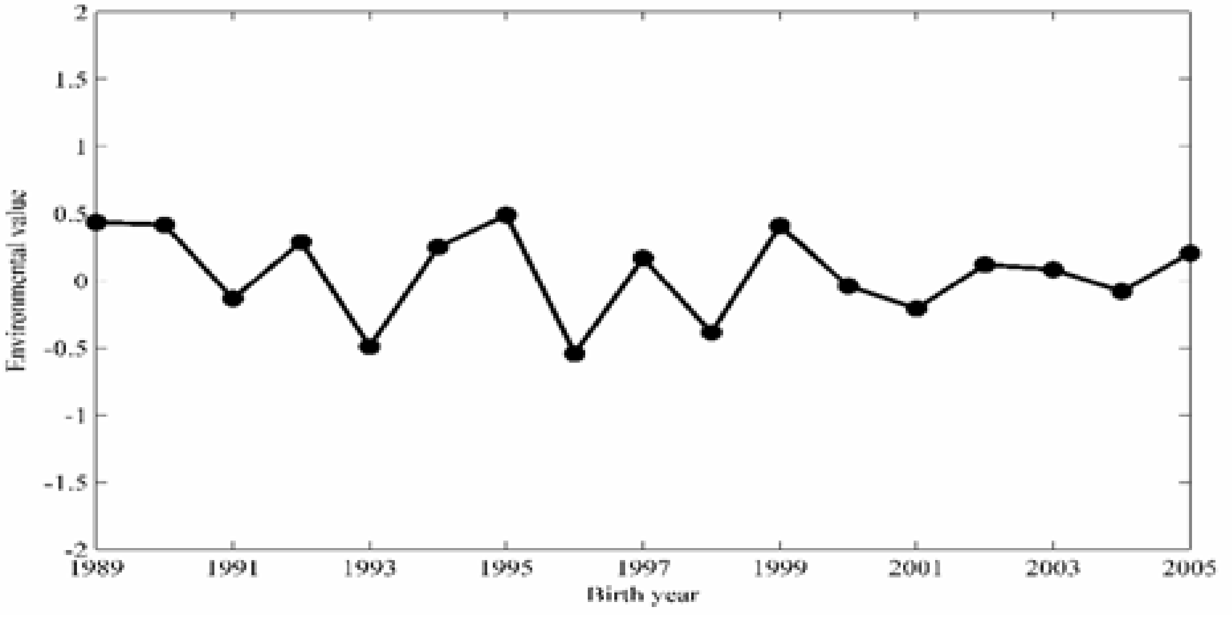

Figure 2 The changes of mean of environmental value

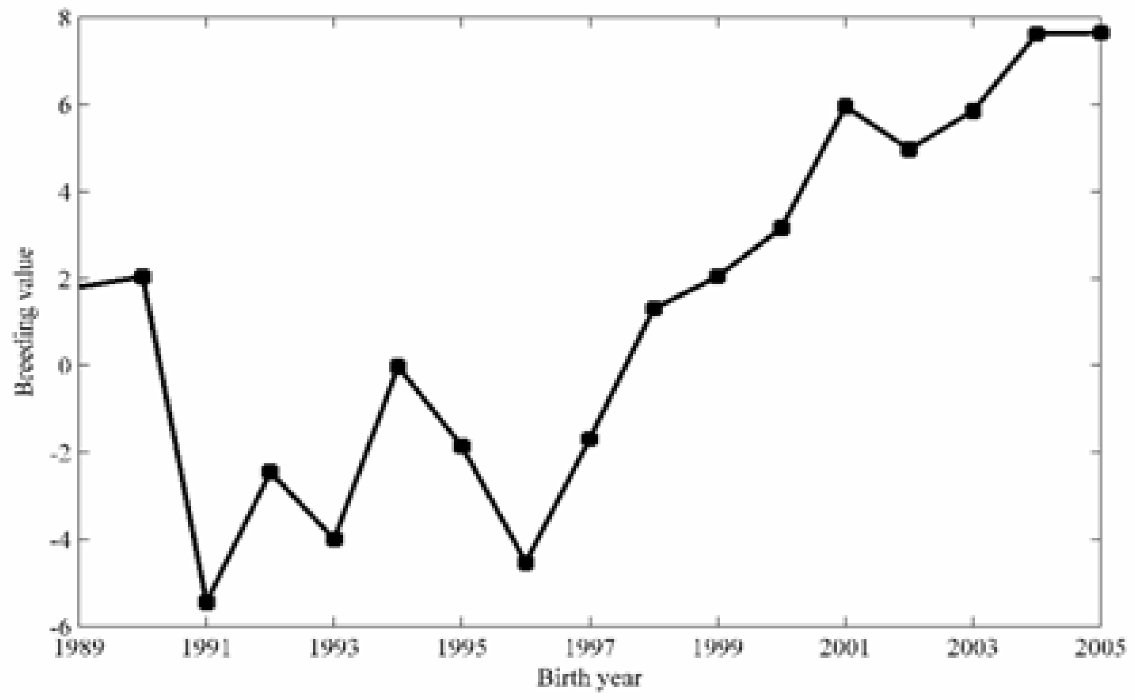

Figure 3 The changes of mean of breeding value

In contrary to the result of Elahi Torshizi *et al*. (2013), in the current study, environmental trend was not significant. Probably the reason is that selection programs had not been implemented for environmental effects and hence it had not made considerable change during the study period.

The increasing genetic and phenotypic trends in the logarithmic form of milk yield over time in this study indicated the effectiveness of selection for improving milk yield.

Genetic trends of sires and dams

Genetic trends of sires and dams based on the logarithmic form of milk yield were estimated. Also, genetic trends of Iranian and imported sires based on linear form of milk yield were estimated separately (Table 3). The genetic trends for Iranian sires were positive and significant while these trends were negative and significant for imported sires.

Total genetic trends in sires were not significant, therefore genetic trends for total sires were not observed. Total genetic trend of sire is affected by positive genetic trend of Iranian sires and negative genetic trend of imported sires, so it was neutral.

The changes of mean estimated breeding value of total sires, Iranian proof and imported proof are shown in Figure 4. A decreasing trend was observed up to 1990 in Iranian proof. Then the average of the breeding value of Iranian proof had variation up to 2000. After that a considerable increasing trend was observed. The changes of mean of estimated breeding values of imported proof had a decreasing trend up to 1991.

Table 3 Estimation of sire and dam trends for logarithmic form of milk yield

Description	Intercept±SE	B^1±SE
Sire_total	-438.77535±425.65811	0.21822±0.21315
Sire_Iranian proof	-1182.29064^*±466.18833	0.58657^*±0.23344
Sire Imported proof	1492.36303^*±356.03678	-0.73974^*±0.17829
Dam	-716.37184^*±255.12199	0.35939^*±0.12788

[1] Linear regression coefficients (genetic trends).
* (P<0.05).
SE: standard error.

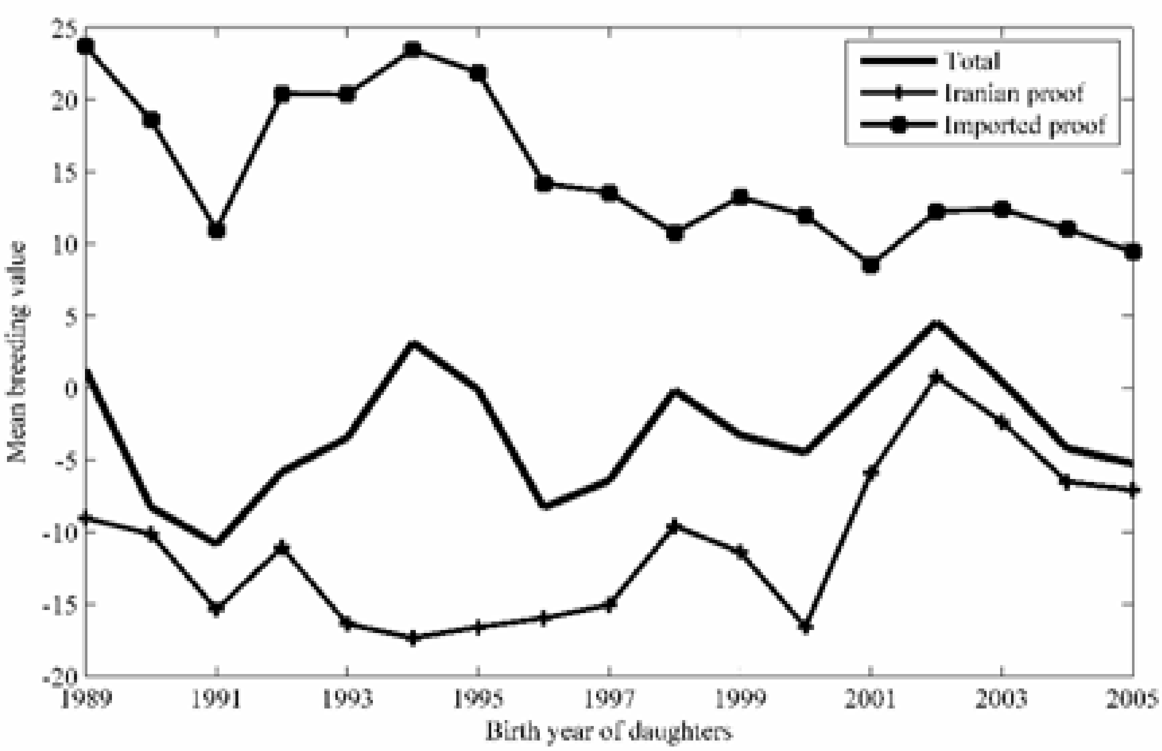

Figure 4 The mean of breeding value of Iranian and foreign sires

Then an increasing trend was observed up to 2004 and it had a moderate decline onwards. The curve related to total sires had a large variation. A decreasing trend was observed up to 1991. Then there was not any considerable change from 1991 onwards.

The reason for the decreasing trend observed for imported sires could be a result of more complex selection indices in exporting countries which rely more on reproductive, health and functional traits (Miglior *et al.* 2005) compared with the applied selection index in Iran that is highly depended to milk yield and milk components (Sadeghi-Sefidmazgi *et al.* 2012).

In general, the average of the breeding value of imported sires was higher than Iranian proof. Savar Sofla and Eskandari Nasab (2008) reported greater average of breeding values of milk yield for daughters of imported proof than daughters of Iranian proof.

The changes of mean estimated breeding values of dams are shown in Figure 5. There was no considerable variation up to 1996. Then genetic trend of dams had an increasing trend from 1997 onwards. Sahebhonar *et al.* (2010) estimated genetic trends of productive traits in Iranian Holstein cows from 1991 to 2006 and reported that the genetic trend of sires has slightly been higher than the genetic trend of dams.

Khorshidie *et al.* (2012) estimated breeding values of milk yield and persistency in Iranian Holsteins from 1991 to 2007 and reported a higher genetic trend for sires compared to the results of Sahebhonar (2007) because the genetic trend for milk production in sires could be larger than cows, due to the more intense selection applied in sires. Koonawootrittriron *et al.* (2009) reported negative genetic trend for sires and positive genetic trend for dams for milk yield in Thai Holstein cows.

Correlations

The phenotypic, environmental and genetic correlation between each DIM and total 305 days are shown in Figure 6. The correlation between the breeding value of the logarithmic form of each DIM and total breeding value based on logarithmic form were estimated. Results indicated that the correlation was low and it was not significant. The DIM 209 has the highest correlation with the total breeding value and was 0.14. Also, the correlation between the environmental value of the logarithmic form of each DIM and total environmental value was estimated. The highest correlation was observed at DIM 172 and it was 0.98. It means that environmental condition in this DIM has high importance and effects on total environmental value and this can impress total milk yield.

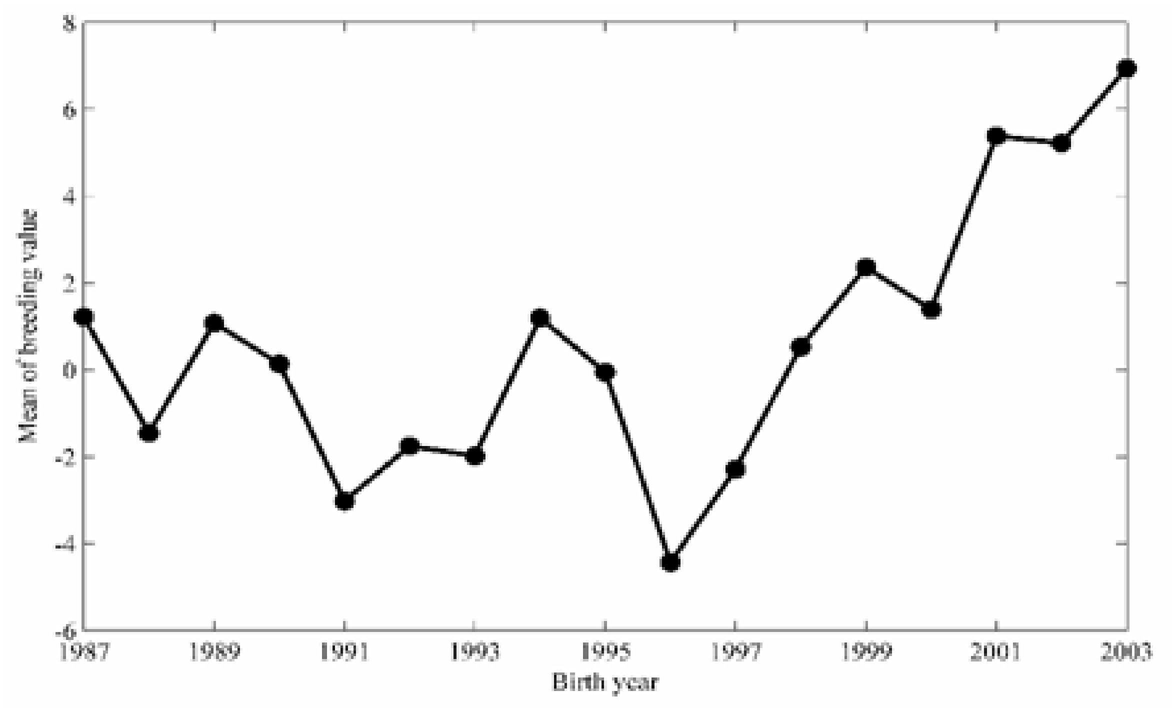

Figure 5 The mean of breeding values of dams

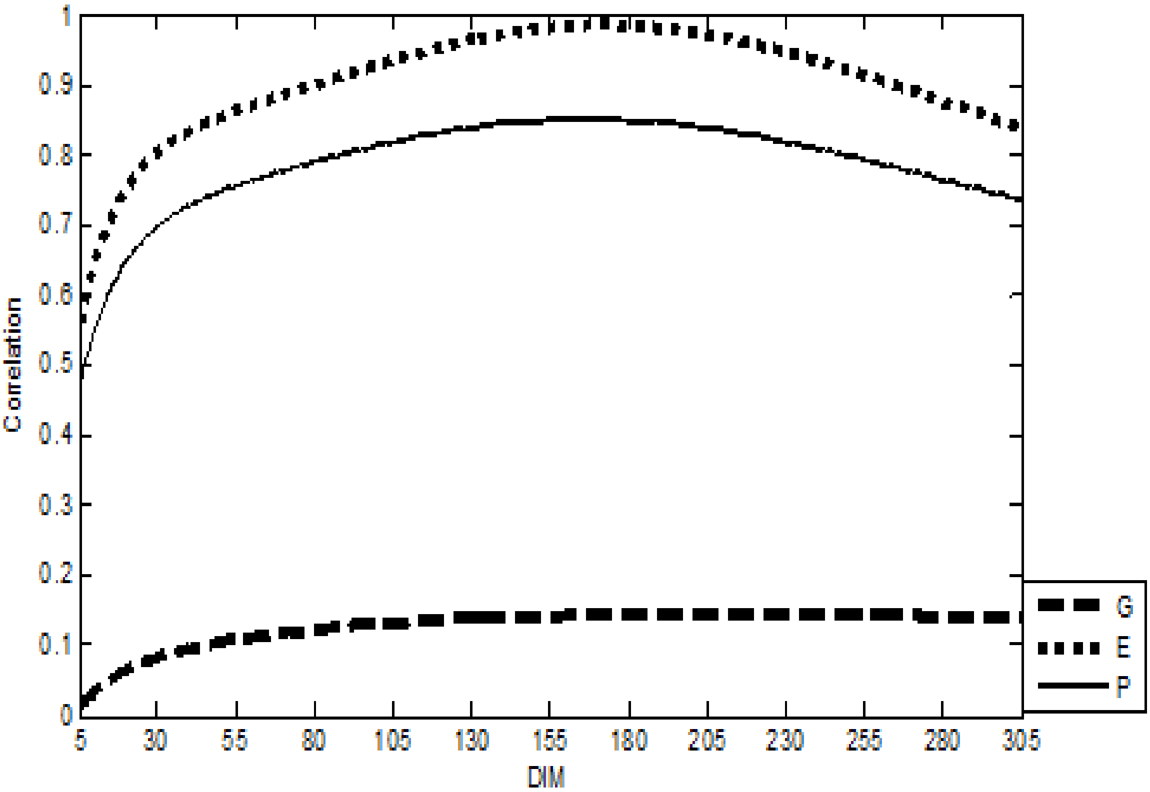

Figure 6 The correlation between breeding value of each DIM and total breeding value (G), between environmental value of each DIM and total environmental value (E) and between phenotypic value of each DIM and total phenotypic value (P)

The correlation between the phenotypic value of the logarithmic form of each DIM based and total phenotypic value of was estimated.

The highest correlation belonged to DIM 166 and it was 0.85. It shows that selection based on milk yield of this DIM can lead to better total milk yield.

In addition, the correlation between the total breeding value of the logarithmic form of Wood function and breeding values of the first 100 DIM, the second 100 DIM and the last 100 DIM were estimated and they are shown in Table 4.

Table 4 Correlation between total breeding value and 3 parts of lactation days

Days	Correlation
5-104	0.105361
105-204	0.142677
205-305	0.144262

Correlations were low and the last 100 DIM has a higher correlation with the total breeding value. Moradi Shahrebabak (2001) reported a high correlation between the second 100 DIM and total 305 days in milk in Iranian Holsteins. Based on EBV, the correlation of persistency with the second and third parts of lactation could be used as a criterion to evaluate the persistency criteria regarding improving both persistency and 305 d milk yield using random regression method (Elahi Torshizi *et al.* 2013).

In general the correlations were low. These weak correlations between the total breeding value of the logarithmic form of milk yield and breeding value of the logarithmic form of each DIM or breeding value of the logarithmic form of each section of milk yield showed that with the logarithmic transformation of milk yield, persistency can be improved independently from improving milk production.

CONCLUSION

In conclusion, the results of the present study indicated that genetic and phenotypic trends for the logarithmic form of milk yield were positive and significant. This increasing trend in milk yield over time indicated the effectiveness of selection for improving milk yield in Iranian Holstein cows. Genetic trends of dams were positive and significant. Genetic trends of total sires were not significant. By correct selection of Iranian sires, using suitable sperm of imported sires and performing appropriate breeding programs, genetic trend of Iranian Holsteins can be improved. The correlations related to breeding values were weak and it is possible to improve persistency independent from improving milk yield. Biological explanation, interpretation and usage of the results of logarithmic transformation of Wood function needs to be further investigated.

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