

Full Length Research Paper

Genetic constraints and developments of milk yield in Iranian Holstein population

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The aim of the present study was to estimate the genetic parameters and trends of milk yield, fat yield and fat percentage in Iranian Holstein population using animal model (multiple-traits) and Derivative-Free Restricted Maximum Likelihood (DFREML) procedure. First lactation data of 1128, 1093 and 1093 Mazandaran Holstein cows were collected from National Animal Breeding Center from 1988 to 2004 for milk yield, fat yield and fat percentage, respectively. The numbers of the whole animals were 49776 from 12 generations of studied pedigree. The heritability of milk yield, fat yield and fat percent during 305 days of lactation were 0.22, 0.24 and 0.28, respectively. Genetic correlations between milk and fat yield, milk yield and fat percent, and fat yield and fat percent were 0.99, -0.98 and 0.52, respectively. The genetic trends of all three studied traits were calculated using regression of means of breeding values over the years. The genetic trends were positive for milk (6.791) and fat (0.139) yields and negative for fat percentage (-0.04).

Key words: Production traits, genetic parameter, genetic trend, Iranian Holstein.

INTRODUCTION

The aim of animal breeding is to genetically improve livestock populations for production of more efficient animals to guard against future circumstances. Selection of the best individuals of the current generation and their use as parents of the next generation can be the major goal of an animal breeding scheme. Accurate prediction of breeding value of animals is one of the best tools available for maximizing response to selection program. Success of a breeding program can be assessed by actual change in breeding value expressed as a proportion of expected theoretical change of the breeding value mean for the trait under selection (Jurado et al., 1994). Selection of livestock is usually based on a combination of economically important traits that may be phenotypically and genetically correlated. Multivariate genetic evaluation takes account of the relationship among the traits in question, thus increasing the effectiveness of selection (Mokhtari and Rashidi, 2010).

Genetic trend evaluates genetic variations over time and also explains the variations of breeding values over

consecutive years. A number of methods are available for estimating genetic trends in dairy cattle populations, using either planned selection experiments or data from commercial herds that use control group, regression method and animal model (Nizamani and Berger, 1996; Roman et al., 1999). For dairy cattle improvement, prediction of breeding values with an animal model is becoming common instead of computation of separate genetic evaluations for cows and bulls (Suzuki et al., 1994). Estimation of genetic trends is necessary for monitoring and evaluating selection programs. Several researchers have studied genetic trends in dairy cattle (Nizamani et al., 1996; Roman et al., 1999; Abdallah et al., 2000; Elzo et al., 2004). The precision of genetic trend estimates is enhanced greatly as the number of years in which it has been studied increases (Abdallah et al., 2000). Various methods have been proposed for routine genetic evaluation of dairy cattle for economically important traits. Until 1988 sire models were the method of choice. With the increase in computing capabilities in the 1980s, animal models became computationally feasible

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Table 1. Number of records, unadjusted means, standard deviations and coefficients of variation for milk yield, fat yield and fat percentage of Mazandaran Holstein cows

Trait	Number of record	X	SD	CV (%)
MY (kg)	1128	5662.91	±1251.73	17.74
FY (kg)	1093	169.78	±41.55	18.26
Fat (%)	1093	2.98	±0.55	12.98

MY: Milk yield, FY: fat yield, X: mean.

Table 2. Information of pedigree of Mazandaran Holstein cows.

Number of animal	Number of sire	Number of dam	Number of grand sire	Number of grand mother	Number of inbred animal	Total means of inbreeding	Means of inbreeding in inbred animal
49776	1982	13141	1053	5547	1130	0.07%	3.26%

even for the largest commercial populations (VanRaden and Wiggans, 1991).

The past quarter-century in dairy cattle breeding has been marked by improvement of methodology and computer capacity, expansion in the array of evaluated traits, and globalization. Animal model replaced sire and sire-maternal grandsire models and, more recently, application of Bayesian theory has become standard. The increased capabilities have supported evaluation of additional traits affecting the net profitability of dairy cows (Powell and Norman, 2006).

Relatively high heritability, easy and accurate recording and high economical value make animal geneticist solicitous for milk and milk component (fat and protein) traits. Genetic trend is a major element in the function of breeding programs. In Iran, majority of dairy cattle breeding schemes have been conducted using Holstein breed. The aim of present study was to estimate the genetic trend and genetically analyses of production (milk yield, fat yield and percent) traits in Iranian Holstein cattle.

MATERIALS AND METHODS

First lactation data of 1128, 1093 and 1093 Mazandaran Holstein cows were collected from National Animal Breeding Center from 1988 to 2004 for milk yield, fat yield and fat percentage, respectively. The numbers of the whole animals were 49776 from 12 generations of studied pedigree. Traits were milked twice daily and on 305 days cycle basis. Records were collected and designated using EXCEL, SPSS and ACCESS softwares and the wrong and unusual records were ignored. The first lactation records of milked twice a day and 305 days cycle in the range of 1500 to 8500 milk yield and 18 to 36 months were used for analysis. The records with percentage above 1.5 were used to analyze fat percentage. Mean and overall standard deviations of traits are shown in Table 1. The pedigree file was prepared with consideration of 5 generations of studied animals using EXCEL and ACCESS software's. In pedigree file, number of animals was spotted larger than numbers of sires and dams. Table 2 shows the information derived from pedigree.

Analysis of (co)variance component and genetic parameters

The herd-year-season (HYS) factor which is fixed effect and age of first-parity known as a quantitative variable were used in the following model. The minimum, maximum and average numbers of records for each HYS were 5, 90 and 10, respectively. The analysis model of all three traits was:

$$Y_{ijk} = \mu + HYS_i + \beta (Age) + a_j + e_{ijk}$$

Where, Y_{ijk} is the record of observation k of animal j of herd i ; μ is the overall population means; HYS_i is the fixed effect of herd-year-sire i ; β is the linear regression coefficient of parity age on production traits; age is the effect of age of parity (month); a_j is the random effect (additive genetics) of animal j and e_{ijk} is the random effect of error.

The matrix notation of model was:

$$Y = Xb + Zu + e$$

Where, Y is the vector of observation of all three traits; b is the vector of fixed effects with incidence matrix X ; u is the vector of random animal effects with incidence matrix Z and e is the vector of random residual effects. The variance and covariance components of traits were calculated with DFREML algorithm using multivariate animal model. The analysis was done by DFREML software (Meyer, 1997).

Genetic trend estimates

After best linear unbiased prediction of breeding values of studied animals, the genetic trends of all three studied traits were calculated using regression of means of breeding values over the years. Genetic trends analyses were performed with the regression procedure of the SAS software package (SAS Institute, 1989).

RESULTS

In the present study, the variance component and heritability of studied traits were calculated using maximum likelihood methodology and DFREML algorithm (Table 3).

Table 3. Estimates of variance (var) component, heritability and standard error of studied traits.

Trait	σ^2_g	σ^2_e	σ^2_p	h^2 (%)	SE
MY (kg)	621722.47	787759.63	1409482.1	22	0.09
FY (kg)	233.13	728.09	961.22	24	0.09
Fat (%)	0.012	0.137	0.149	28	0.08

MY: Milk yield, FY: Fat yield, σ^2_g : Genetic variance, σ^2_e : Environment variance, σ^2_p : Phenotypic variance, h^2 : Heritability, SE: Standard error.

Table 4. Estimates of genetic (upon the diagonal) and phenotypic (below the diagonal) correlation of studied traits.

Trait	MY	FY	FP
MY	-	0.99	-0.98
FY	0.94	-	0.52
FP	-0.93	0.37	-

MY: Milk yield, FY: Fat yield, FP: Fat percentage.

Table 5. Linear regression parameters of studied traits.

Indep. var	Dep. var	R^2	df	F	P-value
Year	MY. BV (kg)	0.260	15	5027	0.037
Year	FY. BV (kg)	0.300	15	6.44	0.023
Year	FT. BV (%)	0.064	15	1.03	0.326

Indep. var: Independent variable, Dep. var: Dependent variable, R^2 : R-square, df: Degree of freedom, MY: Milk yield, FY: Fat yield, FP: Fat percentage, BV: Breeding value.

The traits were obtained from first lactation of Mazandaran Holstein cows. In Mazandaran Holstein cattle, the heritability of milk yield, fat yield and fat percentage were 22, 24 and 28%, respectively (Table 3).

Estimation of genetic and phenotypic correlations using multi traits models increases the accuracy of estimations. In Mazandaran Holstein cattle, the genetic correlation between milk and fat yield, milk yield and fat percent, and fat yield and fat percent were 0.99, -0.98 and 0.52, respectively (Table 4).

The genetic trends of all three studied traits were calculated using regression of means of breeding values over the years (Table 5). These values were positive for milk (6.791) and fat (0.139) yields and negative for fat percentage (-0.04) in Mazandaran Holstein cows. Table 6 shows the genetic trends of studied traits for 17 years (1998-2004). The graphs of genetic trends of all three studied traits are shown in Figures 1, 2 and 3. The SAS regression analysis showed that R^2 of means of breeding values of fat yield over the years had highest value (0.300) amongst studied traits (Table 5).

DISCUSSION

Genetic parameters and trends of milk yield, fat yield and

fat percentage were estimated in the present study. The variance components can be used to predict animals breeding value and designation of appropriate selection and breeding program. In Mazandaran Holstein cattle, the heritability estimates of the milk yield, fat yield and fat percentage traits were 22, 24 and 28%, respectively. These values were in the range of some previous reports. Abdallah and McDaniel (2000) estimated the heritability of 25% for 3.7% FCM in North Carolina Holstein cows using multivariate animal model and DFREML program. The estimated heritability of milk yield in our study was lower than those reported by Campos et al. (1994) for Florida Holstein cows (34%), Elzo et al. (2004) for Chilean Holstein cows (31%), Dedkova and Wolf (2002) for Czech Holstein cattle population (30%), Misztal et al. (1992) for U.S Holstein cows (44%), Weller and Ezra (2004) for Israel Holstein dairy cattle (39%), Van Tassell et al. (1999) for U.S Holstein cows (32-44%), Suzuki et al. (1994) for Holstein dairy cattle (26%) and higher than those reported by Strabel and Jamrozik (2006) for polish black and white cattle (18%) and Ben Gara et al. (2006) for Tunisia Holstein cows population (17%) . Also, our estimate of heritability of milk yield was close to that published by Silvestre et al. (2005) for Holstein dairy cattle (22%). Direct heritability estimated for fat yield (24%) was lower than those reported by Abdallah and

Table 6. Estimates of genetic trends for studied traits.

Year	MY (kg)	FY (kg)	Fat (%)
1988	0	0	0
1989	49.694	1.320	-0.4
1990	0	0	0
1991	35.768	0.936	-0.2
1992	28.553	0.104	-0.5
1993	14.748	0.300	-0.1
1994	59.519	0.980	-0.8
1995	1.173	0.352	0.2
1996	10.522	0.259	-0.1
1997	-10.090	-0.804	-0.8
1998	17.794	0.193	-0.3
1999	11.494	0.122	-0.1
2000	58.491	1.631	-0.2
2001	36.860	1.748	-0.05
2002	60.883	2.046	-0.3
2003	50.750	1.480	-0.5
2004	108.669	2.220	-0.7
Genetic trend/year	6.791	0.139	-0.04

Milk yield

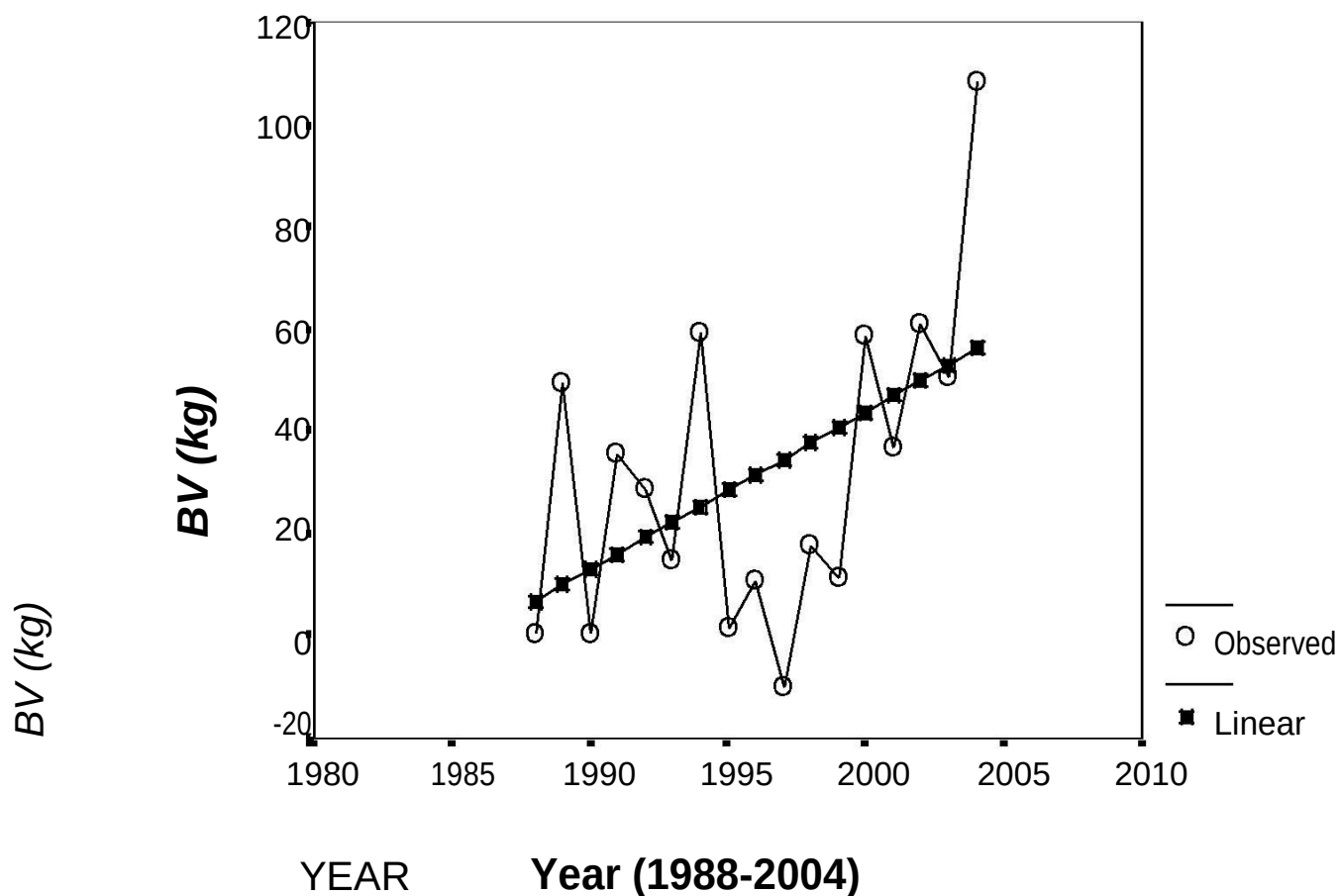


Figure 1. Means of breeding value for milk yield of Iranian Holstein cows at different ages by year of birth.
year (1988-2004)

Fat yeild

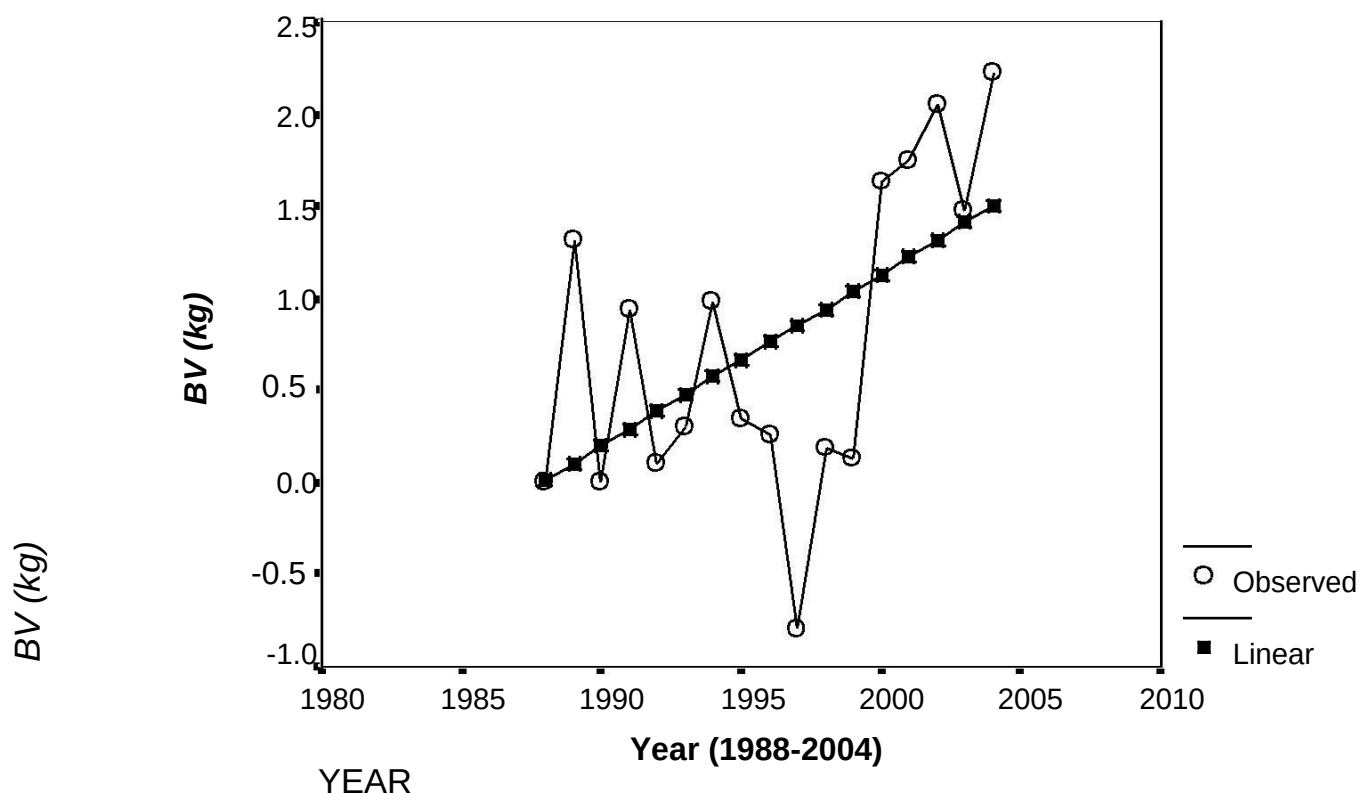


Figure 2. Means of breeding value for fat yield of Iranian Holstein cows at different ages by year of birth.

Year (1988-2004)

McDaniel (2000) for North Carolina Holstein cows (28%), Campos et al. (1994) for Florida Holstein cows (30.4%), Elzo et al. (2004) for Chilean Holstein cows (29%), Misztal et al. (1992) for U.S Holstein cows (42%), Weler and Ezra (2004) for Israel Holstein dairy cattle (42%), Van Tassell et al. (1999) for U.S Holstein cows (35-36%), Suzuki et al. (1994) for Holstein dairy cattle (26%) and higher than those reported by Silvestre et al. (2005) for Holstein dairy cattle (14%) and Strabel and Jamrozik (2006) for polish black and white cattle (12%). Furthermore, our estimate of heritability of fat yield was close to that reported by Dedkova and Wolf (2002) for Czech Holstein cattle population (24%).

The heritability of fat percentage was 28% in our study, higher than that reported by Tehani et al. (2008) for Iranian Holstein population (10%). Also, our estimate was lower than those published by Boujenane, (2002) for Moroccan Holstein-Friesian cows (39%) and Campos et al. (1994) for Florida Holstein cows (38.2%). According to the obtained results, the heritability estimates of all three studied traits in Mazandaran Holstein cattle were lower than previous estimates on Holstein cows in majority of other countries. The low estimate of heritability is due to large amount of phenotypic variance.

In the present study, the genetic correlation between milk yield and fat percentage was -0.98. The negative correlation means that genes that positively influenced milk production had reverse effect on fat percentage.

Direct phenotypic correlation between milk yield and fat percentage was -93%. This estimate was higher than that reported by Boujenane (2002) for Moroccan Holstein-Friesian cows (-28%) and close to that reported by Tehani et al. (2008) for Iranian Holstein population (-93%). In our study, the genetic and phenotypic correlations between milk yield and fat yield were 99 and 94%, respectively. These results were close to those published by Boujenane (2002) for Moroccan Holstein-Friesian cows (96% for each of genetic and phenotypic correlation). Misztal et al. (1992) reported that genetic correlation between milk yield and fat yield was 69% for U.S Holstein cows. Also, Silvestre et al. (2005) published the genetic correlation of 43% between milk yield and fat yield for Holstein dairy cattle. Our estimates of genetic and phenotypic correlation between fat yield and fat percentage (52 and 37%, respectively) were inconsistent with results of Tehani et al. (2008) for Iranian Holstein population. Genetic correlation between important productions traits can be used as a valuable tool for designation of a cheaper breeding project. If the genetic correlation between two or more valuable traits is positive and high, it can help us to improve two traits using correlated response.

The genetic trends for milk yield, fat yield and fat percentage in Mazandaran Holstein cattle were 6.791 kg, 0.139 kg and -0.04%, respectively. Tehani et al. (2008) reported genetic trends of 2.34 kg, 0.02 kg and 0.01% for

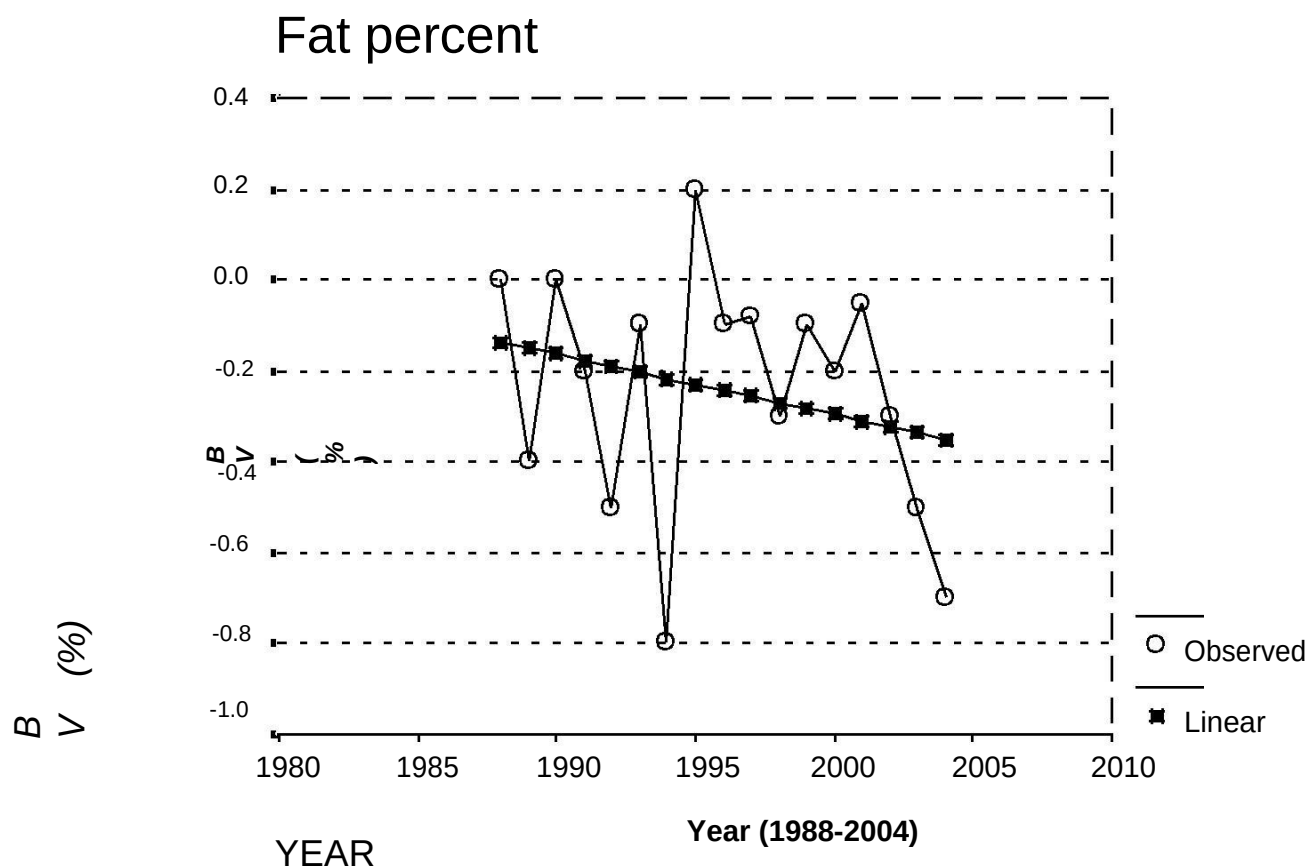


Figure 3. Means of breeding value for fat percentage of Iranian Holstein cows at different ages by year of birth. year (1988-2004)

milk yield, fat yield and fat percentage in Iranian Holstein population, respectively. The values of 39.9 kg, 0.94 kg and -.02% were estimated for these traits, respectively by Roman et al. (1999) for jersey cow population. Abdallah and McDaniel (2000) estimated the genetic trends of -2.5, 27.9, 36.7 and 94.7 kg for milk yield and 0.45, 0.75, 1.23 and 3.64 kg for fat yield from 1950 to 1993 (in ten years period) in North Carolina Holstein cows. In other study, Weler and Ezra (2004) reported genetic trends of 53.7 kg, 2.00 kg and 0.0026% for milk yield, fat yield and fat percentage, respectively in Israel Holstein dairy cattle population. The progress of an animal breeding program can be assessed by calculating genetic trends over the years. Results of the present study showed that designed genetic program has had positive impact on milk and fat yields and negative impact on fat percentage for 17 years in Mazandaran Holstein cattle.

Conclusion

In the present study, genetic parameters and trends of three production traits were estimated using animal model in Iranian Holstein population. Fat yield and milk yield had highest heritability and genetic trend, respectively. Furthermore, genetic correlation between milk yield and fat percentage and phenotypic correlation between milk yield and fat yield had highest values amongst correlation estimates.

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