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Use of Random Regression Test-Day Model to Estimate Genetic Parameters of Milk Yield in Holstein Cows

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Abstract

(Co) variance components and genetic parameters were estimated for milk yield of Iranian Holstein cows. A total number of 68,945 milk test-day records of first, second and third lactations of 8515 animals from 100 sires and 7743 dams originated from 34 herds collected during 2007 to 2009 by Iranian animal breeding center were used. The ASReml computer program was used to analyze the milk test-day records using the random regression procedure. Herd test date (HTD), milking times per day (milking frequency), number of lactations, year of birth, year of calving, age of animal at calving and days in milk (DIM) considered as fixed effects and additive genetic effects and animal permanent environmental effects were considered as the random effects. Additive genetic variance, animal permanent environment variance, residual variance, phenotypic variance, heritability and repeatability were estimated during different months of lactation between 5.7 - 19.6, 15.3 - 27.1, 31.4 - 17.2, 45.8 - 64.83, 0.1 - 0.32 and 0.4 - 0.6, respectively. Genetic correlation and phenotypic correlation were also estimated between months of lactation in range of −0.35 - 0.98 and 0.03 - 0.67, respectively. Genetic correlation and phenotypic correlation both showed the same changing pattern and they decreased as the interval between months of lactation increased.

Keywords

Genetic Parameters, Random Regression Model, Test-Day Records, Milk Yield, Holstein Cows

1. Introduction

Estimates of genetic parameters are important in the design of animal breeding programs aimed to maximizing genetic gain [1]. Heritability of a trait is a fraction of the genetic variation to the phenotypic variation, which indicates, on average, how much of the superiority of selected animals as the next generation parents is passed to the progeny generation [2]. Lactation yield and persistency are two economically important traits in dairy production [3]. Test day records are expressions of a trait that changes over time. These records are used to predict total 305-d yields which are required to evaluate the additive genetic merit of sires and cows in traditional evaluation [4]. The model for test day yields can account more precisely for environmental factors that could affect cows differently during lactation for the genetic evaluation of dairy cows using individual test day yields rather than total lactation production has a number of advantages.

A common approach to investigate genetic associations between test day yields is to consider every yield at each time period as a separate trait and then to estimate the genetic correlations between these traits. This approach has some disadvantages when large numbers of test day yields are considered. The biological interpretation of a large number of correlations is furthermore often difficult [4]. Different statistical models have been used to genetically evaluate milk production using test-day observations [5]. Reference [6] proposed the use of random regression models in animal breeding for genetic evaluations on traits measured over time. Advantages of random regression test-day models over an approach using 305-day lactation yields are now widely acknowledged. Random regressions allow for a different shape of lactation curves for each cow. The random regression model also allows a cow to be evaluated on the basis of any number of test day records during lactation and it can account for different genetic, permanent environmental and residual variances in the course of lactation. References [7] [8] [9] reported that random regression models were more appropriate for estimating the genetic parameters of test-day milk yield than repeatability models, because random regression models are able to fit genetic and environmental changes in milk yield over the time.

The aim of this study is to estimate the genetic parameters (additive genetic and permanent environmental (Co) variances) and heritability values for test day milk yields of Iranian Holstein cows using a random regression Test-Day model.

2. Methods and Materials

2.1. Data Set

Data were provided by the Animal Breeding Center of Iran (ABCI, Tehran) and consisted of a total number of 68,945 milk test-day records of first, second and third lactations of Holstein cows that calved between 22 and 36 month of age during the time period from 2003 to 2009. The records were measured on 8515 animals originated from 100 sires and 7743 dams from 34 herds. More details of the data are presented in Table 1.

2.2. Genetic Analysis

Single trait random regression Test-Day model was applied to estimate the genetic parameters of milk yield of Iranian Holstein Cows in the first, second and third lactations. Herd test date (HTD), milking times per day (milking frequency), number of lactations, year of birth, year of calving, age of animal at calving and days in milk (DIM) were fitted in the model as fixed effects. Linear, quadratic and higher orders of regression were tested for effect of age at calving. Fixed polynomial regression with different order of fit was considered for DIM. For changing scale of days in milk from 5 to 305 day was standardized to the interval [−1, ···, 1] [10]. Additive genetic effects and animal permanent environmental effects were fitted as the random effects. To take heterogeneous residual variances into account, the residual variance was estimated for 10 equally sized groups, based on duration of lactation (Table 2).

The following model was used for analyzing the data:

$$Y_{ij} = Xb + \sum_{m=0}^{K-1} \delta_m \varnothing_{mij} + \sum_{m=0}^{K_a-1} \alpha_{im} \varnothing_{mij} + \sum_{m=0}^{K_{(ide)}-1} \beta_{im} \varnothing_{mij} + \varepsilon_{ij}$$

where:

y_{ij} is the performance of i^{th} cow.

Table 1. Statistics and structure of used data.

Number of Animals	8515
Number of Records	68,945
Number of Sires	100
Number of Dams	7743
Number of Herds	34

Table 2. Groups of days in milking (DIM) and the number of records in each group.

Group	Days in milking	Number of records
1	5 - 35	8076
2	35 - 65	8608
3	65 - 95	8514
4	95 - 125	8912
5	125 - 155	8393
6	155 - 185	7713
7	185 - 215	6528
8	215 - 245	5409
9	245 - 275	4157
10	275 - 305	2635

X is an incidence matrix for fixed effects.

b is the vector for fixed effects.

δ_m is coefficient i of a fixed regression on element i of the polynomials of all environments.

α_{im}, m^{th} degree fitting random regression for additive genetic effects for i^{th} animal.

β_{im}, is a permanent environmental effect of i^{th} animal.

$\varnothing_{mij}$, m^{th} degree of fit of j^{th} day for i^{th} animal.

k_a and $k_{(ide)}$, degree of fit for additive genetic and permanent environmental effects, respectively.

e_{ij} is the temporary or residual environmental random effects associated with y^{ij}.

Models with different order of Legendre polynomials were fitted for both the additive genetic effects and the animal permanent environmental effects. To choose the best order of fit for the random effects, the models were compared using Schwarz's Beysian Information Criterion (BIC) [11].

The variance-covariance matrix for models was assumed to be:

$$\text{var}\begin{bmatrix} u \\ p \\ e \end{bmatrix} = \begin{bmatrix} \boldsymbol{G} \otimes \boldsymbol{A} & & \\ & \boldsymbol{P} \otimes \boldsymbol{I} & \\ & & \boldsymbol{R} \end{bmatrix}$$

where:

$\boldsymbol{G}$ and $\boldsymbol{P}$ are the (co)variance matrices of the random regression coefficients for additive genetic and permanent environmental effects;

$\boldsymbol{R}$ is a diagonal matrix of residual variance;

$\boldsymbol{A}$ is the additive genetic relationship matrix among cows;

$\boldsymbol{I}$ is an identity matrix, and $\otimes$ is the Kronecker product.

The best order of fit for additive genetic effects and animal permanent environmental effects were estimated. The restricted maximum likelihood (REML) procedure, under an average information algorithm, was used to estimate the (co)variance components and corresponding genetic parameters applying ASReml computer program [12].

3. Result and Discussion

Milk yield was significantly affected by the fixed effects of herd test date (HTD), milking times per day (milking frequency), number of lactations, year of birth, year of calving, age of animal at calving and days in milk (DIM) ($p < 0.001$) (Table 3).

$K = 4$ was the best order of fit for the fixed regression of days in milk. Genetic analysis was started with $K = 2$ for both direct additive genetic and animal permanent environmental effects and completed with higher order of fitting up to $K = 4$. The best model was selected using BIC (Table 4). Accordingly, a random regression model fitting Legendre polynomials to order $K = 4$ for direct additive genetic effects and $K = 3$ for animal permanent environmental effects was found to be the best model to describe the genetic (co) variance structure in the data.

Table 3. Fixed effects used in the model for the analysis of milk yield with their significant level, degree of freedom, LSM and SE.

Fixed effects	Significant level	Degree of freedom	Level	LSM ± SE
Milking frequency per day	***	1	3	34.71 ± 0.33
			4	36.85 ± 0.43
Lactation period	***	2	1	34.71 ± 0.33
			2	34/2 ± 0.56
			3	33.07 ± 0.69
Birth year	***	3	2003	34.71 ± 0.33
			2004	35.69 ± 0.56
			2005	36.11 ± 0.67
			2006	37.11 ± 0.82
Calving year	***	2	2007	34.71 ± 0.33
			2008	33.71 ± 0.54
			2009	34.97 ± 0.66
Age	***	3	1	34.71 ± 0.33
			2	40.81 ± 0.74
			3	32.4 ± 0.51
			4	34.02 ± 0.51
Days in milking	***	3	1	34.71 ± 0.33
			2	28.06 ± 0.53
			3	31.88 ± 0.42
			4	37.42 ± 0.42

***: $P < 0.001$.

Table 4. Order of fit for direct additive genetic effects (K_a), animal permanent environment effects (K_{ide}), number of parameters (Np), Log likelihood values (LogL) and Bayesian Information Criterion (BIC) derived from base model (Model 1).

Order of fit		Np	LogL	BIC
K_a	K_{ide}			
2	2	17	4292.67	8774.74
3	2	20	4026.56	8275.93
3	3	23	3929.33	8114.91
4	3	27	3846.15	7993.09[a]
4	4	31	3844.09	8033.54

[a]Best model based on BIC.

3.1. Additive Genetic Variance

Additive genetic variance showed an increasing rate from the first to the 9th month of milking but it was suddenly decreased at the end of lactation period (**Figure 1**). Minimum (5.7 kg^2) and maximum (18.16 kg^2) additive genetic variance were observed in the first and 9th month of lactation, respectively. Generally, the rate of variance changing in the first half of the milking period was less than the second half of the lactation period. The results are in agreement with the results of [13] [14], and are not in agreement with the results of [15] [16].

3.2. Animal Permanent Environment Variance

Animal permanent environment variance had a gradual increasing rate from the first to the 8th month of lactation period and then sharply increased for the later months (**Figure 2**). Minimum (15.3 kg^2) and maximum (27.1 kg^2) animal permanent environment variance were observed in 2nd and 10th months of lactation period. References [13] [16] [17] reported a maximum animal permanent environment variance at the first two months and last two months and a minimum animal permanent environment variance in the middle months of lactation period. Also [18] [19] observed that animal permanent environment variance had increased by increasing the number of the lactation period.

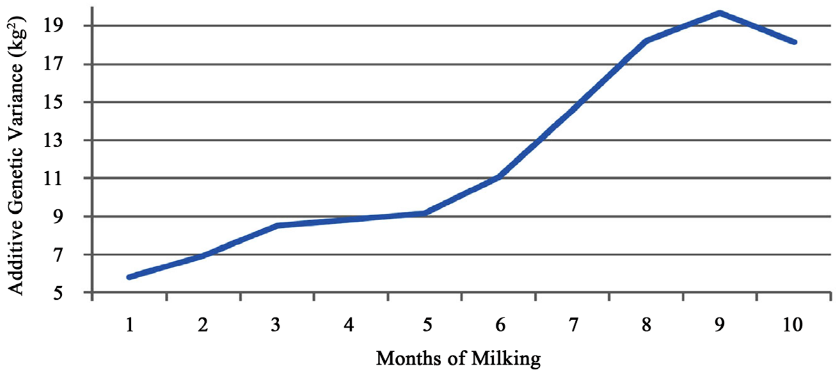

Figure 1. Additive genetic variance of milk yield during month of milking.

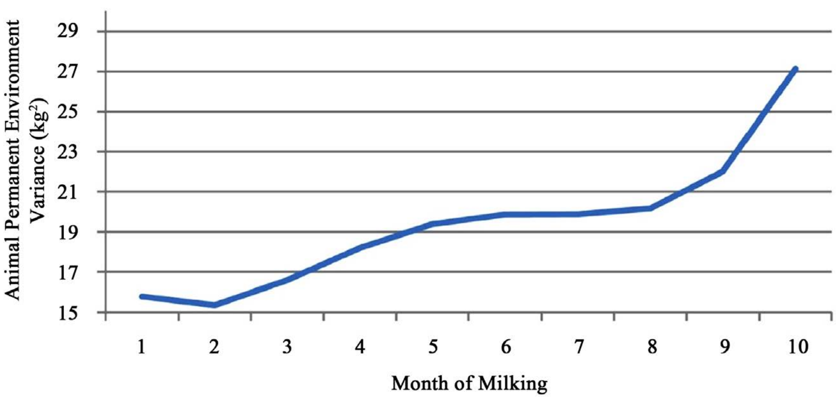

Figure 2. Animal permanent environment variance of milk yield during month of milking.

3.3. Residual Variance

Residual variance had decreased up to the 6th month of lactation period and then smoothly increased to the end of lactation period (**Figure 3**). Maximum residual variance (31.4 kg^2) was observed in the first month of lactation. In a study by [20] in order to estimation of variance components of milk yield using random regression models, the residual variance had an increasing rate from beginning to the end months of lactation period that is not in agreement with the results of this study. Also, [14] [17] reported residual variance changes during the lactation period.

3.4. Phenotypic Variance

Phenotypic variance had a decreasing rate and reached to the minimum level (45.8 kg^2) at the 4th month of lactation and then showed an increasing rate to the later months of lactation period (**Figure 4**). Maximum level of phenotypic variance was observed in the last month of lactation period. These results are in agreement with results of [14] [16] [17] [20] but differ from those observed by [18] that phenotypic variance had a decreasing rate from beginning to the end of the lactation period.

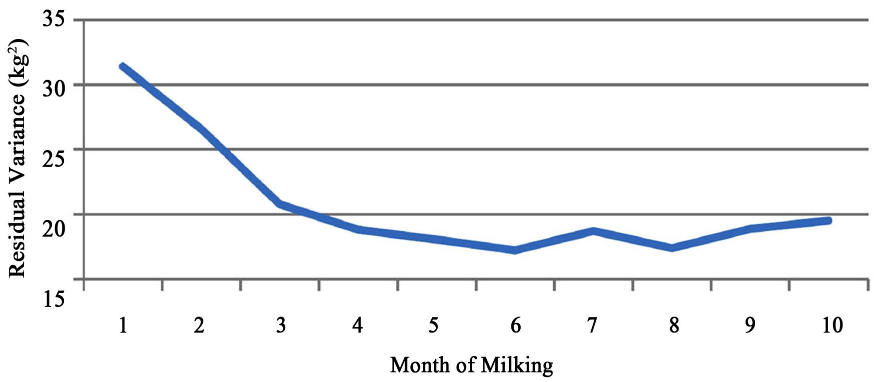

Figure 3. Residual variance for milk yield during month of milking.

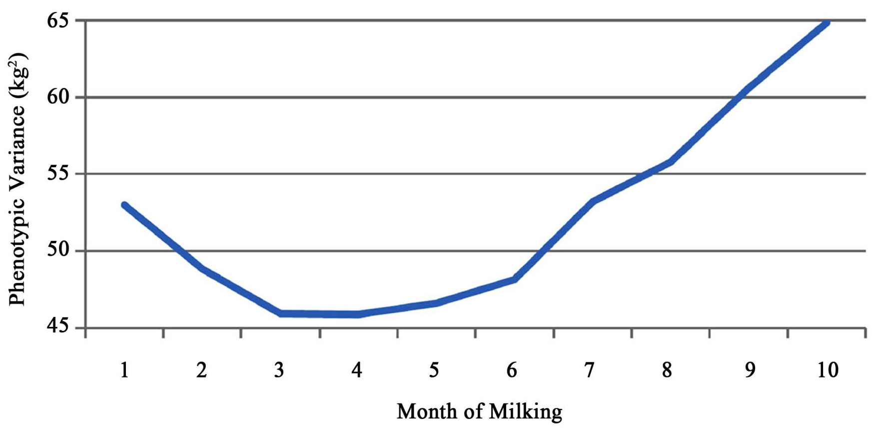

Figure 4. Phenotypic variance of milk yield during month of milking.

3.5. Heritability

Heritability of milk yield estimated between 0.1 to 0.32 and it was different among months of lactation. Minimum heritability (0.1) belongs to the first month of lactation. Heritability had a gradually increasing to 3rd month of lactation followed by smooth increasing up to 5th month of lactation and then reaching to the highest heritability (0.32) at the 8th month of lactation through a sharp increasing rate, and finally, a slight decreasing to the 9th and a sharper decrease in the last month of lactation (**Figure 5**). Low levels of heritability at the beginning months of lactation maybe duo to low additive genetic variance and higher levels of residual variance in the beginning months of lactation period. The average of estimated heritability for entire lactation period is 0.22. These results are in agreement with those reported by [15] [18] [19] [20] [21]. Reference [22] reported minimum heritability (0.26) for the first month and maximum heritability (0.44) for 3rd month of lactation period. In another study by [16] minimum heritability (0.19) was observed in the first month and the maximum heritability (0.23) was observed in the middle months of lactation period.

3.6. Repeatability

Repeatability for milk yield trait was estimated between 0.4 to 0.69 in the months of lactation period (**Figure 6**). Repeatability for milk yield trait had an increasing rate from the beginning to the end of lactation period. Minimum level and maximum level belongs to the first and last month of lactation period, respectively.

Figure 5. Heritability for milk yield during month of milking.

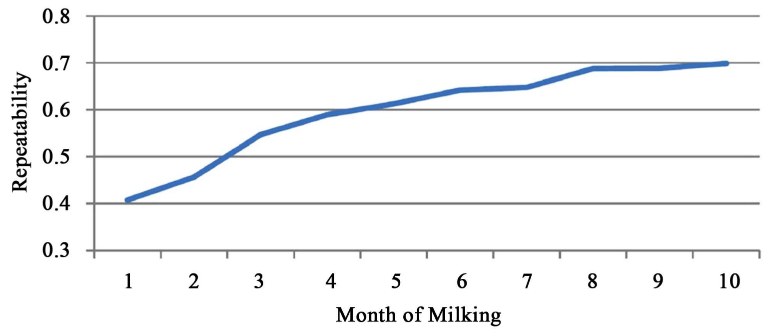

Figure 6. Repeatability for milk yield during months of milking.

3.7. Genetic Correlation

Genetic correlation between months of milking estimated between −0.35 to +0.98 (**Table 3**). Maximum genetic correlation for milk yield trait observed between consecutive months, specially, at the end of lactation period. Genetic correlations between first month of lactation and other months (up to 6th month) estimated between 0.8 to 0.11 that shows genetic correlation had decreased as the intervals between months of lactation increased. Negative genetic correlation shows cows with high performance in milk production at the beginning of lactation have low performance at the end of lactation period. Genetic correlation between consecutive months at the beginning of lactation was less than genetic correlation between consecutive months at the end of lactation period. Genetic correlation between first and second month of lactation was 0.8 and genetic correlation for the four latest months of lactation estimated between 0.96 to 0.98. These results are in agreement with those reported by [13] [17] [20] [21] [22].

3.8. Phenotypic Correlation

Phenotypic correlation for the milk yield estimated between 0.03 to 0.67 during months of lactation (**Table 5**). Maximum phenotypic correlation observed between consecutive months at the end of lactation period. Phenotypic correlation estimated 0.39 to 0.48 for the first three months of lactation and 0.65 to 0.67 for the latest three months of lactation. Results of this study shows that phenotypic correlation between months of lactation had decreased by increasing the interval between months of lactation. The magnitude of phenotypic correlation was less than genetic correlation but it follows the same pattern to the genetic correlation. Estimated phenotypic correlation in this study was similar to those reported by [13] [17] [20] [22].

Table 5. Coefficients for genetic correlation (below diagonal), and phenotypic correlation (above diagonal) for milk yield in different months of lactation.

Month of lactation	1	2	3	4	5	6	7	8	9	10
1	-	0.39	0.36	0.32	0.27	0.22	0.17	0.12	0.07	0.03
2	0.8	-	0.48	0.46	0.41	0.34	0.26	0.19	0.12	0.07
3	0.6	0.94	-	0.55	0.52	0.45	0.37	0.28	0.2	0.14
4	0.44	0.83	0.95	-	0.58	0.54	0.47	0.39	0.31	0.23
5	0.28	0.62	0.79	0.93	-	0.6	0.55	0.5	0.42	0.33
6	0.11	0.33	0.53	0.74	0.93	-	0.62	0.6	0.53	0.44
7	−0.03	0.08	0.27	0.52	0.79	0.95	-	0.65	0.61	0.53
8	−0.14	−0.09	0.09	0.35	0.65	0.88	0.98	-	0.67	0.61
9	−0.24	−0.2	−0.01	0.25	0.56	0.81	0.94	0.98	-	0.66
10	−0.35	−0.25	−0.04	0.21	0.5	0.73	0.86	0.92	0.96	-

4. Conclusion

This research highlighted that milk yield in Iranian Holstein cows significantly affected by milking frequency, number of lactations, year of birth, year of calving, age of animal at calving and days in milk (DIM). Also, we can conclude that additive genetic variance, animal permanent environment variance, phenotypic variance, heritability and repeatability can have different values during the lactation period. Nutrition, management, parturition stress and genotype by environment interaction in Iranian dairy cows may be the most probable factors that change the milk production curve. High magnitudes of genetic and phenotypic correlations between consecutive months of lactation indicated that similar factors (Management, Nutrition, …) with the same pattern can affect the milk production and as the interval increases between months of lactation, the effects of these factors differ from a month to another month in the lactation period.

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