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Estimation of Genetic Parameters for Milk Production Trait in Holstein Cows of the Mazandaran Gavdasht Herd Using Test Day Records

Research Article

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ABSTRACT

Random regression models (RRM) are used for genetic estimations of milk traits in dairy cows. RRM utilize data on traits that are repeated during the time, such as milk trait, which allows of the evaluation of the test day production information. In this study, to estimate genetic parameters for milk production trait, test day records (TDR) were collected from the first lactation of Holstein cows from a Mazandaran Gavdasht herd during the years 2001 to 2012. The data included 14150 TDR of milk production trait of 1460 Holstein cows. Analysis of TDR was performed using the DFREML software. The random regression was fitted according to the Legendre polynomials model from days of lactation. The minimum of heritability (0.04) was estimated for the early lactation period and increased in the late of lactation, about the month 9 of lactation to its peak (0.29). The phenotypic variance was not same during the lactation period and it was too much in the early and late of lactation. The maximum of genetic variance was at the month 10 (19.81) and the minimum at the early of the lactation period (2.51). The residual variances were constant. The maximum of the genetic and phenotypic correlations were observed between adjacent days for milk production trait. Using TDR, accuracy of genetic parameter estimation was increased.

KEY WORDS genetic parameters, heritability, Holstein, RRM, TDR.

INTRODUCTION

The main source of milk production are cows. Over 90% of milk in the world will be produced by the cows (Borquis *et al.* 2013). The data collection management is the most important factor in any decision for the farm manager. The test day records (TDR) for milk are the basic data used for calculation of yields during traditional 305-d lactations. The milk traits for a completed 305-d lactation would be composed of 10 TDR. Random regression models (RRM) are an appealing approach to model repeated measurements and to estimate genetic parameters. Milk production records provide a typical example of repeated measurements data. The main property of measurements data is the evaluation of the genetic properties of one or more variables across a specific dimension, such as time. The TDR will be affected by many factors, such as breed (Borquis *et al.* 2013; Yarinezhad *et al.* 2008). Animal breeders with design of test day model and using relevant data could have done evaluation and selection of genetic in a shorter timeframe and increase response to genetic selection and reduce generation interval and costs**.** In 1994, a RRM was proposed for the analysis of TDR. In this model the covariance structure of repeated data during time or life was considered (Jamrozik and Schaeffer, 1997; Kettunen *et al.* 2000; Emam Jome kashan, 1997). RRM permit the estimation of genetic parameters for the lactation curve as a whole, for any point within the lactation period, and for functions of the lactation curve. In dairy cattle, the regressions are fitted as a function of the lactation period using a base function that permits modeling of the trajectory for both the population mean (fixed regression) and each animal (random regression). Another advantage of RRM is that the covariance structure between measures can be characterized by a function (Jamrozik and Schaeffer, 1997). The aim of this study is the estimation of genetic parameters for milk trait in Gavdasht herd of Mazandaran.

MATERIALS AND METHODS

In the recent study, TDR of the milk production trait from 11430 of the first lactation record of 1460 Holstein cows of the Mazandaran Gavdasht herd were used. The calving of cows were between 2001 and 2012. The number of base animal was 803. The inbreeding coefficient average of herd was 1.60 (Table 1). Data edition was performed using the EXCEL (2007) software. The entire 305-day lactation period was divided into 10 groups. On the other hand, days of lactation was divided into 10 groups of monthly records. The number mean of TDR per cow was 9.

For determining significant factors on the milk production a general linear model (GLM) was fitted using SAS (2003) software. Estimation of variance components was done using the following random regression animal model.

$$y_{ijkn} = cys_i + CA_j + \sum_{n=1}^{2} b_n (TD_{ijn})^n + \sum_{n=0}^{k} \beta_n \phi_n (\dim_{ijkn}) + \sum_{n=0}^{ka-1} \alpha_{p_n} \phi_n (\dim_{ijkn}) + \sum_{n=0}^{kp-1} \gamma_{p_n} \phi_n (\dim_{ijkn}) + e_{ijkn}$$

Where:

y_{ijkn}: amount of each of the daily records of milk production.

cys_i: fixed effect of i the calving year-season.

CA_j: fixed effect of j the age at calving.

b_n: n the regression coefficient for record date.

TD_{ijn}: record date effect (with variable).

$\O_n$: n the Legendre polynomial of lactation.

dim_{ijkn}: days in milk (range -1 to 1).

β_n: n the constant regression coefficient.

α_{pn}: n the random regression coefficient of additive genetic of p the cow.

γ_{pn}: n the random regression coefficient of permanent environmental effect.

e: residual error.

Estimation of genetic parameters was conducted using restricted maximum likelihood with DXMRR DFREML software. Order of fit for genetic effect and permanent environment and the convergence criteria to stop repeating the sequence 3, 3 and 10^{-8} were considered. Basic information about the study population in table 1 has been studied.

RESULTS AND DISCUSSION

The effect of calving year - season and calving age on milk production trait in all months of lactation was significant ($P<0.05$).

Table 1 Pedigree details of the under study herd

Record number	11430
The number of base animals	803
Number of animals with record	1460
Sires	290
The average of inbreeding coefficient	1.60

The effect of calving age on milk production traits were not significant ($P>0.05$). The effect of record date and days in milk on milk production trait in months 2, 4, 5, 8 and 9 were significant ($P<0.05$). The increase of mean in the recent years was due to efficient breeding program and use of best qualify of sperm and sufficient nutrition (Table2).

Table 2 Descriptive statistic of milk production trait

Test day (TD)	Days of record	Sample number	Mean	SD of mean
TD1	5-30	1090	35.11	7.14
TD2	31-60	1210	39.82	6.35
TD3	61-90	1280	39.41	6.42
TD4	91-120	1240	37.26	6.23
TD5	121-150	1150	35.80	6.15
TD6	151-180	1120	34.72	6.31
TD7	181-210	1180	32.83	5.12
TD8	211-240	1050	30.49	5.03
TD9	241-270	1020	28.14	4.90
TD10	271-305	1090	27.20	5.14

TD_1 to TD_{10}: monthly test day of 1 to 10.
SD: standard deviation.

Animals that were calving in winter and fall had the maximum mean of milk production. Important factors that cause of reducing the milk production mean in the summer is the heat tension and subsequent reduced feed intake. The milk production mean of cows that were calving in old age was more than others. The mean, standard deviation and coefficient of variation for milk production trait are presented in Table 2. The milk production means were increased and reached their maximum in TD2 (39.82) and then decreases.

This change has also been reported by other researchers (Kettunen *et al.* 2000; Miglior *et al.* 2009). Heritability of daily milk production (Table 3) decreased during the first months of lactation and then increased (0.29). This trend of heritability changes is similar to those obtained by another researcher (Yarinezhad *et al.* 2008).

Table 3 Genetic parameters of daily milk records in different months of lactation

Month	Additive genetic variance	Permanent environmental variance	Phenotypic variance	Heritability	Repeatability
1	8.97	29.62	71.80	0.13	0.56
2	2.51	26.31	61.90	0.04	0.51
3	3.46	25.71	62.20	0.08	0.51
4	6.72	23.38	63.10	0.13	0.52
5	10.02	20.12	62.12	0.17	0.52
6	12.87	16.12	61.30	0.21	0.50
7	14.98	14.08	61.80	0.24	0.51
8	16.71	14.14	63.84	0.27	0.52
9	18.70	15.80	65.12	0.29	0.54
10	19.81	17.26	68.52	0.28	0.55

Table 4 Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) of daily milk records

Months	1	2	3	4	5	6	7	8	9	10
1	-	0.73	0.01	0.20	0.18	0.07	0.08	0.21	0.28	0.33
2	0.47	-	0.68	0.53	0.54	0.61	0.70	0.76	0.76	0.75
3	0.36	0.47	-	0.97	0.97	0.97	0.95	0.92	0.84	0.81
4	0.29	0.44	0.50	-	0.99	0.98	0.94	0.88	0.81	0.73
5	0.25	0.40	0.47	0.49	-	0.99	0.95	0.92	0.84	0.79
6	0.23	0.35	0.42	0.46	0.49	-	0.98	0.94	0.91	0.81
7	0.22	0.30	0.36	0.41	0.45	0.48	-	0.97	0.95	0.92
8	0.20	0.25	0.30	0.35	0.41	0.46	0.49	-	0.95	0.94
9	0.18	0.21	0.25	0.30	0.36	0.43	0.48	0.50	-	0.97
10	0.13	0.18	0.23	0.28	0.33	0.39	0.45	0.47	0.52	-

However the observed initial decrease in heritability is greater than of other reports but the increasing trend from the second month towards the end of lactation is similar to reports of others (Yarinezhad *et al*. 2008; Moqadaszadeh Ahrabi *et al*. 2005; Bignardi *et al*. 2011).

In a study with similar result, to estimate the genetic parameters for milk production in Yasuj Holstein cows using test day records, the heritability range was from 0.116 to 0.258 (Yarinezhad *et al*. 2008). In a study on Portugal dairy cows, heritability estimates ranged from 0.021 to 0.23 and the maximum value occurred in mid-Lactation (Silvestre *et al*. 2005). In another study on milk production in Holstein cows of North Carolina, the range of heritability was from 0.092 to 0.149 (Bignardi *et al*. 2011). The maximum of heritability estimation obtained by another researcher in months 8 of lactation (Moqadaszadeh Ahrabi *et al*. 2004). With a constant residual variance, the increase in heritability can be a result from an increase in genetic variance and reduction in permanent environmental variance (Table 3). The maximum of repeatability for daily milk production occurred in first month, then reached to minimum in 6th month. The maximum of repeatability was estimated in the first month, but the maximum of heritability was estimated in the 9^{th}. In the study for estimation of genetic parameters of daily milk production of Holstein cows in the Khorasan province, repeatability range estimated from 0.36 to 0.51, in which the minimum and maximum were found in first and fourth month, respectively (Farhangfar *et al*. 2008). The amount of additive genetic variance was high in first month and decreased in second month. Then, additive genetic variance increased with the progress of lactation and at the late of lactation reached to the maximum.

The minimum of additive genetic variance was observed in second month. The trend of additive genetic variance was similar to the heritability trend (Table 3). Residual variance was constant for all days in milk and estimated as 305. Trend of additive genetic variance is similar with reports of several researchers. In its papers, the minimum and maximum of additive genetic variance were estimated in early and end of lactation period, respectively (Yarinezhad *et al*. 2008; Farhangfar *et al*. 2008; Emam Jome kashan, 1997; Lasley, 1987).

Also, others estimated the maximum of additive genetic variance in tenth month (Bignardi *et al*. 2011; Silvestre *et al*. 2005; Olori *et al*. 1999). A number of researchers estimated the maximum of additive genetic variance for the sixth and seventh months (Kettunen *et al*. 2000; Miglior *et al*. 2009) which are not similar with the above studies. The maximum of permanent environmental variance was estimated for the first month. So, the minimum of that estimated for month 8. Other researchers estimated the minimum and the maximum of permanent environmental variance for first tenth month, respectively (Bignardi *et al.* 2011; Silvestre *et al.* 2005). The maximum and minimum of phenotypic variance estimated for the first 6th month, respectively. The researchers showed the maximum and minimum of phenotypic variance in the end and middle of lactation (Yarinezhad *et al.* 2008; Farhangfar *et al.* 2008). Other researchers reported the maximum of phenotypic variance in early of lactation and the minimum in middle of lactation (Kettunen *et al.* 2000; Moqadaszadeh Ahrabi *et al.* 2005; Bignardi *et al.* 2011). With the exception of the first month records and other months, the genetic correlation between all records was high. The estimation of genetic correlation between records in the middle and late of lactation was higher than others. The phenotypic correlation trend is similar with the genetic correlation trend. The minimum phenotypic correlation (0.13) was estimated between records in first and tenth month. The maximum phenotypic correlation (0.52) was estimated between records in ninth and tenth month (Table 4). The researchers estimated the similar correlations (Moqadaszadeh Ahrabi *et al.* 2004; Moqadaszadeh Ahrabi *et al.* 2005; Razmkabir *et al.* 2008; Sobhani *et al.* 2008; Farhangfar and Rezaei, 2007). Genetic and phenotypic correlations are presented in Table 4.

CONCLUSION

Random regression model has been become acceptable for milk trait genetic evaluation. It is widely applicable to model lactation curve using test day records. The model accounts all factors precisely. Currently research should be focused on defining the RRM to be implemented, investigating the environmental effects to be included in the model and estimating the covariance structure among observations and genetic parameters for milk trait to be included in the breeding program for dairy cattle. These are the requisite steps towards adoption of a RRM framework for analysis of dairy TD records. Potential to improve the accuracy of estimated breeding values, reduce the generation interval and the quest to provide management information to dairy farmers are stimulating interest in advancing the conceptual framework of the TDM.

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