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Random Regression Animal Model for Genetic Evaluation of Milking Duration in Holstein Friesian Cows

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ABSTRACT

The main objective of this study was to apply random regression animal model for analyzing the relationships between repeated measurements of milking duration (^{Mk}Dr) across different days in milk. The study analyzed data involving 103563 sample test-day records from multiparous Holstein-Friesian cows. A cubic random regression was applied to represent additive genetic variance in all studied traits across all different days in milk (112 groups). Estimates of heritability were very low during the first 60 days of lactation and did not exceed more than 0.04. During the 2nd half of lactation, the estimates ranged from 0.35-0.39. Results of genetic variations for lactation records during early production life showed that an intermediate milking rate could be achieved. Estimates of expected breeding values for milking duration increased in different rates with progressing days in milk groups. Additive genetic correlations between measures at different lactation months continuously decreased with an increase in interval between the test days. Correlations between expected breeding values ranged from 0.41-0.83 (mean = 0.69) across different lactation months. A detailed estimates of breeding values, estimates of permanent environmental and additive genetic correlations for milking duration were tabulated. Overall, application of random regression animal model proved a useful tool for genetic evaluation of milking duration in Holstein Friesian cows.

Key words: Heritability, random regression model, test day milking duration, milking time, correlation, lactation

INTRODUCTION

Milk production in dairy industries is encountered by a number of factors such as types of cows, animal health, environmental conditions, level of inputs, milking speed of animals, farm inputs namely and labour cost (Dodenhoff *et al.*, 1999; Antalik and Strapak, 2010). The other cost involving factors such as supply of power and milking equipments can also be handled by decreasing the milking time (Boettcher *et al.*, 1998). Considerable economic influence on the success of a dairy enterprise can be attributed to milking speed of dairy cows (Banos and Bunside, 1992). Therefore, dairy farmers would appreciate to lay more emphases on genetic selection against this characteristic. To avoid slow and long milking, cow should be milked gently, quickly and completely with minimal machine stripping or over-milking (Meyer, 1998). Furthermore, milk can also be produced on cost effective basis if the milking cows are classified into different categories on the

basis of total milk production per milking cow. This can be achieved by maintaining daily records of each cow during lactation period (Matthew 2001; Banos and Bunside, 1992; Erf *et al.*, 1992). The objectives of this study were to estimate (co)variance components of the first three lactations data with random regression models and to characterize some genetic aspects of test-day milking duration across lactation in Hungarian Holstein-Friesian cows.

MATERIALS AND METHODS

Data consisted of 103563 Test Day Records (TDR) on milking duration (^{Mk}Dr). The current data set involved the 1st, 2nd and >3rd lactation of Hungarian Holstein Friesian cows provided by Hungarian Holstein Association. All studied traits were recorded on each test day between 5 and 365 days in milk (DIM). Cows must have at least two lactations, while the average was 3.7 lactations with 7.16 test-day records. Data were recorded on cows calving between 1996 and 2000. Number of test day record per lactation was not less than five observations. Days in milk (DIM) were classified into 12 monthly groups with 30 days interval. Structure of the current data is given in Table 1.

Statistical analysis: The random regression model used in this study was:

$$Y_{ijklm} = \text{HTD}_{il} + \sum_{n=1}^{np} \beta_{in} \chi_{k_{lmo}} + \sum_{n=1}^{np} \alpha_{klo} \chi_{k_{lmo}} + \sum_{n=1}^{np} \phi_{klo} \chi_{klmo} + \epsilon_{ijklm}$$

where, Y_{ijkl} is the m th (test-day observation) of the k th cow in the l th lactation, HTD_{il} is the independent fixed effect of j th herd-test date for the l th lactation, n_p is the number of parameters fitted on days in milk function, β_j is the o th fixed regression coefficient on j th days in milk effect within l th lactation, χ_{klm} is the o th dependent trait on days in milk, α_k is the o th random regression coefficient of additive genetic effect of the k th cow in the l th lactation on days in milk, ϕ_k is the o th random regression coefficient of permanent environmental effect of the k th cow in the l th lactation on days in milk, ϵ_{ijkl} is the random residual. Variance-covariance parameters for each of the current longitudinal traits (test-day milk yield and body condition score) were estimated using the software random regression package, DFREML (Meyer, 1998).

RESULTS AND DISCUSSION

Multi-lactation heritability estimates using random regression model: Estimates of heritability for milking duration (h^2_{DR}) (Table 2) were very low during early lactation months (from 0.01 to 0.11) and were intermediate across the 2nd half of lactation (from 0.35 to 0.39). Heritability estimate for milking duration (^{Mk}Dr) was low during the first half of lactation while it increased during the beginning of the 2nd half of lactation. Similar findings were reported by Zwald *et al.*

Table 1: Data Structure for Different Variables Recorded during Study

Parameter	Parity-1 (Pr ¹)	Parity-2 (Pr ²)	Parity-3 (Pr ³)	Parity-4 (Pr ⁴)	Parity-5 (Pr ⁵)
No of cows (COWS)	4173	3012	2660	2017	1843
Test day record (TDR)	39226	24397	19152	13047	7741
Sires (No of males)	453	316	196	174	153
Dams (No of mothers)	3967	2784	2163	1754	1843

Table 2: Heritabilities (h^2), permanent-environmental effect (P_E), additive (σ^2_A) and phenotypic (σ^2_P) variances across days in milk groups (DIM)

^{MK}Dr	Days in milk groups											
	1	2	3	4	5	6	7	8	9	10	11	12
h^2	0.01	0.04	0.11	0.20	0.29	0.35	0.38	0.39	0.39	0.38	0.37	0.36
P_E	0.73	0.64	0.52	0.42	0.36	0.35	0.38	0.42	0.46	0.50	0.53	0.56
σ^2_A	0.02	0.1	0.2	0.3	0.5	0.7	1.0	1.3	1.6	2.0	2.4	2.9
σ^2_P	2.3	2.0	1.7	1.6	1.7	2.1	2.6	3.3	4.1	5.2	6.5	7.9

$P_E = \frac{\sigma^2_c}{\sigma^2_P}$, σ^2_c : is the permanent environmental variance, ^{MK}Dr means milking duration of a cow

Table 3: Heritability (h^2) estimates and permanent environmental effect (p_E) within the 1st, 2nd and >3rd parity

Days in Milk (DIM)	Milking duration					
	Pr^1		Pr^2		$>Pr^3$	
	h^2	P_E	h^2	P_E	h^2	P_E
1	0.21	0.42	0.17	0.17	0.03	0.51
2	0.18	0.45	0.05	0.17	0.04	0.34
3	0.13	0.53	0.03	0.38	0.08	0.28
4	0.09	0.61	0.06	0.50	0.11	0.31
5	0.06	0.68	0.07	0.56	0.11	0.35
6	0.03	0.74	0.08	0.59	0.11	0.39
7	0.01	0.78	0.09	0.59	0.12	0.42
8	0.00	0.80	0.12	0.56	0.14	0.44
9	0.02	0.78	0.17	0.51	0.15	0.50
10	0.06	0.70	0.22	0.46	0.14	0.58
11	0.13	0.59	0.25	0.44	0.14	0.64
12	0.20	0.48	0.27	0.43	0.14	0.67

DIM: Days in milking; Pr^1 : Parity-1; Pr^2 : Parity-2; Pr^3 : Parity-3

(2005) who found that low heritability estimates for milking time may be due to the wideness of the interval between positive and negative predicted transmitting ability or breeding values that is associated with increasing estimates of permanent environmental effect. Moore *et al.* (1983) found that estimated heritability of the "2-min milk" was 0.23 which was significantly higher than the corresponding estimate of 0.13 for milking duration.

Estimates of permanent environmental effect (P_{EDR}) effect (as the ratio between permanent environmental variance and phenotypic variance) for milking duration were high ranging from 0.52-0.73 and 0.50-0.56 during the first and the last three months of lactation, respectively. On the other hand, P_{EDR} decreased greatly at the middle of lactation reaching to 0.35 during the 6th month of lactation. It appears that the environmental conditions contributed appreciably in variations of milking duration among different months of lactation.

Estimate of random regression heritabilities and permanent environmental effects for milking duration within parities across DIM groups are presented in Table 3. Results of heritability estimates of milking duration (h^2_{DR}) within different lactations were mostly near to zero while the corresponding estimates of P_{EDR} were high. Some high values for h^2_{DR} were obtained slightly during

edges of the 1st lactation (from 0.13-0.21 and 0.13-0.20) and during the 2nd half of the 2nd lactation (0.12-0.27). Previous studies showed that milking duration may have an intermediate optimum, because most producers prefer cows with relatively uniform milking duration that do not decrease the flow of cows through the milking parlor. However, selection for extremely short milking duration may be undesirable, because an antagonistic relationship may exist with general udder health (Zhang *et al.*, 1994).

Estimates of P_{EDR} were relatively high reaching 0.80, 0.59 and 0.67 within the 1st, 2nd and the later parity, respectively. These results refer to the impact of some environmental conditions which may affect the extent of genetic improvement of this trait across and within all lactations.

Meyer and Burnside (1987) concluded that several environmental factors affecting the milk ability characteristics of individual cows may vary during lactation or between subsequent lactations. Zavadilova *et al.* (2005) found that variances in milking time of the small permanent environmental effect went up substantially between the first and subsequent lactations, with the differences between the 2nd and the 3rd lactations.

Correlations between repeated measures of milking duration across different days in milk: Estimates of additive genetic (R_A) and permanent environment correlations (R_{Pe}) between measures of milking duration in different months of lactation are illustrated in Fig. 1. Estimates of additive genetic correlations between repeated measures of milking duration decreased in magnitude with increasing interval between measurements. Additive genetic correlations between early and late measures of $MkDr$ were low and directly changed to negative direction. Therefore, $MkDr$ in early and late stages of lactation could be considered as different traits.

Multi-lactations expected breeding values using random regression analysis: Estimates of expected breeding value for milking duration ranged from 0.15 to 0.81 and -0.10 to -0.67 across 360 days in milk. Estimates of breeding values ($^+E_{BV}$) increased rapidly within the 2nd half of lactation (Table 4). Similar findings were reported by Zwald *et al.* (2005) who found that the

Table 4: Estimates expected breeding value (E_{BV}) that generated from random regression analysis for milk duration using pooled lactation data set

	Days in milk											
	30	60	90	120	150	180	210	240	270	300	330	360
$^+E_{BV}$	0.15	0.15	0.27	0.35	0.37	0.42	0.45	0.57	0.68	0.68	0.72	0.81
$^-E_{BV}$	-0.10	-0.10	-0.21	-0.21	-0.32	-0.33	-0.41	-0.44	-0.51	-0.51	-0.66	-0.67

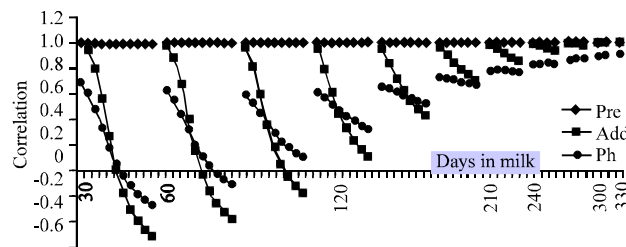


Fig. 1: Relationship (Pre: permanent environmental, Add: additive, Ph: phenotypic correlations) between repeated measures of milking duration across different days in milk

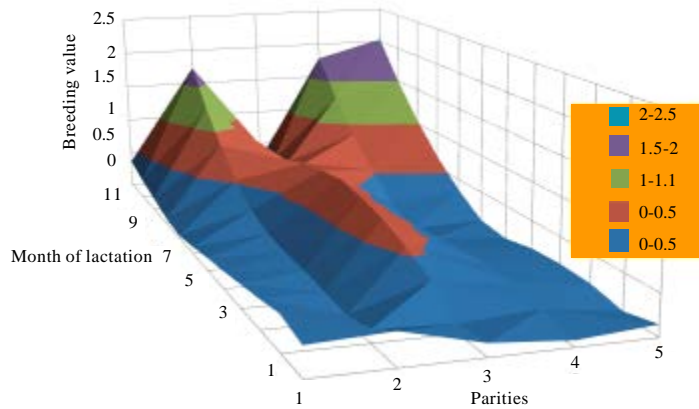


Fig. 2: Random regression positive expected breeding values (BV) across months of lactation within different parities

estimated heritability of milking duration was 0.17 and predicted transmitting abilities of individual sires ranged from -0.48 min for sires with the short time milking daughters to 0.59 min for sires with the long time milking daughters.

Changes of ($-E_{EV}$) were slightly lower than the corresponding positive estimates during the 2nd half of lactation. These results indicate to mass selection especially during the late of lactations could reduce the goal of milk production genetic improvement. These results indicate that the best individual selection results will be achieved during the late part of lactation. In general, results of expected breeding values indicate that high estimate of heritability is not a measure of genetic improvement rate. However, the positive or negative breeding values in the herd could increase estimates of heritability. Therefore, breeding strategies must be practiced based on the individual breeding value.

The floor (blue) area in Fig. 2 shows the widest area for $+E_{EV}$. These estimates were obtained within the first 5 lactations and ranged from 0.0-0.5. The second category of $+E_{EV}$ ranging from 0.5-1.0 were mainly distributed with the 3rd lactation across most of lactation curve. High breeding value for milking duration >1.0 was mainly obtained within early and late of productive life during end of lactation. Therefore successful breeding strategies for improving milking duration could be possible during the late part of productive life within the late area of lactational curve. While, the results of random regression on Breeding Values (BV) shows development of additive genetic effect on milk duration (^{Mk}Dr) during the end of lactations. On the other hand, the analysis of heritability results from different studied models showed weakness in the inheritance of ^{Mk}Dr .

CONCLUSION

Estimates of h^2_{DR} were very low during early lactation months (from 0.01-0.11) and were intermediate across the 2nd half of lactation (from 0.35-0.39). Heritability estimate for milking duration was low during the first half of lactation while it increased during the beginning of the 2nd half of lactation. Estimates of expected breeding values for milking duration increased in different rates with progressing days in milk groups. Additive genetic correlations between measures at different lactation months continuously decreased with an increase in interval between the test days. Correlations between expected breeding values ranged from 0.41-0.83 (mean = 0.69)

across different lactation months. Overall, application of random regression animal model proved a useful tool for genetic evaluation of milking duration in Holstein Friesian cows.

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