

Genetic Parameters of Milk Yield and Milk Fat Percentage Test Day Records of Iranian Holstein Cows

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ABSTRACT : Genetic parameters for first lactation milk production based on test day (TD) records of 56319 Iranian Holstein cows from 655 herds that first calved between 1991 and 2001 were estimated with restricted maximum likelihood method under an Animal model. Traits analyzed were milk yield and milk fat percentage. Heritability for TD records were highest in second half of the lactation, ranging from 0.11 to 0.19 for milk yield and 0.038 to 0.094 for milk fat percentage respectively. Estimates for lactation records for these traits were 0.24 and 0.26 respectively. Genetic correlations between individual TD records were high for consecutive TD records (>0.9) and decreased as the interval between tests increased. Estimates of genetic correlations of TD yield with corresponding lactation yield were highest (0.78 to 0.86) for mid-lactation (TD3 to TD8). Phenotypic correlations were lower than corresponding genetic correlations, but both followed the same pattern. For milk fat percentage no clear pattern was found. Results of this study suggested that TD yields especially in mid-lactation may be used for genetic evaluation instead of 305-day yield. (*Asian-Aust. J. Anim. Sci.* 2005. Vol 18, No. 9 : 1231-1236)

Key Words : Genetic Parameters, TD Records, Animal Model, Iranian Holstein

INTRODUCTION

The genetic evaluation of dairy sire and cows for production traits has been based on the analysis of 305-day lactation yield. A completed 305-day lactation yield is based on 7 to 10 test day (TD) yields are usually taken approximately at monthly intervals. TD yields are affected by factors such as breed, herd management and management group within a herd, regions of country, days of the calving year, age at calving and test, pregnancy status, days in milk and milking times per day (Swalve, 1995a; Jamrozik and Schaeffer, 1997). The effects of environmental factors on each TD yield have been averaged together for the lactation yield. Averaging would be appropriate if the factors were the same for each TD and represented random environmental variation, but many of these factors for a cow vary from one TD to the next and it would be difficult to model for 305-day yields (Swalve, 1995b; Jamrozik et al., 1997).

Advantages of utilization of TD yields for genetic evaluation are more accurate estimation of environmental effects, more accurate definition of contemporary groups, reduced recording costs (due to possibility of using of reduced recording systems) reduced generation interval, more flexibility, no need for extension part lactation records, no need for normal length of lactation period and improved accuracy of evaluation for production traits (Swalve, 1998; Van der Werf et al., 1998; Strabel and Misztal, 1999).

The use of TD records depends on the heritability and genetic correlations with 305-day throughout a lactation.

Many authors have estimated genetic parameters for TD yields. Based on result of these researches, heritability estimates were highest for mid-lactation and genetic correlations between TD records from mid-lactation and 305-day were high (Auran, 1976; Kettunen and Mantysaari, 1996; Machado et al., 1998).

The main purpose of present study was to estimate the genetic and phenotypic parameters for TD records of Iranian Holstein cows under a TD model. The effect of model on the genetic parameters was examined. The possibility of using TD records for cow evaluation instead of 305-day lactation records was also investigated.

MATERIALS AND METHODS

Data consisted of TD and 305-day milk yield and milk fat percentage records of Iranian Holstein cows that calved at first between 1991 and 2001 and were obtained by Animal breeding center of Iran. There were 4.1 million TD records. Recording was approximately monthly but intervals varied somewhat. The first ten tests were used for this analysis. Data restricted to first lactation and only from complete lactation (cows with 305-day yield record in original files) were considered. The TD information was stored in data files that included cow identification number, calving date, days in milk (DIM), proportion of Holstein blood in the animal, milk yield and milk fat percentage. Edits were based on lack of identification number, lack of birth, calving or test date. Data were included only those animals which their first test was taken between 4 and 45 days after calving and interval between their consecutive tests were between 20 and 45 days. If the TD record did not fulfil this requirements, the test record in question and all

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Table 1. Structure of final data set

Variable	Average	Min.	Max.
Number of lactation per herd	85.98	4	4,764
Number of sire per herd	21.14	2	256
Number of TD records per herd	668	25	39,720
Lactation length (day)	200	309	400
Age at first calving (mo)	18	26.37	36
Proportion of Holstein blood (%)	70	87	100

tests of the cow later in lactation were excluded. Age of calving was restricted to 18 to 36 months and length of lactation was in the range of 200 to 400 days. The TD yields were limited to range of 2 to 50 kg for milk yield and 1.5 to 8.5% for fat content. After edits, 418480 TD records on milk yield and 368,061 records on milk fat percentage on 56,319 cows in 655 herds and daughters of 601 sires were extracted. In pedigree file, the total number of animals evaluated was 92,991 and no phantom parent groups were formed for unknown parents in this study. On average, sires had 95.6 and dams 2.2 daughters in the data. Proportion of Holstein blood in cows varied from 70 to 100 percent with average value of 87 percent. Summary of the data is given in Table 1, 2 and 3.

Heritability for single TD and 305-day yield estimated under univariate model. The following model was used for TD records:

$$y_{ijkl} = \text{HYST}_i + M_j + a_k + \sum_{n=1}^2 b_n \text{DIM}_{ijkl}^n + \sum_{n=1}^2 b_{(n+2)} \text{AGE}_{ijkl}^n + b_5 \text{HF}_{ijkl} + e_{ijkl}$$

where,

y_{ijkl} = TD record on milk yield or milk fat percentage,

HYST_i = fixed effect of herd-year-season of test. Season was defined as spring, summer, autumn and winter,

M_j = fixed effect of milking times ($j = 1, 2$),

DIM = fixed covariate of days in milk at test,

Age = fixed covariate of age of calving,

HF = fixed covariate of proportion of Holstein blood in the animal,

Table 3. Structure of pedigree file

Number of individuals with record	56,319
Number of individuals in pedigree	92,991
Number of sires	601
Minimum number of sire per herd	2
Maximum number of sire per herd	256
Average number of sire per herd	21.14
Minimum number of progeny per sire	2
Maximum number of progeny per sire	1,736
Average number of progeny per sire	95.60
Number of sires which were also garandsire	98
Number of dams	45,289
Number of dams with records	9,218
Number of dams which were also garanddam	31
Average number of progeny per dam	2.20

a = animal's random additive genetic effect, and

e = random residual effect.

The model for the analysis of 305-day yield was:

$$y_{ijk} = \text{HYS}_i + a_j + \sum_{n=1}^2 b_n \text{AGE}_{ijk}^n + b_3 \text{HF}_{ijk} + e_{ijk}$$

where HYS was fixed effect of herd-year-season of calving and covariates were similar to single TD model. Variance components were estimated with restricted maximum likelihood (REML) method using REML 3.1 software (Meyer et al., 1989). Animal model were applied throughout the analysis.

For estimation of genetic and phenotypic covariance between TD records and between individual TD and 305-day records, a multiple trait model was used. To enable the computation to be made with a multiple trait model data were reduced. Thus only cows with the first 10 TD records had remained and cows with lower than 10 tests were excluded from data file. Reduced data file consisted of 196,050 and 164,190 TD records for milk yield and milk fat

Table 2. Number of subclasses, average and maximum number of records per subclass for TD, 305-days milk yield and fat percentage records

Trait	Fixed effect	Number of subclass		Average number of records per subclass		Maximum number of records per subclass	
		Milk yield	Fat %	Milk yield	Fat %	Milk yield	Fat %
TD1	HYST*	4,652	4,541	11.65	11.34	270	262
TD2	HYST	4,506	4,404	11.42	11.02	240	203
TD3	HYST	4,344	4,251	11.37	10.93	240	211
TD4	HYST	4,198	4,111	11.22	10.83	256	248
TD5	HYST	4,013	3,926	11.16	10.83	240	229
TD6	HYST	3,874	3,802	11.04	10.75	237	227
TD7	HYST	3,695	3,621	11.01	10.77	256	248
TD8	HYST	3,427	3,360	10.82	10.60	235	233
TD9	HYST	3,001	2,946	10.35	10.15	238	224
TD10	HYST	2,305	2,250	8.69	8.54	175	174
Lactation	HYS**	4,640	4,610	11.66	11.62	253	253

* Herd-year-season of test. ** Herd-year-season of calving.

Table 4. Phenotypic mean, standard deviation and coefficient of variation of traits, days in milk and test interval

Trait*	TD1	TD2	TD3	TD4	TD5	TD6	TD7	TD8	TD9	TD10	305-day
DIM											
Mean	19.75	50.19	80.56	111.11	141.55	171.99	202.30	232.57	262.27	291.81	
SD	9.60	9.85	10.01	10.20	10.22	10.42	10.46	10.41	10.22	10.18	
TI											
Mean	19.75	30.45	30.48	30.51	30.47	30.49	30.46	30.47	30.45	30.36	
SD	9.60	2.57	2.59	2.57	2.56	2.51	2.51	2.49	2.47	2.43	
MILK											
Mean	24.26	27.14	26.83	25.99	25.10	24.08	23.10	21.98	20.73	19.65	7,082.37
SD	6.21	6.50	6.62	6.65	6.63	6.58	6.54	6.36	6.24	6.13	1,292.76
CV%	25.60	23.95	24.67	25.59	26.41	27.33	28.31	28.94	30.10	31.20	18.25
Fat %											
Mean	3.34	2.94	2.90	2.93	2.99	3.06	3.14	3.22	3.32	3.39	3.04
SD	0.93	0.77	0.75	0.76	0.77	0.79	0.81	0.82	0.84	0.86	0.52
CV%	27.84	26.19	25.86	25.94	25.75	25.82	25.80	25.47	25.30	25.37	17.11

* DIM = days in milk, TI = test interval, MILK = milk yield, Fat % = milk fat percentage.

Table 5. Estimated additive genetic variance, environmental variance and heritability and its standard error of TD and 305-day milk yield and milk fat percentage

	TD1	TD2	TD3	TD4	TD5	TD6	TD7	TD8	TD9	TD10	305-day
Milk yield											
V_A	2.71	3.09	3.50	4.10	4.38	4.69	4.45	4.86	4.55	4.31	324,206.76
V_E	22.54	23.43	22.28	21.53	21.36	21.16	21.32	20.12	20.08	20.10	1,022,788.82
h^2	0.11	0.12	0.13	0.16	0.17	0.18	0.17	0.19	0.19	0.17	0.24
SE (h^2)	0.01	0.01	0.01	0.01	0.02	0.02	0.02	0.02	0.02	0.02	0.02
Fat percentage											
V_A	0.023	0.020	0.023	0.029	0.039	0.042	0.046	0.045	0.049	0.050	0.038
V_E	0.570	0.420	0.400	0.410	0.410	0.424	0.447	0.453	0.476	0.507	0.108
h^2	0.038	0.044	0.054	0.066	0.087	0.090	0.090	0.090	0.094	0.089	0.260
SE (h^2)	0.006	0.006	0.007	0.008	0.010	0.011	0.012	0.012	0.013	0.016	0.020

percentage respectively. To simplify the computation, 2-traits models were used.

RESULTS

Overall phenotypic means, standard deviation and coefficient of variation for TD and complete lactation records are presented in Table 4. On average first test was taken 20 days after calving with subsequent test taken at average intervals of approximately 30 days. The peak milk yield occurred at TD2 and subsequently, yield decreased as lactation progressed. The coefficient of variation (CV%) of milk yield increased as lactation progressed. The milk fat percentage was greater at the beginning of lactation but decreased and became lowest at TD3 and subsequently was increased steadily. The CV% of fat percent in TD1 was higher than other TDs. It is probably related to very early tests, when the milk composition is still not typical.

Additive genetic and residual variance components and heritability estimates for TD and complete lactation records of milk yield and milk fat percentage are presented in Table 5. Additive genetic variance was increased as lactation progressed for milk yield and was highest in mid-lactation (i.e. TD6-TD8) and subsequently decreased at the end of lactation. Residual variance was decreased steadily and was

lowest at the end of lactation. For milk fat percentage additive genetic variance decreased from TD1 to TD2 and subsequently increased steadily during lactation period. Residual variance for milk fat percentage was low at the beginning of lactation and increased as lactation progressed. Heritability estimates for TD records were highest in second half of lactation and ranged from 0.11 to 0.19 for milk yield and 0.038 to 0.094 for milk fat percentage. The highest and the most stable heritability estimates from one TD to next appeared in the interval 6th-10th TD. Heritability estimates for 305-day were 0.24 and 0.26 for milk yield and milk fat percentage respectively. In all cases the heritability for TD records was lower than the corresponding complete lactation. For both traits the heritability estimates have slightly declined from TD9 to TD10. In general, for milk fat percentage the heritability estimates of TD records were lower than for milk yield. However 305-day heritability estimate was slightly higher for fat percentage than for milk yield.

Genetic and phenotypic correlations between TD records and between TD and 305-day records are presented in Table 6 and 7. The genetic correlations between individual TD records varied from 0.46 to 0.99. Genetic correlations between individual TD records were high (>0.9 and on average 0.95) and decreased as the distance between

Table 6. Genetic (above diagonal) and phenotypic (below diagonal) correlations between TD and 305-day milk yield

	TD1	TD2	TD3	TD4	TD5	TD6	TD7	TD8	TD9	TD10	305-days
TD1		0.90	0.83	0.70	0.69	0.69	0.69	0.60	0.59	0.46	0.60
TD2	0.52		0.95	0.87	0.84	0.82	0.80	0.82	0.72	0.61	0.62
TD3	0.44	0.61		0.98	0.97	0.97	0.88	0.92	0.90	0.81	0.83
TD4	0.40	0.54	0.63		0.99	0.97	0.96	0.93	0.88	0.77	0.78
TD5	0.35	0.50	0.59	0.67		0.99	0.99	0.95	0.95	0.83	0.78
TD6	0.35	0.47	0.55	0.62	0.69		0.99	0.97	0.96	0.84	0.77
TD7	0.34	0.45	0.54	0.58	0.64	0.71		0.99	0.99	0.92	0.86
TD8	0.33	0.47	0.51	0.54	0.60	0.66	0.73		0.99	0.93	0.83
TD9	0.32	0.40	0.47	0.51	0.56	0.61	0.67	0.73		0.98	0.37
TD10	0.25	0.35	0.42	0.45	0.50	0.54	0.58	0.65	0.72		0.35
305-days	0.59	0.54	0.61	0.77	0.79	0.79	0.74	0.73	0.59	0.42	

Table 7. Genetic (above diagonal) and phenotypic (below diagonal) correlations between TD and 305-day milk fat percentage

	TD1	TD2	TD3	TD4	TD5	TD6	TD7	TD8	TD9	TD10	305-days
TD1		0.75	0.47	0.68	0.54	0.83	0.59	0.39	0.77	0.68	0.68
TD2	0.09		0.78	0.88	0.90	0.88	0.85	0.85	0.87	0.81	0.74
TD3	0.09	0.16		0.92	0.99	0.97	-0.58	-0.76	0.98	0.94	0.83
TD4	0.08	0.15	0.21		-0.51	0.96	0.93	0.75	0.94	0.88	0.96
TD5	0.08	0.14	0.19	0.18		0.99	0.96	0.93	0.97	0.95	0.97
TD6	0.07	0.15	0.18	0.22	0.28		0.99	0.98	0.99	0.99	0.99
TD7	0.07	0.16	0.11	0.21	0.24	0.28		0.54	0.99	0.92	0.98
TD8	0.06	0.14	0.08	0.22	0.21	0.25	0.28		0.96	0.89	0.94
TD9	0.08	0.14	0.16	0.21	0.21	0.24	0.25	0.29		0.99	0.85
TD10	0.08	0.13	0.16	0.21	0.22	0.23	0.25	0.27	0.23		0.56
305-days	0.35	0.38	0.49	0.53	0.55	0.55	0.47	0.24	0.55	0.46	

tests increased but always were positive. As lactation progressed genetic correlations between tests were increased but for the last month this correlation dropped. The genetic correlations between TD and 305-day records for both traits were high at mid-lactation (for TD3 to TD7). The first two and the last two TD yields had lower correlations with complete lactation yield. Genetic correlations between individual TD records and 305-day record were always more than 0.6. Phenotypic correlations followed a similar pattern but were lower than the corresponding genetic correlations.

For milk fat percentage no clear pattern was found. Genetic correlations between individual TD records ranged from -0.76 to 0.99. Genetic correlations between TD lactation records at mid-lactation records were high but smaller than 1.

DISCUSSION

In this study heritability estimates increased as lactation progressed and were highest in second half of lactation. This pattern is in agreement with some reported results (Danell, 1982; Ptak and Scaeffler, 1993; Baffour-Awuah et al., 1996). Choi et al. (2003) studied the trend in heritability of daily milk yield by period in Korean cattle and observed dramatic increase in the heritability by periods. Heritability estimates in mid-lactation were high and were in agreement with other studies. Generally in this study heritability

estimates were lower than previous estimates on Iranian Holstein cows (Moradi Shahre Babak, 2001; Farhangfar et al., 2001). There are several factors that might influence level of heritability estimates. Among the many reasons which cause the differences in heritability estimates are different models and different ways for computing 305-day yield and different yield are defined. In earlier works on Iranian Holstein, random regression models were used for estimation of genetic parameters (Moradi Shahre Babak, 2001). Usually in random regression models heritability is higher than ordinary TD models (Jamrozik and Schaeffer, 1997). By using two different random regression sub-models which described individual lactation curves Kettunen et al. (1998) showed that both random regression models gave higher estimates of heritability than that of multiple trait models.

In this study herd-year-season of test (HYST) was used as a contemporary group. Some published reports on genetic parameters were based on herd-test date (HTD). Comparing results from present study and the others indicated that fitting HTD effect resulted in lower residual variance and higher heritability than models with effect of HYS of test (Pander and Hill, 1993; Swalve, 1995b; Jamrozik and Schaeffer, 1997).

In this study cows with complete lactation records are selected for estimation of variance components. Hence, estimates of genetic parameters are expected to be biased downward, caused by culling of cows during the course of

lactation. Auran (1976) compared heritability estimates for sample of cows having at least 3, 6 or 8 tests and reported a decline in estimates for a given test as the minimum number of records for each cow increased. The main tendency was that the heritability estimate decreased with increasing selection intensity. Danell (1982) evaluated the expected bias for a culling rate of 5% for low production and found about 30% decrease in heritability estimate. Wilmlink (1988) studied genetic parameters for cumulative production at different part lactations both including and excluding incomplete lactations and showed that where incomplete lactation was included in the analysis, due to the removal of selection bias, heritability estimates increased by up to 36%. Meyer et al. (1989) suggested that culling bias would not have been important up to about days 210-240 of lactation.

Another possible reason is that the presence of non-additive effects in the present model. In the current study, the proportion of Holstein blood of the sire was included as a co variable. It ranged from 70% to 100% and averaged at 87%. In this study the effect of proportion of Holstein blood on milk yield was estimated as 6.4 kg/%. Its average effect on fat percent was estimated as 0.022. It seems accounting for this effect may bias the heritability downward, (Van der Werf and De Boer, 1989) although some studies such as Baffour-Awuah et al. (1996) resulted in different views.

Heritability estimates for milk yield were higher than milk fat percentage. Estimates for fat and protein traits when TD records are used are lower than milk yield (Swalve, 1995b). Heritability estimates of TD were lower than of 305-day yield. This result was in agreement with most studies (Kettunen and Mantysaari, 1996; Kettunen et al., 1998). Heritability estimate for 305-day milk yield was 0.24. It was very close to most of estimates reported in other works (e.g. Swalve, 1995b; Moradi Shahre Babak, 2001; Lee and Han, 2004).

Genetic correlations between consecutive TD records were high and decreased as distance between them increased. All correlation values were positive for milk yield. Genetic correlations between TD records in mid-lactations and 305-day yield were lower than corresponding genetic correlations but both have the same pattern. The correlation estimates and their pattern of change reported here were similar to those found in other studies (Auran, 1976; Danell, 1982; Meyer et al., 1989; Baffour-Awuah et al., 1996).

As a final conclusion, due to lower additive genetic variance and higher residual variance, the heritability at the beginning of lactation (TD1 and TD2) were lower than other records. The first TD yield often sampled only a few days after calving and is less reliable measurement than other later TD yields. First TD affected by many environmental factors such as feeding before calving. This was indicated by larger variance at the beginning of the

lactation. Prediction of lactation yield from TD records is a function of their heritability and genetic correlations with complete lactation yield. Therefore it may not be sufficiently accurate to predict the complete lactation from earlier tests (TD1, TD2) due to low heritability and genetic correlations that are less than 0.7. The high estimated heritability of TD yields and their genetic correlations with 305-day yields during mid-lactation indicated that TD records especially in mid-lactation may be used for genetic evaluation instead of 305-day yield.

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