

Estimation of Genetic and Phenotypic Parameters for Productive Life, Milk Yield and Constituents and Milk and Fat Persistency in Holstein Dairy Cows

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ABSTRACT

Genetic and phenotypic parameters were estimated for first parity Holstein cows with records from April 1991 to May 2006 for 305-d milk (Milk305), fat (Fat305), and protein (Pro305) yields, fat (Fat%) and protein (Pro%) percentage, productive life (PL), natural logarithm of somatic cell score (LSCS), lactation length (LL) and milk (Milk3:1), and fat (Fat3:1) persistency. The (co)variance components and genetic parameters were estimated using restricted maximum likelihood (REML) method. Among production traits, the highest heritability (0.26) was for Fat% and the lowest one (0.048) was for Fat3:1 persistency. Heritability estimate for PL was low (0.035). Genetic correlations of PL with production traits were relatively high and positive (except for Fat% and Pro%). PL had the highest genetic correlation with Fat3:1 and Milk3:1 persistency (0.56 and 0.45, respectively). In general, phenotypic correlations between traits were lower than genetic correlations. Milk3:1 and Fat3:1 persistency had favorable genetic correlation with LSCS (-0.34 and -0.36, respectively). It can be suggested to include a combination of production and persistency traits in selection index in order to increase PL and improve udder health.

Keywords: productive life, somatic cell score, persistency, restricted maximum likelihood.

INTRODUCTION

Estimates of genetic parameters for traits of economic importance in dairy cattle are necessary for implementing efficient breeding programs. Accurate heritability and correlation estimates are required to predict expected selection response and to obtain predicted breeding values using mixed model Best Linear Unbiased Prediction (BLUP) procedures. Traits related to milk, fat, and protein production, conformation, length of productive life,

reproduction, workability and health are included in breeding programs of dairy cattle in many countries (Mark, 2004; VanRaden, 2004) to maximize improvement of a breeding goal involving traits related to income and costs (Dekkers and Gibson, 1998).

The productive life (PL) of a cow refers to the length of time between first calving and culling from the herd (VanRaden and Klaaskate, 1993). No adjustment is made for level of milk production, so PL, which is also commonly referred to as true herd life, reflects both voluntary and involuntary culling. Genetic selection for increased PL is expected to result in improved general health, production, and reproduction, which can increase dairy farm profitability by decreasing the number of replacement heifers needed, by allowing rearing costs to be dispersed over a longer period, and by increasing the

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number of cows producing at a mature level (Rogers et al., 1988; Allaire and Gibson, 1992). Many countries include some measures of longevity in their national breeding objectives (VanRaden, 2002). Because culling decisions are not made until several months or years into a cow's life, early predictions of PL are necessary to obtain an evaluation on young bulls and cows. Genetic evaluation of PL in Holsteins is obtained by combining direct predicted transmitting ability (PTA) for PL along with an indirect prediction of PTA for PL from correlated traits (Weigel et al., 1998). Weigel et al., (1998) calculated genetic correlations of PL with type and production traits for bulls born up to 1983. Their estimates of genetic correlation between PL and milk, fat and udder traits ranged from 0.22 to 0.46. Tsuruta et al., (2004) calculated genetic correlations using data on younger animals and a model where genetic correlations were assumed as functions of year of birth.

Also, persistency has been shown to be an economically important trait in dairy cattle (Solkner and Fuchs, 1987). At the same total yield, cows with lower peak yield and greater persistency may experience less energy imbalance and thus less reproductive and health problems than cows with higher peak yield (Solkner and Fuchs, 1987).

Despite remarkable changes in selection indices in different countries in the last fifteen years (VanRaden, 2002; Miglior et al., 2005) the main emphasis in selecting bulls and cows in Iran is focused on estimated breeding value of milk yield. To our knowledge, estimation of the genetic correlations between PL and production traits (especially with persistency measures) and LSCS has rarely been investigated in Iran until now. Therefore, The objectives of this study were to estimate

heritabilities as well as genetic and phenotypic relationships between 305-d milk (Milk305), fat (Fat305) and protein (Pro305) yield, fat (Fat%) and protein (Pro%) percentage, productive life (PL), natural logarithm of somatic cell score (LSCS), lactation length (LL) and milk (Milk3:1) and fat (Fat3:1) persistency in Holstein cows of Iran.

MATERIALS AND METHODS

Dataset

Records of Milk305, Fat305 and Pro305 yield, Fat% and Pro%, LSCS and calving events of Holstein cows were obtained from the Animal Breeding Center of Iran. Data were restricted to cows that calved for the first time between 19 and 40 months of age. Also, lactation lengths lower than 180 or more than 600 days were excluded from the data set. To achieve an approximate normal distribution of test-day records, these were \log_e -transformed to somatic cell score ($SCS = \log_e(SCC/1000 \text{ cells/ml})$) as SCC has a lognormal distribution (Schukken et al., 1992). Finally, lactation mean of SCS (LSCS) was calculated as the arithmetic mean of all observations per cow. The latter variable was used for the estimation of variance components. Records of cows with unknown parents or cows with registration number smaller than their parent's number were also discarded. The final dataset consisted of records of 27,019 cows with first calving from April 1991 to May 2006 in 86 herds. The average number of daughters per sire was 19.73 and about 4% of the sires had more than 100 daughters. The total number of sires was 1369. A summary of pedigree information is shown in Table 1.

Table 1. Summary of pedigree information in this study

Description	Total
Total number of animals	46094
Animals with record	27019
Animals without progeny	21591
Animals with progeny	24503
Base animals	18969
Sires	1369
Dams	17600
Average inbreeding coefficient	0.0101 (%)
Number of herd-year-season	1601

Statistical methods

The WOMBAT1.0 software (Meyer, 2007) was used to estimate the (co)variance components. Lactation length was calculated by subtracting date of calving from date of first day of subsequent dry period and also PL was calculated by subtracting date of first calving from date of culling.

An easy calculating type of persistency measure was used in this study (ratio of total milk and fat yields in the third 100 days to the first 100 days of lactation, namely Milk3:1 and Fat3:1, respectively). Model selection was based on reports of literature on which factors affect under study traits. The fixed part of the model included the effect of herd-year-season (four seasons i.e. winter, spring, summer, fall were assumed) and calf sex, with age at first calving (months), and percentage of genetic contribution from the Holstein breed was considered as a covariate effect. The following linear model was used for the analysis of data:

$$Y = XB + ZA + E$$

Where Y is the vector of observation; B is the vector of the systematic effects and linear regression coefficients with association matrix of X; A is the vector

of additive genetic with incidence matrix of Z; E is the random vector of residual effects. The model equation is based on the following assumptions:

$$E \begin{bmatrix} Y \\ a \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \end{bmatrix}; \text{V} \begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix}.$$

$$G = \sigma_a^2 A; R = I_n \sigma_e^2.$$

Where, A is the additive numerator relationship matrix and σ_a^2 and σ_e^2 are additive and residual variances, respectively. I_n is identity matrix with order equal to the number of individual records. In the first step, data were analysed using single-trait analyses to obtain variance components and heritabilities. Then, estimated variance components were used as starting values in two-trait analyses in order to avoid bias and converge faster. The (co)variance components and genetic parameters were estimated using the Average Information (AI) Restricted Maximum Likelihood (REML) algorithm.

RESULTS AND DISCUSSION

Descriptive Statistics

Summary of descriptive statistics of phenotypic values for studied traits are shown in Table 2.

Table 2. Estimated means and standard deviations of traits in dataset^a

Trait	Mean	SD	Min.	Max.	CV (%)
PL (mo)	34.89	21.78	22	143	62.42
Milk305 (kg)	6884.3	1388.5	1216	12464	20.17
Fat305 (kg)	219.61	49.53	52.4	447.2	22.55
Fat%	3.216	0.494	1.47	6.07	15.36
Pro305 (kg)	213.66	40.09	55.8	407	18.76
Pro%	3.131	0.303	1.64	5.62	9.68
LSCS	4.629	0.9977	2.053	8.660	21.55
LL (day)	347.47	82.65	180	600	23.79
Milk3:1	0.904	0.185	0.140	2.503	20.46
Fat3:1	0.980	0.267	0.197	3.236	27.24

^a PL: Productive life; Milk305: 305-day milk yield; Fat305: 305-day fat yield; Fat%: fat percent; Pro305: 305-day protein yield; Pro%: protein percent; LSCS: $\frac{1}{n} \sum_{i=1}^n \left(\ln \left(\frac{\text{SCC cells}}{1000 \text{ ml}} \right) \right)$, where n = number of records per cow; LL: Lactation length; Milk3:1: [(milk yield third 100 days)/(milk yield first 100 days)]×100; Fat3:1: [(fat yield third 100 days)/(fat yield first 100 days)]×100.

The Average of PL in the investigated population (34.89 mo) was higher than the average of PL in the Holstein cows of US (27.1 mo) (Tsuruta et al., 2004), but averages for Milk305, Fat305, and Pro305 were much lower (6884.3 vs. 10074, 219.61 vs. 373 and 213.66 vs. 299, respectively) this indicate that high-producing cows have shorter PL. Mean of age at first calving of this population (26.26 mo) was slightly lower than estimated mean of 26.77 mo in the United States (Tsuruta et al., 2005) and estimate of 26.48 mo by Ghavi Hossein-Zadeh (2011) that used records from a large

segment of the Iranian Holstein population. Mean of LSCS (4.629) was higher than that reported by Ødegard et al., (2003) for Norwegian dairy cattle (4.11) indicating that more cows in Iran subjected to subclinical mastitis. Persistency of fat yield (0.980) was higher than persistency of milk yield (0.904) that shows at the end of lactation depression in fat yield is lower relative to other content of milk (e.g., water content).

Variance components and heritabilities

Estimates of variance components and heritabilities for studied traits are shown in Table 3.

Table 3. Estimates of variance components and heritabilities of the traits obtained from single-trait analyses^a

Trait	Additive Variance	Residual Variance	Phenotypic Variance	$h^2 \pm SE$
PL (mo)	13.6363	374.481	388.117	0.035±0.010
Milk305 (kg)	351,870	1,073,810	1,425,680	0.247±0.023
Fat305 (kg)	258.628	1,093.92	1,352.55	0.191±0.021
Fat%	0.0411524	0.117081	0.158233	0.260±0.023
Pro305 (kg)	264.731	873.510	1,138.241	0.233±0.023
Pro%	0.0116046	0.0335259	0.0451305	0.257±0.023
LSCS	0.0446775	0.537781	0.582459	0.077±0.016
LL (day)	349.499	5,954.97	6,304.47	0.055±0.013
Milk3:1	0.003522	0.026087	0.029609	0.120±0.020
Fat3:1	0.00268865	0.0533940	0.0560827	0.048±0.013

^a PL: Productive life; Milk305: 305-day milk yield; Fat305: 305-day fat yield; Fat%: fat percent; Pro305: 305-day protein yield; Pro%: protein percent; LSCS: $\frac{1}{n} \sum_{i=1}^n \left(\ln \left(\frac{SCC \text{ cells}}{1000 \text{ ml}} \right) \right)$, where n = number of records per cow; LL: Lactation length; Milk3:1: [(milk yield third 100 days)/(milk yield first 100 days)]×100; Fat3:1: [(fat yield third 100 days)/(fat yield first 100 days)]×100.

Heritability of milk305 (0.247) was lower than reports of Tsuruta et al., (2005) and Loker et al., (2012) for Holstein cows of US and Canada, respectively, but it was higher than the estimates of Schutz et al., (1990). Discrepancy among studies can be due to difference in population, accuracy of recording and statistical model. Heritability of PL was estimated as 0.035 in the current study. Consistent with the result of this study, previous researches (Weigel et al., 1997; Tsuruta et al., 2004; Tsuruta et al., 2005) estimated a low heritability (ranging from 0.06 to 0.10) for PL. Low heritability of PL shows the high effect of environment on variation of this trait (e.g., voluntary culling, nutritional and climate factors). However, with allocating relatively high number of progeny per sire in progeny testing, regarding that

increase in reliability with addition of each record for low heritability traits is higher relative to high heritability traits (Mrode, 2005), considerable improvement can be obtained. Heritabilities for Fat% and Pro% were higher than the heritabilities of Fat305 and Pro305 (0.260 vs. 0.191 and 0.257 vs. 0.233, for fat and protein yields, respectively). Heritability estimates for milk constituents were lower than reports of other studies (Schutz et al., 1990; Miglior et al., 2007; Loker et al., 2012). Heritability can be affected by many factors including accuracy of recording, environmental condition and model of analysis.

Genetic correlations

Estimates of genetic and phenotypic correlations between traits are shown in Table 4.

Table 4. Estimates of genetic (above diagonal), and phenotypic correlations (below diagonal) for PL, milk yield and constituent, LnSCS, LL, milk persistency and fat persistency by two-trait analyses^a

Trait	PL	Milk305	Fat305	Fat%	Pro305	Pro%	LSCS	LL	Milk3:1	Fat3:1
PL		0.34±0.12	0.41±0.12	-0.01±0.13	0.35±0.12	-0.18±0.12	0.06±0.13	0.27±0.17	0.45±0.15	0.56±0.17
Milk305	0.23±0.01		0.71±0.04	-0.56±0.05	0.92±0.01	-0.57±0.05	-0.07±0.13	0.62±0.09	0.66±0.06	0.46±0.10
Fat305	0.17±0.01	0.75±0		0.18±0.07	0.80±0.03	-0.07±0.07	-0.01±0.13	0.55±0.10	0.49±0.08	0.58±0.10
Fat%	-0.10±0.01	-0.46±0.01	0.22±0.01		-0.35±0.06	0.70±0.04	0.12±0.13	-0.15±0.11	-0.32±0.08	0.11±0.12
Pro305	0.22±0.01	0.94±0	0.77±0	-0.34±0.01		-0.21±0.07	-0.04±0.13	0.65±0.08	0.62±0.07	0.46±0.11
Pro%	-0.09±0.01	-0.51±0.01	-0.22±0.01	0.49±0.01	-0.20±0.01		0.07±0.12	-0.14±0.11	-0.34±0.08	-0.14±0.11
LSCS	0.04±0.01	-0.17±0.01	-0.12±0.01	0.08±0.01	-0.13±0.01	0.17±0.01		-0.10±0.22	-0.34±0.15	-0.36±0.29
LL	0.19±0.01	0.31±0.01	0.27±0.01	-0.12±0.01	0.32±0.01	-0.13±0.01	0.05±0.01		0.63±0.09	0.64±0.12
Milk3:1	0.10±0.01	0.27±0.01	0.19±0.01	-0.11±0.01	0.25±0.01	-0.10±0.01	-0.10±0.01	0.24±0.01		0.85±0.06
Fat3:1	0.06±0.01	0.11±0.01	0.05±0.01	-0.08±0.01	0.11±0.01	-0.01±0.01	-0.08±0.01	0.13±0.01	0.59±0.01	

^a PL: Productive life; Milk305: 305-day milk yield; Fat305: 305-day fat yield; Fat%: fat percent; Pro305: 305-day protein yield; Pro%: protein percent; LSCS: $\frac{1}{n} \sum_{i=1}^n \left(\ln \left(\frac{\text{SCC cells}}{1000 \text{ ml}} \right) \right)$, where n = number of records per cow; LL: Lactation length; Milk3:1: [(milk yield third 100 days)/(milk yield first 100 days)]×100; Fat3:1: [(fat yield third 100 days)/(fat yield first 100 days)]×100.

Genetic correlations of Milk305 with Fat305 and Pro305 were high and positive (+0.71 and +0.92, respectively), but corresponding values with Fat% and Pro% were negative (-0.56 and -0.57, respectively). This implies that selection for milk yield can increase fat and protein yield. These estimates were similar to those reported by Montaldo et al., (2010) for Mexican Holsteins. Although, heritabilities of Fat% and Pro% were higher than those of Fat305 and Pro305, their negative genetic correlations with Milk305 should take into consideration while constructing selection index. Similar to the previous studies (Solkner and Fuchs, 1987; Haile-Mariam et al., 2003), cows with longer LL and greater persistency had higher milk305 (genetic correlations between Milk305 and persistency measures ranged from +0.46 to +0.66). Genetic correlations of Milk305, Fat305 and Pro305 with PL were +0.34, +0.41 and +0.35, respectively. Weigel et al., (1997) and Tsuruta et al., (2005) reported similar genetic correlations for corresponding values. Clearly, milk

yield and constituents have a large influence on voluntary culling decisions. Productive life had the highest genetic correlation with Fat3:1 and Milk3:1 (+0.56 and +0.45, respectively). This indicates that selection based on higher estimated breeding values of Fat3:1 and Milk3:1 can genetically increase PL through indirect response. Because data for the production traits are available relatively early in life and because those traits are more highly heritable than culling traits, production traits may provide useful additional information for many bulls that have recently been progeny tested. LSCS had low genetic correlation with high standard error with most of the traits (except with Milk3:1 and Fat3:1). Negative genetic correlations between persistency traits and LSCS were consistent with the estimates of Haile-Mariam et al., (2003) and Weller et al., (2006). Appuhamy et al., (2009) investigated the relationship of milk and fat persistency with mastitis in first and later lactations. They concluded that incidence of mastitis decreased with increasing

persistence of milk yield and persistence of fat yield in the present and previous lactations. On the other hand, since the genetic correlation between clinical mastitis and lactation average somatic cell score is known to be high it can be stated that more persistent cows had lower SCC, more udder health and lower incidence of mastitis. Also, genetic correlation of Milk3:1 with milk constituents and percentage of milk constituents implies that cows with higher breeding value for Milk3:1 have higher breeding value for Fat305 and Pro305 but not for Fat% and Pro%.

CONCLUSIONS

Regarding the high importance of animal welfare and

also high costs for rearing heifers it can be deduced that allocating proper weights to milk production traits and milk and fat persistence in selection index, can lead to faster and more efficient results by lengthening PL and improving udder health, despite increasing milk and fat yields, through correlated response. The moderate to large positive genetic correlation of lactation yield with milk and fat persistence suggest that one of those traits could be used as a selection criterion to improve all three traits.

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تقدير المعايير الوراثية والظاهرية للحياة الإنتاجية وانتاج ومكونات الحليب وثبات الحليب والدهن في أبقار الهلستين

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ملخص

تم تقدير المعايير الوراثية والظاهرية لأبقار الهلستين للولادة الأولى حسب السجلات المتوفرة من عام 1991-2006 ولمدة 305 يوم حليب ودهن وبروتين وكذلك نسبة الدهن والبروتين والحياة الإنتاجية (PL) واللوغاريتم الطبيعي للخلايا الجسدية (LSCS) وفترة الإدرار (LL) وثبات الحليب (حليب 1:3). كما تم تعيين المعايير الوراثية ومكونات المتغيرات باستخدام طريقة (restricted maximum likelihood) حيث تبين أن عامل الوراثة كان الأعلى لنسبة الدهن (0.26) والأدنى لثبات الدهن (3:1) كما كان متدني للحياة الإنتاجية (0.035). كما تبين أيضاً إن هناك علاقة وراثية عالية وإيجابية (باستثناء نسبة الدهن والبروتين) للحياة الإنتاجية مع الصفات الإنتاجية. كان للحياة الإنتاجية أعلى نسبة علاقة مع الوراثة لثبات الدهن (3:1) والحليب (3:1) (0.56 و 0.45) على الترتيب. وبشكل عام كانت العلاقة مع الصفات الظاهرية متدنية مقارنة مع الصفات الوراثية. يوجد توافق مفضل بين ثبات الحليب (3:1) والدهن (3:1) مع العلاقة الوراثية لكل من (LSCS) (-0.34&-0.36) على التوالي. يمكن الاقتراح بأن تمزج الصفات الإنتاجية مع صفات الثبات عند استعمال مؤشر الاختيار الذي قد يزيد من الحياة الإنتاجية وتحسين صحة الغدة اللبنية عند الإبقار.

الكلمات الدالة: الحياة الإنتاجية، مؤشر الخلايا الجسدية، الثبات، Restricted Maximum Likelihood.

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