

GENETIC PARAMETERS FOR MILK PRODUCTION TRAITS OF IRAN HOLSTEINS

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INTRODUCTION

Improvement of milk and fat yields is the most important breeding goals in dairy cattle in Iran. BLUP evaluation of the animals for these traits, which has been implemented currently, is based on repeated-records animal model. In spite of large data set for milk and fat yields of Iran Holstein, there is no single-trait or repeated-records animal model estimates of variance components for these traits. Since, the available genetic parameters were estimated from few herds with small number of observations, using Henderson's methods (Henderson, 1953) and sire model, pooled values of variance components, derived from literature, are used for national genetic evaluation program.

For implementation of any procedures in evaluation and selection of animals based on single trait or repeated records, genetic parameters should be known, preferably similar to a model for prediction of breeding values. Also, It has been noted that such evaluation can be accurately increased by considering each lactation records as a different trait using multiple-traits BLUP animal model (Ducrocq, 1994). Therefore, the objective of this study was to estimate genetic parameters for the first three lactations of milk and fat yields, using single-trait, repeated-records and multiple-traits animal model by restricted maximum likelihood procedures.

MATERIAL AND METHODS

Data. The first three lactation records of milk (M_1 , M_2 , and M_3) and fat (F_1 , F_2 , and F_3) yields (305 day and twice daily milking) of Holstein cows, collected by Animal Breeding Center of Iran from 1991 to 1999, were used for the present study. The cows with milk yield less than 800 and more than 11000 kg were discarded. Also, cows first calving between 20 to 40 months of age were included in the analysis. The second lactation records were included only if the cows had a first lactation record in the data set. The third lactation records included in the analysis for cows with known two first lactation records. A numerator relationship matrix based on pedigree information tracing back to three generations before 1991, was used in all analyses. The structure of data for first (L_1), second (L_2) and third (L_3) lactation of milk ($\text{kg} \pm \text{s.e.}$) and fat ($\text{gr} \pm \text{s.e.}$) yields are presented in Table 1.

Statistical analysis. Data were analysed by restricted maximum likelihood procedures, using the DFREML program (Meyer, 1997). The following animal models were used for repeated-records (Model 1) and univariate (Model 2) analyses :

$$y = \mu + \text{HYS} + \beta(\text{AGE}) + a + pe + e \quad (1)$$

$$y = \mu + \text{HYS} + \beta(\text{AGE}) + a + e \quad (2)$$

where y is repeated observations for cow, containing first, second and third lactation records in Model 1 and the observations for the first, second and or third lactation in Model 2, μ is the overall mean, HYS is fixed effect of herd-year-season, β is linear regression on age at calving (AGE), a is random additive genetic effects of animal in both models, pe is permanent environmental effects of animal for Model 1, and e is random residual errors.

Table 1. Structure of data for first three lactation records of milk and fat yields

	L ₁	L ₂	L ₃
No of animals in data	86488	86205	85968
No of records	60589	31367	14265
No of sires	1116	747	483
Mean (Standard deviation)			
Milk	5943.0±1269.4	6609.7±1451.2	6929.6±1542.8
Fat	175.7±41.8	192.0±46.4	201.93±49.0

Multivariate analyses of milk or fat yield were carried out within lactation records with Model 2, considering each lactation performance as a different trait. Due to heavy computational requirements, analyses were splitted into three bivariate analyses (e.g., M₁M₂, M₁M₃, and M₂M₃ for milk yield, and F₁F₂, F₁F₃, and F₂F₃ for fat yield). For repeated-records and single-trait analyses, maximization of the likelihood function was done by the Simplex method. The iterations were stopped when the maximum change in parameter value was less than 10⁻⁹ and the estimation was performed in one step. For multiple-trait analyses, the estimation of parameters were carried out in two steps, using Powell's method. In the first step, variance components were fixed at their univariate estimates and the likelihood was maximized only with respect to the covariances, then a second run was performed to estimate all parameters. The convergence criterion was set at 10⁻⁴ and 10⁻⁶ for the first and second steps, respectively.

RESULTS AND DISCUSSION

Repeated-records model. The estimates of variance components, heritabilities and repeatabilities for milk and fat yields are presented in Table 2. Heritability estimates for milk and fat yields were 0.22. The corresponding estimates for repeatability were 0.47 and 0.43 for milk and fat yield, respectively. These estimates were, in general, lower than the results reported by Visscher and Thompson (1992) for Holstein-Friesian of UK (0.36 and 0.33 for heritabilities and 0.56 and 0.53, respectively for repeatabilities of milk and fat yields, using first and second lactation records) and Suzuki and Van Vleck (1994) for Japanese Holsteins (0.30 for heritabilities and 0.54 and 0.52, respectively for repeatabilities of milk and fat yields, using first three lactation records). These differences can be attributed to the level of milk and

fat production. It has been reported that heritability for higher yielding herds was larger than for lower yielding herds (Van Vleck, *et al.*, 1988).

Table 2. Estimates of variances^A, heritability and repeatability for milk and fat yields from repeated-records animal model

Traits	σ_a^2	σ_{pe}^2	h^2	R
Milk	301086.07	341825.19	0.22±0.02	0.47±0.02
Fat	261.10	233.57	0.22±0.02	0.43±0.02

^A σ_a^2 = additive genetic variance; σ_{pe}^2 = permanent environmental variance; h^2 = heritability (\pm s.e.); R = repeatability (\pm s.e.).

Univariate and bivariate analyses. Univariate and pooled bivariate (the average of three bivariate analyses) estimates of variance components, and derived parameter for each lactation are given in Table 3. In general, the results of additive genetic variance and heritability estimate obtained from bivariate analyses were almost similar to the univariate estimates, except for the third lactation records. The average estimate of additive genetic variance obtained from bivariate analyses for M_3 and F_3 were 14.05% and 12.21% higher than the counterpart estimates from univariate analyses. It seems additional lactation records has resulted in a substantial increase in additive genetic variance. Similar findings (but with higher estimates of heritability) have been reported by Visscher and Thompson (1992).

Table 3. Estimates of additive genetic variance and heritability for first three lactations of milk (M) and fat (F) yield from univariate and bivariate animal models

Traits	M_1	M_2	M_3	F_1	F_2	F_3
Univariate						
σ_a^2	291528.41	351401.66	256211.38	210.50	269.00	209.24
h^2	0.27±0.01	0.23±0.02	0.14±0.02	0.23±0.01	0.21±0.02	0.14±0.02
Bivariate						
σ_a^2	293724.91	349022.95	292208.61	207.78	259.74	234.79
h^2	0.27	0.23	0.15	0.23	0.21	0.15

The additive genetic and phenotypic correlations between the first three lactations for milk and fat yields are presented in Table 4. Additive genetic correlations between lactation records of each trait were high and ranged from 0.92 (for M_1M_2) to 0.98 (for M_2M_3) for milk yield and 0.85 (for F_1F_2) to 0.98 (for F_2F_3) for fat yield. The strong additive genetic correlation between M_2M_3 and F_2F_3 suggest that they could be considered as the same performance. Phenotypic correlations were lower than the corresponding genetic correlations and ranged from 0.40 (for F_1F_3) to 0.55 (for M_1M_2). Visscher and Thompson (1992) and García-Cortés, *et al.* (1995) also

reported similar results for genetic and phenotypic correlations between the first three lactations for milk and fat yield.

Table 4. Additive genetic and phenotypic correlations^A between first three lactations for milk and fat yield

Parameters	M ₁ M ₂	M ₁ M ₃	M ₂ M ₃	F ₁ F ₂	F ₁ F ₃	F ₂ F ₃
r _a	0.94	0.92	0.98	0.85	0.93	0.98
r _p	0.55	0.46	0.53	0.45	0.40	0.46

^A r_a = additive genetic correlation; r_p = phenotypic correlation.

CONCLUSION

The results of present study indicate that repeated-records animal model is incorrect for Iran Holstein dairy cattle evaluation, since the additive genetic correlations between all lactations are not unity and their additive genetic variances are different. Also, estimates of additive genetic variances for second and third lactations from univariate analysis can be biased, because selection on correlated traits is not accounted for. Furthermore, since multivariate analysis has been performed by several bivariate analyses, estimates of additive genetic variance and heritability of second and especially third lactation performances may be biased due to culling animals on the basis of first lactation performance.

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