

Prediction Breeding Value and Genetic Parameter in Iranian Holstein Bulls for Milk Production Traits

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Abstract: Data set included records of 43303 cows for first lactation. Records were collected from 2000 to 2006 in Animal Breeding Center of Iran. Studied traits were yield of milk, fat, protein and percentage of fat and protein. Total number of animal was 197561 individual in pedigree. Genetic and phenotypic parameters were estimated with REML method under single trait Animal Model. Breeding values were predicted with BLUP procedure. The model for the analyses included the factors herd-year-season as fixed factor (1694 levels), animal as random effect and age at calving as co variable with minimum and maximum of 23 and 36 month. Respectively the estimated heritabilities were 0.35 (± 0.02), 0.33 (± 0.02), 0.31 (± 0.017), 0.28 (± 0.02), 0.27 (± 0.016) for milk, fat, protein yield, percent of fat and protein. Mean of breeding values of sires were 180.2 (± 28.2), 3.7 (± 1.26), 2.3 (± 1.06), -0.036 (± 0.014) and -0.028 (± 0.009) for milk, fat, protein yield, percent of fat and protein, respectively.

Key words: Breeding value, genetic parameter, milk production, holstein

INTRODUCTION

For improving genetic merit for milk production traits in dairy cattle, Animal Breeding Center of Iran have started to recorded the data from 1975. Now more than 1000 herds in the country are under recording. The increase in results is because of concerted efforts by Agriculture and Jihad ministry and Animal Breeding Center (Karaj) and many private dairy cattle organization. They were screened Dairy cattle herds and select best of male calve based on genetic criteria for using in national progeny testing program. About 1620 sires have been tested in this program from 1984 up to now. About 145 sires were proved based on the highest breeding value for production traits.

Dairy cattle have a long generation interval and a low reproductive rate. In addition, it is costly and time-consuming to carry out dairy cattle selection on a large experimental scale (Togashi *et al.*, 2004). Methods to determine variance component have been greatly improved over the last three decades. Maximum Likelihood based methods have been introduced by Patterson and Thompson (1971) and making use of mixed

models equation by Henderson (1984). Animal models have some clearly defined and useful genetic properties for prediction of genetic values and estimation of genetic parameter in selected and inbred population. This model incorporate all relatives with and without phenotypic observation. Sire evaluation are almost exclusively based on field data, which are highly affected by a large array of environment factors. Therefore, it becomes very important to adjust for those environmental effects in order to accurately estimate the genetic merits of sires and cows. Genetic evaluation of dairy sires and cow has evolved greatly over the years. The Best Linear Unbiased Prediction (BLUP) procedure under animal model has quickly become the method of choice for genetic evaluation based on national field data (Togashi *et al.*, 2004).

Genetic parameter estimates from REML-AM analysis have been reported by several authors. Swalve and Van Vleck (1987) and Albuquerque *et al.* (1994) analyzed the milk yield in 1st, 2nd and 3rd lactation. Van Vleck and Dong (1988), Dong *et al.* (1988) and Albuquerque *et al.* (1995) performed a multivariate analysis of milk, fat and protein yield in the first lactation. Visscher and Thompson

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(1992) reported results from univariate and multivariate analyses for milk production traits in 1st, 2nd and 3rd lactation. Prediction of BLUP breeding values requires known variance components.

BLUP solutions were also proven to vary with the data quality (Winkelman and Schaeffer, 1988), the inclusion of all or part of the data, the use of pedigree information (Van Der Werf and De Boer, 1990). A variety of factors may influence the estimation of co-variances and consequently affect genetic evaluations. Continuous selection was theoretically proven to reduce the genetic variance (Bulmer, 1971). Variance component estimates were also shown to depend on the level of production (Meyer, 1991; Misztal *et al.*, 1992). The effects of heterogeneous variances and selection on the BLUP breeding values were discussed by Wiggans and Van Raden (1991).

The aim of the present study was to estimate genetic parameters for milk, fat, protein yield, percent of fat and protein in the first lactation of Holstein dairy cattle in Iran, based on REML method under single traits animal model and prediction breeding value of proven sires with BLUP procedure.

MATERIALS AND METHODS

Data and pedigree information: Records of first lactation of Holstein cows were used to estimate variance component. The data were recorded in animal breeding center of Iran (Karaj) from 2000 to 2006. The pedigree was traced back to cows born in 1993. Total number of animal in pedigree were 197561. Traits analyzed were 305 day lactation milk (MY), fat (FY) and protein yield (PY), percent of fat (FP) and percent of protein (PP). All of traits were adjusted for 305 day and two times milking. Phenotypic means, standard deviation, maximum and minimum of traits, levels of fixed effect and the number of the individual data sets for each trait are given in Table 1.

Table 1: Summary of the milk production traits

Parameters	MY (kg)	FY (kg)	PY (kg)	FP (%)	PP (%)
Mean±SD	6947±1229	225.0±41.8	216.0±35.0	3.2±0.41	3.07±0.22
Maximum	12511	492.2	379.6	4.48	4.91
Minimum	2195	40.4	51.3	1.45	1.77
Levels of fixed effects	1694	1692.0	1034.0	1686.00	1034.00
Number of records	43303	43293.0	39181.0	42989.00	39172.00

Table 2: Pedigree information for milk production traits

Parameters	MY	FY	PY	FP	PP
No. of base animals	70506	70506	70502	70506	70502
No. of animals with records	43303	43293	39181	42989	39172
No. of animals with unknown sire	02426	02426	1707	02395	1707
No. of animals with unknown dam	11565	11557	8923	11443	8919
No. of sires with progeny records	01305	01304	1218	01301	1218
No. of dams with progeny records	27163	27161	24273	27035	24273
No. of grand-sires with progeny records	01162	01162	994	01161	0994
No. of grand-dams with progeny records	13200	13199	11162	13134	11162

Age of cows at calving was considered as a co variable that minimum and maximum were 23 to 36 month with average of 25 (±2.4) month. Number of base animals was 70506 and animals with records were about 43303 individual. Pedigree information of each trait is presented in Table 2.

Statistical analysis: The model equation for milk production traits was:

$$Y = Xb + Za + e$$

Where, Y is the vector of observations ordered by traits with in animals, b is the unknown vector of fixed effects, a is the unknown vector of animal's genetic effects and e is the vector of random residual effects. X, Z, is known incidence matrices connecting the observations to the respective fixed and random effects.

The structure of variance-covariance matrix is:

$$\text{Var} \begin{bmatrix} y \\ a \\ e \end{bmatrix} = \begin{bmatrix} V & ZA' \sigma_a^2 & R \\ AZ' \sigma_a^2 & G & 0 \\ R & 0 & R \end{bmatrix}$$

Where:

$$V = ZGZ' + R$$

If $R = I\sigma_e^2$ and $G = A\sigma_a^2$, the MME for animal model becomes:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}k \end{bmatrix} \begin{bmatrix} a \\ b \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

Where:

$$k = \frac{\sigma_e^2}{\sigma_a^2} = \frac{1 - h^2}{h^2}$$

The estimation method was REML (Patterson and Thompson, 1971) under single traits Animal Model. The software used was DFREML 3.1.000 (Meyer, 2000).

RESULTS AND DISCUSSION

For all traits residual variances were higher than the genetic variances. The phenotypic coefficient of variation for traits was in range from 7 for percent of protein to 18.5 for fat yield (Table 3).

Estimated heritabilities and standard errors were 0.35 (± 0.02), 0.33 (± 0.02), 0.31 (± 0.017), 0.28 (± 0.02), 0.27 (± 0.016) for milk, fat, protein yield, percent of fat and protein, respectively. Mean of breeding value were 180.2 (± 28.2), 3.7 (± 1.26), 2.3 (± 1.06), -0.036 (± 0.014) and -0.028 (± 0.009) for milk, fat, protein yield, percent of fat and protein, respectively (Table 4).

Heritability of milk yield was higher than other traits. These values for fat and protein yield compare with percent of fat and protein were higher. Mean of breeding value for milk, fat and protein yield were positive but for fat and protein percentage were negative.

The estimated heritabilities were in good agreement with the results from the literature. Van Vleck and Dong (1988) using REML methods with an animal model reported heritabilities of 0.36, 0.35 and 0.33 for milk, fat and protein yield in the first lactation. Similarity, Albuquerque *et al.* (1994) reported heritability estimates of 0.34, 0.35 and 0.4 for milk, fat and protein yield in the first lactation. REML sire model gave usually lower estimates than the animal model, as only a part of relationships in included in the sire model (Dong *et al.*, 1988). Meyer (1984) reported heritabilities of 0.34, 0.35 and 0.28 for milk yield, 0.32, 0.33, 0.23 for fat yield and 0.24, 0.29, 0.12 for protein yield in 1st, 2nd and 3rd lactations, respectively. Also, Dedkova and Wolf (2001) reported heritability of 0.30, 0.28 and 0.30 for milk yield, 0.24, 0.25 and 0.25 for fat yield and 0.25, 0.25 and 0.27 for protein yield in 1st, 2nd and 3rd lactations,

respectively. They used five subset data of large dataset of Holstein. Ben Gara *et al.* (2006) used BLUP procedure for prediction breeding value of sires they estimated heritabilities lower than those commonly found in the literature probably because of limited production levels and missing information on the current data. Jamrozik *et al.* (2000) reported that reliabilities of predicting breeding values of sires increased with the number of progenies per sires.

Heritabilities were estimated, using the complete data set, for milk production traits ranged from 0.22 (± 0.042) for milk yield to 0.70 (± 0.049) for milk fat concentration (Evans *et al.*, 2002; Atil *et al.*, 2001).

Comparable heritability estimates were published for other cattle. In Montbeliarde cattle, Beaumont (1989) reported heritability estimates of 0.27, 0.24 and 0.27 for milk yield, 0.26, 0.20 and 0.24 for fat yield and 0.18, 0.18 and 0.22 for protein yield in the 1st, 2nd and 3rd lactation, respectively from REML sire model. In Swedish Red and White, Standberg and Danell (1989) received the following REML sire model estimates of heritability: 0.29, 0.27 and 0.24 for milk yield and 0.24, 0.20 and 0.21 for fat yield in the first, second and third lactation, respectively. For Dutch Red and White, Van Veldhuizen *et al.* (1991) estimated heritabilities of 0.31, 0.37 and 0.34 for milk, fat and protein yield, respectively in first lactation. Low values 0.23, 0.19 and 0.16 for first lactation milk, fat and protein yield, respectively) were found by Linamo *et al.* (1999) for Finnish Ayrshire. Using Henderson's method III, Soliman *et al.* (1990) reported high value of heritabilities (0.40, 0.39 and 0.41) for the 1st lactation milk, fat and protein yield, respectively for Pinzgauer cattle in Austria.

Kaya *et al.* (2003) estimated additive genetic, residual and permanent environment variances, heritabilities and breeding value for 305 day and test day milk yield by REML method using animal models. The reported heritabilities were 0.25 and 0.11 for 305 day and test day milk, respectively.

Table 3: Genetic and phenotypic parameter

Parameters	MY	FY	PY	PF	PP
Genetic variance	534658	582.70	397.8	0.048	0.013
Residual variance	976402	1167.32	852.0	0.120	0.035
Phenotypic variance	1511060	1750.00	1249.8	0.168	0.048
Coefficient of variation (%)	17	18.50	16.0	12.500	7.00

Table 4: Heritabilities and breeding value

Parameters	MY	FY	PY	PF	PP
Heritabilities \pm SE	0.35 \pm 0.02	0.33 \pm 0.02	00.31 \pm 0.017	0.280 \pm 0.02	0.270 \pm 0.016
Mean of BV \pm SE	180.20 \pm 28.8	03.70 \pm 1.26	02.30 \pm 1.06	-0.036 \pm 0.014	-0.028 \pm 0.009
Max of BV	1287.00	27.30	26.90	0.505	0.190
Min of BV	-265.00	-27.50	-29.00	-0.310	-0.300

In the literature in agreement with the present findings, slightly lower estimates were reported for heritabilities of fat and protein yield compared with heritabilities of milk yield (Jakobsen *et al.*, 2000).

CONCLUSION

Present result showed that estimated heritabilities of milk compare to these values for fat and protein were higher. heritabilities of fat and protein percentage were lower than fat and protein yield that probably reason were for structure of data and record of these traits.

Mean of breeding value of sires for milk, fat and protein yield were positive. These results imply that for genetic improvement of production traits on Iranian Holstein population, selection of sires could be based on highest breeding value for using them in mating system on different herd on the country.

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REFERENCES

- Albuquerque, L.G., J.F. Keown and L.D. Van Vleck, 1994. Covariances among lactation yield for milk, fat and protein, using an animal model. In: Proceeding of the 5th World Congress on Genetic Applied to Livestock Production, 7-12 August, Guelph, Canada.
- Albuquerque, L.G., G.M. Dimov, J.F. Keown and L.D. Van Vleck, 1995. Estimates using an animal model of (co) variances for yield of milk, fat and protein for the first lactation of Holstein cows in California and New York. *J. Dairy Sci.*, 78: 1591-1596.
- Atil, H., A. Salah Khattab and C. Yakupoglu, 2001. Genetics analysis for milk traits in different herds of Holstein cattle in Turkey. *Online J. Biol. Sci.*, 1: 737-741.
- Beaumont, C., 1989. Restricted maximum likelihood estimation of genetic parameter for the first three lactation in the montbeliarde dairy cattle breed. *Genet. Sel. Evol.*, 21: 493-506.
- Ben Gara, A., B. Rekik and M. Boualle'gue, 2006. Genetic parameters and evaluation of the Tunisian dairy cattle population for milk yield by Bayesian and BLUP analyses., *Livestock Sci.*, 100: 142-149.
- Bulmer, M.G., 1971. The effect of selection on genetic variability. *Am. Nat.*, 105: 201-211.
- Dedkova, L. and J. Wolf, 2001. Estimation of genetic parameters for milk production traits in Czech dairy cattle population. *Czech. J. Anim. Sci.*, 46: 298-307.
- Dong, M.G., L.D. Van Vleck and G.R. Wiggans, 1988. Effects of relationship on estimation of variance component with an animal model and restricted maximum likelihood. *J. Dairy Sci.*, 71: 3047-3052.
- Evans, R.D., F. Buckley, P. Dillon and R.F. Veerkamp, 2002. Genetic parameters for production and fertility in spring-calving Irish dairy cattle. *Irish. J. Agric. Food Res.*, 41: 43-54.
- Henderson, C.R., 1984. *Linear Models in Animal Breeding*. University of Guelph Press. Guelph, Canada.
- Jakobsen, J.H., P. Madsen, J. Jensen, P.H. Pedersen and G.A. Pedersen, 2000. Genetic correlation between beef traits measured on young performance test bulls and daughter milk yield. *Acta. Agric. Scand., Sect. A. Anim. Sci.*, 50: 39-46.
- Jamrozik, J., L.R. Schaeffer and G.B. Jansen, 2000. Approximate accuracies of prediction from random regression models. *Livest. Prod. Sci.*, 66: 85-92.
- Kaya, Ü., Y. Akbaş and C. Uzmay, 2003. Estimation of breeding values for dairy cattle using test-day milk yields. *Turk. J. Vet. Anim. Sci.*, 27: 459-464.
- Liinamo, A.E., M. Ojala and J. Van Arendonk, 1999. Relationships of body weight and carcass quality traits with first lactation milk production in Finnish Ayrshire cows. *Livest. Prod. Sci.*, 60: 271-279.
- Meyer, K., 1984. Estimation of genetic parameter for milk and fat yield for the first three lactation in British Friesian cows. *Anim. Prod.*, 38: 313-322.
- Meyer, K., 1991. Estimating variances and covariances for multivariate animal models by restricted maximum likelihood. *Genet. Sel. Evol.*, 23: 67-83.
- Meyer, K., 2000. DFREML 3.1.000. (<http://agbu.une.edu.au/~kmeyer/dfreml.html>)
- Misztal, I., T.J. Lawlor, T.H. Short, P.M. Van Raden, 1992. Multipletrait estimation of variance component of yield and type traits using an animal model. *J. Dairy Sci.*, 75: 544-551.
- Patterson, H.D. and R. Thampson, 1971. Recovery of inter-block-information when block sizes are unequal. *Biometrika.*, 52: 545-554.
- Soliman, A.M., K.H. Khalil, A.A. Ashmawy and A. Essl, 1990. Analysis of milk production traits of Pinzgauer cattle in Austria. II. Genetic parameter. *J. Anim. Breed. Genet.*, 107: 43-51.
- Standberg, E. and B. Danell, 1989. Genetic and phenotypic parameter for production and days open in the first three lactation of Swedish dairy cattle. *Acta. Agric. Scand.*, 39: 203-215.

- Swalve, H. and L.D. Van Vleck, 1987. Estimation of genetic (co)variances for milk yield in first three lactation using an animal model and restricted maximum likelihood. *J. Dairy. Sci.*, 70: 842-849.
- Togashi, K., C.Y. Lin and K. Yokouchi, 2004. Overview of genetic evaluation in dairy cattle. *Anim. Sci. J.*, 75: 275-284.
- Van Der Werf, J.H.J. and I.J.M. De Boer, 1990. Estimation of additive genetic variance when base populations are selected. *J. Anim. Sci.*, 68: 3124-3132.
- Van Veldhuizen, A.E., H. Bekman, J.K. Oldenbrok, J.H.J. Van der Werf, D.S. Koom and J.S. Muller, 1991. Genetic parameters for beef and milk production in Dutch Red and White dual-purpose cattle and their implications for a breeding program. *Livest. Prod. Sci.*, 29: 17-30.
- Van Vleck, L.D. and M.C. Dong, 1988. Genetic (co)variances for milk, fat and protein yield in Holstein using an animal model. *J. Dairy Sci.*, 71: 3040-3046.
- Visscher, P.M. and R. Thompson, 1992. Univariate and multivariate parameter estimates for milk production traits using an animal model. I. Description and results of REML analyses. *Genet. Sel. Evol.*, 24: 415-430.
- Wiggans, G.R. and P.M. Van Raden, 1991. Method and effect of adjustment for heterogeneous variances. *J. Dairy. Sci.*, 74: 4350-4357.
- Winkelman, A. and L.R. Schaeffer, 1988. Heterogeneity of variances among herds and its effects on dairy sire evaluation. *J. Dairy Sci.*, 71(Suppl.2): 84.