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## 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 ( $\pm 0.02$ ), 0.33 ( $\pm 0.02$ ), 0.31 ( $\pm 0.017$ ), 0.28 ( $\pm 0.02$ ), 0.27 ( $\pm 0.016$ ) for milk, fat, protein yield, percent of fat and protein. Mean of breeding values of sires were 180.2 ( $\pm 28.2$ ), 3.7 ( $\pm 1.26$ ), 2.3 ( $\pm 1.06$ ), -0.036 ( $\pm 0.014$ ) and -0.028 ( $\pm 0.009$ ) for milk, fat, protein yield, percent of fat and protein, respectively.

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

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### 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 ( $\pm 0.02$ ), 0.33 ( $\pm 0.02$ ), 0.31 ( $\pm 0.017$ ), 0.28 ( $\pm 0.02$ ), 0.27 ( $\pm 0.016$ ) for milk, fat, protein yield, percent of fat and protein, respectively. Mean of breeding value were 180.2 ( $\pm 28.2$ ), 3.7 ( $\pm 1.26$ ), 2.3 ( $\pm 1.06$ ), -0.036 ( $\pm 0.014$ ) and -0.028 ( $\pm 0.009$ ) 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 ( $\pm 0.042$ ) for milk yield to 0.70 ( $\pm 0.049$ ) 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 | 0.31 $\pm$ 0.017 | 0.28 $\pm$ 0.02    | 0.27 $\pm$ 0.016   |
| Mean of BV $\pm$ SE     | 180.2 $\pm$ 28.8 | 3.7 $\pm$ 1.26  | 2.3 $\pm$ 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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