# Genetic analysis of milk production traits of Iranian Holstein dairy cattle using multi-trait random regression model

**A. Mohammadi, M. Bohlouli and S. Alijani**

Department of Animal Science, University of Tabriz, Tabriz, Iran

E-mail: alimohamadi36@gmail.com

**Abstract**

This research was carried for estimating of genetic parameters of production traits (milk yield, fat yield and protein yield) in Iranian Holstein dairy cattle. Data set was included first lactation records of109574 cows. These data were collected from2001 to 2010 by the national breeding center of Iran. Multi-trait random regression model was used based on restricted maximum likelihood method. Permanent environmental variances for the traits were higher at the early of lactation. Heritability estimates based on days in milk, for milk yield, fat yield and protein yield ranged from 0.09 to 0.22, 0.07 to 0.09 and 0.07 to 0.23, respectively. Genetic correlations between traits were calculated from covariance components for parameters estimated in bivariate analyses. Genetic correlations for same days in milk between milk and protein yield (0.84-0.94) were higher than between milk yield and fat yield (0.63-0.90). The genetic correlations between 305-d production of milk and fat, and milk and protein were 0.81 and 0.94, respectively. Therefore selection to improve the milk yield has been the better response to selection of protein yield.

**Key words**: Dairy cattle - Milk production - Genetic parameter -Heritability- Genetic correlation

**Introduction**

The use of appropriate method for the genetic components evaluation of dairy cattle is an important program of dairy animal production. In conventional method, lactation yields are calculated based on the test day (TD) records. TD records are actually repeated observations measured along a trajectory days in milk (DIM) and the mean and covariance between measurements change gradually along the trajectory (Schaeffer, 2004). Among the models that consider TD production, random regression model (RRM) has been widely observed to increase the accuracy of breeding value predictions (Strabel et al. 2004). Therefore, the purpose of this study is estimation of genetic parameters of milk production traits of Iranian Holstein Dairy cattle using multi-trait RRM.

**Materials and methods**

The TD milk yield records obtained from a national breeding center of Iran, belonged to the first lactation dairy cows from 2001 to 2010.The age of cows in the first lactation was from 21 to 46 months. Edited data included the following: The TD data were excluded before $5^{th}$ day and after the $305^{th}$ day of lactation. In addition, irregular data for milk yield (<1.5 and >75 kg), fat yield (<1.5% and >9 %), and protein yield (<1% and >7 %) were excluded. Cows had also, only cows with more than 5 TD records were kept. The sires having progeny fewer than 5 were eliminated. Finally edited

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data included 866084 TD records of 109574 cows that were 1616sire progeny. The RRM used to fit yield records was:

$$y_{tijklpq} = HTD_i + YC_j + MT_k + \sum_{n=1}^{5} Age_{ln} Z_n + \sum_{m=0}^{4} s_{qm} Z_n + \sum_{m=0}^{4} pe_{pm} Z_n + e_{tijklpq}$$

Where $y_{tijklpq}$ is the $t^{th}$ record of $p^{th}$ cow in $i^{th}$ herd-test-date ($HTD$) effect, $j^{th}$ calving year ($YC$) and $k^{th}$ milking frequency ($MT$); $AS_{ln}$ is the $n^{th}$ fixed regression coefficient of $l^{th}$class of cows calving age-season; $s_{qm}$ and $pe_{pm}$ are regression coefficients $m^{th}$ for sire and permanent environment effect on $p^{th}$ cow respectively; $z_n$ is $n^{th}$ legendre polynomial for $t^{th}$ day; $e_{tijklpq}$ random residual. Number of records of and other descriptive statistics are summarized in Table 1.

$$\text{var} \begin{bmatrix} \mathbf{s} \\ \mathbf{pe} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G \otimes A} & 0 & 0 \\ 0 & \mathbf{P \otimes I} & 0 \\ 0 & 0 & \mathbf{I}\sigma_e^2 \end{bmatrix}$$

Where, $G$ is sire genetic (co)variance matrix among random regression coefficients and $A$ is additive numerator relationship matrix between sires. The matrix $P$ was the cow effects variance-covariance matrix among random regression coefficients, $\sigma_e^2$ and was residual variances for each traits and $I$ represents an identity matrix with ones on the diagonal. In two trait model $G$ and $P$ are $10 \times 10$ (co)variances matrix of regression coefficients. Additive genetic correlation for 305-days production were calculated as:

$$r_{g305d(i,j)} = \frac{q_{305d} \mathbf{G}_{(i,j)} q'_{305}}{\sqrt{q_{305d} \mathbf{G}_{(i,i)} q'_{305} \times q_{305d} \mathbf{G}_{(j,j)} q'_{305}}}$$

Where $\mathbf{G}_{(i,j)}$, is genetic covariance matric for considered trait in $i^{th}$ and $j^{th}$ trait, $\mathbf{G}_{(i,i)}$ and $\mathbf{G}_{(j,j)}$ are genetic (co)variance matrices $i^{th}$ and $j^{th}$ trait, respectively and $q_{305d}$, Vector of 305-days legendre polynomial were obtained by summing up the coefficients from day 5 to day 305.

For estimated heritability for $i^{th}$ DIM was calculated as: $h_t^2 = \frac{4\sigma_{s(t)}^2}{\sigma_{s(t)}^2 + \sigma_{pe(t)}^2 + \sigma_e^2}$, Where $\sigma_{S(t)}^2 = \mathbf{q}G\mathbf{q}'$, $\sigma_{pe(t)}^2 = \mathbf{q}P\mathbf{q}'$, where $\mathbf{q}$ is the vector of the associated legendre polynomial respectively. Diagonal of above (co)variance matrices were sire additive genetic variances ($\sigma_{s(t)}^2$) and permanent environmental ($\sigma_{pe(t)}^2$) for $5^{th}$ day to $305^{th}$ DIM.

**Results and Discussion**

Number of record and other descriptive statistics are summarized in Table 1. Heritability estimate of fat yield were lowest than other traits. In this study, minimum heritability of milk and protein yields in early lactation was observed, that associated with the increase values of permanent environmental and residual variance in early lactation. Maximum heritability for all traits the end of lactation was observed (Figure 1). However, the trends in the heritabilities in this study was similar to the results obtained by Mohammadi et al (2012) for Iranian Holsteins. The genetic correlation between TD yields were higher when periods were closer to each other (Figure 3). The genetic correlation between milk and fat yields was low in the early lactation and then trend increase the end of lactation was observed. However, genetic correlation between milk and protein yields was high (Figure 2). Genetic correlations between milk and fat yields 0.65 to 0.90 was estimated that was higher than results presented by Jakobsen et al (2002). Moreover, genetic correlation between milk

**Table 1. Descriptive statistics of data sets for milk production traits in different TD**

| TD | Trait | Milk yield (kg) | | Fat yield (kg) | | Protein yield (kg) | |
|---|---|---|---|---|---|---|---|
| | **Records** | **Mean** | **SD** | **Mean** | **SD** | **Mean** | SD |
| 1 | 84720 | 28.53 | 6.83 | 1.029 | 0.333 | 0.862 | **0.222** |
| 2 | 88701 | 32.33 | 6.83 | 1.057 | 0.331 | 0.953 | **0.224** |
| 3 | 91186 | 32.63 | 6.80 | 1.053 | 0.323 | 0.955 | **0.224** |
| 4 | 92948 | 32.28 | 6.81 | 1.039 | 0.315 | 0.952 | **0.225** |
| 5 | 93554 | 31.44 | 6.94 | 1.026 | 0.312 | 0.952 | **0.228** |
| 6 | 93201 | 30.65 | 6.94 | 1.014 | 0.311 | 0.940 | **0.228** |
| 7 | 90869 | 29.79 | 6.98 | 1.002 | 0.311 | 0.925 | **0.229** |
| 8 | 87790 | 28.73 | 6.93 | 0.978 | 0.303 | 0.902 | **0.227** |
| 9 | 81022 | 27.55 | 6.92 | 0.957 | 0.301 | 0.857 | **0.228** |
| 10 | 64469 | 26.63 | 6.94 | 0.938 | 0.298 | 0.857 | **0.230** |
| **Total** | **868460** | **30.20** | **6.89** | **1.012** | **0.319** | **0919** | 0.227 |

and protein yields 0.84 to 0.95 obtained, this results agreeing with the results presented by Jakobsen et al (2002) and Veerkamp et al (1998).Genetic correlation 305 day between milk and fat yield 0.81 and between milk and protein yields 0.94 was estimated. Therefore, genetic correlations trends in this study was similar to the results obtained by Sahebhonar et al (2010) for Iranian Holsteins.Therefore genetic selection to improve and increase of milk yield has been the better response than genetic selection of protein and fat yields.

The Using of multi-trait models can Studied genetic relationships different traits. It seems to be more research on records for the second and third lactation will be required to more accurately estimate.
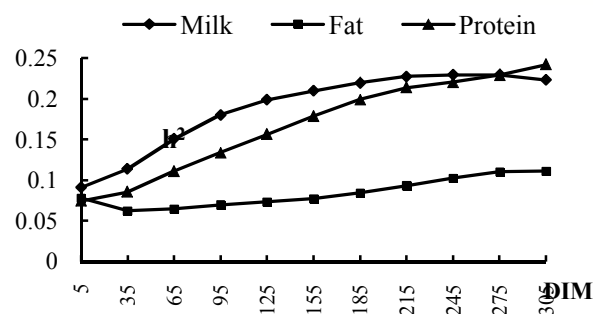


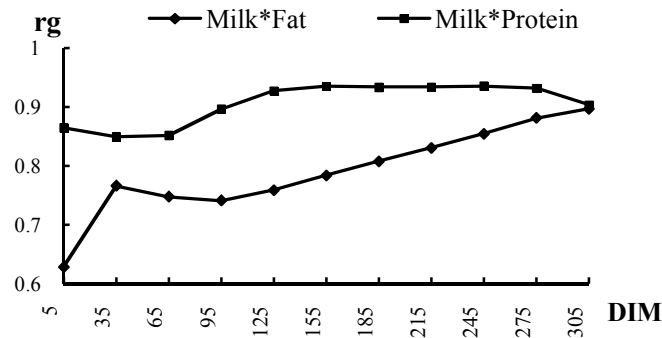**Figure1. Estimated heritability (h2) as a function of DIM**

**Figure2. Genetic correlation (rg)
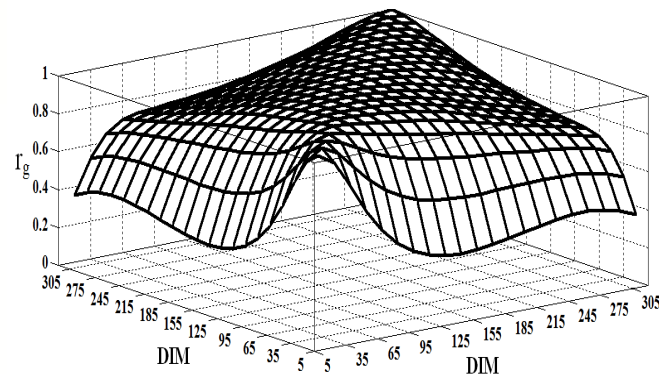between different traits as a function of DIM**



**Figure3. Genetic correlation (rg) milk yield as a function of DIM**

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