

Short Communication

Estimation of genetic parameter in Iranian Holstein crossbred dairy cattle

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The performance of Holstein × Indigenous (H×I) crossbred dairy cattle in Iran was considered between 1991 and 2003. Milk, fat yield and fat percentage traits were considered in this research. Variance components were estimated using animal model (single trait) and derivative-free restricted maximum likelihood method for different traits. Crossbred animals with 50 to 70% of Holstein gene ratio have shown higher performance. The average performances for the mentioned traits were 2722.68, 122.97 and 3.97%, respectively. The estimation of the heritability for milk yield, fat yield, and fat percentage were 0.332, 0.3277 and 0.145. The research results showed that production potential has been increased by crossbreeding.

Key word: Genetic parameter, crossbreeding, Holstein.

INTRODUCTION

The use of modern technology in developed countries at animal husbandry, nutrition genetics and also improvement of farm animal with regards environmental and health conditions has caused the actual production of animals be close to their physiological and genetic potential (Rukui et al., 2000; Singh et al., 1986). Thus, production in these countries is economical. However, the use of these technologies in developing countries like Iran where most farming systems are located in the villages is impossible (Soldatov and Dutsheev, 1991). Crossbreeding of European *Bos taurus* dairy breeds with indigenous *Bos indicus* cattle is a well-documented method to improve milk production traits. Crossbreeding optimizes the additive and non additive genetic breed effects of *Bos taurus* and *Bos indicus* cattle (Meyer, 1998). Knowledge of the kind and amount of genetic variance and its distribution in the population structure can lead to the design of optimum breeding plans. Since forty years ago, genes from European dairy cattle have been imported to Iranian populations in the different regions. Heritability estimates in crossbred population were adjusted to various degrees for fixed additive effects

of breed contribution. Meyer (1998) found higher heritability for first lactation milk and fat yield when data from imported Canadian sires were included, and breed effects were not accounted for.

Other authors considering the breed of sire also found high heritabilities in crossbred data (Albu and Kennedy, 1999; Rukui et al., 2000; Touchberry, 1992). Van der Werf et al. (1989) found heritabilities of 0.41 and 0.79 for milk yield and fat yield respectively. Recent year studies in Iranian crossbred dairy population were limited to production and type of characteristics consideration. Rukui et al., (2000) carried out a primary estimation of heritability and repeatability estimation in Esfahan Province crossbred population. The aim of this study was to estimate genetic parameter in Iranian Holstein crossbred dairy population.

MATERIALS AND METHODS

Data were obtained from Animal Breeding Centers of the Agriculture Ministry. Records were sampled from Holstein × Indigenous (H×I) and their backcross progeny between 1991 and 2003 from all herds in all provinces. Data on the following four traits were obtained for each cow: milk yield (Kg), fat yield (Kg) and fat percent traits. Breed composition (%H genes) was known for all sires and their progeny. Editing data included checks on breed

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Table 1. Pedigree information.

Total	Pronounced dam	Pronounced sire	None pronounced dam
12425	2620	1900	1853

Table 2. Estimation of genetic parameter (σ_P^2 , σ_A^2 and h^2) in Iranian Holstein crossbreds.

Genetic parameter	σ_P^2	σ_A^2	σ_{pe}^2	h^2	r
Milk yield	391313.94	193694.70	67605.62	0.332(0.01)	0.505
Fat yield	702.96	462.93	0.0000158	0.3415(0.003)	0.3416
Fat percent	0.1742	0.129	0.008	0.2361(0.002)	0.2539

code of sires and progeny. Data set contained 15524 records.

Pedigree data were iteratively retrieved in seven loops for all cows with records and for their parents no additional pedigree was after this time. Ninety-five percent of the pedigree was found after three loops; given a total of 12445 animals in the model. Nine genetic groups were defined according to the percentage of H genes at intervals of 12.5%. The distribution of progeny over groups of the dam is expressed in Table 1.

Software

EXCEL (XP), SPSS (9) and FOXPRO (2.6) Software for editing and preparing data and for genetic analysis were used; SAS (8.2) and DFREML (2000, Meyer) Software.

Models for analysis

Records were analyzed with the following model proposed by Van der werf (1989).

$$y_{ijklmnop} = \mu + L_i + H_j + (YS)_k + g_l + Het_m + RE c_n + MHet_o + a_p + e_{ijklmnop}$$

where μ is population mean, L_i is lactation number $i = 1 \dots 8$, H_j and YS_k are fixed environmental effects of herd and year season with $j = 1 \dots 295$ and $k = 1 \dots 4$, g_l is fraction of Holstein gene in crossbred progeny with $l = 1 \dots 8$ that equal to $[(P_s + P_d)/2]$ (P_s and P_d are imported genes percent in two parent), Het_m is hetrosis percent in progeny equal to degree of heterozygosity of animal, Rec_n is interaction between presence of imported gene in two parents, $Mhet_o$ is maternal hetrosis, a_p is the additive genetic effect of cow making record, and $e_{ijklmnop}$ is a residual effect.

The model can be written in matrix notation as:

$$y = Xb + Z_1a + Z_2Pe + e$$

where b is a vector of fixed effects, a is a vector of genetic effects of the animals, Pe vector of permanent environmental effect and e is a vector of residual effects. X , Z_1 and Z_2 are design matrices for fixed, genetic and permanent environmental effect, respectively. Expectation and variance matrices for model are:

$$E(y) = Xb + Z_1a + Z_2Ad_a + Id_e$$

$$Var(y) = Xb + Z_1a + Z_2Ad_a + Id_e$$

Variance components are estimated by REML. A univariate procedure was used for the analysis of each trait.

RESULT AND DISCUSSION

Analysis of variance revealed that herd, year, season, Holstein gene, individual heterosis, maternal heterosis and recombination effect in all traits were significant. REML estimation of variance component is presented in Table 2. Results show that estimations of the heritability for different traits are low to moderate. Permanent variance percent in milk trait is moderate and for fat yield and fat percent traits are low. Another research in Holstein and native crossbred population reported heritability for milk yield, fat yield and fat percent traits which are 0.2-0.38. 0.334 and 0.367 (Rukui et al., 2000) respectively and repeatability for the mentioned traits are 0.55, 0.335 and 0.38 (Miraei-Ashtiani et al., 2001; Rukui et al., 2000). Although there are many studies regarding the genetic parameter estimation in different country but results are inconsistent (Singh et al., 1986; Soldatov and Dutsheev, 1991; Swan and Kinghorn, 1992; Touchberry, 1992; Van der werf, 1989; Van der werf and Deboer, 1989).

Some researchers reported high value, whereas another reported low to moderate value. The contradictory results may be associated with differences in local breed, number and composition of used animals in the estimation procedures and differences in methods and software used in genetic parameter estimation.

Crossbreeding as a mating method has been used in different countries for years. This method has increased the performance of the local production systems. Crossbred animal performance is a combination of

additive and non-additive genetic factors. Therefore, determining the portion of each factor can help the breeder when the performance of crossbred population is increased.

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