

Comparison of Additive Genetic Parameter in Two Iranian Crossbred Population

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Abstract: The performance of crossbred cattle in Iran was considered across years 1991-2003. Crossbred animals were results of Holstein×Indigenous (H×I) and Brown Swiss×Indigenous (B×I) crossbreeding systems. These two population were considered separately. The research results showed that production potential has been increased by crossbreeding, and crossbred animals with 50-70% of Holstein or Brown Swiss blood ration have showed higher performance. Variance component were estimated using animal model (single trait) and Derivative-free restricted Maximum Likelihood method for different traits. The estimation of the heritability for milk yield, fat yield, and fat percentage and milk days were 0.332, 0.34, 0.23 and 0.26, respectively for single models in (H×I) population. In (B×I) population the estimation heritability were 0.2374, 0.1629, 0.17 and 0.338, respectively for milk yield, fat yield, fat percentage and milk days traits. The result showed that additive genetic variance share in Holstein crossbred higher than others.

Key word: Brown Swiss, crossbreeding, genetic parameter, heterosis

INTRODUCTION

Crossbreeding is widely used to improve productivity of dairy cattle in Iran. Desirable effects of crossbreeding are heterosis and the utilization of differences between breeds to optimize genetic merit of performance traits under various environmental conditions (Gregory and Cundiff, 1980; Koch *et al.*, 1985). Since the re-discovery of Mendel's laws in 1920, many scientists believed that genetic variations in traits such as milk and milk content traits is determined by one or perhaps as well as two separate loci and by environmental changes (Van Vleck, 1993). Knowledge of genetic parameters is necessary to evaluate the suitability of breeds for crossbreeding.

Crossbreeding program in Iran is started since 80 years ago. However, lack of proper scientific and practical interpretation on crossbred cows data have been prevented properly planning for continuity of breeding programs. First genetic parameter estimation conducted by Hydarpour (1996) that reported that heritability for milk yield in brown Swiss crosses is 0.2-0.46. Rukui (2000) showed heritability and repeatability in Esfahan province crossbred population for milk production traits are low to moderate. However, since a comprehensive study has not been done in Iranian crossbred dairy cattle. The aim of this study was genetic parameter estimation in Iranian 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 herd in all province. 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 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; give a total of 12445 animals in the model. Nine genetic groups were defined according to the percentage of H genes at intervals 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 prepare data and for genetic analysis were used of SAS (8.2) and DFREML (Meyer, 1998) Software.

Models for analysis: Records were analyzed with following model that proposed by Van der werf (1989).

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 crossbreds

		σ_p^2	σ_A^2	σ_{PE}^2	h^2	r
milk	H	391313.94	130013.62	67605.62	0.332	0.505
	B	296601.23	177365.29	48825.76	0.24	0.406
Fat yield	H	702.96	240.032	0.0000158	0.3415	0.3416
	B	652.914	106.81	99.113	0.1629	0.3147
Fat percent	H	0.174	0.036	0.008	0.236	0.254
	B	1.39	0.243	0.095	0.175	0.18
Milk days	H	1536.04	409.46	75.74	0.266	0.304
	B	1804.22	602.26	0.25	0.334	0.334

$$y_{ijklmnop} = \mu + L_i + H_j + (YS)_k + g_i + Het_m + Rec_n + MHet_o + a_p + e_{ijklmnop}$$

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_i 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 heterosis percent in progeny is equal to degree of heterozygosity of animal, Rec_n is interactions between presence of imported gene in two parents, $Mhet_o$ is maternal heterosis, 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:

$$E \begin{bmatrix} y \\ a \\ e \end{bmatrix} = \begin{bmatrix} Xb \\ 0 \\ 0 \end{bmatrix} \quad Var \begin{bmatrix} a \\ Pe \\ e \end{bmatrix} = \begin{bmatrix} Ad_a^2 & & \\ & Id_{pe}^2 & \\ & & Id_e^2 \end{bmatrix}$$

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

RESULTS AND DISCUSSION

Best linear unbiased prediction is used widely for genetic evaluation because it has many desirable properties

(Henderson, 1953). The point of departure for BLUP is usually a mixed linear model for phenotypic values.

Analysis of variance revealed that herd, year, season, direct genetic effect, 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 estimation of the heritability in two populations for different traits are low to moderate.

The estimation of Heritability in Holstein population has been greater than Brown Swiss population in all traits except for the milk day traits. Therefore, additive variance share in Holstein population is high and predicted selection response and breeding value is accurate.

Rukui (2000) reported that heritability for milk yield, fat yield, fat percent and milk days traits were 0.28, 0.33, 0.37 and 0.37 for Holstein population and 0.24, 0.3, 0.41 and 0.32 for brown Swiss population respectively. The Holstein result is agreed to current study and Brown Swiss is consisting especially in fat yield and percent traits. The reasons of this consistent are a low sample size and different native breed in Reku studies. Also there are many studies regarding the genetic parameter estimation in different country but results are inconsistent (Singh *et al.*, 1986; Van der werf, 1989, Van der werf and Deboer, 1989; Soldatov and Dutsheev, 1991; Freitas, 1991; Swan *et al.*, 1992; Touchberry, 1992; Albu and Kennedy, 1999; Elzo *et al.*, 2002).

Even so, estimation of repeatability in Brown Swiss population is higher than other except fat percent trait. However, the proportion of permanent variance in Brown Swiss population is great and therefore, in this population producing ability and prediction of further lactation production is accurate. Rukui (2000) reported that heritability for milk yield, fat yield, fat percent and milk days traits were 0.56, 0.35, 0.38 and 0.53 for Holstein population and 0.52, 0.44, 0.58 and not estimate for brown Swiss population, respectively. The Holstein result is agreed to our study and in brown Swiss is inconsistent.

Crossbreeding as a mating method is used in different countries for years. This method has been increases the performance of the local production systems. Crossbred animal performance is combination of additive and non-additive genetic factors. Therefore, determine the portion of each factor can be helped to breeder that the performance of crossbred population is increased.

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