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Heritability and Repeatability Estimation in Iranian Brown Swiss Crossbred Dairy Cattle Population

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Abstract: The aim of this study was genetic parameter estimation in Iranian Brown Swiss crossbred dairy population. The performance of Brown Swiss crossbred cattle in Iran was considered across years 1991-2003. 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 0.24, 0.163, 0.175 and 0.334, respectively for single models. Repeatability estimation for mentioned traits was 0.41, 0.31, 0.18 and 0.334. The result showed that the additive genetic variance share in milk yield and milk day's traits and permanent environmental variance in milk and fat yield are high.

Key words: Brown Swiss, crossbreeding, genetic parameter

INTRODUCTION

The Brown Swiss breed has been used in crossbreeding program in Iran. The choice of B. taurus breeds has been determined by several factors. For example, higher milk volume. In crossbreeding systems, selection and mating system is critical keys. In order to design efficient breeding systems, information on additive and non additive genetic effect are required (Kahia *et al*., 1999). Predicted performances of untested genotypes and breeding systems are also required because crossbreeding experiments for dairy and beef cattle are long term and expensive (Dickerson, 1969). Genetic variance is used by breeders to change animal population. 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. Heritability is usually estimated with animals of known relatedness reproduced using a controlled breeding program (Falconer and Mackay, 1996). 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 were considered the breed of sire, also thus found high heritabilities in crossbred data (Soldatov and Dutsheev, 1991; Swan *et al*., 1992; Albu and Kennedy, 1999). Van der Werf (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 characteristics consideration (Hydarpour, 1996). Rekui (2000) carried out a primary estimation of heritability and repeatability estimation in Esfahan Province crossbred population. The aim of this study was genetic parameter estimation in Iranian Brown Swiss 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 is 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 (%B 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.

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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 crossbreds

Genetic parameter	σ_p^2	σ_A^2	σ_{pe}^2	h^2	r
Milk yield	296601.23	177365.29	48825.76	0.24	0.406
Fat yield	652.914	106.81	99.113	0.1629	0.3147
Fat percent	1.39	0.243	0.095	0.175	0.18
Milk days	1804.22	602.26	0.25	0.334	0.334

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

$$y_{ijklmnop} = \mu + L_i + H_j + (YS)_k + g_l + Het_m + Rec_n + \mathrm{Mhet}_o + a_p + e_{ijklmnop}$$

where μ is population mean, L_i is lactation number i = 1…8, H_j and YS_k are fixed environmental effects of herd and year season with j = 1…295 and k = 1…4, g_l is fraction of Brown Swiss gene in crossbred progeny with l = 1…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 is equal to degree of heterozygosity of animal, Rec_n is interactions 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:

$$y = Xb + Z_1 a + Z_2 Pe + e$$

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:

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

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

RESULTS AND DISCUSSION

Analysis of variance revealed that herd, year, season, Brown Swiss 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 estimation of the heritability for different traits are low to moderate.

Additive genetic variance proportion in milk and milk day's trait than fat traits is high. The trend in repeatability is different. Milk and fat yield repeatability than the fat percent and milk days traits are high. In other words, permanent variance share in milk and fat yield traits are high and for fat percent and milk days traits are low. Hydarpour (1996) reported that heritability for Brown swiss cross in first and second lactation is 0.36 and 0.26, respectively. In Esfahan provianc, Rekui (2000) showed that the heritability for milk, fat, fat percent and milk days are 0.24, 0.3, 0.41 and 0.32, respectively. These results in fat yield and milk days are agreed and in milk yield and fat percent are consisted with current study. Rekui (2000) also reported that repeatability for milk, fat and fat percent traits are 0.52, 0.46, and 0.59 than higher than result in this research. The native cattle population and sample size difference are the main reasons for result disparity.

Although there are many studies regarding the genetic parameter estimation in different country but results are inconsistent (Dickerson, 1969; Singh *et al*., 1986; Van der werf, 1989, Soldatov and Dutsheev, 1991; Swan *et al*., 1992; Touchberry, 1992; Rekui, 2000; Elzo *et al*., 2002). Some researcher 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 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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