

HERITABILITY ESTIMATES OF SOME PRODUCTIVE TRAITS IN SAHIWAL CATTLE

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ABSTRACT

Data on 8948 performance records of Sahiwal cows kept at the Livestock Experiment Station, Jahangirabad (Khanewal) were used in the present investigation. The heritability was estimated by using Restricted Maximum Likelihood (REML) procedure fitting an Individual Animal Model. The heritability estimates by univariate analysis were 0.013 ± 0.022 for first lactation milk yield, 0.062 ± 0.039 for first lactation length and 0.028 ± 0.027 for first dry period. The heritability estimates considering all lactations (repeatability model) were 0.052 ± 0.032 , 0.027 ± 0.013 and 0.029 ± 0.018 for milk yield, lactation length and dry period, respectively. Pedigree and performance recording of dairy animals for more precise genetic evaluation programmes is suggested.

Keywords: Animal Model, Heritability, Pedigree, Sahiwal, cattle

INTRODUCTION

The genetic composition of a population can be studied by considering the relative importance of heredity and environmental factors affecting the performance of individuals in that population. The most commonly used parameters are repeatability, heritability and genetic correlations. The genetic parameter estimates are helpful in determining the method of selection, to predict direct and correlated response to selection, choosing a breeding system to be adopted for future improvement as well as in the estimation of genetic gains. The genetic sources of variation include all differences that may be attributed to heredity. The concept of heritability is important for dairy cattle breeders since it is a limiting factor in the rate of genetic change possible in a trait (Wilcox, 1992). The heritability of a metric character is one of its most important properties which express the proportion of the total variance attributable to average effects of genes and its most important function is its predictive role expressing reliability of the phenotypic value as a guide to its breeding value (Falconer and Mackay, 1997). In the past heritability estimates for production traits of Sahiwal cattle (Ahmad *et al.*, 1976; Mohiuddin *et al.*, 1994) have been estimated through paternal halfsib correlation or intrasire regression of daughter on dam techniques, with pre-adjustment of fixed effects. Furthermore, all these studies were based on small datasets. This may have added bias to the estimates due to

the omission of systematic environmental effects in the models, for example, year and season of calving and due to sampling error.

Best Linear Unbiased Predictions (BLUP) procedure using the Individual Animal Model (IAM0) has become the world wide standard for the prediction of breeding values of farm animals. Also, the basis for estimation of variance components using restricted maximum likelihood (REML) by virtue of the properties, provides minimum variance for unbiased predictors of genetic merit, estimates genetic and environmental effects simultaneously, takes into account the relationship between all animals to account for the effects of selection and non-random matings. Animals can also be compared across herds and years and evaluations across years facilitate monitoring of the rates of genetic progress (Hill and Meyer, 1988). This technique has not been widely used for the genetic evaluations of Sahiwal cattle in Pakistan. The present investigation was aimed to find out genetic parameters of some productive traits in a pure-bred herd of Sahiwal cattle.

MATERIALS AND METHODS

Data on 8948 pedigree, breeding and performance records of a purebred Sahiwal herd maintained at Livestock Experiment Station, Jahangirabad, Khanewal during the period 1939-97 were utilized for the present study. The data on milk yield, lactation length and dry

period were analyzed to estimate the magnitude of various genetic sources of variation in these traits. Incomplete lactations (614 records) for any recorded reason or lactations showing any abnormality were not utilized in the analysis. In addition to the basic edits of consistency for dates and animal identities, the following edits were conducted on the data set by eliminating the out layer records having $+3\sigma$ from the mean values of the corresponding traits, lactations having less than 120 days (421 records) were also removed. All of the available pedigree information was included in the analysis.

The heritability was estimated by using Restricted Maximum Likelihood procedure (Patterson and Thompson, 1971) fitting an Individual Animal Model. For the purpose Derivative Free Restricted Maximum Likelihood (DFRML) set of computer programmes (Meyer, 1997) was used. The fixed effects (year and season of calving, lactation length and lactation number for lactation milk yield, year and season of calving and lactation number for lactation length and year and season of calving for dry period) found significant (reported elsewhere, Javed *et al.*, 2000) were fitted in the model. The mathematical model assumed was:

$$Y_{ijk} = \mu + F_j + A_i + e_{ijk}$$

Where,

Y_{ijk} = measurement of a particular trait

μ = population mean

F_j = fixed effects observed to be significant from the initial analysis

A_i = random additive genetic effect of i th animal with mean zero and variance σ^2A

e_{ijk} = random error with mean zero and variance σ^2E

Phenotypic variance (σ^2p) = additive genetic variance (σ^2A) + residual variance (σ^2E)

The heritability was calculated by the following formula

$$\text{Heritability } (h^2) = \sigma^2A / \sigma^2P$$

RESULTS AND DISCUSSION

The least squares means for first lactation milk yield (kg), first lactation length (days) and first dry period (days) were 1579.04 ± 18.17 , 260.52 ± 2.64 and 221.68 ± 5.20 , respectively. The corresponding values for traits considering all lactations were 1862.42 ± 42.08 , 317.71 ± 3.24 and 198.30 ± 5.56 days, respectively. The performance of an individual is influenced by various environmental and genetic factors. The influence of various environmental factors on the traits under study has been reported elsewhere (Javed *et al.*, 2000).

The estimates of heritability for various first lactation and considering all lactations as obtained by

restricted maximum likelihood (REML) procedure using animal model technique are summarized in Table 1.

Table 1: Heritability estimates for productive traits

| Traits | First lactation traits | | All lactation traits | |
|------------------|------------------------|-------------------|----------------------|-------------------|
| | No. of obs. | $h^2 \pm SE$ | No. of obs. | $h^2 \pm SE$ |
| Milk yield | 1535 | 0.013 ± 0.022 | 7913 | 0.052 ± 0.032 |
| Lactation length | 1619 | 0.062 ± 0.039 | 7913 | 0.027 ± 0.013 |
| Dry period | 1909 | 0.028 ± 0.027 | 6787 | 0.029 ± 0.018 |

Milk yield

The estimate of heritability for lactation milk yield based on 1535 first lactation and 7913 all lactation records of 1615 cows progeny of 138 sires were 0.013 ± 0.022 and 0.052 ± 0.032 , respectively (Table 1). The overall heritability estimate by a repeatability model was slightly higher (0.052 ± 0.03) but was also in the lower range. Although, analysis with an animal model generally gives higher estimates than with a sire model (Sorensen and Kennedy, 1984; Visscher and Thompson, 1992), the estimates were at the lower end of the range, in comparison with most other studies on tropical breeds. However, the low estimates for lactation milk yield as obtained in the present study were fairly close to those of Yadav and Rathi (1991) and Yadav *et al.* (1994) who reported the heritability estimates for lactation milk yield as 0.03 and 0.07 in Sahiwal and Tharparkar cattle, respectively. The estimates reported by Mohiuddin *et al.* (1994) Tallbot *et al.* (1997), Dahlin *et al.* (1998) and Ahmad *et al.* (2001) ranged from 0.1 ± 0.07 to 0.20 in Pakistan Sahiwals were higher than that obtained in the present study. The estimated heritability of milk yield was reported to be 0.52 ± 0.16 in Indian Sahiwal cattle reviewed in the literature. Higher heritability estimates for lactation milk yield in other *Bos indicus* cattle herds like Red Sindhi (0.25 ± 0.10), Tharparkar (0.35 ± 0.18) and Haryana (0.26 ± 0.15) were also reported by various workers (Ruvuna *et al.*, 1984; Taneja and Bhatnagar, 1985; Pundir and Raheja, 1994), which were not in agreement with the estimate of heritability for milk yield obtained in the present study. But almost in all these studies the breeds were different and the size of data set was small. Also, the methodology used was different (Paternal half-sib correlation and Intra-sire regression of daughter on dam).

Lactation length

The heritability estimates for first lactation length based on data on first lactation records of 1619 cows was 0.062 ± 0.039 (Table 1). The heritability estimate for

lactation length considering all lactations was 0.027 ± 0.013 based on 7913 lactations of 1615 cows (Table 1). These estimates were in close agreement with those of Mohiuddin *et al.* (1994) and Gandhi and Gurnani (1995) who reported the heritability estimates for lactation length as 0.06 ± 0.05 and 0.032 in Pakistani and Indian Sahiwals, respectively. However, higher estimates (0.16 , 0.44 and 0.11) for lactation length were also reported by Reddy and Nagarcenkar (1989), Pundir and Raheja (1994) and Ahmad *et al.* (2001) in Indian and Pakistan Sahiwals. In an earlier study the highest estimate for lactation length was reported as 0.83 ± 0.29 (Singh and Desai, 1961). These estimates were not in agreement with the results of the present study.

The difference in the estimates of heritability of present study and those of other investigations might be due to breed, herd, the environmental conditions as well as the method of estimation. Low estimate indicated that the variation due to additive gene action was probably small and that the variation due to environmental factors was more important.

Dry period

The estimates of heritability for dry period on the basis of first and all lactations records were 0.028 ± 0.027 and 0.029 ± 0.018 , respectively. These estimates were based on 1909 first lactation and 6768 lactation records, respectively. Similar heritability estimates for dry period were reported by other workers. Mohiuddin (1987) reported the heritability estimates for dry period as 0.04 ± 0.05 using 811 records by paternal halfsib correlation technique in Sahiwal cattle in Pakistan. Recently, Talbott *et al.* (1997) reported heritability estimate for dry period in Pakistani Sahiwals as 0.16 after analyzing 1771 lactational records of 732 cows using animal model technique. In a more recent study, Ahmad *et al.* (2001) reported heritability estimates (0.07 ± 0.02) for dry period in combined data set of Sahiwal and their crossbreds with Holstein-Friesian and Jersey breeds of cattle. Whereas Ahmad and Ahmad (1974) reported negative estimates of heritability for dry period in Sahiwal cattle by the methods of paternal halfsib correlation (-0.09 ± 0.02) and intrasire regression of daughter on dam (-0.10 ± 0.05) using 900 paternal halfsibs and 556 daughter-dam pairs in Pakistan. Higher estimates of heritability for dry period as 0.16 ± 0.13 (Sahiwal), 0.11 ± 0.10 (Haryana) and 0.49 (Holstein Friesian) were also reported by Reddy and Nagarcenkar (1989), Pundir and Raheja (1994) Majuja and McDaniel (1996), respectively. These estimates are not in conformity with the estimates obtained in the present study. However, the data set in these studies was small except for Holstein Friesian. The low heritability estimate for dry period indicates that dry period is probably not under the influence of additive gene action

and is an environmental trait. For genetic improvement in this trait, some special procedures of selection would be applied.

The heritability estimates varied between breeds, herds, level of productivity, method of estimation and even periods of time for a particular trait. Inbreeding (Falconer and Mackay, 1997) might reduce the genetic variance, whereas, different management and environmental factors in different breeds, herds and years might increase the phenotypic variation. The low estimate of heritability could also be a function of lower production, misidentification (Cristensen *et al.*, 1982) and for animal model, incomplete pedigrees (Sorensen and Kennedy, 1984) might also have contributed to the lower heritabilities.

The heritability estimates of almost all the traits under study were low. The low heritability is caused not only by a low genetic variance but rather by a higher phenotypic variance due to small size of the herd and also by random or unidentified environmental factors. Considering that climate, disease and other environmental factors exert greater effects on performance in subtropical and tropical regions than in temperate regions, it is not surprising that heritability might be lower.

Genetic improvement in Sahiwal cattle has been negligible over the past five decades in Pakistan. Ahmad *et al.* (1978) reported 0.18 per cent genetic improvement in a purebred herd of Sahiwal cattle. Similarly, Talbott *et al.* (1997), Dahlin *et al.* (1998) and Javed (1999) observed no genetic change in Sahiwal cattle in Pakistan indicating that the selection strategy as well as the breeding programme in the past was ineffective and roughly similar trend will be expected in the presence of random mating. In the presence of low population of recorded Sahiwals in Pakistan (Dahlin *et al.*, 1995) and low heritabilities, it is important to utilize all information as efficiently as possible for better genetic evaluations. Selection schemes for genetic improvement of dairy animals also require both pedigree and performance recording more precisely. The recording system in Pakistan has been limited to institutional herds only. Its extension to field is required because institutional herds do not have sufficient number of animals that can provide enough accuracy to genetic evaluation programmes.

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