

A NOTE ON ESTIMATION OF HERITABILITIES OF DIFFERENT DAIRY CHARACTERISTICS OF KANKREJ BREED BY DIFFERENT METHODS

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ABSTRACT

Age at 1st calving, lactation yield and lactation length are important characters in dairy cattle. Different methods such as ANOVA, ML, REML, MIVQUE are used to estimate variance components and in turn, heritability which is one of the most important genetic parameter for selection of sires for breeding purpose. In this paper, heritabilities of age at 1st calving, lactation yield and lactation length in Kankrej breed have been estimated using the above 4 methods and estimates so obtained are compared.

An important aspect of formulation of breeding plan for animal or plant improvement is selection which amounts to choice of parents to produce the next generation. A basic prerequisite to the planning of breeding programme is that of the total variability existing in the population and how much of this is caused by differences in the genetic make-up of the individuals. A quantitative measure of this is provided by heritability. With the help of heritability one can predict the breeding value of the individual. The magnitude of heritability dictates the choice of the selection method and breeding system. Several methodologies for estimation of heritability are available in the literature.

In this paper a critical look on the estimation of heritability by different methods of estimation of genetic variance components for different milking characteristics of Kankrej breed has been made.

For the present study, the data relating

to age at first calving, lactation length and lactation yield of 143 daughters of 11 sires during the period from 1941 to 1965 were taken from the records of Kankrej herd maintained at the Institute of Agriculture, Anand and have been used. As the heritability is a function of variance components, so the 4 methods of estimation of variance components have been used as under :

- (1) ANOVA as per Henderson (1953),
- (2) Maximum Likelihood (ML) as per Harville (1977),
- (3) Restricted Maximum Likelihood (REML) as per Patterson and Thompson (1971). Further, Meyer (1986) showed its extensive use in estimation of genetic parameter.
- (4) Minimum Variance Quadratic Unbiased Estimation (MIVQUE) as per Rao (1971).

The analysis of the data using half-sib analysis in SAS software package was carried out and the results obtained are presented in Table 1.

Table 1. Estimation of heritability by different methods

	ANOVA	ML	REML	MIVQUE
Age at 1st calving	1.1253 (0.1143)	0.7236 (0.0951)	0.7902 (0.0989)	1.8746 (0.1272)
Lactation length	0.3089 (0.0661)	0.2503 (0.0613)	0.2909 (0.0647)	0.4397 (0.0763)
Lactation yield	0.3079 (0.0660)	0.2553 (0.0617)	0.2986 (0.0653)	0.3878 (0.0724)

Figures in brackets indicate Standard Errors of the estimates.

From the data which is highly unbalanced and from Table 1, it is noticed that the ANOVA and MIVQUE methods gave inadmissible estimates of heritability with relatively high standard errors for the character age at 1st calving. ML and REML methods, however, gave good results for all the characters considered for the study in the sense that the standard errors obtained are less as compared to those obtained by ANOVA and MIVQUE methods. It is thus suggested that when data are unbalanced, then it is desirable to use ML method or REML method as compared to ANOVA and MIVQUE methods. This will ensure comparably precise and accurate estimates of heritability.

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