A GENETIC INTERPRETATION OF RESULTS OBTAINED IN *BOS INDICUS* X *BOS TAURUS* CROSSBREEDING FOR MILK PRODUCTION

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SUMMARY

The simplest genetic model which explains the results for milk yield in *Bos indicus* x *Bos taurus* crosses is one which assumes that *Bos taurus* animals are homozygous for one or more sets of dominant genes which are complementary to one another.

INTRODUCTION

In a review of reports on *Bos indicus* (zebu) x *Bos taurus* (European type) cattle crossbreeding for milk production, means of the various groups were extracted and summarized by fitting constants to sets of data and genetic groups simultaneously. Main results are reported elsewhere (Syrstad 1988). The purpose of the present paper is to suggest a genetic interpretation of the findings.

DATA

Altogether 54 sets of data were included in the study. The traits studied were age at first calving, lactation yield and calving interval. The least squares means for various genetic groups are presented in Table 1.

Table 1 Performance of *Bos indicus* x *Bos taurus* crosses. Least squares means, summary of 54 sets of data.

Proportion *Bos taurus*[1]	Age at first calving, months	Milk kg	Calving interval, days
0	43.6±0.6	1052± 39	459± 5
1/8	40.1±2.8	1371±170	450±21
1/4	37.5±2.9	1310±158	435±23
3/8	36.1±1.4	1553±100	435±12
1/2 (F_1)	32.4±0.5	2039± 28	429± 4
5/8	33.8±1.1	1984± 75	432± 9
3/4	33.9±0.7	2091± 45	450± 6
7/8	34.4±1.2	2086± 84	459±11
1	31.6±0.9	2162± 50	460± 7
1/2 (F_2)	33.7±1.3	1523± 92	449±12

[1] All groups except F_2 were sired by purebred bulls.

GENETIC MODELS

In the first crossbred generation, F_1, a significant heterosis was observed in all traits, demonstrating the presence of dominance. Also the other genetic groups performed approximately according to the additive + dominance model, except F_2 (from F_1 x F_1), which had much lower milk yields than expected. With additive and dominance effects only, the performance of F_2 would be expected to be midway between midparent mean and F_1, as one half of the extra heterozygosity in F_1 is lost in F_2. The discrepancy between predicted and actual milk yield in F_2 was 300±94 kg. This suggests that also non-allelic gene interaction (i.e. epistasis) is involved, and that some of these effects are lost in F_2 (recombination loss). However, when the data of all genetic groups were analysed in a multiple regression analysis including additive effects, heterozygosity and additive x additive epistasis (Dickerson 1973, Koch et al. 1985), the coefficient for epistasis was not significantly different from zero. By this method the recombination loss in F_2 was estimated at 103±61 kg. The disagreement between the two estimates suggests that the genetic model of epistasis underlying the regression analysis might be inadequate.

Visual inspection of the least squares means reveals that the main deviation from the additive x additive epistasis model is in the performance of the *Bos taurus* backcross. This group is midway between pure *Bos taurus* and F_1 in both additive effects and heterozygosity, and should suffer one half of the recombination loss in F_2. In fact no loss is observed in this group, the mean is almost exactly midway between F_1 and the *taurus* parent. In contrast the mean of the Bos *indicus* backcross suggests a recombination loss of about 15% in this group.

The lack of recombination loss in the *taurus* backcross can be explained by assuming that epistatic effects are dominance x dominance rather than additive x additive. This is a simplified version of the parental epistasis model proposed by Sheridan (1981). Assume that the *taurus* parent was homozygous for two dominant genes, say A and B, which are complementary to one another. This combination of genes would be intact in F_1 and other crosses having one *taurus* parent. Among the crosses with less than 1/2 *taurus* inheritance the proportion of individuals carrying both A and B genes would be 1/16 (for 1/8 *Bos taurus*), 1/4 (for 1/4 *Bos taurus*) and 9/16 (for 3/8 *Bos taurus*). The proportion of F_2 individuals having the AB combination would be 9/16, i.e. the proportion of epistasis lost would be 7/16. In general the proportion of dominance x dominance epistasis in one of the parental breeds which is retained in a composite population equals $[1-(1-p)^2]^2$, where p is the proportion of inheritance originating from the breed in question.

RESULTS AND DISCUSSION

A statistical model including additive gene effects, heterozygosity and dominance x dominance epistasis was fitted to the means for milk yield in Table 1. The various means were weighed by the inverse of their variance. When the independent variables were considered in the above order all effects were highly significant, and the model accounted for more than 99% of the total sum of squares. However, the partial effect was significant only for the epistasis, which alone explained 98% of the sum of squares.

The partial regression coefficients obtained in the multiple regression analysis were used to construct the graph in Fig. 1.

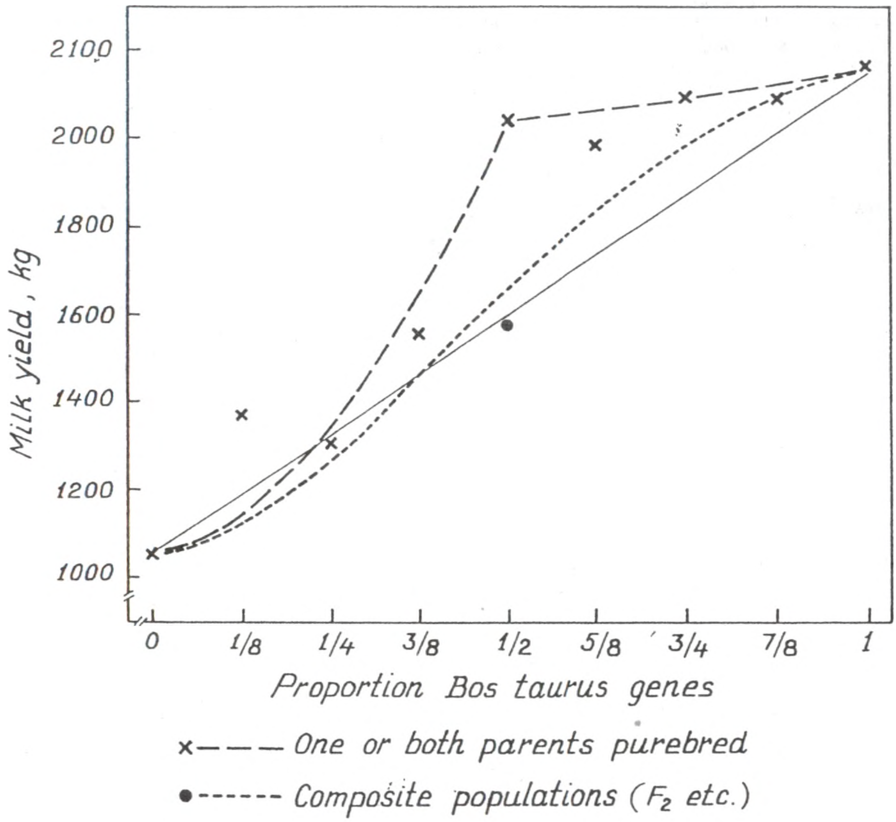

Fig. 1. Milk yield in various Bos indicus x Bos taurus crosses. The curves are fitted to the data in a model including additive gene effects, heterozygosity and dominance x dominance epistasis.

The amount of heterosis expressed in a particular cross is shown by the deviation of this cross from the straight line. It is seen that heterosis in a composite population reaches a maximum when the proportion of taurus genes is around 3/4, and that it is negative if this proportion is less than about 3/8. If more than two loci are involved the loss would be even larger, resulting in a negative heterosis in F_2 (Sheridan, 1981).

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