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GENETIC VARIABILITY AND SIRE X MATING SYSTEM INTERACTION
FOR MILK YIELD IN HOLSTEIN-SAHIWAL CROSSES

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SUMMARY

The average first lactation milk yield of crossbreds in northern region was higher than that in southern region with heritability estimates being 0.16 ± 0.06 and 0.04 ± 0.04 . The heritability estimates according to production level were 0.28 ± 0.14 , -0.02 ± 0.04 and 0.36 ± 0.15 for low, medium and high level herds in northern and -0.05 ± 0.01 and 0.03 ± 0.12 for low and high level herds in southern region, suggesting more genetic variability in relation to total variance in high level herds. The reasons for low estimates in medium level herds have been discussed. The sire x genetic group interaction was estimated from (i) two way analysis of variance, and (ii) genetic correlation between the same trait expressed in two genetic groups. The sire x genetic group interactions were non-significant and the genetic correlations were 0.87 and 1.00 in northern and southern region, respectively. The sire x breed of dam interaction was non-significant for all breed group combinations.

INTRODUCTION

A popular opinion is that it is easier to distinguish between genotypes under better environmental conditions. The validity of this opinion depends on the answers to two questions (1) whether the genetic variability of dairy records is different under different levels of herd management and (2) is it easier to detect sire differences at some management levels than others? The present study, accordingly, was undertaken to examine genetic variability at different levels of production and to study the sire x genetic group interactions for milk yield in Holstein-zebu crosses.

MATERIALS AND METHODS

The milk yield data on 1403 Holstein-Friesian (H) x Sahiwal crossbred cows from 10 farms in the central and northern and 986 Holstein-Friesian X Sahiwal crosses from 6 military farms in southern India were used. Records from 1967 to 1975 were studied. The analysis of data for the two regions was carried out separately as the sires used were different. The farms were stratified into three production levels as low (milk yield less than 2500 kg), medium (milk yield between 2500 and 2600 kg), and high (milk yield more than 2600 kg) in northern and two production levels as low (milk yield less than 2500 kg), and high (milk yield more than 2500 kg) in the southern region. The records corrected for significant environmental effects were used for estimation of heritability. The sire x genetic group interaction for milk yield was estimated from (1) two way analysis of variance and (2) the genetic correlation between the same trait expressed in two genetic groups (Yamada, 1962). Apart from Holstein-Sahiwal crosses, 1/2 Holstein-1/2 Tharparkar (Thp), 1/2 Holstein-1/2 Sindhi (Sdi) and 3/4 Holstein-1/4 Hariana (Har) in the northern and 1/2 Holstein-1/2 Gir crosses in the southern region, sired by the same set of bulls, were used to study the combining ability of

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UK	107.6	107.9	100.3	101.0	106.2	103.0	101.6
Sweden	109.8	110.8	100.8	102.3	107.1	106.4	99.6
W.Germany	108.2	107.8	99.8	102.3	104.6	103.9	100.1
Netherlands	106.0	106.4	100.4	101.6	98.2	99.1	100.9
Israel	116.1	116.1	100.1	103.4	112.9	110.4	98.7
New Zealand	110.6	113.5	102.6	102.7	105.1	107.3	100.9
Poland	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	3047.1kg	120.0 kg	3.93%	277.4days	3067.5kg	120.8kg	3.90%
							277.2days

Minimum number of observations was 144 and maximum 279 per strain

Holstein sires with different Indian breeds.

RESULTS AND DISCUSSION

The average production of the crossbred grades in northern region was higher than that in the southern region. Accordingly, it was assumed that the southern region represented a lower environmental level than the northern region. The heritability estimates for milk yield in the northern and southern region were 0.16 ± 0.06 and 0.04 ± 0.04 , respectively suggesting that genetic variability was higher at higher production levels. In view of the fact that the sires used in the two regions were entirely different and the number of records in the southern region were much less; these considerations seem to hamper the validity of the comparisons. Nevertheless, these estimates do indicate the trend of variability at different levels of production. In order to take care of this inadequacy, the heritability estimates were made for different production levels in each region. The heritability estimates for different herd levels in the northern region were higher in high level (0.36 ± 0.12) than low level herds (0.28 ± 0.14). The heritability was very low in medium level herds (-0.02 ± 0.04). Similarly, in the southern region, the heritability in the high level herds was higher (0.03 ± 0.12) than the low level herds (-0.05 ± 0.01). Both sets of estimates (intra and inter-regional) seem to support the view that there is more genetic variability relative to total variance in high level herds. More genetic variability in high level herds has been reported by Mason and Robertson (1956), and Van Vleck (1963). On the other hand Robertson *et al.* (1960), Burnside and Rennie (1961), Legates (1962) and Touchberry (1963) reported increase in size of both genetic and residual variability, so that heritability was constant at all levels. The low sire variance in the medium level herds probably was due to the reason that the level of feeding in the medium level herds was not able to aid the fullest expression of the best genotypes, but at the same time was not as unfavourable as in the low level herds. In consequence, the performance of all the animals was uniform at the medium level, thus leading to very low genetic differences. It may be mentioned that sire x herd and sire x herd-level interactions for milk yield in the present study were non-significant. The differences therefore, in genetic variability at different levels of production suggest the manifestation of a second type of genotype-environment interaction.

Evaluation of sires used in crossbreeding programmes entails the use of information on crossbred daughters of different genetic groups (e.g. 1/2, 5/8, 3/4 etc.). Occasionally, sires evaluated on the basis of performance of daughters belonging to a particular genetic group may be used to improve the performance of other genetic groups as well. The success of such sire selection programmes and the rate of improvement in the crossbred populations on account of sires thus selected depends on whether the sire x genetic group interactions are important or not. If interactions are important the sires evaluated on the performance of daughters belonging to a particular genetic group may not rank the same when evaluated using daughters belonging to another genetic group. Conversely, the sires evaluated on the performance of daughters of a particular genetic group may not be equally effective in improving the performance of other genetic groups. This situation is referred to as sire x mating system interaction and specific combining ability of sires. In the present data, the same set of Holstein sires were used to produce 1/2, 5/8, 3/4 and 7/8 Holstein crosses, making this data suitable for the study of sire x genetic group interaction. The data corrected for all non-genetic significant effects were used to study the sire x genetic group interaction.

The sire x genetic group interaction for milk yield was non-significant both in the northern and southern region (Table 1). The corresponding estimates of genetic correlations for milk yield were 0.87 and 1.0 respectively, thus suggesting that sire x genetic group interactions are not important to be reckoned with in sire evaluation

Table 1 . Sire x genetic

Source	Northern df
Sires	14
Genetic groups	3
Sire x genetic group	42
Error	1343

programme and that the crossbred grades can safely be combined to estimate the breeding values were made by Allair and Henderson. The sires ranked the same, when used to produce cattle. Robertson and Fairlie (1973), who evaluated the basis of purebred and crossbred daughters, found similar in both the evaluations.

The crosses of Holstein sires with various Indian breeds. The combining ability of Holstein sires with various Indian breeds of dam interaction was non-significant for milk yield. It was found that Holstein sires combined equally well with all the Indian breeds.

Table 2 . Sire x breed o

Source	Northern region			
	1/2 H-1/2 Sh vs 1/2 H-1/2Thp	MS	1/2 H-1/2 S vs 1/2 H-1/2 S	M
	df		df	M
Sires	8	499145	3	8196
Genetic groups	1	17147	1	5594
Sire x genetic group	8	620415	3	2388
Error	120	374283	86	2242

sire x mating system interaction for milk yield. The data were corrected for all non-genetic significant effects and Touchberry (1966).

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Table 1 . Sire x genetic group interaction effects

Source	Northern region		Southern region	
	df	MS	df	MS
Sires	14	890135	8	398379
Genetic groups	3	829227	3	835850
Sire x genetic group	42	440753	24	349997
Error	1343	426688	840	384244

programme and that the crossbred daughters with varying levels of exotic inheritance can safely be combined to estimate the breeding value of sires. Almost similar observations were made by Allair and Henderson (1963). Young *et al.* (1969) observed that sires ranked the same, when used to produce outcross inbred or line crosses in Holstein cattle. Robertson and Fairlie (1973), while evaluating the purebred Ayrshire bulls on the basis of purebred and crossbred daughters, observed that ranking of the sires was similar in both the evaluations.

The crosses of Hostein sires with various indigenous breeds were used to study the combining ability of Holstein sires with various Indian breeds. The sire x breed of dam interaction was non-significant for all combinations (Table 2), thus suggesting that Hostein sires combined equally well with all indigenous breeds. Non-significant

Table 2 . Sire x breed of dam interaction effects

Source	Northern region						Southern region	
	1/2 H-1/2 Sh		1/2 H-1/2 Sh		3/4 H-1/4 Sh		1/2 H-1/2 SH	
	vs		vs		vs		vs	
	1/2 H-1/2Thp	1/2 H-1/2 Sdi	3/4 H-1/4 Har	1/2 H-1/2 Gir				
	df	MS	df	MS	df	MS	df	MS
Sires	8	499145	3	81960	8	334499	7	183391
Genetic groups	1	17147	1	559459	1	82979	1	225547
Sire x genetic group	8	620415	3	238875	8	489421	7	189318
Error	120	374283	86	224256	102	386550	290	376267

sire x mating system interaction for milk yield has also been reported by Bereskin and Touchberry (1966).

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CROSSBREEDING OF CATTLE

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SUMMARY

Sri Lanka is an island in the tropics with a population of about 1.7 million. In order to improve the dairy production crossbreeding trials were initiated about 1960.

The indigenous cows were bred to Shorthorn breeds. Imported Zebu breeds were also bred to bulls of temperate breeds.

The article describes the findings of the trials and discusses the usefulness in formulating breeding policies for different agroclimatic zones of the country.

INTRODUCTION

Sri Lanka has an area of about 65,000 square miles, about 5.5 degrees above the equator. The population is about 1.7 million and the average production of an indigenous cow is about 1000 kg of milk in a 280 day lactation period. A Jersey cow produces about 55 kg of boneless meat.

The country can be divided into three agroclimatic zones. The ecology of these areas is shown in Table 1. The central region having an elevation of 915 metres above sea level is the zone bordering the hill country. The hill country is from 305 - 919 metres above sea level. Jersey, Friesian, Shorthorn, Ayrshire and Jersey crosses do well in the mid country while their crosses do well in the mid country.

The terrain in the coconut growing zone is such that pasture can be grown under coconut. Coconut is grown from the hot sun. More than 50% of the national population lives in the hill country. These animals forage on natural pastures. Diseases such as haemorrhagic septicaemia are common. Farmers sell their surplus stock to butcher shops in towns where abattoirs are located.

Crossbreeding research was directed to determine the best policies for different agroclimatic zones. This paper discusses the experiments carried out in the hill country.

Karagoda Uyangoda Experiment

This farm is situated in the south central region of Sri Lanka. The annual rainfall is 2500 mm and the relative humidity is high. The experimental design is shown diagrammatically in Figure 1.