ADDITIVE AND NON-ADDITIVE GENETIC EFFECTS IN FRIESIAN, JERSEY AND SAHIWAL CROSSES IN PAKISTAN

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SUMMARY

Data on 4,023 lactation records (parity 1 to 5) on purebred Sahiwal cows and 2,391 lactation records of Holstein Friesian X Sahiwal (FS) and Jersey X Sahiwal (JS) crossbreds in Punjab, Pakistan were analysed to study additive and non-additive breed effects for production and reproduction traits: lactation milk yield (LMY), calving interval (CI), milk yield per day of calving interval (MCI), days open and days dry. Heterosis effects were significant and in a favourable direction for all production and fertility traits. Compared with the mid-parent mean, the F_1 would increase LMY by 31 % in FS and by 41 % in JS crosses. The MCI would be increased in these crosses, by 49 % and 51 %, respectively. For reproduction traits there was a decrease in days open: 35 and 60 %; days dry: 41 and 72 % and CI: 15 and 20 % for FS and JS crosses, respectively. Heterosis effects were larger than breed additive effects. Additive breed effects for FS crosses were larger than for JS crosses, and FS crossbreds were superior to JS crossbreds in LMY and MCI. The effects of recombination loss were found significant in this study.

Keywords: *Bos indicus*, *Bos taurus*, crossbreeding, heterosis, recombination loss

INTRODUCTION

For developing a dairy programme in Pakistan, Sahiwal cattle could provide germ plasm for crossbreeding with *Bos taurus* (*BT*: Friesian or Jersey) breeds. The Sahiwal breed is considered more productive among indigenous species (Khan *et al.* 1992). The improvement in genetic potential through within breed selection is very slow (<1 % per year), and such rates are insufficient to improve production from indigenous breeds for a fast growing human population in the country. A possible solution is to crossbreed, combining the desired characteristics of both species; milk production from *BT* and adaptability from *Bos indicus* (*BI*: indigenous) cattle. Cunningham and Syrstad (1987) noted that the improvement in genetic potential in *BT* X *BI* crossbreeding could be equal to 100 years of selection. The present investigation was undertaken to calculate the additive and non-additive breed effects in Friesian, Jersey and Sahiwal crosses in Pakistan. These parameters would be needed to predict the possible improvement made in crossbreds with respect to various production, reproduction and fitness traits and would help to assess the potential for crossbreeding programmes.

MATERIALS AND METHODS

The data set included 4,023 lactation records (parity 1 to 5) on 1,172 purebred Sahiwal cows, 2,182 lactation records on 748 Friesian crossbreds and 209 records on 76 Jersey crossbreds from LPRI Bahadurnagar and from Qadirabad in Punjab, Pakistan. Five economically important traits: lactation milk yield (LMY), calving interval (CI), milk yield per day of calving interval (MCI), days open and days dry were included in this study. Data was split in two sets, one for Sahiwal and its crossbreds with Holstein Friesian (FS) and another for Sahiwal and its crossbreds with Jersey (JS). Two models were compared: a regression model where additive breed, heterosis and epistatic (recombination loss) effects were fitted as regression coefficients, and a breed group model. Fixed effects of herd-year-season and calving age within parity and random cow effects were common in both models. The models were fitted using ASREML (Gilmour and Thompson 1998). Breed group representation is given in Table 1.

Table 1. Representation of different breed groups and their non-additive genetic effects

Breed groups	% BT*	% heterosis	% recomb.	Friesian x Sahiwal No. of records	Jersey x Sahiwal No. of records
3/4	75	50	25	161	21
5/8	62.5	50	44	113	8
F1	50	100	0	934	138
F2	50	50	50	465	12
F3	50	50	50	300	-
F4	50	50	50	75	-
3/8	37.5	50	44	43	5
1/4	25	50	25	91	25
Sahiwal	0	0	0	4,023	4,023

* BT = Bos taurus (Friesian or Jersey breeds).

RESULTS

Heterosis effects were highly significant for all traits of the Sahiwal crosses with Holstein Friesian and Jersey (Tables 2 and 3). Additive genetic differences between Sahiwal and Jersey were not significant for any of the traits but between Holstein and Sahiwal they were significant for most of the traits. Generally, heterosis effects were larger than breed differences, especially for Jersey crosses. The effect of recombination was also significant for both crosses except for JS crosses where there was little information available about this parameter (Table 3).

The regression model and the breed group model were compared for MCI, having the highest level of heterosis (49 %) in Friesian crossbreds. The predicted least square means for this trait in Friesian crosses from both models is given in Figure 1. This figure shows that predicted means for both models were reasonably similar.

Table 2. Additive and non-additive breed effects for Friesian crosses

Trait	Sahiwal means	Additive est	± se	Heterosis est	± se	Recombination est	± se
LMY (kg)	1,770	783**	200	670**	110	-650**	143
CI (days)	482	32.3	24.0	-76.9**	11.4	-93.7**	10.7
MCI (kg)	3.94	1.52**	0.48	2.32**	0.26	-0.46	0.35
Days open	196	60.7*	25.8	-80.4**	14.0	-98.1**	19.3
Days dry	209	11.4	26.4	-88.0*	14.2	-80.4*	19.5

** P < .01   * P < .05

Table 3. Additive and non-additive breed effects for Jersey crosses

Trait	Sahiwal means	Additive Est	± se	Heterosis Est	± se	Recombination est	± se
LMY (kg)	1770	379	422	813**	230	-560	484
CI (days)	482	-42.4	68	-94.1**	36	-136	81
MCI (kg)	3.94	1.90	1.12	2.50**	0.60	-1.47	1.25
Days open	196	3.0	69	-118 **	37	-138	81
Days dry	209	11.4	771	-154**	41	-150	92

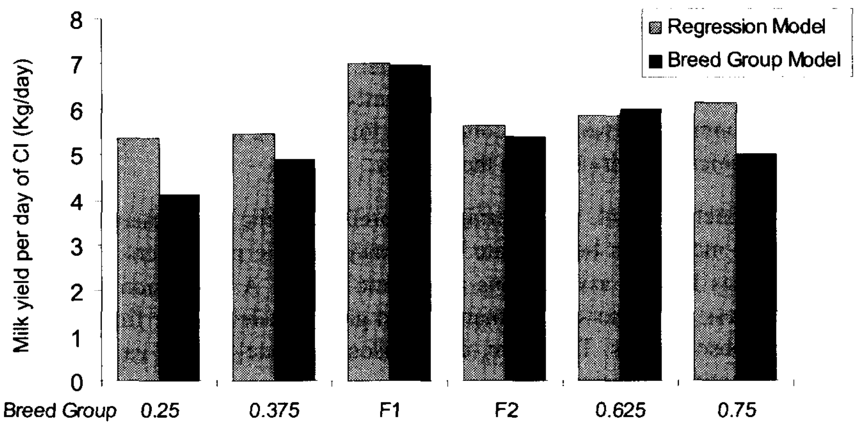

Figure 1. Comparison of two models for prediction of MCI in Friesian crossbred groups.

Differences with the least square estimates obtained from breed group model were larger for Jersey (not shown). An explanation is that breed group estimates from the regression model were inaccurate due to the fact that regression coefficients in Jersey crossbreds had very high standard errors and some genetic groups had a small number of observations.

Least squares means indicate that almost all crossbreds were superior to Sahiwals for having shorter CI, less days dry and days open. MCI was also improved in all the crossbreds. LMY was better in crosses having ≥ 50 % *BT* in case of FS crosses. In case of JS crosses there was an improvement in LMY only in F_1 crosses. FS crosses were superior to JS crosses for production and MCI but JS were better for reproduction traits.

DISCUSSION

In our study, heterosis effects were larger than additive breed effects, indicating that a 50 % composite breed would outperform purebred Friesians. This might be typical for harsh tropical environments. Martinez *et al* (1988) reported higher estimates for the additive genetic than for the heterosis effects in farms where management practices appeared to support higher level of production (>2,800 kg /lactation). The substantial milk depression observed in the F_2 relative to F_1 (indicated as recombination) has been well documented by others (McDowell 1985 and Syrstad 1989). Syrstad (1989) attributes this decline to a reduction in the epistatic effects. An F_2 cross would retain only 50 % of the heterosis and have an additional loss due to recombination effects. Significant recombination effects would have negative effects on composites. However, such losses might be recovered by a selection program within the composite.

CONCLUSION

This study emphasises the importance of developing a breeding strategy that maintains a high level of heterosis to maximise both milk production and fitness in sub tropical environment of Pakistan, where inputs are limited. Heterosis effects were significant and in a favourable direction for all traits, whereas additive effects from BT were smaller. Continuously producing F_1 crosses is not a practical solution because producers have to constantly rely on external sources to purchase replacements. The development of two breed composite, for example an FS composite, is a more practical way for improvement of dairy stock in the country.

The fitting of a good genetic model, is important for predicting the performance of crossbred progeny. The regression model can be accurate to estimate genetic parameters. A breed group model is robust and relies less on assumptions of genetic model. A regression model is more accurate since there are less parameters to estimate. Breed group models suffer from inaccuracy if some groups have few observations. Therefore, comparison of models is not easy for crossbred experiments that are not optimally designed.

REFERENCES

Cunningham, E.P. and Syrstad, O. (1987) *FAO Anim. prod. health paper* No.**68**, Rome, Italy

Gilmour, A.R. and Thompson, R. (1998) *Proc. 6th World Congress on Genetics Applied to Livest. Prod.* **27**:453

Khan, U. N., Olsson, A. and Philipsson, J. (1992) *Proc. 6th AAAP Anim.Sci. Cong.* Vol.**I**:171. Bangkok

Martinez, M.L., Lee, A.J. and Lyn, C.Y. (1988) *J.Dairy Sci.* **71**: 80

McDowell, R.E. (1985) *J.Dairy Sci.* **68**: 2418

Syrstad, O. (1989) *Livest. Prod. Sci.* **23**:97