



Sire evaluation of milk producers' co-operative union limited of Bangladesh

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Abstract

Data on 3637 cows of seven genetic groups at Baghabarighat milk shed area, from 1991 to 2000 were analyzed. The genetic groups were Pabna Milking (PM) cows, $\frac{1}{2}$ PM \times $\frac{1}{2}$ Sahiwal (PM \times SL), $\frac{1}{2}$ PM \times $\frac{1}{2}$ Friesian (PM \times FN), Australian Friesian Sahiwal (AFS), $\frac{1}{2}$ Sahiwal \times $\frac{1}{4}$ PM \times $\frac{1}{4}$ Friesian [SL(PM \times FN)], $\frac{1}{2}$ Friesian \times $\frac{1}{4}$ PM \times $\frac{1}{4}$ Sahiwal [FN(PM \times SL)] and $\frac{1}{2}$ Friesian \times $\frac{1}{4}$ Sahiwal \times $\frac{1}{4}$ Jersey [FN(SL \times JR)]. The purpose of this study was to predict breeding values (PBV) of dairy sires using individual daughters performance (birth weight, lactation yield, fat% and SNF%) records at Baghabarighat milk shed area. The heritability values were estimated as 0.27 ± 0.05 for birth weight, 0.45 ± 0.03 for lactation yield, 0.37 ± 0.04 for fat% and 0.46 ± 0.01 for SNF%. The high genetic variability of birth weight, lactation yield, fat and SNF% indicates that there is a great opportunity or genetic improvement when these traits are included in a selection scheme. The first 3 top sires were 24, 14 and 20 for birth weight; sire number 19, 36 and 23 for lactation yield; sire number 16, 11 and 26 for fat % and sire number 14, 19 and 16 for SNF% were ranked on the basis of PBV.

Key words: Dairy cows, heritability, prediction of breeding values

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Introduction

Genetic improvement of dairy cattle has become a global venture. Farmers routinely use semen of foreign sires and breeding companies acquire genetic information from a variety of countries. With the international exchange of cattle and of different genotypes there arise a need for evaluation animals that differ in housing conditions, feeding programs and genetic composition of mates. Genetic differences between countries and strains are smaller and statistical evaluations are needed to compare animals fairly and accurately. The genetic gain associated with the production performance mainly comes through sires because of its favorable reproductive differential and higher selection intensity. Therefore, the success of any breeding strategy depends on the identification of genetically superior sires and their maximum utilization. Suitable methodology of selection, which gives best discrimination among sires, should be formulated to evaluate the sires based on their progeny performance. Bangladesh Milk Producers' Cooperative Union Limited (BMPCUL) was established in 1973 with the Government initiative as an emerging mega cooperative society. With the passage of time, considering the well adaptability of Sahiwal breeds under

ecological conditions, BMPCUL has been carrying out an upgrading program from 1987 using deep frozen Sahiwal semen. For improving genetic merit for milk production the BMPCUL used deep frozen semen of Australian Friesian Sahiwal, Friesian and Jersey breeds. As a result, temperate dairy inheritance level of cattle of these areas became elevated.

Literature concerning comparative evaluation among sires used in Baghabarighat milk shed area is in extreme paucity. Thus it is important to prediction of breeding values of dairy sires using individual daughters' performance records at Baghabarighat milk shed area to compare them with the existing literatures. Generally, selection of sire is based on complete lactation yields, which are predicted from individual test day milk records taken at monthly intervals (Pander et al. 1992). Selection on test day milk records in the early part of lactation would result in a reduction in generation interval, cost of recording and maintaining cows and bulls with low breeding values. The object of this study was to assess breeding values of different productive traits like birth weight, lactation yield, fat% and solids-not-fat % of the progeny of dairy sires used in the Baghabarighat milk shed area since 1990.

Materials and Methods

The study was conducted at the Baghabarighat milk shed area under Bangladesh Milk Producers' Co-operative Union Limited (BMPCUL) of Pabna and Sirajgonj districts in Bangladesh. BMPCUL has been carrying out intensive cattle breeding program through AI using deep frozen semen collected from bulls of different genetic merits since 1987. Deep frozen semen from 31 breeding bulls of different breeds was used as sire line in the present study (Table 1). Out of them, 14 were SL, 10 were FN, 5 were AFS, 2 were JR and 1 was PM.

Table 1. Breeding bulls used in this study

Sire ID	Source	Genetic Composition	No. Progeny
11	Pabna, Bangladesh	PM	115
12	NDDDB, India	FN	120
13	NDDDB, India	FN	119
14	New-Zealand	SL	125
15	New-Zealand	SL	105
16	New-Zealand	SL	110
17	New-Zealand	SL	135
18	New-Zealand	SL	110
19	CCBDF, Bangladesh	FN	110
20	CCBDF, Bangladesh	FN	135
21	CCBDF, Bangladesh	SL	115
22	NDDDB, India	JR	120
23	NDDDB, India	JR	125
24	CCBDF, Bangladesh	FN	110
25	CCBDF, Bangladesh	SL	115
26	CCBDF, Bangladesh	SL	105
27	CCBDF, Bangladesh	SL	115
28	CCBDF, Bangladesh	SL	105
29	Pakistan	SL	110
30	Pakistan	SL	115
31	Pakistan	SL	115
32	Pakistan	SL	125
33	Australia	FN	125
34	Australia	FN	135
35	Australia	FN	115
36	Australia	FN	120
37	Australia	AFS	118
38	Australia	AFS	120
39	Australia	AFS	115
40	Australia	AFS	120
41	Australia	AFS	110

NDDDB, National Dairy Development Board; CCBDF, Central Cattle Breeding and Dairy Farm; PM, Pabna milking; FN, Friesian; SL, Sahiwal; JR, Jersey; AFS, Australian Friesian Sahiwal

In this study, sires were ranked according to the predicted breeding values calculated using their daughters' performance. Most of the cows at study area were of PM and graded type, owned by farmers. The performance records of 3637 cows of seven genetic groups like PM, PM×SL, PM×FN, AFS, SL(PM×FN), FN(PM×SL) and FN(SL×JR), sired by 31 breeding bulls were collected from the study area.

The effects and ranks of 31 sires were estimated on the basis of performance of their daughters. The sires were evaluated for four production traits viz. birth weight, lactation yield, fat and SNF%. The total quantity of collected milk throughout the lactation period was defined as lactation yield of the cow. The use of test day yield instead of 305-d lactation yield has recently become the focus of many researchers on evaluation systems for dairy cows. Each cow was hand milked on every 30th d (test day) up to last day of lactation. The first milk production was recorded at the 10th day of parturition and lactation yield was calculated by summing up the milk of test days (excluding first nine days). The first nine days were needed for adjustment of suckling and proper milking of the cows. Finally, the lactation yield of individual cow was estimated by test day method as described by Chacko and Schneider (2005).

The variance components for each trait were estimated by the Residual Maximum Likelihood (REML) method with the variance component estimation (VCE) computer program (Neumaier and Groeneveld 1998). The optimization in VCE was done with Quasi-Newton procedure and included setting up the mixed model equation, numerical factorization, solving the triangular system, computing the sparse inverse and assembling the gradients. The following model described the analyzed traits:

$$Y_{ij} = F_i + b(A_j - A) + a_j + e_{ij}$$

where Y_{ij} =phenotype of j^{th} cow in i^{th} genetic group; F_i =fixed effect of i -th genetic group; b =linear regression coefficient of observation on age; A_j =age of the cow; A =average age of cow; a_j =random additive genetic effect; e_{ij} =random residual term.

Results and Discussion

The variance components (additive genetic, environmental and residual) and heritabilities along with their SE for different productive traits are summarized in the Table 2.

Crossbred sire ranking

Table 2. Variance components and heritability estimates for productive traits using pooled dataset (n=3637)

Traits	σ^2_P	Variance components ¹			Heritability (h ²)
		σ^2_A	σ^2_E	σ^2_e	
Birth weight (kg)	17.22	4.69	7.84	4.69	0.27±0.05
Lactation yield (liters)	192436.14	87753.82	104681.79	0.53	0.45±0.03
Fat %	0.08	0.03	0.02	0.03	0.37 ±0.04
SNF%	0.04	0.02	0.004	0.02	0.46 ±0.01

¹ σ^2_P , phenotypic variance; σ^2_A , additive genetic variance; σ^2_E , environmental variance; σ^2_e , residual variance

The variance components estimates for birth weight ranged from 4.69 to 7.84 for additive genetic, residual and environmental variance. The h² estimate for birth weight was found to be (0.27±0.05) moderate. The h² estimate of birth weight of calves in the present study was within the range of the published literatures. However, Khan et al. (1992), Tosh et al. (1999) and Bhuiyan (1999) obtained higher h² estimate for birth weight of calves compared with the results of the present study. Higher environmental variance (Table 2) for birth weight obtained in the current study signifies that environment plays partial role in expressing the trait.

The σ^2_A of lactation yield of the experimental cows was found to be 87753.82 (0.45% of σ^2_P). It means that the trait in the population deserve high transmittable potency. Medium to high h² estimates of the present study would allow breeder to go for selection of better cows for milk yield on the basis of mass selection. The estimated h² for lactation yield was found to be moderate (0.45±0.03). The estimates seem to be relatively reliable because of its small SE. The h² estimate for lactation yield in present study was almost similar to the estimate for FN×SL (0.46±0.18) found by Gaur et al. (1999). The medium estimates of h² were reported by Harris et al. (1992), Pander et al. (1992) and Hibner (1993) in different crossbreds and exotic breeds and also as reported by Hossain et al. (2002) for SN cattle in Bangladesh. Ageeb and Hillers (1991) reported h² of lactation yield as 0.68±0.30 for FN crossbred.

The additive genetic, environmental and residual variances for fat % were found to be 0.03, 0.02 and 0.03, respectively, The h² estimate of fat % of milk was found to be 0.37±0.04. Among the variance components of fat %, both σ^2_A and σ^2_e were found to be 0.38 % of σ^2_P . The h² estimate was almost similar with the observation of Arai et al., (1976) in Japanese crossbred cows (0.29) and of Abdallah and McDaniel (2000) in North Carolina experimental cow herds (0.28).

The variability in the performance of different genetic groups of cows for fat yield suggested that there is a scope for improvement of this trait. The estimated h² for SNF% was found to be moderate. In the present study, the σ^2_A and σ^2_e for SNF% were similar having a value of 0.02 against 0.04 for σ^2_P , which indicates magnificent transmitting ability of the trait in the population. The h² estimate was in agreement with the estimate as 0.53±0.25 of Guernsey cows reported by Armstrong (1959), as 0.50±0.19% of crossbred cows in Japan by Arai et al. (1976) and as 0.46±0.11% of FN×SL cows by Chowdhury et al. (1994). In the present study, the h² estimate of SNF% of milk was within the range of these findings.

Ranking of sires

Breeders are always interested to realize maximum economic return from the animals. In reality, total aggregate merit of the sire is often sought. Breeder has to choose many traits simultaneously to arrive at the aggregate breeding value. The individuals with higher-ranking values are selected for producing progeny. Sire evaluation is generally aimed at selecting first few top ranking sires. A total of 31 sires were ranked according to their PBV based on their daughter's performance for each of the economic traits (birth weight, lactation yield, fat and SNF%) separately and presented in Figure 1, 2, 3 and 4.

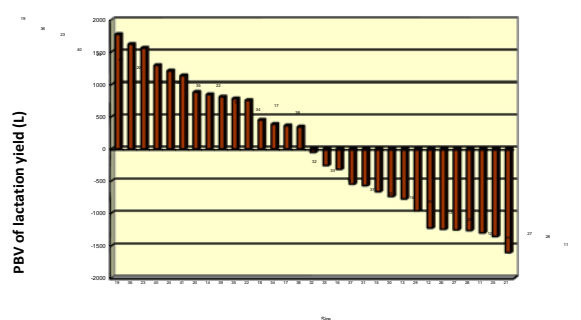


Figure 1. Predicted breeding value (PBV) of sires for progeny birth weight (h² = 0.27; μ = overall mean; No. of sires = 31)

Birth weight: Among 31 sires, best one was Sire No. 24(FN), followed by Sire No. 14 (SL) and 20 (FN) in order, while worst one was Sire No. 11(PM), followed by Sire No. 25(SL) and 21(SL) in order for birth weight (Figure 1). Among top three sires, Sire No. 24 showed extra ordinary superiority over second best and third best sires. Of all, 11 sires stood above average while 17 sires have fallen below average PBV.

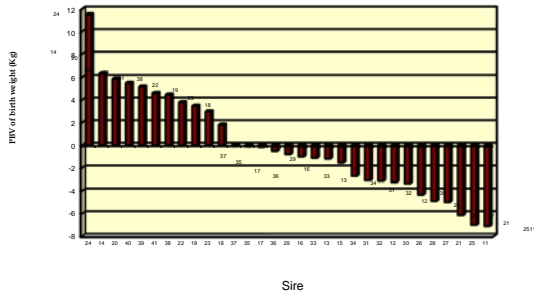


Figure 2. Predicted breeding value (PBV) of sires for progeny lactation yield ($h^2 = 0.45 \pm 0.03$; $\mu =$ over all mean; No. of sires = 31)

Lactation yield: Unlike PBV for birth weight, PBV of sires for lactation yield of their progeny varied according to different sires. According to the PBV of lactation yield of daughters, Sire No. 19 (FN) ranked the highest in order followed by Sire No. 36(FN) and 23(JR). The poorest performer was Sire No. 21(SL) followed by Sire No. 25 (SL) and 11(PM). According to the performance of daughter's lactation yield 31 sires were ranked (Figure 2). Among the 31 sires 15 sires stood above average PBV, whereas, 16 sires stood below PBV

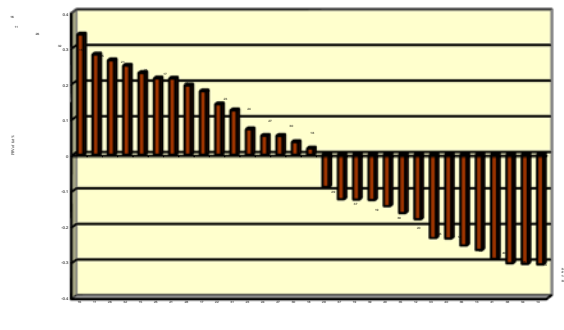


Figure 3 Predicted breeding value (PBV) of sires for progeny fat % ($h^2 = 0.37 \pm 0.04$; $\mu =$ over all mean; No. of sires = 31)

Fat %: The PBV of sires for fat % of daughters ranged from -0.531 to +0.455. The highest breeding value of fat % was found in the progeny of Sire No. 16(SL), followed by Sire No.11 (PM) and 26(SL). The lowest breeding value of fat % was found from the progeny of Sire No. 14(SL), followed by 34(FN) and 38(AFS). From the result it was observed that SL germplasm might be responsible for higher PBV of sires for fat%. It was also remarkable that PM sire had the third highest PBV for fat% (Figure 3)

Solids not fat %: Maximum (0.745) and minimum (-0.650) breeding value of sire for SNF% of daughters are presented in Figure 4. As per breeding value of the trait merit of sires was ordered to be 14(SL) > 19(FN) > 16(SL).... > 21(SL).

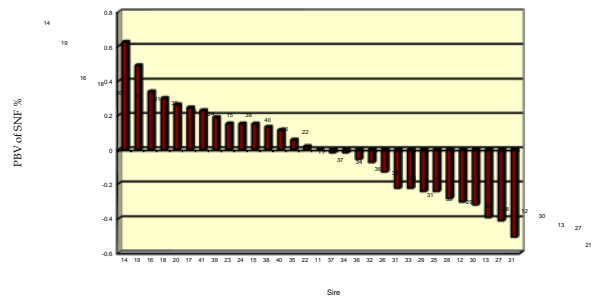


Figure 4. Predicted breeding value (PBV) of sires for progeny SNF% ($h^2 = 0.46$; $\mu =$ over all mean; No. of sires = 31)

PBV of sires increases with the increase of SL blood. Among 31 sires, 15 sires stood above the average and 15 sires stood below the average PBV. Sire evaluation is generally aimed at selecting first few top-ranking sires although it depends on the selection intensity desired for the breeding program. For progeny birth weight, lactation yield, fat and SNF% top prioritized sires were Bull No. 24, 14 and 20; Bull No.19, 36 and 23; Bull No. 16, 11 and 26 and Bull No. 14, 19 and 16, respectively.

Conclusion

The moderate heritabilities for birth weight of calves, lactation yield, fat and SNF % of different genetic groups of cows for suggested that there is a scope for improvement of these traits. The PBV of sires increases with the increase of SL blood. Considering the progeny birth weight, lactation yield, fat and SNF % top prioritized sires were Bull No. 24, 14 and 20; Bull No. 19, 36 and 23; Bull No. 16, 11 and 26 and Bull No. 14, 19 and 16, respectively.

Crossbred sire ranking

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