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A Comparative Study of Productive and Reproductive Performance and Estimates of Heritability for Economic Traits in Different Genetic Groups of Cattle Available at Baghabarighat Milk Pocket Area of Bangladesh

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Abstract: The study was conducted at Baghabarighat milk pocket area to observe the productive and reproductive performance of the crossbred of Sahiwal × Friesian, Sahiwal × Pabna, Friesian × Pabna and Pabna × Pabna during the period from 1990 to 1998. Comprising four genetic groups data of 41 Sahiwal × Friesian, 72 Sahiwal × Pabna, 55 Friesian × Pabna and 18 Pabna × Pabna were considered to evaluate birth weight of calves, age at puberty, gestation length, service per conception, post partum heat period, lactation length, and daily milk yield. Five Sahiwal and four Friesian sires were used for the crossbreeding. The exotic sire effect of individuals on their daughters were also evaluated in this study. Statistical analysis of the results showed that the genetic group had a significant effect on birth weight ($P<0.001$), age at puberty ($P<0.001$), post partum heat period ($P<0.01$), lactation length ($P<0.01$) and daily milk yield ($P<0.001$). But genetic group had no significant effect on gestation length and number of services per conception. The performance of SL × F cows with regard to birth weight of calves (26.35±0.35 kg), age at puberty (25.21±0.55 months), lactation length (260.38±4.48 days) and daily milk yield (10.56±0.14 litres), was found to be better among the other genetic groups. The best performance for the trait service per conception (1.29±0.13) and post partum heat period (104.82±6.53 days) was observed in Pabna × Pabna cows. F × Pabna grades had a slightly shorter gestation length (280.59±0.91 days) than the other genetic groups. So it can be concluded that SL × F crossbred are well ahead to other genetic groups in respect of productive aspect, whereas F × Pabna crosses show the remarkable performance both for production and reproduction. Under this consideration the F × Pabna grades ranked first in over all merit followed by SL × F, SL × Pabna and then Pabna × Pabna cows. Individual sire effect was found significant on birth weight ($P<0.05$) and average daily milk yield ($P<0.05$) in SL × F genetic group, on birth weight ($P<0.05$), age at puberty ($P<0.05$) and lactation length ($P<0.05$) in SL × Pabna genetic group and on lactation length ($P<0.05$) and average daily milk yield ($P<0.05$) in F × Pabna genetic group. The pooled estimates of heritability for birth weight, age at puberty, gestation length, service per conception, post partum heat period, lactation length and daily milk yield were 0.44±0.30, 0.14±0.17, 0.25±0.21, 0.03±0.12, 0.33±0.26, 0.46±0.33 and 0.43±0.27 respectively. In this study the h^2 estimates of reproductive traits were found lower than that of productive traits which indicate that these traits are mostly influenced by managemental factors rather than genetic variability.

Key words: Reproductive performance, crossbred, genetic groups

Introduction

Most of our indigenous cattle are of the ***Bos indicus*** type and with certain exceptions are on the whole, poor producers, exhibiting poor milk production even under the good dietary and managemental condition and characterized by poor weight gains and late maturity. But they often exhibit remarkable heat tolerance, the ability to maintain body condition on poor quality feed stuff and to a certain degree of resistance to local diseases. On the other hand, exotic breeds from temperate zone though are more productive in favourable environment, cannot adjust to our hot and humid condition. Vacarro (1979) stated that the performances of exotic breeds have often disastrous with retarded growth, high mortality, poor fertility and susceptibility to diseases. According to Taneja and Bhat (1986) the performance of temperate genotypes in tropical environment like Bangladesh is 30-40% lower than that of the countries of their origin. The annual milk production is about 1.62 million metric tons which is far below the normal requirement of 9.9 million metric tons per year (DLS, 1997-98). It is therefore, necessary to speed up the production potential of the cattle to meet the growing needs of the country.

In order to increase the productive efficiency of indigenous cattle, specially at the small holder level, for developing countries like Bangladesh aiming at increasing self sufficiency in milk production, there are two ways to improve the genetic potentials of our native stocks: (I) selecting the best performing existing genetic resource from indigenous cattle and (ii) out-crossing with high yielding cattle breeds from temperate zones. Although, there are some authorities who mention that selection from within the native is preferable, the consensus is that this method is slow for the urgent and growing need for increased production and instead, out crossing is preferable (Ansell, 1985).

It is an important to maintain the right genotypes in the right environment for expressing the full genetic potentiality. Any deviation in the genetic-environment interaction causes serious consequence on productivity. Bandoc ***et al.*** (1989) reported that with the increase of ***Bos taurine*** blood in ***Bos indicus*** cattle at the level of onward second generation there have been a notable decrease in milk yield and lactation length and increase in age at first calving. So it is the most crucial factor for the breeder to maintain optimum proportion of exotic blood in our indigenous stock to suit the limited feed resources in our traditional production system.

Selection when based on accumulation of favourable additive effects of genes from generation to generation, leads to a permanent change with change in gene frequency. Out-breeding is largely based on the arrangement of favourable dominant effects of genes in each generation. These dominant effects are not cumulative from one generation to the next, though they can be enhanced by appropriate selection. Out-breeding is often regarded as an alternative to selection in some cases. It, therefore, needs to be stressed that these are not mutually exclusive strategies and that any out-breeding programme requires a supporting selection programme (Matin, 1993). It is agreed that whatever systems and breed combinations are adopted in a particular environment, the ultimate target of a breeder is to maintain a high rate of genetic improvement after the first generation of crossing. Progeny testing and selection of superior bulls for widespread use by artificial insemination in this connection are the principle means by which the genetic gains are made in modern breeding program.

Estimates of heritability is one of the essential genetic parameter which is required in animal breeding research and in the design and application of practical breeding programme (Koots ***et al.***, 1994). Heritability estimates (h^2) tell something about the amount of progress that might be made in selection for a particular trait. When the h^2 of a trait is high, the correlation between the phenotype and the genotype of the individuals, on an average, should also be high, and selection on the basis of own phenotype should be effective. High h^2 estimates also indicate that additive gene action is important for that trait. To make progress in selection when the h^2 of a trait is low much more alternation must be paid to aids to selection like the performance of the collateral relatives and the progeny. Low h^2 estimates ensure that variations due to additive gene action are probably small whereas non additive gene action such as dominance, over dominance and epistasis may be important. So in this case it is necessary to use special methods for selection and mating for greater improvement in the herd (Lasely 1978). In terms of variance component the heritability is expressed as (Falconer, 1989):

$$\text{Heritability } (h^2) = \frac{V_A}{V_P} = \frac{V_A}{V_G + V_E} = \frac{V_A}{V_A + V_D + V_I + V_E}$$

Where, V_A= Variance due to additive gene action
V_D= Variance due to dominant gene action
V_I= Variance due to epistatic gene action
V_E= Variance due to environment

Records of cattle breeding operations at the private enterprise in this country are limited or not available at all. Bangladesh Milk Producers' Co-operative Union Limited (BMPCUL) in this respect is self sufficient and profitable milk producing organization. In this respected it is believed that, exploitation of suitable genetic resource could be the most important elements of successful story behind the BMPCUL. Crossing of local cows with Sahiwal, Hariana and Red Sindhi by generations, has enabled the farmers of Baghabarighat milk pocket area to develop a type of cattle notable for milk and the type has been popularly known as Pabna type (Hoque, ***et al.***, 1999). Genetic theory also stresses that improvement through breeding is green positive, accumulating overtime and appreciable in the long-term basis (Smith, 1984). Therefore, quantitative investigation of the performance of genetic materials used in the BMPCUL programme deems it an economic justification and this requires first of all an evaluation of reproductive and lactation potentials in the prevailing environment.

The present study was designed to monitor the productive, reproductive performances and heritability estimates of various performance traits of genetic groups reared under Baghabarighat milk pocket area.

Materials and Methods

The study was confined at Baghabarighat milk pocket area under Bangladesh Milk Producers' Co-operative Union Limited (BMPCUL), a large dairy pocket located at Sirajgong district. The data were collected from the record sheets of several primary milk producing societies namely: Kanai, Barabil, Shak Tala, Potagia, Haturia and Banagram during the period from 1990 to 1998. The information on productive and reproductive parameters of a total of 181 healthy cows of different genetic groups were accumulated from the record sheets maintained by relevant Livestock Field Assistant- Inseminator (LFAI). The parameters considered were birth weight, Age at puberty, Gestation length, service per conception, post partum heat period, lactation duration and daily milk yield. The records were obtained from herd of Sahiwal (SL) × Friesian (F), Sahiwal (SL) × Pabna, Friesian (F) × Pabna and purebred Pabna. To determine individual sire effect on performances within genetic group, the progeny records of five Sahiwal bulls (Nos. 101, 102, 103, 104 and 107) and four Friesian bulls (Nos. 111, 113, 115 and 121) were considered. Information of cows used to estimate the heritability were from the daughters of 10 sires representing three breeds- Sahiwal (5), Friesian (4) and Pabna (1). Sib analyses arranged on parental half-sib basis were confined to first lactation only.

Two types of feeding and management system were available in Baghabarighat milk shed area, such as "Bathan" feeding and stall-feeding. From December- June each year cattle were fed and managed in "Bathan" which is a large legume pasture (about 600 hectares) along the sides of river Baral. In addition to grazing during that period all animals were provided with a concentrate mixture of rice polish, mustard oil cake and common salt once a day. From July to October animals were fed and managed in the stall with straw supplemented with a similar concentrate mixture as given to each animal twice a day (Hoque ***et al.***, 1999). Milk Vita (Baghabarighat) provides services for improved husbandry practices, veterinary care, artificial insemination (AI). Artificial insemination is done by 37 trained Livestock Field Assistant Inseminators (LFAI) with deep frozen semen of Sahiwal, Friesian and Jersey bulls.

The collected data were subjected to statistical analysis using the technique of a completely randomized design to compute analysis of variance and to calculate the means of each variance with standard error (SE) according to Steel and Torrie (1980) as follows:

$$Yij = \mu + Bi + Eij$$

Where,

Yij = measurement of ith genetic group in jth animal
μ = general mean
Bi = effect of genetic group
Eij = random error

Analysis of variance for obtaining intra-class correlation was used to estimate the h^2s of the traits, for meaningful comparison of sub-class means, a Least- Significant Difference (LSD) test was performed. Variance components from analysis of variance were computed as outlined by Beaker (1975). The statistical model used to estimate the components of variance was as follows:

$$Yij = \mu + Si + Eij$$

Where,

Yij = the observation on the jth individual from the ith sire
μ = effect common to all animals
Si = effect due to ith sire
Eij = effect variable of the jth individual of the ith sire

As the number of offspring per sire was not equal the co-efficient K was estimated according to the formula described by Beaker (1975). The co-efficient K was calculated as follows:

$$K = \frac{1}{S-1} \left(n - \frac{\sum n_i^2}{n.}\right)$$

Where,
K = average number of offspring per sire
S = number of sires
n_i = number of offspring of the ith sire
n. = total number of offspring

The analysis of variance (ANOVA) of traits for h^2 estimation was designed as follows:

Sources of variation	d.f	S.S.	M.S.	Estimated mean squares
Between individuals	S-1	SS_s	MS_s	$6^2_w + K6^2_s$
Within individual	n.-S	SS_w	MS_w	6^2_w

Variance components were estimated as:

$6^2_w = MS_w$ = within sire component of variance

$6^2_s = \frac{MS_s - MS_w}{K}$ = Between sire component of variance

$6^2_w + 6^2_s$ = Total phenotypic variance

From the above variance components heritability was estimated by paternal half-sib correlation method using the following formula:

$$h^2 = \frac{46_s^2}{6^2{}_w + 6_s^2}$$

Standard error of estimated heritability was calculated according to the formula outlined by Becker (1975).

$$\text{S.E. } (h^2) = 4\sqrt{\frac{2(n.-1)(1-t)^2[1+(k\ -1)t]^2}{k\ ^2(n.-S)(S-1)}}$$

Where,

t= intra class correlation

Results and Discussion

Highly significant differences between genetic groups ($P<0.001$) were observed for birth weight of calves (Table 1). In the present study, the highest birth weight was observed in SL × F (26.35±0.35 kg) and the lowest was in Pabna × Pabna (16.58±0.63 kg) cows. The mean birth weight for Pabna calves is consistent with the findings of Hossain and Routledge (1982), Udo ***et al.*** (1990) and Hoque ***et al.*** (1999) who reported 16.37, 15.60 and 17.92 kg respectively. According to Islam ***et al.*** (1997) and Hoque ***et al.*** (1999) the average birth weight of Sahiwal × Pabna graded cattle were 23.70 and 21.26 kg respectively which supports the present findings but higher than the results of Nahar ***et al.*** (1989) who obtained the birth weight of ½ Sahiwal × ½ Local graded cattle to be 17.6 kg. The average birth weight of F × Pabna calves was found to be 22.5 kg by Hoque ***et al.*** (1999) which was similar to Nahar ***et al.*** (1992) who also found the same birth result (22 kg) in F × Local calves. This result is consistent with the present study. Khan ***et al.*** (1992) found that the mean birth weight of SL calves was 20.04 kg. Hussain and Mostafa (1985) also stated that the birth weight of SL calves was 36.1 and 37.9 kg under rural and urban condition, respectively.

The individual sire effect on birth weight was significant ($P<0.05$) in SL × F and SL × Pabna graded cattle (Table 2 and 3). Non-significant sire effect was found only in F × Pabna calves (Table 4). So within genetic group selection of individual superior sire could be an important factor in terms of improving birth weight of calves. Estimated h^2 of birth weight along with standard error are presented in Table 5. The heritability estimate for birth weight for SL × F crossbred was 0.50±0.70 which was a little lower than the estimate of 0.61±0.13 and 0.62±0.19 reported by Taneja ***et al.*** (1977) for SL × F crossbred with two different ratio of Friesian inheritance. The pooled estimate based on all crosses was 0.44±0.30 (Table 6) whereas for SL × Pabna and F × Pabna graded cattle the corresponding estimates were 0.37±0.45 and 0.32±0.49, respectively. The estimated h^2 of the present findings differ with Verma and Johar (1985) who reported the estimates to be 0.21±0.05 for crossbred cattle. In general these high heritability estimates in crossbred groups were indicative of increase in genetic variability due to

Table 1: Comparison of mean±S.E of productive and reproductive traits in different genetic groups of dairy cattle

	Genetic group				
Trait	Sahiwal (SL) × Friesian (F)	Sahiwal (SL) × Pabna	Friesian (F) × Pabna	Pabna × Pabna	Level of significance
Birth wt. (kg)	26.35±0.35a (41)	21.83±0.29b (72)	23.40±0.20ab (55)	16.58±0.63c (18)	***
Age at puberty (month)	25.21±0.55c (40)	33.68±0.93b (73)	28.12±0.29bc (52)	38.58±1.48a (18)	***
Gestation length (day)	284.33±1.26 (40)	281.04±0.49 (75)	280.59±0.91 (52)	287.21±0.81 (14)	NS
Service per conception (number)	1.43±0.08 (40)	1.37±0.06 (70)	1.36±0.06 (56)	1.29±0.13 (14)	NS
Post partum heat period (days)	145.39±5.50a (36)	126.66±4.42b (58)	131.73±4.70ab (55)	104.82±6.53c (17)	**
Lactation length (day)	260.38±4.48a (39)	227.98±7.31bc (66)	249.84±7.62ac (49)	225.93±8.26c	**
Daily milk yield (liters)	10.56±0.14a (40)	6.78±0.19b (72)	8.28±0.22ab (55)	4.27±0.24c (15)	***

Table 2: Comparison of mean±S.E of progeny of the individual sire (Friesian) showing difference amongst themselves in SL × F genetic group

	Friesian Bulls		
Trait	111	113	121
Birth wt. (kg)	27.11±0.39a (20)	25.15±0.45ab (10)	26.06±0.96b (11)
Age at puberty (month)	24.36±0.81 (19)	26.37±1.20 (10)	25.6±0.87 (11)
Gestation length (day)	286.45±1.53 (20)	283.90±2.63 (10)	280.50±3.07 (10)
Service per conception (no.)	1.30±0.11 (20)	1.50±0.17 (10)	1.60±0.16 (10)
Post partum heat period (days)	145.22±7.83 (18)	159.44±10.59 (9)	131.67±10.49 (9)
Lactation length (day)	253.47±6.60 (19)	261.40±8.48 (10)	272.5±8.13 (10)
Daily milk yield (liters)	10.50±0.19a (19)	10.20±0.26b (10)	11.09±0.23b (11)

crossbreeding. This also suggests that mass selection may be effective to achieve increased gain in birth weight.

Pabna × Pabna had the highest age at puberty (38.58±1.48 months) and lowest in SL × F (25.21±0.55 months). The present study indicated that genetic group had significant effect (P<0.001) on this trait (Table 1). These results are supported by those of Hoque ***et al.*** (1999) who noted that the ages at puberty of SL × Pabna (35.10 months), F × Pabna (25.53 months), and Pabna × Pabna (39.23 months) did differ significantly (P<0.05). Khan and Khatun (1998) found no

Table 3: Mean comparison of progeny of the individual sire (SL) showing difference amongst themselves in SL × Pabna genetic group

	Sahiwal bulls				
Trait	101	102	103	104	107
Birth wt. (kg) (Mean, SE, No)	21.62±0.48ab (16)	20.94±0.65b (16)	23.13±0.44a (15)	22.46±0.79ab (14)	20.88±0.69b (11)
Age at puberty (month) (Mean, SE, No)	35.42±1.88a (16)	34.09±2.66a (16)	36.961±1.99a (15)	31.25±1.42ab (14)	29.68±1.57b (11)
Gestation length (day) (Mean, SE, No)	282.25±0.93 (16)	279.75±0.96 (16)	279.53±1.38 (15)	281.53±1.19 (15)	282.31±0.85 (13)
Service per conception (no.) (Mean, SE, No)	1.25±0.11 (16)	1.38±0.13 (16)	1.47±0.13 (15)	1.18±0.12 (11)	1.58±0.15 (12)
Post partum heat period (days) (Mean, SE, No)	126.23±9.23 (13)	133.88±12.24 (9)	110.23±9.70 (13)	142.09±6.28 (11)	125.33±10.63 (12)
Lactation length (day) (Mean, SE, No)	267.06±14.61a (16)	227.91±17.78ab (11)	220.00±18.20b (12)	216.93±14.25b (14)	199.23±12.57b (13)
Daily milk yield (liters) (Mean, SE, No)	7.06±0.42 (16)	6.12±0.32 (13)	7.25±0.49 (14)	6.60±0.40 (15)	6.82±0.40 (14)

Table 4: Mean comparison of progeny of the individual sire (Friesian) showing difference amongst themselves in F × Pabna genetic group

	Friesian Bulls			
Traits	111	113	115	121
Birth wt. (kg) (Mean, SE, No)	23.09±0.29 (16)	24.14±0.48 (12)	22.78±0.43 (12)	23.65±0.39 (15)
Age at puberty (month) (Mean, SE, No)	27.53±0.66 (16)	27.33±0.58 (12)	29.07±0.58 (12)	28.63±0.41 (15)
Gestation length (day) (Mean, SE, No)	278.07±1.80 (15)	283.18±1.46 (11)	282.72±2.11 (11)	279.67±1.64 (15)
Service per conception (no.) (Mean, SE, No)	1.26±0.12 (15)	1.25±0.13 (12)	1.57±0.14 (14)	1.33±0.13 (15)
Post partum heat period (days) (Mean, SE, No)	116.56±9.11 (16)	133.85±10.76 (13)	135.08±9.40 (12)	144.21±7.38 (14)
Lactation length (day) (Mean, SE, No)	267.13±12.13ab (15)	231.58±11.56bc (12)	219.45±10.82c (11)	276.54±21.02a (11)
Daily milk yield (liters) (Mean, SE, No)	8.50±0.44ab (15)	7.90±0.47ab (11)	7.43±0.41b (14)	9.13±0.39a (15)

Means with uncommon superscripts differ significantly (p<0.05) from each other.
Figures in the parenthesis indicate the number of observations

significant difference (P<0.05) among SL × Pabna (37.29 Months), F × Pabna (33.57 months) and Pabna × Pabna (38.8 months) and this is more less close to present study. This result also supports those of Islam ***et al.*** (1997) who found significant (P<0.01) effect on ½ SL × ½ Pabna (38.53 months) and ¾ SL × ¼ Paban (31.12 months), Chowdhury ***et al.*** (1994), Majid ***et al.*** (1995) reported the birth age at puberty of SL × F cattle ranging from 606.4 days (20.2 months) to 770.31 days (25.68 months). The results obtained from SL × F cattle of the present study fall within the

Table 5: Heritability (h^2) estimates of the productive and reproductive traits in different genetic groups

	Genetic group					
	SL × F		SL × Pabna		F × Pabna	
Trait	h^2	SE	h^2	SE	h^2	SE
Birth wt.	0.50	0.70	0.37	0.45	0.32	0.49
Age at puberty	0.07	0.39	0.27	0.38	0.29	0.46
Gestation length	0.26	0.57	0.14	0.28	0.25	0.45
Service per conception	0.11	0.43	0.12	0.29	0.09	0.31
Post partum heat period	0.22	0.56	0.17	0.37	0.20	0.40
Lactation length	0.18	0.49	0.25	0.45	0.41	0.58
Daily milk yield	0.65	0.77	0.14	0.29	0.39	0.47

Table 6: Pooled average estimates of heritability (h^2) of all cattle herd

	All cattle	
Trait	h^2	SE
Birth weight	0.44	0.30
Age at puberty	0.14	0.17
Gestation length	0.25	0.21
Service per conception	0.03	0.12
Post partum heat period	0.33	0.26
Lactation length	0.46	0.33
Daily milk yield	0.43	0.27

range. In the present study individual sire had a significant effect ($P<0.05$) on this trait belonging to SL × Pabna graded cattle (Table 3). Progeny of SL bull no 103 reached sexual maturity much earlier than those of the other 4 bulls of that genetic group. Progeny of individual sire belonging to other genetic groups did not differ significantly for this trait (Table 2 and 4). Genetic make up is the main factor which influences this trait remarkably. Environmental condition, nutrition, cares and management may also effect this trait. For age at puberty the h^2 estimate was 0.07±0.39, 0.27±0.38 and 0.29±0.56 for SL × F, SL × Pabna and F × Pabna graded cows respectively, whereas, the pooled estimate based on all crosses was 0.14±0.17. These results were in close agreement with the reports of Pal ***et al.*** (1996), Singh ***et al.*** (1990); Patel and Parekh (1982) and Souza ***et al.*** (1995). The h^2 estimates from their experiment were 0.28 for Holstein crossbreds, 0.21±0.63 for Sahiwal corssbreds, 0.11±0.21 for Friesian crossbreds and 0.11±0.21 for Jersey crossbreds. The present estimate of h^2 differs with Silva and Pareira (1987) who found the estimate to be 0.42±0.12 for Chiana × Zebu cattle. The polled estimate of h^2 of all genetic groups is supported by Mostafa (1971) who reported the estimates to be 0.18±0.28 for entire herd comprising different genetic groups.

The gestation length of different genetic groups varied form 281 to 287 days (Table 1). There were no significant effects of genetic groups on this trait. Similar results were obtained by Khan and Khatun (1998), Sultana (1995) and Rahman ***et al.*** (1993). Gestation length of SL × Pabna cattle in this study is almost similar to the work done by Islam and Bhuiyan (1997) who found the corresponding figure for ½ SL × ½ Pabna and ¾ SL × ¼ Pabna genetic groups to be 282.35 days and 282.94 days respectively. Khan and Khatun (1998) reported the gestation length of SL × Pabna group to be 285.61 days, which differs a little with the present findings. In case of F × Pabna and Pabna × Pabna genetic groups the present study was supported by Khan and Khatun (1998) who reported that the gestation length of the two genetic groups was 282.75 days and 286.20 day respectively. The effect of individual sire on gestation length was non-significant (Table 2, 3 and 4), because it is the species characteristic which is fixed genetically. But the variation may occur due to maternal influence. The h^2 estimate of gestation length for SL × F, SL × Pabna and F × Pabna was 0.26±0.57, 0.14±0.28 and 0.25±0.45 respectively (Table 5), whereas the pooled estimate was 0.25±0.21 (Table 6). Baco ***et al.*** (1998) found the h^2 of this trait to be 0.17 for Japanese cows while Choi ***et al.*** (1998) reported the estimates to be 0.11±0.06 for HF herd. Chandrak and Psenica (1994) observed that the h^2 estimate of this trait was 0.28±0.10 and 0.39±0.13 for Slovakian Pied and Slovakian Pinzau breed respectively. The h^2 of gestation length of Ontario Holstein cattle was found to 0.33 (Nadarajah ***et al.***, 1989). All of these results more or less support the present findings. A maximum estimate of h^2 was found by Oliveira (1990) whose finding was to be 0.62 for Santa Gertrudis cattle.

Number of services per conception were almost similar in all genetic groups (Table 1) and sire effect was non-significant (Tables 2, 3 and 4). These results are in agreement with Hoque ***et al.*** (1999), Khan and Khatun (1998) and Sultana (1995) who found a non-significant effect (P<0.05) of genetic groups on this trait. Hoque ***et al.*** (1999) reported that the average number of services required per conception for SL × Pabna, F × Paban and Pabna × Pabna cows was 1.59, 1.35 and 1.32 whereas Khan and Khatun (1998) found 1.08, 1.18 and 1.20 for the same. Number of services per conception for SL × F cows in this study is in close agreement with the findings of Chaudhury ***et al.*** (1994) who reported the average of 1.6 for the same genetic group. It therefore appears that service per conception is mostly determined by environmental attributes rather than by heredity. For number of services per conception the h^2 estimate was 0.11±0.43, 0.12±0.29 and 0.09±0.31 for SL × F, SL × Pabna and F × Pabna genetic group (Table 5) whereas the pooled estimation was 0.03±0.12 (Table 6). Singh ***et al.*** (1997) reported that the h^2 of this trait ranged from -0.06±0.11 to 0.27±0.22 in different lactation for Jersey crossbred cows. All of the estimates of service per conception in the present study fall into that range which partially supports the present study.

The lowest number of PPHP was found in the Pabna × Pabna (104.82±6.53 days) followed by SL × Pabna cows (126.66±4.42 days). The highest PPHP was obtained in SL × F (145.39±5.5 days) cows (Table 1). Statistical analysis showed that there was highly significant (P<0.001) difference within the PPHP of different genotypes. Islam and Bhuiyan (1997) found no significant difference between ½ SL × ½ Pabna (4.33 months) and ¾ SL × ¼ Pabna (3.38 months) genetic groups, whereas Majid ***et al.*** (1995) found a little variation in PPHP between different genetic groups which was not statistically significant. They reported that the PPHP for ½ local × ½ Friesian cows was 117.24 ± 7.20 days. Nahar ***et al.*** (1992) found a significantly shorter PPHP for Holstein × Local cows (123 days) than from Sahiwal × Local cows (149 days). All these results are in agreement with the present study. The individual sire effect for all genetic groups was also non-significant for this trait. In the present study a longer PPHP was probably due to improper heat detection, reproduction disorder or improper nutrition. For post partum heat period the h^2 estimate for SL × F, SL × Pabna and F × Pabna was 0.22±0.56, 0.17±0.37 and 0.20±0.40 respectively which are presented in table 5. The pooled estimates based on all crosses was 0.33±0.26 (Table 6). These results differ with the finding of Freitas ***et al.***, (1997) who reported that the h^2 estimates of this trait was 0.05 for European × Zebu crossbred. Spasic (1997); Rico and Planas (1990) reported that in cases of Belgradian Zebu and Cuban Zebu cattle the h^2 ranged from 0.10±0.09 to 0.17±0.12 and 0.08±0.06 to 0.16±0.10 respectively. These results partially support the present study. The present results are in agreement with Reddy and Nagarcenkar (1989) who reported that the estimated h^2 for this trait ranged from <0 to 0.49±0.19 for Sahiwal herds. The present result for SL × F crossbred cows is similar to those reported by Taneja ***et al.*** (1977), where they found the h^2 estimates to be 0.21±0.09 and 0.23±0.12 in SL × F crossbred with different Friesian inheritance.

Genetic group had a significant effect (P<0.01) on lactation length in the present study (Table 1). Hoque ***et al.*** (1999) also found a significant (P<0.05) variation among SL × Pabna (282.8±32.02 days), F × Pabna (238.33±40.12 days) and Pabna × Pabna (197.41± 21.38 days) genetic groups. But Khan and Khatun (1998) observed no significant difference among those genetic groups. According to them lactation lengths of those three genetic groups were 213.70±25.85 days, 206.92±22.74 days and 208.75±18.15 days. This is slightly lower than the present findings. The lactation length of SL × Pabna cows in this study is almost in agreement with Islam and Bhuiyan (1997) who reported that the lactation length was 216.88 days for ½ SL × ½ Pabna genetic group. Sultana (1995) also found a highly significant (P<0.001) effect between genetic groups and reported the lactation length to be 241.18±10.53 and 247.41±5.88 days for SL × F and Local × F cattle respectively which almost support the present study. Individual sire effect was also significant (P<0.05) in SL × Pabna and F × Pabna genetic group (Table 3 and 4), whereas insignificant result was found in case of SL × F (Table 2) genetic group. For lactation length the heritability estimate was 0.18±0.49, 0.25±0.45 and 0.41±0.58 for SL × F, SL × Pabna and F × Pabna genetic groups respectively which are presented in the Table 5. The present result for SL × F group is similar to those reported by Taneja ***et al.*** (1977), in which they found the corresponding figure of this trait to be 0.15±0.09 and 0.08±0.21 in SL × F crossbreds with two different proportion of Friesian inheritance. Much higher heritability estimate (0.34±0.29) has been reported for SL × F crossbred cattle by Tomar ***et al.*** (1996). According to Reddy and Nagarcenkar (1989), the corresponding figure ranged from <0 to 0.19±0.20 which partially supports this present study. There was no published reports for SL × Pabna and F × Pabna graded cattle. But Tekade ***et al.*** (1994) and Ageeb and Hillers (1991) had some research work with different crossbreds where they noted that the value of h^2 was 0.33±0.11 for Jersey × Sahiwal crossbred and 0.34±0.25 for Friesian × Sudanese local crossbreds respectively. The h^2 based on all genetic groups (pooled) was 0.46±0.33 (Table 6). The h^2 estimates of lactation length indicated higher genetic variability among individuals and was also effected by environment and managemental interaction.

The least squares mean with SE for daily milk yield presented in Table 1 shows that genetic group had a significant effect (P<0.001) on this trait. Daily milk yield was highest in SL × F

(10.56±0.14 litres) followed by F × Pabna (8.28±0.22 litres), while SL × Pabna (6.78±0.19 litres) crosses took third position. The significant effect of genetic group on daily milk yield was also found by Khan and Khatun (1898), Chowdhury ***et al.*** (1994), Bhuiyan and Sultana (1994), Nahar ***et al.*** (1992), Bhuiyan ***et al.*** (1992), Nahar ***et al.*** (1989), Rahman ***et al.*** (1987), and Husain and Mostafa (1985), Khan and Khatun (1998) observed that the daily milk yield was 8.10, 9.74 litres and 7.35 litres for SL × Pabna, Fx Pabna and Pabna × Pabna genetic groups respectively. This result is almost similar to the present findings. The daily milk yield of Pabna cows in this study differ with Ali (1994) who found the average of 2.50 litres per day and with Hossain and Routledge (1982) whose findings gave 2.81 litres per day. The present result was supported by Ahmed and Islam (1987) who summarized that the daily milk yield was 7.62 liters in F × Local cattle. In the present finding daily milk yield for SL × Pabna cows was 6.78±0.189 litres. Islam and Bhuiyan (1997) noted the corresponding yield for the same trait to be 8.37 litres and 7.49 litres in ½ SL × ½ Pabna and ¾ SL × ¼ Pabna graded cattle respectively. Individual sire had significant ($P<0.05$) effect on this trait within SL × F (Table 2) and F × Pabna (Table 4) genetic groups. In case of SL × Pabna (Table 3) cattle the sire effect did not differ significantly. This indicates that there is much variability in the milk production potentiality of bulls within breeds and therefore a response can be obtained from sire selection even in a well defined breed in a grading programme. For daily milk yield the h^2 estimate was 0.65±0.77, 0.14±0.29 and 0.39±0.47 for SL × F, SL × Pabna and F × Pabna graded cows respectively (Table 5). The pooled estimates of h^2 of all groups was 0.43±0.27. The present result is higher than the estimates of Zarnecki ***et al.*** (1990), Garcha ***et al.*** (1989) and Butte and Deshpande (1987). The h^2 estimates from their experiment was 0.22 for Fresian × Polish Black grades, 0.065±0.07 for F × SL crossbred, 0.14±0.07 for F × SL crossbred cattle and this was higher than the present finding except in case of Sahiwal × Pabna grades. In Sahiwal herd Reddy and Nagarcenkar (1989) found the h^2 of this trait to rang from <0 to 0.81±0.19. Results obtained in the study falls within the range. The high magnitude of heritability of this trait confirms that good response from selection can be achieved for this trait.

When values for all the productive and reproductive traits studied are considered, the F × Pabna grades ranked first in overall merit followed by SL × F, SL × Pabna and then Pabna × Pabna cows. Significant variations between the performance of progeny within the SL and F sire groups in several important traits: age at puberty lactation length, milk yield- indicates the scope for sire selection to improve dairy merit. The results of this study provides guidelines, but it is desirable that they be confirmed by further studies on the performance of pure and crossbred Pabna cows in a wider context with large number of animals in each group.

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