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Genetic trends of some important dairy traits of crossbred cows at Baghabarighat milk shed area in Bangladesh

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Abstract

Data on 3637 cows of seven genetic groups at Baghabarighat milk shed area during the period from 1991 to 2000 were analyzed. The genetic groups were Pabna Milking (PM) cows, ½PM×½ Sahiwal (PM×SL), ½PM×½Friesian (PM×FN), Australian Friesian Sahiwal (AFS), ½Sahiwal×¼PM×¼ Friesian [SL(PM×FN)], ½Friesian×¼PM×¼Sahiwal [FN(PM×SL)] and ½Friesian×¼Sahiwal×¼Jersey [FN(SL×JR)]. The purpose of this study was to estimate genetic trends of some dairy traits (birth weight, lactation yield, fat% and SNF %). 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 genetic trends for the dairy traits were computed as average of breeding values using all data for cows born during 1991-2000. It was observed that the genetic trend of birth weight of calves increased in PM×SL, PM×FN, AFS and FN(SL×JR) at the rate of 0.08, 0.10, 0.12 and 0.05 kg per year, respectively. The same for lactation yield of genetic group PM×FN, AFS, SL(PM×FN) and FN (SL×JR) rose up at the rate of 6.78, 5.20, 4.14 and 5.19 liters per year, respectively. The genetic group PM, PM×SL and PM×FN showed negative trend for fat % at the rate of 0.0005, 0.002 and 0.004% per year, respectively. But the same increased in AFS, SL(PM×FN), FN(PM×SL) and FN(SL×JR) at the rate of 0.002, 0.013, 0.011 and 0.004% per year, respectively. The genetic trend of SNF % in only one group showed negative trend in PM×SL at the rate of 0.01 % per year. On the contrary, PM, PM×FN, AFS, SL(PM×FN), FN(PM×SL) and FN (SL×JR) increased at the rate of 0.005, 0.010, 0.011, 0.0002, 0.014 and 0.003% per year, respectively. The high genetic variability of birth weight, lactation yield, fat and SNF% indicated that there are good opportunities for genetic improvement when including these traits in a selection scheme.

Key words: Pabna milking cows, heritability, genetic trends

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Introduction

Bangladesh is a developing country in South East Asia. In the districts of Pabna and Sirajgonj a specialized dairy type animal was developed through natural mating of local cows with Hariana, Sindhi and Multani bulls. The cattle of this area became notably dairy type cattle popularly known as Pabna Milking (PM) cows. At present the Pabna Milking cows have been using as dam line for further upgrading of cows by Taurus blood. Bangladesh Milk Producers' Cooperative Union Limited (BMPCUL) was established in 1973. BMPCUL has been carrying out an upgrading program from 1987 using deep frozen Sahiwal semen. For improving genetic merit as well as milk production for 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.

Estimation of variance components, heritability and breeding value are important to animal breeders because these components are required for estimation of genetic parameters as well as genetic trends and to design animal breeding program.

The genetic trend, which is the change in production per animal per unit of time due to change in mean breeding value of the animals would be an indicator to determine the direction of change brought about as a result of any kind of breeding program operated. Commercially valuable traits in the field of dairy cattle industry include birth weight, lactation length, lactation yield, fat% and solids-not-fat% given primary emphasis for the present study. These traits are integral part of the profit-loss equation in dairy production.

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Materials and Methods

The present study was conducted at the Baghabarighat milk shed area under Bangladesh Milk Producers' Co-operative Union Limited in Bangladesh, which is a model of dairy development in Bangladesh along with many developing countries with similar agro-livestock production system (Hoque et al. 1999). Herd management and feeding practices were maintained almost equally throughout the study period. The experimental area consists of fertile medium lowland. Heavy silts deposited by rivers streams during the rainy season are thus continuously enriching the alluvial soil. The study area enjoys generally monsoon climate.

The data were collected on 3637 cows of seven different genetic groups. Most of the cows at study area were of PM and graded type owned by farmers. For estimating variance components, a pedigree file was constructed and the total number of animals including pedigreed ones was 10,920. In the present study, productive traits included birth weight of calves, lactation yield, fat % and SNF% in milk. These traits were taken into consideration with a view to estimate the effects of genetic groups to estimate variance components, heritability, breeding value and genetic trends.

Data analyses and statistical models

The collected data were analyzed with Generalized Linear Model (GLM) procedure of Statistical Analysis System (SAS, 1991) computer package. The least squares analysis of variance (LSANOVA) and difference between least squares means were calculated for all the traits to test for Least Significant Difference (LSD) with the help of SAS. The following statistical model was used to describe the traits studied:

$Y_{ijl} = \mu + G_i + B_j + e_{ijl}$

where Y_{ijl} = observation; μ = common mean; G_i = effect of i^{th} genetic group (i = 1 - 7); B_j = effect of the j^{th} birth year (j= 1991- 2000); e_{ijl} = random error associated with each measurement normally distributed with mean '0' and variance σ^2_e.

The variance components for each trait were estimated by the Residual Maximum Likelihood (REML) method with the variance component estimation (VCE) computer program by 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 conversion was defined to be reached when a change was less than 0.005 over the last 9 iterations and followed by the current estimates of the ratios. 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 =additive genetic effect; e_{ij} = random error.

Heritability values were estimated for birth weight, lactation yield, fat % and SNF%. The variance component estimation was done solely via a parameter file, a data file and a file for common pedigree. The total variance was stored into additive and non-additive genetic components for the REML analysis of animal model. However, variance components for all the traits were estimated over the genetic groups.

Breeding value of animals for the traits was estimated using Best Linear Unbiased Prediction (BLUP) method. The BLUP in turn was carried out by computer program prediction and estimation (PEST) proposed by Groeneveld et al., (1998). A single trait animal model was used for the PEST program considering the animal and genetic group as a random effect considering year of birth and generation as fixed effects. However, the matrix of variance components from the VCE results for each of the traits considered was used in the matrix for PEST program to estimate breeding values of each animal for each trait separately.

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. The h^2 estimate for birth weight (0.27±0.05) was found to be moderate and reliable as indicated by its small SE.

Table 2. Variance components and heritabiliies for productive traits using pooled data set (n = 3637)

Traits	σ^2_P	Variance components[†]			Heritability
		σ^2_A	σ^2_E	σ^2_e	(h^2)
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

[†] *σ^2_P, phenotypic variance; σ^2_A, additive genetic variance; σ^2_E, environmental variance; σ^2_e, residual variance*

There was no difference between the value of additive genetic variance and residual variance but environmental variance was observed higher than aforesaid components. Khan et al., (1992), Tosh et al. (1999) and Bhuiyan (1999) obtained higher h^2 estimate for birth weight of calves compared with the results of the present study. Therefore, the h^2 estimate of birth weight of calves in the present study was within the range of the published literatures. Higher environmental variance (Table 2) for birth weight obtained in the current study signifies that environment plays a greater 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 additive genetic variance and h^2 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 highest and the lowest values were observed for environmental and residual variance, respectively. The estimated h^2 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 h^2 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 h^2 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 higher estimate than the result of the present study for the same trait. They found h^2 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 h^2 estimate of fat % of milk was found to be 0.37±0.04 and it indicates that the trait is moderately heritable. 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 h^2 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). Moderate h^2 of fat % showed that this trait is not much influenced by environment. 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 h^2 for SNF% (0.46±0.01) 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 h^2 estimate for SNF% of milk was found to be (0.46±0.01). The h^2 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 h^2 estimate of SNF% of milk was within the range of these findings.

Range of predicted breeding values (PBV) indicates a degree of additive genetic variation, which exists in a population. Enough variation for a trait in the population is needed so that the level for the trait can be changed along with the breeding objectives. Pooled PBV obtained for each of the traits assuming genetic group as a population is provided in Table 3.

A general trend of genetic variability can be seen in birth weight of calves. Cows with more number of genotypes were shown to give calves with wider range of birth weight. However, AFS exceptionally showed highest range (8.32) in this ranged. Range of PBV for lactation yield showed that cows of composite genotype (pooled data) had more variation than PM cows. PM×FN possessed highest range of variation with smaller population size. Genetic variation in fat % of milk had very narrow range in all the genetic groups of cows. However, FN (PM×SL), FN(SL×JR) and SL(PM×FN) cow population manifested relatively wider range of genetic variation compared to other groups. It bears testimony to the existence of more genetic homogeneity among cows of all genetic groups for fat%. PM and PM×FN cow population had smaller range of PBV of SNF% than other genetic groups. Negative pooled mean signifies that majority of cows had negative PBV, in other words, only a few cows showed above average genetic performance.

Regression co-efficient of mean breeding values for each of the traits on year of birth for seven different genotypes as estimated and presented in Table 4.

Table 3. Predicted breeding values for productive traits for animals born from 1991 to 2000

Traits	Genetic groups†	n	Pooled PBV±SE	Range of PBV		
				Range	Maximum	Minimum
Birth weight (kg)	PM	674	-0.101±0.05	4.392	1.980	-2.412
	PM×SL	659	-1.047±0.12	5.749	2.636	-3.113
	PM×FN	361	-0.012±0.04	6.892	4.584	-2.308
	AFS	515	0.574±0.12	8.320	5.115	-3.205
	SL(PM×FN)	626	0.260±0.15	7.361	3.792	-3.569
	FN(PM×SL)	441	0.273±0.12	7.961	3.971	-3.990
	FN(SL×JR)	361	0.114±0.10	7.634	4.217	-3.417
Lactation yield (liters)	PM	674	12.08±2.81	578.06	282.69	-295.37
	PM×SL	659	-66.15±2.70	727.63	426.01	-301.62
	PM×FN	361	-45.02±2.19	916.88	439.47	-477.42
	AFS	515	4.26±0.17	854.85	435.57	-419.28
	SL(PM×FN)	626	44.60±12.25	868.44	434.64	-433.81
	FN(PM×SL)	441	9.64±3.78	899.20	438.41	-460.79
	FN(SL×JR)	361	-45.991±5.02	838.80	525.44	-313.36
Fat%	PM	674	0.07±0.04	0.78	0.405	-0.376
	PM×SL	659	0.11±0.04	0.88	0.408	-0.470
	PM×FN	361	-0.01±0.01	0.72	0.375	-0.345
	AFS	515	-0.01±0.01	0.85	0.435	-0.415
	SL(PM×FN)	626	0.01±0.01	0.88	0.358	-0.526
	FN(PM×SL)	441	-0.03±0.01	0.98	0.455	-0.529
	FN(SL×JR)	361	-0.06±0.02	0.95	0.419	-0.531
SNF%	PM	674	0.01±0.04	0.44	0.268	-0.172
	PM×SL	659	0.04±0.04	1.35	0.700	-0.650
	PM×FN	361	-0.07±0.01	0.81	0.423	-0.391
	AFS	515	0.08±0.03	1.11	0.810	-0.299
	SL(PM×FN)	626	0.03±0.01	1.21	0.602	-0.604
	FN(PM×SL)	441	-0.03±0.01	1.06	0.502	-0.555
	FN(SL×JR)	361	-0.07±0.01	1.34	0.745	-0.591

†PM, Pabna Milking; SL, Sahiwal; FN, Friesian; AFS, Australian Friesian Sahiwal; JR, Jersey; n, number of observation

Table 4. Regression coefficient (b) of economic traits on year of birth (1991-2000) in different genetic groups of cows

Genetic groups†	Regression coefficient (b)			
	Birth weight (kg)	Lactation yield (liters)	Fat (%)	SNF (%)
PM	-0.0389	-5.1374	-0.0005	0.0050
PM×SL	0.0846	-0.7209	-0.0024	-0.0104
PM×FN	0.1045	6.7770	-0.0040	0.0099
AFS	0.1245	5.195	0.0029	0.0111
SL(PM×FN)	-0.0598	4.1362	0.0130	0.0002
FN(PM×SL)	-0.1634	-4.1992	0.0111	0.0144
FN (SL×JR)	0.0463	5.1909	0.0043	0.0034

†PM, Pabna Milking cows; SL, Sahiwal; FN, Friesian; AFS, Australian Friesian Sahiwal; JR, Jersey

Table 4 shows that birth weight of calves of PM, SL(PM×FN) and FN(PM×SL) cows decreased at the rate of 0.04, 0.06 and 0.16 kg per year, respectively. It was observed that the genetic trends of lactation yield of genetic group PM×FN, AFS, SL(PM×FN) and FN (SL×JR) rose up to the rate of 6.78, 5.20, 4.14 and 5.19 liters per year, respectively, whereas, the genetic trends of lactation yield of genetic group PM, PM×SL and FN(PM×SL) declined at the rate of 5.14, 0.72 and 4.20 liters per year, respectively. The genetic trends of fat % in three of seven genetic groups showed negative trend and four genetic groups showed positive trend. The genetic group PM, PM×SL and PM×FN showed negative trend for fat %. The genetic trends of SNF% in only one group showed negative trend in PM×SL at the rate of 0.01% per year. On the contrary, PM, PM×FN, AFS, SL(PM×FN), FN(PM×SL) and FN (SL×JR) were increased.

Mean breeding values were calculated by summing up the breeding values of all animals born in a particular year for each of the traits of interest and dividing the aggregate value by the total number of animals born in a given year. Mean breeding values of different genetic groups of cows for various traits from 1991-2000 are furnished in Figure 1, 2, 3 and 4. The rate of genetic change for each of the trait per year of birth of cows was either in the positive or in the negative direction.

The genetic trends constructed from PBV of birth weight of different genetic groups are presented in Figure 1. Genetic trends of birth weight of calves in AFS and SL(PM×FN) cows did not follow a definite pattern rather they showed an erratic fashion. In 1994, the shapes severely dropped bellow than rest of the years, of that time flood severely affected to experimental area and crisis of concentrate cattle feed. Due to flood affection, supply less amount of concentrate feed of pregnant animal. On the contrary, the same for PM×FN, FN(PM×SL) and FN(SL×JR) maintained more or less an upward trend of direction.

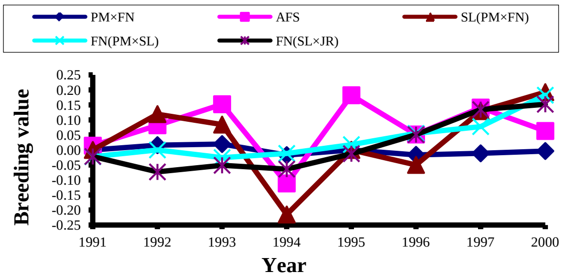

Figure 1. Genetic trends of birth weight of calves for five genetic groups of cows

From the Figure 1, it can be seen that mean breeding value for birth weight of calves of AFS and SL(PM×FN) cows did not maintain consistency rather both declined in 1994 and 1996. The rest three lines more or less remained parallel to the horizontal base line. However, in the year 2000 mean PBV for SL(PM×FN), FN(PM×SL), FN(SL×JR) and AFS cows made a little progress in comparison to 1991. The reasons behind the fluctuation are difficult to explain. However, variation from individual sires within each genetic group might cause sudden drop in AFS and SL(PM×FN) lines.

The genetic trends of lactation yield of genetic groups PM×FN and AFS randomly fluctuated especially a distended drop can be seen in the year 1994 and for AFS only in 1996. But the genetic trend of lactation yield in other groups such as SL(PM×FN), FN(PM×SL) and FN(SL×JR) showed somewhat a regular and slightly upward trend.

The genetic trends of mean PBV of lactation yield are presented in Figure 2. In spite of slight up–down of the curves, general trend was that overall PBV for lactation yield increased from 1991 to 2000. It signifies that genetic potential of cows steadily increased over the period for milk yield irrespective of the breeding program carried out by the BMPCUL in Baghabarighat milk shed area.

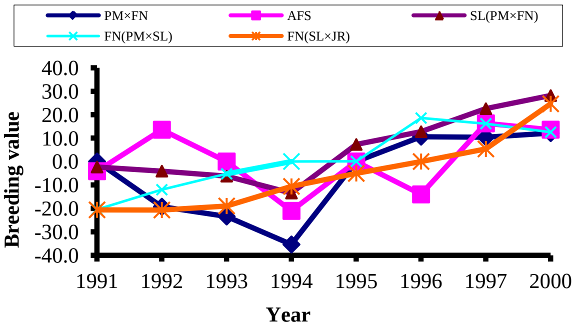

Figure 2. Genetic trends of lactation yield for five genetic groups of cows

The genetic trends for fat% of different genetic groups are presented in Figure 3. The genetic trends of fat% of cows belonging to genetic group PM×FN and FN(SL×JR) showed zigzag pattern instead of having regular fashion. On the contrary, the genetic trends of fat% in AFS, SL(PM×FN) and FN(PM×SL) groups declined in 1992 and they gradually rose up to 1994 sharply but finally SL(PM×FN) and AFS cows produced remarkably higher fat% than PM×FN cows.

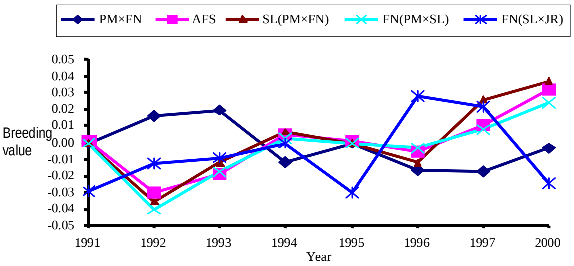

Figure 3. Genetic trends of fat % for five genetic groups of

From the Figure 3, it can be seen that mean PBV of fat % of PM×FN genetic group showed steady rise up to 1993 but declined in the subsequent years. AFS, SL(PM×FN) and FN(PM×SL) cows maintained very close PBV up to 1996 and later all of them gradually got inclined. FN(SL×JR) cows steadily rose up till 1994 and then followed very erratic fashion. FN(SL×JR) cows gave maximum lactation yield which might affect PBV for fat %. Although breeding of cows were not intended to enhance fat %, but pressure for increasing milk yield inversely might reduce fat% in milk.

The genetic trends for SNF% of different genetic groups are shown in Figure 4. The genetic trends for SNF% of genetic group PM×FN and FN(SL×JR) did not follow normal shape i.e. the magnitude sometimes rose up and sometimes fell down. On the other hand, the genetic trends of AFS, SL(PM×FN), FN(PM×SL) followed the normal shape of promotion for the trait.

Figure 4 demonstrates that all the mean PBVs for SNF% were close in 1991 but at the end of the period of study (in the year 2000) the lines ended apart each other. However, in general, the trend was not in negative mode. Augmented pressure for increasing milk over the years could not be found, at least, to reduce SNF% in milk.

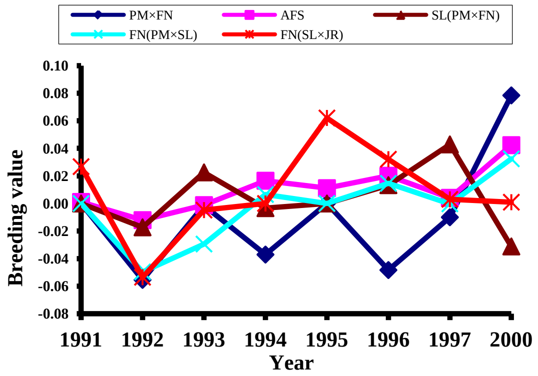

Figure 4. Genetic trends of SNF % for five genetic groups of cows

For reliable and accurate analysis of data, large number with minimum missing cells, complete pedigree information, better genetic connection among animals is also important to meet up the purpose. In fact, in this study, such requirements were poorly met. However, cows constituting the population displayed somewhat erratic type of genetic trends for birth weight, lactation yield, fat% and SNF%. The FN(SL×JR) and AFS cows maintained an upward genetic trend for all the traits under investigation during 1991-2000.

Conclusion

Heritability values were estimated to be medium to high (0.27 to 0.46) for the traits like birth weight, lactation yield, fat%, and SNF%. From the results of this study, it is revealed that birth weight, lactation yield and SNF% increased significantly with the increase of exotic inheritance level of cows. Regression analyses reveal that birth weight, lactation yield, fat% and SNF% were maximally increased per year at the rate of 0.12 kg, 6.78 L, 0.01% and 0.01% in genetic group AFS, PM×FN, SL(PM×FN) and FN(PM×SL), respectively.

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