

Full Length Research Paper

Within-herd phenotypic and genetic trend lines for milk yield in Holstein-Friesian dairy cows

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A total of 937 pedigree, breeding and performance records of 567 Friesian cows at the Livestock Experiment Station Bhunikey Dist. Kasur (Pakistan) spanning the years 1982-2001 were analyzed using Best Linear Unbiased Predictions procedure. Individual animal models were fitted to total milk yield from all lactations to estimate breeding values by Restricted Maximum Likelihood methodology. Milk yield and lactation length averaged 3391.66 ± 137.97 kg and 278.40 ± 90.17 days, respectively. The estimated breeding values for milk yield ranged from -354 to 503 kg. The corresponding values for the standing herd ranged from -209 to 294 kg. The genetic trend for milk yield was slightly positive indicating that the sires used during the last 20 years were of better breeding values. Phenotypic reduction in milk yield over time was observed, a probable reflection of the inability of the cows to adapt to the local environment and other environmental inadequacies.

Key words: Friesian, pedigree, genetic, phenotypic, trend lines, Estimated Breeding Value (EBV), animal model

INTRODUCTION

Out of Pakistan's 26 million heads of cattle (Anonymous, 2007), about 72% are of non-descript type. These animals are late-maturing and poor milkers. To improve their lactation performance, a crossbreeding programme with exotic temperate dairy breeds was initiated in the early seventies by importing frozen semen of Jersey and Friesian cattle. To cope with the demand of exotic cattle semen, a herd of 86 pregnant Friesian cows was also imported for the production of genetically superior bulls to ensure the regular and adequate supply of semen for crossbreeding in canal-irrigated areas of the Punjab and other parts of the country. About 4 - 5 generations of these imported cows have been produced in the sub-tropical environment of central Punjab. The genetic evaluation of the performance of these animals has not yet been carried out.

Ranking breeding animals according to their genetic merit for desirable traits adds value and efficiency in a breeding programme. Therefore, an accurate identification and genetic evaluation of breeding animals is of vital significance for genetic improvement. Estimated breeding values (EBVs) are estimates of the true

breeding value of an animal and Best Linear Unbiased Predictions (BLUP) procedure using the Individual Animal Model (IAM) is one of the global favourite methodologies for the prediction of breeding values of farm animals (Hill and Meyer, 1988).

A graphic historical perspective of a within-herd breeding program using phenotypic and genetic trend lines can convey a quick assessment of a breeder's selection success in previous generations. Trend lines may be used to compare alternative methods of selection or management for breeders involved with large herds. Trend lines may reinforce selection and management goals established by a breeder. However, such trend lines may also signal the need for changes in selection and/or management schemes. Trend lines resulting in a direction and (or) at a rate contrary to the anticipated result could mean that projected responses to selection were made with inappropriate assumptions or that expectations were too optimistic. Trend lines may also demonstrate how much (or little) selection was actually applied (Wilson and Willham, 1986).

The aim of this investigation was to present the phenotypic and genetic trend lines of total milk yield and also to estimate the breeding values of the cows for comparative ranking within a purebred herd of Holstein-Friesian cattle in the Punjab Province of Pakistan. The

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Figure 1. The genetic trend for milk yield.

information so generated will be useful in the future direction of the cross breeding programme for the genetic improvement of the local cattle population.

MATERIALS AND METHODS

Data on 937 pedigree, breeding and performance records of a pure bred Holstein-Friesian herd (567) maintained at the Livestock Experiment Station Bhunikey (Pattoki) Distt. Kasur during the period 1982 - 2001 were analyzed. The data on milk yield and lactation length were analyzed to estimate the breeding values and genetic trends in milk yield. Records with incomplete or abnormal lactations less than 100 days, inconsistent cow identity, unknown birth dates and $\pm 3 \sigma_P$ from the mean were treated as outliers and excluded from analysis. A total of 114 records were edited. All pedigree information was included in the analysis to minimize the bias due to selection and non-random mating.

Breeding values of animals for milk yield were estimated by Best Linear Unbiased Prediction (BLUP) procedure (Henderson, 1973) using an animal model. The genetic parameters used were the same for genetic evaluations. The fixed effects, year of birth/calving (19 years), season of calving (5 seasons), lactation length (823 records) and lactation number (No. 8) found significant in an initial analysis (Javed et al., 2004) were fitted in the model. In matrix notation, model assumed can be written as under:

$$Y = XB + Z\mu + e$$

Where,

Y is the vector of observations of the animal for a trait (No. of records x 1)

X is the known design matrix relating fixed effects to (No. of records x total No. of fixed effect levels)

B is the vector of unknown fixed effects including the covariables (total No. fixed effect levels)

Z is the known design matrix relating animals direct additive genetic effects to Y (total No. of records x total No. of animals)

μ is the vector of random animal solutions i. e. breeding values (total No. of animals x 1)

'e' is the vector of unknown random residual effects (total No. of records x 1)

The random effects were assumed to be normally distributed with mean zero and (Co) variances:

$$V(\mu) = A \sigma_A^2 \quad V(e) = I \sigma_E^2 \quad \text{and} \quad \text{Cov}(\mu, e) = 0$$

$$V(y) = Z A Z \sigma_A^2 + I \sigma_E^2$$

Where,

A is the numerator relationship matrix (total No. of animals x total No. of animals)

I is the identity matrix (total No. of records x total No. of records)

σ_A^2 is the estimate of direct additive genetic variance

σ_E^2 is the estimate of residual variance.

BLUP equations (Henderson's mixed model equations) for the above mixed model can be represented as follows:

$$\begin{array}{ccc|c|c} XX & XZ & & b & X \\ \hline & & & & \\ \hline ZX & ZZ+A^{-1} \lambda & & \mu & Z \end{array} =$$

Where;

A^{-1} is the inverse of the numerator relationship matrix and

$$\lambda = \sigma_E^2 / \sigma_A^2$$

The estimates of σ_A^2 and σ_E^2 used here were from the same analysis.

The derivative free restricted maximum likelihood (DFREML) Set of Computer programmes (Meyer, 1997) was used which also generated Estimated Breeding Values (EBVs) as a by-product. Breeding values thus estimated were fitted in a fixed effect model (Harvey, 1990) having year of birth as the only fixed effect. The least squares solutions of breeding values were drawn against year of birth to depict the genetic trend. Phenotypic values of milk yield were plotted against the year of birth to determine phenotypic trend.

RESULTS AND DISCUSSION

The least squares means for lactation milk yield and lactation length in the herd under study were 3391.66 ± 137.97 kg and 278.40 ± 90.17 days, respectively (Javed et al., 2004). The estimated breeding values for milk yield from animal model evaluations ranged from -354 to 503 kg for all the cows of Friesian breed maintained under the period of study. The corresponding values for the cows present alive in the herd under study ranged from -209 to 294 kg (Table 1). The genetic trend for milk yield depicted a slightly positive trend (Figure 1) indicating a slight genetic improvement in the present herd overtime. It might be due to the use of imported semen from the sires having some better breeding values for milk yield. However, there was some deteriorating trend in milk yield during the years 1996 and 1997 which might be due to the use of semen for some inferior quality sires. However, a deteriorating genetic trend has been observed in Jersey cows in Pakistan which might be due to the use of semen from the sires produced from the same herd (Javed et al., 2003).

The genetic difference among the individuals is a factor, which determines the rate of genetic improvement that can be accomplished through selection. With low estimate of heritability, the improvement in milk yield is much less through selection as compared to what could

Table 1. Genetic ranking of standing herd of Friesian cows at LES, Bhunikey.

Year of birth	Cow #	Lactations.	Av. Milk yield (Kg)	Estimated breeding values	rank
1996	317	1	3500	294	1
1990	123	6	4044	289	2
1999	403	0	0	273	3
1996	307	1	7689	246	4
1993	201	3	3279	239	5
1995	245	2	5748	230	6
1999	397	0	0	207	7
1995	246	2	3879	182	8
1996	311	1	5208	157	9
1996	314	2	5124	153	10
1994	234	3	3342	140	11
1994	233	2	2615	137	12
1999	390	0	0	130	13
1995	286	1	6921	129	14
1996	321	1	3710	126	15
1991	150	3	3718	124	16
1999	393	0	0	122	17
1999	401	0	0	115	18
1995	274	1	3521	105	19
1995	257	2	4557	102	20
1996	293	1	3148	101	21
1999	391	0	0	91	22
1998	363	1	5838	84	23
1999	385	0	0	74	24
1998	374	1	4506	63	25
1999	395	0	0	62	26
1998	368	1	3052	60	27
1993	203	2	3133	60	28
1994	215	3	3352	53	29
1998	370	1	2110	51	30
1996	309	2	3465	42	31
1998	362	1	3920	35	32
1997	347	1	4305	35	33
1995	277	1	3001	35	34
1996	310	1	4788	32	35
1999	377	1	2527	22	36
1995	269	1	5621	17	37
1999	418	0	0	15	38
1999	416	0	0	15	39
1997	349	1	4072	8	40
1999	405	0	0	2	41
1999	406	0	0	1	42
1999	379	0	0	0	43
1996	304	2	4848	0	44
1999	410	0	0	0	45

Table 1. Contd.

1996	303	1	2996	-1	46
1998	367	1	3717	-7	47
1999	408	0	0	-9	48
1999	372	2	2099	-11	49
1999	413	0	0	-12	50
1999	404	0	0	-17	51
1992	179	4	3045	-17	52
1994	229	3	2644	-18	53
1998	375	1	3128	-18	54
1994	208	2	3150	-18	55
1992	157	2	3459	-20	56
1994	241	2	1153	-24	57
1994	211	2	3934	-25	58
1994	223	2	2639	-26	59
1997	346	1	3659	-29	60
1998	360	1	574	-29	61
1999	412	0	0	-33	62
1995	265	2	4004	-34	63
1996	319	2	2836	-36	64
1999	386	0	0	-54	65
1996	327	2	3488	-56	66
1999	380	0	0	-56	67
1995	244	1	1668	-57	68
1999	381	1	1199	-62	69
1999	392	0	0	-70	70
1995	284	1	2429	-71	71
1997	351	1	5903	-71	72
1997	345	2	3531	-83	73
1998	359	1	3430	-86	74
1993	192	2	2541	-88	75
1997	330	1	3290	-88	76
1998	361	1	4492	-91	77
1998	353	2	3776	-93	78
1999	398	0	0	-104	79
1998	356	2	2434	-106	80
1998	355	1	1939	-107	81
1998	373	1	3906	-109	82
1996	313	3	1703	-110	83
1996	316	2	3529	-111	84
1996	318	2	928	-131	85
1998	366	1	2401	-209	86

be attained by other environmental changes (Javed et al., 2002a). The culling in the herd under investigation was not according to the recommended level and mostly ani-

mals unfit for breeding, repeaters or sick were disposed off. The culling on the basis of low production was rarely practiced. It could be inferred from the present study that

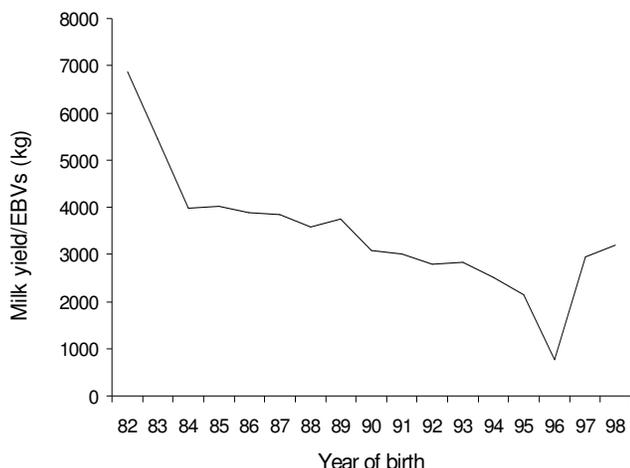


Figure 2. Phenotypic trend for milk yield.

in the presence of various factors, the rate of genetic improvement is much less than the desired level over 20 years.

Phenotypic reduction in milk yield was noticed (Figure 2) in the present herd during the period under study. The deterioration in this trait may largely be attributable to environmental factors. The major reason for this deterioration may be the fact that different diseases like foot and mouth and other hazards occurred during different years. Another factor may be that these animals could not adapt to the subtropical environment. The herd under study was imported from the temperate zone and was kept in the subtropical environment of central Punjab where ambient temperature often rises up to 45°C in summer months. Genotype X Environment interaction (G x E) is potentially extremely important in cattle breeding in the tropics. The animals of temperate regions maintained in tropical conditions cannot behave similar in both the environments (Javed et al., 2002b). The importation of temperate breeds to tropical environments in often trouble making. Payne and Hodges (1997) have reported that nucleus units of Friesian cows established by Governments, when improved management was not given, the pure imported cattle often die. Javed et al. (2002a) also observed similar findings in a pure bred herd of Jersey cattle in Pakistan.

Conclusion

The phenotypic trend line revealed that the import of dairy cattle breeds of temperate zone to the tropical and subtropical regions is not a viable option. However, the genetic trend line was slightly in positive direction. It indicates that use of semen from the bulls having better breeding values and provision of improved management can be a better option for the production of better quality breeding male animals which can be used in crossbreeding program for genetic improvement of local low producing non-descript animals

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