

Response to Selection for Milk Yield and Lactation Length in Buffaloes

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ABSTRACT : A multiple trait animal model having milk yield and lactation length was used to estimate genetic parameters using data from four institutional herds and four field recording centers. Response to selection for milk yield alone and in combination with lactation length was estimated by using principles of genetic theory. Lactation records (n = 2,353) adjusted for age at calving to 60 months were utilized. Milk yield was 17% heritable

with repeatability of 0.44. Lactation length had a low heritability of 0.06 with repeatability of 0.16. Genetic correlation between the two traits was 0.70. Selection response in milk yield can be improved slightly (103.8 vs 102.8 kg) when information on covariance with lactation length is used together with the information on milk yield. (**Key Words**: Selection, Milk Yield, Lactation Length, Buffaloes)

INTRODUCTION

Water buffalo is a unique beast. Due to preference of their milk with higher butter fat, they have been and are likely to be part and parcel of village life in future. Current projections of their population indicate that their share of 70% in the milk supply of the country is also likely to increase in the future.

Breeding value estimation in these and other dairy animals has traditionally been done after pre-adjusting milk yield records for environmental factors like lactation length and age at calving. Age at calving is not exclusively an environmental trait as 15-20% variation is due to additive genes. Lactation length however, varies widely in terms of the kind of genes controlling variation in it. Few studies have reported genetic parameters of lactation length. Salah-ud-Din (1989) reported that lactation length was 4% heritable with repeatability of 0.18 in Pakistani buffaloes. It was, however, moderately heritable (0.15 to 0.22) with genetic correlation of 0.42 to 0.56 with milk yield in Indian buffaloes (Raheja, 1992a). Present study deals with the genetic parameter estimation of milk yield and lactation length in a multiple trait situation and estimation of expected response to selection in milk yield and lactation length by considering milk yield and lactation length as separate traits.

MATERIALS AND METHODS

Data for this study were collected from Nili-Ravi

buffaloes at the Livestock Production and Research Institute, Bahadurnagar, Okara, Pakistan. Data on the daughters of the bulls being progeny tested were also available from three other institutional herds and four field data collection centers (progressive private farms and village populations) involved in the project. A total of 3,892 lactations of 1,235 buffaloes were recorded. Records were edited to exclude those lactations that ended by abortion or sickness. Lactations in which the first part of lactation was not recorded or the lactation length was less than 180 days were also not included. Dates of birth of the offspring were matched with the dates of calving of the dams to confirm the pedigrees wherever possible. Buffaloes with missing dates of birth were also not included in the analyses. After editing, 2,353 lactations from 901 daughters of 66 sires had information on milk yield, lactation length and age at calving.

A multiple trait animal model, having lactation length as a separate trait along with the milk yield was used with following mathematical representation.

$$Y = (I_t \otimes X)b + (I_t \otimes Z_1)a + (I_t \otimes Z_2)p + e$$

where Y is a matrix of dependent variables having vectors of unadjusted milk yield and lactation length; b is vector of fixed effects; t is number of traits, i. e. 2; \otimes is Kronecker product, a, p, and e are random animal, permanent environment and temporary environment effects; X, Z₁, and Z₂ are incidence matrices for vectors b, a, and p. Fixed effects included two parity groups (1st or later parities), 89 herd-year-season combinations, 85 age

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classes (made by two month interval starting from ≤ 30 months to ≥ 200 month of calving).

Random effects were assumed to have expectations and (co)variances as follows:

$$E \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix} \quad \text{Var} \begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A_{q_1} \otimes G & 0 & 0 \\ 0 & A_{q_2} \otimes P & 0 \\ 0 & 0 & I_N \otimes R \end{bmatrix}$$

where G, P and R are genetic, permanent environment and residual variance-covariance matrices for the t traits. A and I are additive relationship and identity matrices; q_1 , q_2 , and N were 1,030, 901, and 2,353. For the relationship matrix, when one or both parents of any buffalo with a production record were missing, phantom parents were assigned which were assumed to be average representatives of the genetic groups of similar animals selected to be parents at the same time (Westell and Van Vleck, 1987). The time period for the genetic group was defined by subtracting the average generation interval from the year of birth of the animal with the missing parent to estimate the year of birth of the missing parent. The generation intervals used were calculated from these data for four selection paths i. e. sire to sire, sire to dam, dam to sire and dam to dam and were 7.4, 6.6, 9.6 and 6.9 years, respectively.

A multiple trait expectation-maximization algorithm for animal model using canonical transformation (Miszta, 1993) was used. Convergence was assumed when change in the ratio of random variances (G and P) to residual variance was less than .001. The convergence criterion was met at 150 iterations.

RESULTS AND DISCUSSION

Milk yield averaged 2,114 kg with coefficient of variation of 33%. Lactation length averaged 283 days with 11 % as coefficient of variation. Lower variation in lactation length was due to restriction of length between 180 and 305 days.

Genetic parameters

Heritability and repeatability estimates of lactation length and milk yield are in table 1. Values from single trait analysis for milk yield (Khan et al., 1996) are also presented here for complacence. Milk yield analyzed as a single trait, adjusted for lactation length and age at calving (as covariables) had heritability of 0.18 and a repeatability of 0.43. Heritability and repeatability

estimates of milk yield from multiple trait analysis (0.17 and 0.44) were not different from those of the single trait model. Lactation length had low heritability (0.06) with moderately low repeatability (0.16). The model used for multiple trait analysis was not exactly the same as that of single trait analysis. Lactation length (deviated from 305 days) was included as a second degree polynomial in the single trait analysis while it was a separate trait (linear) in the multiple trait analysis. Also, age at calving was used as a covariable in the single trait analysis but was a classification variable in the multiple trait analysis.

Table 1. Genetic parameters of milk yield (kg) and lactation length (days)

Parameter	Single trait model*	Multiple trait model	
	Milk Yield (kg)	Milk Yield (kg)	Lactation Length (days)
Breeding Values (SD)	219	251	7.9
Permanent Environment (SD)	257	320	9.8
Temporary Environment (SD)	391	457	28.5
Heritability	0.18	0.17	0.06
Repeatability	0.43	0.44	0.16
Correlations			
Phenotypic		0.54	
Genetic		0.70	
Environmental		0.53	

* Khan et al. (1996).

The values for genetic parameters are within the range of estimates reported elsewhere for buffaloes (Tulloh and Holmes, 1992). Milk yield was 10-15% heritable in Egyptian buffaloes (Mohamed et al., 1993, Metry et al., 1994) and 17-18% in Indian buffaloes (Cheema and Basu, 1991, Tailor et al., 1992a). Both, higher and lower estimates have also been reported for these breeds in other studies. Heritability is higher than reported by Salahud-Din (1989) for Nili-Ravi buffaloes in Pakistan. In that study lactation length of >150 days was considered as the production potential of buffaloes and thus no adjustments were made for records with lactation length between 150 and 300 days. The estimates are, however, similar to those (0.179) reported by Cady et al. (1983) for milk yield of >250 days of lactation duration. Inclusion of records from field data collection centers in the present study may have inflated the proportion of environmental

variance causing lower heritability estimates. Estimates of heritability under the animal model are expected to be higher than sire models (Miształ et al., 1992).

The repeatability estimate of milk yield was higher than Cady et al. (1983) but same as that reported by Salah-ud-Din (1989) for Pakistani buffaloes. Estimates are also similar to some of reports on Indian buffaloes (Ulaganathan et al., 1983, Raheja, 1992a). Repeatability of milk yield was 0.48 for Egyptian buffaloes (Ashmawy, 1991) and 0.47 for Italian buffaloes (Pilla and Moioli, 1992). Repeatability estimates of lactation length for Pakistani buffaloes have been reported in the range of 0.18 to 0.22 (Salah-ud-Din, 1989, Khan, 1986). Estimates for Egyptian buffaloes have been reported to be higher (0.21 to 0.28) by Ashmawy (1991) and Metry et al. (1994).

The phenotypic correlation between milk yield and lactation length was 0.54 (table 1). Genetic and environmental correlations were also positive. Genetic synergism between the milk yield and lactation length ($r_g = 0.70$) is in agreement with most of the studies on buffaloes (Vij and Tiwana, 1986; Tailor and Jain, 1987; Raheja, 1992a; Tailor et al., 1992b). Breeding values of sires for milk yield from single and multiple trait models had a very high correlation which is represented in Figure 1.

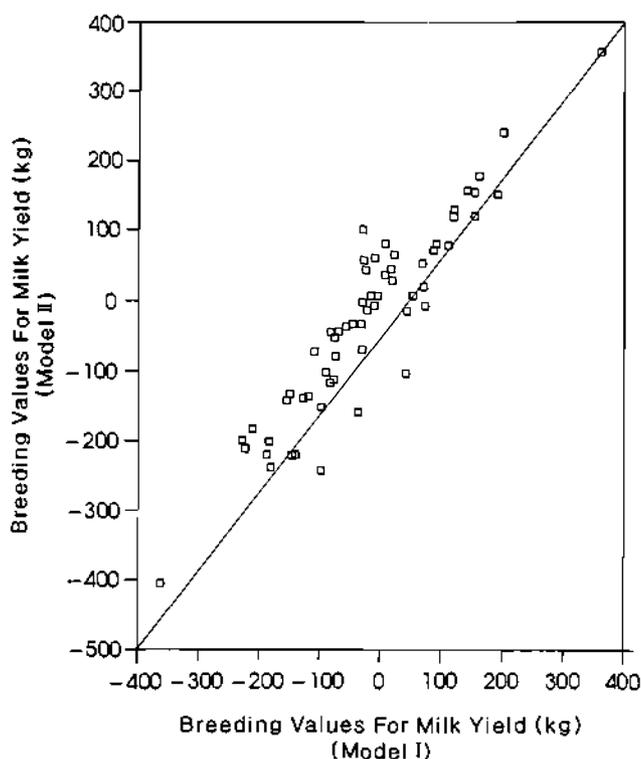


Figure 1. Breeding values of milk yield (kg) from single trait (Model I) and multiple trait (Model II) models.

Response to selection

Using parameter estimates from the multiple trait analysis, direct response in milk yield (table 2) would be 102.77 kg for a selection intensity of 1.0, approximating 337 kg over a period of 25 years. This assumes a generation interval of 7.6 years calculated from the data and averaged over the four selection paths. This would also result in 2.3 days of increase in lactation length as a correlated response or 7.5 days over a period of 25 years. If, however, information on (co)variance of lactation length were used with the information on milk yield, response in milk yield could be improved to 103.83 kg per generation (table 2, G1 based on X1, X2).

Table 2. Response to selection in milk yield and lactation length*

Selection for	Based on	Genetic change in	
		Milk yield (kg)	Lactation length (days)
1G1 + 6G2	X1, X2	103.63	2.21
1G1 + 12G2	X1, X2	103.20	2.26
1G1 + 32G2	X1, X2	101.34	2.35
G1	X1	102.77	2.25
G1	X1, X2	103.83	2.14

*X1 and X2 are phenotypic values of milk yield and lactation length while G1 and G2 are additive genetic values of milk yield and lactation length.

Selecting milk yield and lactation length in an index may not be beneficial in the absence of well founded selection weights. Relative economic weights of <12 for lactation length would cause better response in milk yield than if selection for milk yield was based only on milk yield information. A higher weight, e. g. 1:32, which would mean equal weight in terms of standard deviation of the traits, would result in 101.34 kg increase in milk yield and 2.35 days increase in lactation length per generation. Thus, information on lactation length can marginally improve the selection response in milk yield. Results are comparable with the studies on selection for milk yield in buffaloes where milk yield and lactation length have been used in an index. El-Arian and Tripathi (1990) and Gajbhiye and Tripathi (1991) suggested the relative economic values of 1:12 and 1:6 for milk yield and lactation length for Indian buffaloes.

Genetic parameter estimates under multiple trait model were not different from those of single trait animal model. Milk yield was moderately heritable (0.18) with repeatability estimates of 0.43. Selecting buffaloes for higher milk yield will result in increased lactation length

due to high positive genetic correlation between the two traits. Lactation length had heritability of only 0.06 and repeatability of 0.16. Genetic correlation between lactation length and milk yield was 0.70. Genetic response in milk yield was increased by < 1% by including lactation length with milk yield in a selection index. This small improvement may not justify the complexity of a multiple trait model for selecting buffaloes.

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