Original Article

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GENETIC AND PHENOTYPIC CORRELATIONS OF SOME PERFORMANCE TRAITS OF *Nili-Ravi* BUFFALOES IN TROPICS

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ABSTRACT

Many traits in livestock and associated with each other positively or negatively where selection for trait effectively causes changes in the associated traits. This study was conducted to find such associations of genetic and phenotypic origin known as genetic and phenotypic correlations for some productive and reproductive traits of *Nili-Ravi* buffaloes kept under tropical environment. In this context data of 9003 lactation records of *Nili-Ravi* buffaloes (n=2050) daughters of 173 sires over a period of 30 years were collected from four buffalo herds maintained by the Livestock and Dairy Development Department. Data were analysed by using the BLUP techniques by DFREML (univariate) and ASREMAL (bivariate) analysis. Heritability estimates for 1st to 5th lactation milk yields ranged from 0.06 to 0.18, and 305-day milk yield was 0.09. The genetic correlations (r_g) between 305-day milk yield and LMY for five parities ranged from 0.55±0.22 to 0.95±0.02 (all lactations), whereas respective phenotypic correlations ranged (r_p) from 0.63 to 0.70. However, the bivariate analysis showed genetic correlation (rg) of 1st lactation milk yield with 1st dry period, 1st calving age, 1st calving interval, 1st service period and 1st service per conception as 0.15±0.25, -0.03±0.21, -0.33±0.22, -0.23±0.22 (0.00±0.39, respectively. Whereas, genetic correlation (rg) of 1st lactation length with 1st dry period, 1st calving age, 1st calving interval, 1st service period and 1st service per conception were .14±0.29, 0.31±0.21, 0.22±0.31, 0.31±0.33, 0.15±0.25, -0.03±0.21, -0.33±0.22, -0.23±0.22,-0.56±0.22, respectively. The higher values rg for milk yield help to select in early lactation for higher lifetime productive traits. However, reproduvtive traits had little genetic correlations, signifying that progressive management would be suitable to acquire better performance.

Keywords: *Bubalus bubalis*, buffaloes, genetic, correlation, productive, reproductive, traits, *Nili-Ravi*, genetic parameters

INTRODUCTION

Buffalo is one of the leading specie in the tropics producing food like milk and meat and used as source of the draught power (Faraz *et al.*,

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2021a) thus, serving in the economy of Pakistan (Faraz *et al*., 2021b). The genetic improvement in performance traits depend upon genetic and phenotypic correlations with other traits along with its heritability and repeatability.

A phenotypic correlation is a function of genetic and environmental correlations. However, genetic correlations are of importance to the breeder for the following reason, they indicate how traits are likely to change in the next generation due to selection. If the correlation is positive, selection for the improvement of one trait will also results in the improvement in the other, even though direct selection for its improvement has not been practiced; if the correlation is negative, selection for improvement of one would result in a decline in the other correlated trait. Prior knowledge of a negative genetic correlation would be helpful to plan counter. Selection measures to prevent any undesired correlated changes; Knowledge of a genetic correlation may also be helpful in a situation where one trait may be difficult to improve through direct selection and selection for another correlated trait could be used. The “difficult” trait may be so because of its low heritability or practical problems associated with obtaining accurate measurements. Most of the reproductive traits have low heritabilities, and thus direct selection would bring about slow or even no improvement. Selection based on pedigree, progeny and family information for desirable correlated traits with high positive correlation would be helpful for improvement of such traits.

Genetic correlation was large and positive between lactation length and milk yield. It ranged from 1.0±0.09 to -0.15 (Peeva, 1997). The phenotypic correlation was also high and positive. The high value 1.00±0.09 was reported by Mohamed *et al.* (1993) while low value 0.36±0.13 was reported by Sharma and Basu (1985). Tailor *et al.* (1992) analyzed 580 production records on Surti buffaloes, the genetic correlation of lactation length with milk yield was reported to be high and positive.

For dairy selection program, milk yield traditionally has been the most important trait. However, several studies have shown that reproductive efficiency declines with the increased milk production. Reproductive performance despite being an important part of dairy production costs generally has not been considered to be important for selection program. The genetic correlation between milk yield and calving interval was very low with the highest value of 0.50 and lowest value of -0.93±0.09 reported by (Velea *et al*., 1991), whereas the phenotypic correlation ranged from 0.13 to 0.5 (Salah-ud-Din 1989; Velea *et al.* 1991). The genetic correlation and phenotypic correlation for milk yield and age at first calving was reported very low and found to be non-significant. The genetic and phenotypic correlation between the milk yield and lifetime traits was reported moderate to high but the correlation between the milk yield and breeding efficiency was -0.22±0.43 Sharma and Chaudhary (1986). Raheja (1992) analysed the production and reproduction records of first three lactations on 716 Murrah buffaloes using a multi trait maximum likelihood procedure. It was reported that the genetic correlations of milk yield with calving interval were very low. The negative effect of production on fertility for interval between first and second services was totally compensated by better management (Bagnato and Oltenacu, 1993).

The studies on buffalo are scarce in the literature and relatively less research work has been done in characterizing buffaloes particularly in Pakistan. Studies on association between different productive and reproductive traits are useful in designing selection programs for breed improvement. Hence this study was designed to investigate and find genetic and phenotypic correlations among difference performance traits (including milk production and reproductive traits) of *Nili-Ravi* buffaloes.

MATERIALS AND METHODS

This study is based on performance records of *Nili-Ravi* buffaloes (n=2050). Data were collected about date of calving; sire date of birth, date of drying, dam date of birth, date of disposal, dates of service, number of services per conception and lactation milk yields. The derived variables were 305-day lactation milk yield, lactation length, dry period, age at first calving, calving interval, service period and gestation period. Data on milk yield (305-day and total) were based upon actual weekly milk records. Shorter lactations less than 60 days were excluded (5.23%). Incomplete lactation records of buffaloes due to culling, abortion or due to some other diseases were also excluded. The records of animals were excluded having calving interval <300 or >730 days, gestation period <285 or >335 days, age at first calving <900 or >2400 days according to Cady *et al*. (1983).

The months of calving were arranged into four groups keeping in view the seasonal effects as winter (December to February), spring (March to May), summer (June to Aug) and autumn (Sep to Nov) as reported by Dahlin (1998).

The (Co) Variance components were estimated with both univariate and bivariate models. The basic model used was:

$$Y = Xb + Zu + e$$

Where Y is response vector variable, X and Z are the design matrices for fixed and random effects respectively, b is vector of fixed effects having herd - year of calving, calving season and the age code (Iqbal, 1996), u is a vector of individual animal breeding values and e is a vector of random error terms. When combined analysis was performed for first five parities, u in the model also had permanent environment effect.

Genetic and phenotypic correlations

The performance traits were analyzed statistically for the estimation of phenotypic and genetic correlations among all plausible combination of traits. Bivariate analysis was carried out using individual Animal Model applying REML technique (Patterson and Thomson, 1971). While their fixed effects were the same as considered in the univariate analysis.

The genetic correlation was estimated as follows:

$$r_{GX_1X_2} = \frac{\sigma_{SX_1X_2}}{\sqrt{\sigma^2_{SX_1} \cdot \sigma^2_{SX_2}}}$$

Where;

$\sigma_{SX_1X_2}$ is the animal covariance component for the two traits under consideration.

$\sigma^2_{SX_1}$ is the animal variance component for the first trait; and

$\sigma^2_{SX_2}$ is the animal variance component for the second trait.

The standard error of the estimates of genetic correlation was calculated, and the phenotypic correlations were estimated as under:

$$r_{P(X1X2)} = \frac{\sigma_{S\,X1X2} + \sigma_{W\,X1X2}}{\sqrt{(\sigma^2_{SX1} + \sigma^2_{WX1})(\sigma^2_{SX2} + \sigma^2_{WX2})}}$$

Where;

$\sigma_{W\,X1X2}$ is the within animal covariance component for the two traits.

σ^2_{wx1} is the within animal variance component for first trait.

σ^2_{wx2} is the within animal variance component for second trait; and other symbols are same as described before.

All the analysis was performed using Derivative Free Restricted Maximum Likelihood (DFREML) set of computer program (Meyer, 1997). The approximate standard errors of the genetic correlation were not estimated by the DFREML. The DFREML software failed to estimate the sampling errors. For purpose of estimation of the standard error for genetic correlation Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) set of computer program was used.

RESULTS AND DISCUSSIONS

Genetic and phenotypic correlations

Genetic correlations (r_g) between 305-day milk yield and lactation length were 0.95±0.02 (Table 1). Analysis of individual parities indicated that it increased from 1st (0.55±0.20) to 5th parity (0.81±0.16). The overall phenotypic correlation between the two traits was 0.69 with no major difference among parities.

The r_g between the first lactation 305-day milk yields with other lactation length trait i.e. dry period, calving age, calving interval, service period and services per conception are presented in Table 2. The r_g between 305-day milk yield and dry period was close to zero while with other reproductive traits r_g were also close to zero but favourable.

First lactation length generally has close to zero r_g with reproductive traits (Table 2). Phenotypically, it was positively correlated with calving interval and service period. Genetic correlation between milk yield and lactation length has generally been reported to be high and positive (Mohamed *et al*., 1993; Raheja, 1992; Das and Sharma, 1993; Sharma and Basu, 1985; Khan *et al*., 1997; Velea *et al*., 1991; Tailor *et al*., 1992) which is similar to cattle studies (Dahlin, 1998). The studies which disagree with the above conclusion either have few observations or model are incomplete. Peeva (1997), for example, reported negative r_g between 1st lactation milk yield and lactation period. The population under study was crossbred buffalo population and paternal half-sib correlation was the method utilized. Level of milk production and length of lactation were not reported in the study. Non-additive genetic variation was also assumed zero.

Reproductive parameters are generally reported to have low or negative r_g with milk yield. Genetic correlation between milk yield and calving interval (Raheja, 1992) and between milk yield and 1st calving age, it was also close to zero (Raheja, 1992; Dutt and Taneja, 1994). Between milk yield and service period similar extent of relationship has been reported (Khan *et al*., 1997; Raheja, 1992). Similarly, relationship between milk yield and dry period (Sharma and Chaudhry, 1986; Khan *et al*., 1997) has been reported to be low. Lactation length on the other hand has been reported to have variable genetic relationship with other traits such as dry period, age at first calving and calving interval. Relationship between dry period and age at first calving is week (Raheja, 1992; Khan *et al*., 1997) but most reports agree that lactation length and calving interval are positively correlated phenotypically (Aziz *et al*., 2001; Ayyat *et al*., 1996) and genetically (Khan *et al*., 1997; Dahama *et al*., 1991).

The negative effect of production on

fertility can be compensated for by better management (Bagnato and Oltenacu, 1993). When the genetic correlations are very close to 0; then it is evident that each trait is controlled by different sets of genes and the selection for single trait have a little effect on the other one. If these are different from 0 then, both traits affected by more of the same genes and selection for one increase the other if genetic correlation is positive and vice versa. Weak association or genetic antagonism between milk yield and reproductive traits may be of limited consequence in buffaloes because of heritability of reproductive traits are low (Raheja, 1992; Khan *et al*., 1997; Thevamanoharan *et al*., 2002). The negative r_g of service period and calving with milk yield suggested that selection for increased milk yield would be expected to reduce reproductive traits such as service period and calving interval, which is desirable.

The present study depicted lower but positive genetic correlations with milk yield, and this trait might be considered in the selection program for *Nili-Ravi* buffaloes. In case of heart girth, genetic correlation with milk-yield although not so much high but it seems to be important for consideration of indirect selection for the trait milk yield.

Table 1. Genetic (r_g) and phenotypic (r_p) correlations of 305-day milk yield with lactation length in different parities.

Parity	**Genetic correlation ±SE**	**Phenotypic correlation**
1st	0.55±0.22	0.69
2nd	0.66±0.18	0.65
3rd	0.74±0.18	0.63
4th	0.73±0.12	0.67
5th	0.81±0.16	0.70
Overall	0.95±0.02	0.69

Table 2. Genetic (r_g) and phenotypic (r_p) correlations of first lactation 305-day milk yield and lactation length with different productive and reproductive traits from bivariate analysis.

		r_g ±SE	$\mathbf{r_p}$
First lactation milk yield	1st dry period	0.15±0.25	-0.15
	1st calving age	-0.03±0.21	0.02
	1st calving interval	-0.33±0.22	0.14
	1st service period	-0.23±0.22	0.12
	1st services per conception	0.00±0.39	0.001
First lactation length	1st dry period	0.14±0.29	-0.05
	1st calving age	0.31±0.21	0.03
	1st calving interval	0.22±0.31	0.41
	1st service period	0.31±0.33	0.35
	1st services per conception	-0.56±0.22	-0.03

CONCLUSION

Milk production and reproductive traits showed moderate to high genetic correlations. Compared to univariate analysis, multi-trait analysis slightly improved heritability estimates. This showed that using multi-trait model for selection could be more effective than univariate model because it corrects selection bias by utilizing information from the correlated traits. Therefore, it is suggested to verify lower estimates of certain traits in the future using a large dataset and a multivariate model for the both.

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