

ESTIMATES OF GENETIC PARAMETERS FOR PRODUCTION AND REPRODUCTION TRAITS IN MURRAH BUFFALOES (RIVERINE BUFFALO) IN INDIA

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ABSTRACT

Murrah is a predominant milch breed of buffalo in India with superior genetic potential for milk production. Estimation of genetic parameters for production and reproduction traits is prerequisite for making breeding plan and efficient management decisions. This work was undertaken to understand the influence on performance traits by various factors (genetic and non-genetic) along with assessment of genetic parameters in Murrah buffaloes. The genetic parameters were figured using mixed model least-squares analysis. The results revealed that season and period in which animals calved, affects the performance of Murrah breed and may be considered during its evaluation. The heritability estimates for first lactation 305 days/less milk yield (305FLMY), first lactation total milk yield (FLTM Y), first Lactation Length (FLL1), Wet average (WA), Herd average (HA), Age at first calving (AFC1) and Age at first service (AFS1) were 0.39 ± 0.10 , 0.29 ± 0.09 , 0.14 ± 0.09 , 0.29 ± 0.09 , 0.3 ± 0.11 , 0.27 ± 0.09 and 0.22 ± 0.09 , respectively. The phenotypic and genetic correlation amid 305FLMY and majority of another production trait were positive and significant. Thus,

it may be concluded that appropriate estimation of genetic parameters leads to robust selection for performance traits for genetic improvement in Murrah buffalo.

Keywords: *Bubalus bubalis*, buffaloes, Murrah, non-genetic factors, genetic parameters

INTRODUCTION

India has endowed with major buffalo population (108.70 millions) of the world and this figure is rising continuously (BAHS, 2018). Buffaloes are multipurpose livestock species occupying an important place in Indian dairy industry and contributing approximately 49% of total milk production of India (BAHS, 2018). Among the various Indian buffalo breeds, Murrah breed is essentially the cynosure for dairy type. Murrah breed has reached almost every place of the world and is being used for improving local or no-descriptive buffaloes.

Improvement of dairy buffaloes mainly depends on estimating decisive genetic parameter for production and reproduction traits (Eskandari

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and Karimpour, 2012). These estimates suggest different methods of selection to be included in the breeding programme for the estimation of genetic response and future improvement. Heritability determines the potential rate of progress given the selection differentials (Falconer and Mackay, 1996) and genetic correlations among different traits is required for correct planning and conduct of any breeding program (Biegelmeyera *et al.*, 2017). Monitoring of the genetic advancement helps us for designing the more appropriate breeding strategies to maximize the genetic gains. In the current study an effort has been made to estimate genetic parameters (heritability and genetic correlations) using mixed model least-squares analysis which further would be utilized for making breeding plan and efficient management decisions.

MATERIALS AND METHODS

Collection, editing and normalization of data

The data consisted of production and reproduction characters of 1,334 Murrah animals and were collected from the animal history sheets maintained at record room of AGB Division, NDRI, Karnal. Only those buffaloes that have calved normally and completed normal lactation (greater than 90 days of lactation and over 500 kg of milk yield in lactation) were considered in the study. The outliers beyond two-standard deviation (mean±2SD) on both the tail of the distribution were excluded from the data (Singh *et al.*, 2016).

Traits under study

During first lactation, following production traits i.e. 305/less days milk production (305FLMY), total milk production (FLTMY), lactation length (FLL1), dry days (FLDP), wet

average (WA), herd average (HA) were considered. For reproduction traits, age of animals at first calving (AFC1), age at first service (AFS1), first service period (FSP) and first calving interval (FCI) were used.

Data classification

Data were divided into different seasons and periods on the basis of animal calved in particular month and year for all the traits except AFC1 and AFS1. For studying AFC1 and AFS1, the data were divided on the basis of birth of animals. Seasons were considered to be one of the most important environmental effects which have considerable impact on production and reproduction traits in Murrah buffaloes. Twelve months of year were divided into four seasons, *viz.* winter includes December to March; summer includes April to June; rainy includes July to September and autumn includes October and November (Singh *et al.*, 2016). Finally, the whole data from 1971 to 2018 (48 years) were classified into 10 periods of 5 consecutive years and age at first calving groups (9 groups).

Statistical analysis

Effects of various factors (genetic and non-genetic) on selected traits

The analysis of normalized data was performed by using LSML method to see the effect of various factors (genetic and non-genetic) on selected traits in Murrah buffaloes. The following models were considered:

$$Y_{ijklm} = \mu + S_i + P_j + A_k + X_l + e_{ijklm}$$

Here, Y_{ijklm} , trait of m^{th} individual of l^{th} sire in k^{th} age group of j^{th} period and i^{th} season; μ represents population mean; S_i , fixed effect of i^{th}

season ($i=1-4$); P_j , fixed effect of j^{th} period ($j=1-10$); A_k , fixed effect of k^{th} age group ($k=1-9$); X_l , random effect of l^{th} sire; e_{ijklm} , random error~NID ($0, \sigma^2e$). The statistical significance of aforesaid fixed effects in the mixed model least squares analysis was done by using 'F' test.

Estimation of genetic parameters

Non-genetic factors were considered for their significant effects before estimation of genetic parameters. To estimate heritability of selected traits and genetic correlation between them, Model-2 of the 'Mixed Model Least Square analysis' was used (Harvey, 1990). The following models were used except AFC1 and AFS1:

$$Y_{ijklm} = \mu + S_i + P_j + A_k + X_l + e_{ijklm}$$

Here, Y_{ijklm} , trait of the m^{th} individual of l^{th} sire in k^{th} age group of j^{th} period and i^{th} season; μ , population mean; S_i , fixed effect of i^{th} season ($i=1-4$); P_j , fixed effect of j^{th} period ($j=1-10$); A_k , fixed effect of k^{th} age group ($k=1-9$); X_l , random effect of l^{th} sire; e_{ijklm} , random error~NID ($0, \sigma^2e$).

The model used for AFC1 and AFS1 was:

$$Y_{ijkl} = \mu + S_i + P_j + X_k + e_{ijkl}$$

Here, Y_{ijkl} , AFC1 and AFS1 of the l^{th} individual of k^{th} sire of j^{th} period and i^{th} season; μ , population mean; S_i , fixed effect of i^{th} season ($i=1-4$); P_j , fixed effect of j^{th} period ($j=1-10$); X_k , random effect of k^{th} sire; e_{ijkl} , random error~NID ($0, \sigma^2e$).

RESULTS AND DISCUSSIONS

Descriptive statistics of first lactation traits

The mean with standard error, coefficient

of variation and number of observations has been summarized (Table 1).

In present investigation, the average 305FLMY was $1,890.55 \pm 14.32$ kg with 27.23% coefficient of variation. Recently, Singh *et al.* (2016) has reported 1,806.45 kg 305FLMY with 29.21% coefficient of variation in Murrah buffaloes; which is slightly lower than our findings. Some other researchers (Borquis *et al.*, 2010; Wakchaure *et al.*, 2011) also estimated average 305FLMY which were again slightly lower than our estimated values. Therefore, our findings have showed increase in average 305FLMY during course of time. The FLTMY was found to be $2,046.17 \pm 18.515$ with coefficient of variation 32.525, which was again higher than previous studies (Gupta *et al.*, 2012). The other managemental traits like FLDP, FCI, FLL1 and FDP were found to be 143.82 ± 2.19 , 458.44 ± 3.39 , 330 ± 1.985 and 143.82 ± 2.193 days, respectively. The previous studies showed FLDP from 164.18 ± 4.70 days (Wakchaure *et al.*, 2008) to 331.30 ± 9.2 days (Sharma *et al.*, 2010); FCI from 461 ± 13.54 days (Suresh *et al.*, 2004) to 528 ± 2.9 days (Kuralkar and Raheja, 1997); FLL1 from 373.10 ± 5.80 days (Sharma *et al.*, 1988) to 286.06 ± 1.72 days (Jamuna, 2012); and FLDP from 164.18 ± 4.70 days (Wakchaure *et al.*, 2008) to 331.30 ± 9.2 (Sharma *et al.*, 2010). These finding indicates towards the improvement in the management practices followed at dairy farm.

Effect of various factors (genetic and non-genetic factors)

Single genetic factor i.e. sire was considered to see its effect on selected traits of first lactation in Murrah buffaloes. Effect of sire was significant on 305FLMY, FLTMY, FLL1, WA, HA, AFC1 and AFS1 while there was non-significant effect on FSP, FCI and FDP. The season

of calving had significant effect on 305FLMY, FSP, WA, FDP, FSP, FCI while non-significant on FLTMY, FLL1 and HA. The other non-genetic factor, period of calving, had significant effect on almost all the traits except FLL1 and FDP. Mean sum of squares values from 'mixed model analysis of variance' for selected traits for Murrah buffalo has been summarized in Table 2.

Estimates of heritability, genetic and phenotypic correlations for selected traits

Genetic parameters (heritability, genetic and phenotypic correlations) for selected traits have been mentioned in Table 3 and Table 4. The estimate of additive genetic variability for economically important traits gives an opportunity for genomic improvement through selective breeding. The assessments of genetic parameters (heritability, genetic and phenotypic correlation) for economically important traits are prerequisites for developing optimum breeding strategies for genetic improvement of buffaloes. In present analysis, significant heritability were estimated in 305FLMY (0.392 ± 0.10), FLTMY (0.286 ± 0.09), WA (0.289 ± 0.09), HA (0.295 ± 0.12), AFC1 (0.246 ± 0.10) and AFS1 (0.232 ± 0.10) traits. The heritability estimated revealed the amount of genetic variance present among the selected trait and suggest the measures to be taken for effective genetic improvement. Many researchers have reported varying ranges of heritability i.e. from 0.10 ± 0.01 to 0.47 ± 0.12 for 305FLMY and FLTMY traits (Sharma, 1979; Kuralkar and Raheja, 1997; Chakraborty *et al.*, 2010; Sahoo *et al.*, 2014; Singh *et al.*, 2016). The medium to high value of heritability of these production and reproduction traits suggest that good opportunities do exist for further genetic improvement. The correlations (genetic and phenotypic) between 305FLMY and

other production traits were positive and significant. This correlation indicated that improvement in one trait simultaneously resulted in the improvement of other trait. The lower estimates of heritability suggested that the particular traits were affected largely through environmental effects and can be improved by better management practices in the herd.

In summary, our findings indicate that non-genetic factors (season and period of calving) affect the performance of Murrah breed and should be considered during its evaluation. The heritability estimates of reproductive traits were low except for AFC1 and AFS1, which indicated that these traits were influenced largely by environmental effects. Further, the heritability estimates of production traits were medium to high in Murrah herd of ICAR-NDRI, Karnal, which suggests that good opportunities do exist for further genetic improvement. The trait 305FLMY showed positive and significant genetic correlation with FLTMY, WA and HA per year.

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Table 1. Descriptive statistics of first lactation traits.

Trait	Mean/standard error	Coefficient of variation	Observation
305FLMY	1,890.55±14.321	27.228	1,292
FLMY	2,046.17±18.515	32.525	1,292
FLLI	330±1.985	21.539	1,282
WA	6.22±0.0383	22.025	1,273
HA	4.41±0.407	29.206	1,003
FDP	143.82±2.193	47.058	952
FSP	160.77±3.219	61.516	944
FCI	458.44±3.392	19.577	700
AFCI	1,316.24±4.726	12.816	1,274
AFSI	1,012.30±4.836	16.277	1,161

Table 2. Mixed model ANOVA showing mean sum of squares for factors affecting production and reproduction traits in Murrah buffalo.

Source of variation	305FLMY	FLTMV	FLLI	FLDP	WA	HA	FSP	FCI
Sire	278,846.42**	466,249.68**	5,509.35*	9,587.10 ^{NS}	1.75**	1.72**	4,519.31 ^{NS}	7,667.6 ^{NS}
Season of calving	530,244.03*	768,927.68 ^{NS}	7,639.52 ^{NS}	40,874.84*	3.41*	0.93 ^{NS}	15,254.77*	19,978.51*
Period of calving	1,077,705.38**	1,470,642.57**	8,345.67 ^{NS}	25,305.48*	9.06**	4.35**	2,965.30 ^{NS}	28,649.57**
Age of animal at first calving	263,884.17 ^{NS}	500,832.24 ^{NS}	5,199.64 ^{NS}	14,859.07 ^{NS}	2.54*	3.46**	12,661.73**	13,818.94 ^{NS}
Error	185,058.04	343,080.58	4,688.07 ^{NS}	8,816.00	1.28	1.30	4,325.89	7,469.56

*P<0.05; **P<0.01; NS, Non-significant.

Table 3. Estimates of heritability (at diagonal), phenotypic (below diagonal) and genetic (above diagonal) correlations among first lactation production and reproduction traits in Murrah buffaloes.

Traits	305FLMY	FLTMY	FLL1	WA	HA	FDP	FSP	FCI
305FLMY	0.392*±0.10	1.0*±0.022	0.685*±0.20	0.976*±0.04	0.854*±0.11	-0.881±1.0	-0.24±0.69	1.0
FLTMY	0.928*±0.01	0.286*±0.09	0.707*±0.16	0.993*±0.09	0.774*±0.17	-0.869±1.0	-0.154±0.62	1.0
FLL1	0.526*±0.02	0.707*±0.16	0.144±0.09	0.583±0.33	0.435±0.32	-0.688±1.0	-0.258±0.73	1.0
WA	0.853*±0.01	0.703*±0.02	0.117*±0.03	0.289*±0.09	0.671*±0.15	-0.645±1.0	0.1±0.82	1.0
HA	0.732*±0.02	0.613*±0.02	0.162*±0.03	0.781*±0.02	0.295*±0.12	-0.915±1.0	-2.53±0.79	1.0
FDP	-0.11*±0.03	-0.021*±0.03	0.155*±0.03	-0.203*±0.03	-0.595*±0.03	0.003±0.108	0.378±0.93	1.0
FSP	0.408*±0.03	0.22*±0.03	0.684*±0.02	-0.106*±0.03	-0.287*±0.03	0.717*±0.02	0.083±0.11	0.733±1.0
FCI	0.262*±0.04	0.466*±0.03	0.741*±0.03	-0.09*±0.04	-0.246*±0.04	0.695*±0.03	0.983*±0.01	0.023±0.118

Table 4. Estimates of heritability (at diagonal), phenotypic (below diagonal) and genetic (above diagonal) correlations between AFS1 and AFC1.

Traits	AFC1	AFS1
AFC1	0.246*±0.10	0.954*±0.02
AFS1	1.0*±0.02	0.232*±0.10

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