

Original Research Article

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Estimation of Genetic Parameters for Production and Reproduction Traits in Murrah Buffaloes

Vikram Jakhar*, A.S. Yadav and S.S. Dhaka

Department of Animal Genetics & Breeding, Lala Lajpat Rai University of Veterinary and Animal Sciences, Hisar, Haryana, India

*Corresponding author

ABSTRACT

The data records of Murrah buffaloes from history cum pedigree sheets maintained over a period of 24 years (1992-2015) at Buffalo research centre (BRC), LUVAS, Hisar and Animal farm ICAR-CIRB, Hisar, were analysed to estimate heritability (h^2), genetic and phenotypic correlation among various production and reproduction traits. Production traits whose genetic parameters analysed were Total lactation milk yield (TLMY), 305 days milk yield (305MY), Peak yield (PY) and Lactation length (LL) whereas, reproduction traits include Dry period (DP), Service period (SP) and Calving interval (CI). Data set analysed includes records of 2959 buffaloes which were progeny of 219 sires. Based upon analysis, higher heritability estimates for TLMY, 305MY, PY ($h^2=0.392\pm 0.114$, 0.348 ± 0.118 , 0.328 ± 0.122 respectively) were recorded. Comparatively lower estimates of heritability for LL, DP, SP, CI ($h^2=0.090\pm 0.08$, 0.224 ± 0.09 , 0.211 ± 0.0 , 0.211 ± 0.09 respectively) were recorded. High heritability estimate of production traits help to conclude their significance in selection decision and it also indicate that production traits will serve as a better tool for selective breeding, expected to lead to rapid aggregate genetic gains in Murrah production. Further analysis on genetic correlation of production traits we found higher values of genetic correlation as 0.998 ± 0.01 (TLMY/305MY), 0.728 ± 0.09 (TLMY/PY) and 0.801 ± 0.06 (305MY/PY) whereas reproduction traits have lower and negative genetic correlation. Low and negative genetic correlation of reproduction traits indicate their little genetic role. Positive higher genetic correlations for production traits indicated role of production traits in selection programmes. Further critical analysis revealed that selection based on PY simultaneously will improve total lactation milk yield and 305 days or less milk yield of Murrah buffaloes. Selection based on peak yield also helpful for selection of buffalo at an early stage as compared to 305 days milk yield. It helps to conclude that peak yield may be the best trait to be taken in to selection criteria in for improvement of milk production in Murrah buffaloes.

Keywords

Production traits,
Reproduction traits,
Murrah,
Heritability,
Genetic correlation,
Phenotypic
correlation.

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Introduction

India ranks first in total milk production in world. Out of which almost half (55%) of milk production in country is shared by buffaloes. Murrah is one of the best milch breed in India. Murrah breed of buffalo is considered to be the best milk-cum-meat

breed. The home tract of breed is around the Southern part of Haryana comprising the districts of Rohtak, Jind, Hisar, Gurgaon and Delhi. Home tract has relatively hot and dry climate. Success of dairy industry depends on the selection of high producing animals.

Therefore, in any breeding programmes it is important to study the traits which have importance in selection. Adequate knowledge of genetic parameters namely heritability, genetic and phenotypic correlations are prerequisite for genetic improvement. The estimates of heritability and genetic correlations are important population parameters required in planning of selection experiments and various breeding strategies. Therefore the present study was conducted to investigate the genetic parameters for various production and reproduction traits and also to make a conclusive idea about the role of different traits in selection programmes.

Materials and Methods

The data for present investigation was collected from history cum pedigree sheets maintained at Buffalo Research Centre (BRC), Lala Lajpat Rai University of Veterinary and Animal Sciences and Central Institute for Research on Murrah Buffaloes (CIRB) Hisar over a period of 24 years from 1992 to 2015. Production traits included in the study were total lactation milk yield (TLMY), 305 day milk yield (305MY) and peak yield (PY). Whereas reproduction traits were Lactation length (LL), Dry period (DP), Service period (SP) and Calving interval (CI).

Buffaloes having lactation length of less than 100 days, having incomplete or incorrect record were discarded. In general, group feeding system followed except feeding of pregnant animals and breeding bulls, which were kept in individual pens. Ration fed to lactating animals was computed on the basis of milk production, live weight and stage of pregnancy. The green fodder consisted of maize and jowar during the months of June to October and green berseem, mustard and oat from November to March, whereas dry fodder generally consisted of wheat bhosa. Also the silage prepared from jowar and oat offered

during non-availability of green fodder in May, June, October and November. Genetic and phenotypic parameters were estimated by paternal half sib correlation method using mixed model analysis.

Genetic correlation: Genetic correlation between two traits was obtained by dividing the sire component of covariance between two traits divided by the square root of the product of sire component of variance for the two traits. The standard error of genetic correlation was estimated using formula given by Robertson (1959).

Phenotypic correlation: Phenotypic correlation between two traits was the sum of sire and residual component of covariance between two traits divided by the square root of the product of the sire plus residual component of variance for the two trait. The standard error of phenotypic correlation was computed by the formula given by Snedecor and Cochran (1967).

Results and Discussion

The heritability estimates for TLMY was 0.392 ± 0.114 (Table 1). Heritability values for 305MY, PY, LL, DP, SP and CI were 0.348 ± 0.118 , 0.328 ± 0.122 , 0.090 ± 0.08 , 0.224 ± 0.09 , 0.211 ± 0.0 and 0.211 ± 0.09 respectively. Moderate estimates for heritability for TLMY was reported in present study.

Estimates of similar magnitude were also reported by Raheja *et al.*, (2000), Chakraborty *et al.*, (2010), Chaudhari (2015) in Murrah buffaloes. However, lower estimates were reported by Kumar (2000) in Murrah buffaloes. Higher estimates were reported by Jakhar *et al.*, (2016) in murrah buffaloes. Moderate estimate of heritability indicate the there is existence of genetic variance for TLMY in Murrah buffaloes.

Heritability for 305MY of value 0.348 ± 0.118 was reported which was in accordance with the findings of Chakraborty *et al.*, (2010), Chaudhari, M. (2015) in Murrah buffaloes. Higher values than the present reports was given by Jakhar *et al.*, (2016) in Murrah buffaloes. However, lower heritability estimates were reported by Nath (1998) in Murrah buffaloes.

Heritability estimates for PY was moderate in Murrah. Similar estimates were also reported by Kumar (2000), Dass and Sadana (2000), Chaudhari, M. (2015) in Murrah buffaloes. However, lower heritability estimates were reported by Chakraborty *et al.*, (2010) in Murrah buffaloes. Higher estimate for PY was reported by Jakhar *et al.*, (2016) in Murrah buffaloes. These moderate estimates of heritability suggest that good possibility exists

for further improvement of these traits through proper selection programme. Selection using PY give rapid response to direct selection as compared based on TLMY, 305MY as these traits takes long time to measure. Optimal environment would however, be a prerequisite for exploiting full genetic potential of the animal. Also, the moderate estimates in the present study indicated that progeny testing along with collateral relatives will help to make improvement in these traits.

Low estimates of heritability for L was supported by the findings of Nath (1998), Kumar (2000) and Chaudhari (2015) in Murrah buffaloes. However, higher heritability estimates were reported by Singh *et al.*, (2011) in Nili-Ravi buffaloes and Jakhar *et al.*, (2016) in Murrah buffaloes.

Table.1 Estimates of heritability for different production and reproduction traits

Sr no.	Traits	Heritability
1.	TLMY	0.392 ± 0.114
2.	305MY	0.348 ± 0.118
3.	PY	0.328 ± 0.122
4.	LL	0.090 ± 0.086
5.	DP	0.224 ± 0.096
6.	SP	0.211 ± 0.095
7.	CI	0.211 ± 0.095

Table.2 Genetic correlation between production and reproduction traits

	TLMY	305MY	PY	LL	DP	SP	CI
TLMY		0.998 ± 0.011	0.728 ± 0.092	0.807 ± 0.212	-0.224 ± 0.230	0.175 ± 0.229	0.172 ± 0.201
305MY			0.801 ± 0.068	0.783 ± 0.292	-0.288 ± 0.226	0.140 ± 0.226	0.138 ± 0.201
PY				0.148 ± 0.323	-0.385 ± 0.228	-0.098 ± 0.223	-0.087 ± 0.310
LL					0.582 ± 0.441	0.793 ± 0.305	0.645 ± 0.145
DP						0.774 ± 0.129	0.701 ± 0.110
SP							0.210 ± 0.110
CI							

TLMY=Total lactation milk yield; 305DMY=305 Days milk yield; PY=Peak yield; LL=Lactation length; DP=Dry period; SP=Service period; CI=Calving interval.

Table.3 phenotypic correlation between different production and reproduction traits

	TLMY	305MY	PY	LL	DP	SP	CI
TLMY		0.928±0.11**	0.554±0.092**	0.710±0.21**	-0.067±0.230*	-0.367±0.229*	-0.347±0.189*
305MY			0.672±0.068**	0.473±0.292**	-0.008±0.226*	-0.229±0.226*	-0.212±0.206*
PY				0.028±0.323*	-0.091±0.228*	-0.023±0.223*	-0.019±0.203*
LL					0.190±0.441**	0.530±0.305*	0.513±0.285*
DP						0.765±0.129**	0.685±0.109**
SP							0.210±0.110**
CI							

*p<0.05, **p<0.01.TLMY=Total lactation milk yield; 305DMY=305 Days milk yield; PY=Peak yield; LL=Lactation length; DP=Dry period; SP=Service period; CI=Calving interval.

Furthermore, the estimates of heritability for DP, SP and CI were low. Estimates of similar magnitude were also reported by Kumar (2000), Raheja *et al.*, (2000), Chander (2002), Godara (2003), Chakraborty *et al.*, (2010), Chaudhari, M. (2015) and Jakhar *et al.*, (2016) in Murrah buffaloes. However, higher heritability estimates were reported by Saha *et al.*, (2000) in Murrah buffaloes. The lower values of heritability estimates of various reproduction traits in the present study revealed that these traits were largely under the influence of environmental effects. Therefore improvement in the environmental condition might help in more precise estimation of these reproduction traits.

Genetic and phenotypic correlations along with standard errors of various production and reproduction traits were presented in Tables 2 and 3, respectively.

The TLMY had a high positive genetic correlation with 305MY, PY and LL of the order 0.998±0.011, 0.728±0.092 and 0.807±0.212 respectively and low and negative genetic correlation with DP. The phenotypic correlation of TLMY was found to be positive and highly significant (p<0.01) with 305 MY, PY and LL. whereas, negative and significant with DP. Higher genetic correlation among TLMY, 305MY and PY revealed that selection can be done based on any of the milk production trait. Selection for

higher TLMY will also result in higher values for 305MY and PY. Whereas, low negative genetic correlation with DP shows that higher TLMY will lead to decreased DP thus reducing unproductive life. In affinity the present findings Dass and Sadana (2000), Chander (2002) and Chakraborty *et al.*, (2010) estimated high and positive genetic and phenotypic correlations between lactation yield and PY. High and positive genetic correlations of TLMY with LL were in close agreement with that reported by Malhado *et al.*, (2013) and Galsar *et al.*, (2016) in Murrah buffaloes. 305MY had high and positive genetic correlation with PY and LL, whereas, non-significant negative genetic correlation with DP. The phenotypic correlations of 305DMY were significant and positive with PY and LL. Whereas, negative and significant with DP. Peak yield (PY) had low and positive genetic correlation with LL while, low and negative with DP. The phenotypic correlations of PY were positive and significant with LL and negative and significant with DP. Similar findings were reported by Tailor (1995), Kumar (2000), Chaudhari (2015), Dev (2015) and Jakhar *et al.*, (2016). Further, Singh *et al.*, (2011) also reported higher but comparatively low estimates of genetic correlation TLMY and PY. Present study revealed stronger relationship among PY, TLMY and 305 DMY. Kumar and Tailor (2010); Singh *et al.*, (2011) also reported high and positive genetic

and phenotypic correlations between various production traits. The PY had high significant and positive genetic correlation with TLMY (0.93 ± 0.04) and 305 DMY (0.874 ± 0.046) had negative correlation with DP. These findings indicated that PY was found as a good indicator of productivity for improving TLMY and SLMY. Similar association was observed among LL and lactation milk yield. The high positive genetic and phenotypic correlations of PY and LL with TLMY and 305 DMY whereas, negative genetic and phenotypic correlation with DP. These results indicated the selection on the basis of PY and LL will not only reduces the unproductive life in the form of DP but also increases the TLMY. Present study revealed that TLMY had positive and significant phenotypic correlation with LL and PY these results are supported by the reports of Suresh *et al.*, (2004). Lactation length (LL) had non-significant positive genetic correlation with DP of the order 0.582 ± 0.441 . The corresponding phenotypic correlation was positive with high standard error. Service period (SP) had high and positive genetic correlation with CI whereas; the corresponding phenotypic correlation was positive and significant. TLMY had low and positive genetic correlation with SP and CI of the order 0.175 ± 0.229 and 0.172 ± 0.201 and negative and significant phenotypic correlation with SP and CI. Similar higher values of genetic and phenotypic correlation of TLMY with LL and lower values for TLMY with CI was reported by Malhado *et al.*, (2009), Suhail *et al.*, (2009), Seno *et al.*, (2010) and El-bramony (2014). Higher correlation of TLMY with the LL is expected indicating higher milk yield leading to longer lactation length. Similarly shorter CI is also desirable. 305 Day milk yield had low and positive genetic correlation with reproduction traits (SP and CI). The corresponding phenotypic correlations were negative and significant. The genetic correlations of PY

were low and negative with SP and CI. The phenotypic correlations were negative and significant. Lower and negative genetic and phenotypic correlation among production and reproduction traits is favorable as selection for high values of production traits will reduce the unproductive life in the form of DP, SP and CI. Lactation length (LL) had high and positive genetic correlation with SP and CI. The phenotypic correlation of LL was positive and significant. These results are in close agreement with the findings of Kumar *et al.*, (2001) and Suresh *et al.*, (2004). Higher and positive genetic correlation between LL and CI was supported by the findings of Barross *et al.*, (2016) indicating that increase in LL will result in selection for longer CI. Tonhati *et al.*, (2000b) and Aziz *et al.*, (2001) found low genetic correlations between these traits (-0.20 and 0.09 , respectively). Dry period was found to have high positive genetic correlation with SP and CI. The phenotypic correlation of DP with SP and CI was positive and significant. These findings were supported by the reports of Nath (1998), Kumar (2000) and Kumar *et al.*, (2001). The high genetic and phenotypic correlation between SP and CI was also reported by Suresh *et al.*, (2004) and Singh and Barwal (2012) in Murrah buffaloes. Low genetic and phenotypic correlation values for different reproductive traits were also reported by Chaudhari (2015), Jakhar *et al.*, (2016) in Murrah buffaloes.

Moderate estimate for production traits and lower heritability estimations for reproduction traits were obtained. Moderate estimate of production traits indicate there sufficient scope for improvement in milk production of Murrah buffaloes through proper selection criteria in any breeding programmes. Also the lower estimates for reproductive traits reveals more environmental effect on SP and CI indicating importance of better management and environment on reproduction traits.

Analysis of genetic and phenotypic correlation revealed that milk production traits especially PY serve as a better criteria in selection programmes for Murrah buffaloes.

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