

Estimate the Genetic Parameters of Major Economic Traits of Crossbred Murrah Buffalo in Nepal

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Abstract

Purpose: The main objective of this research was to estimate the genetic parameters of major economic traits of crossbred Murrah Buffalo in Nepal.

Methods: The performance records of 16912 buffaloes from the year 2017 to 2020 at mid-hill and Terai and maintained at the Veterinary Hospital Livestock Specialties Center, Artificial Insemination records, buffalo farm were used for analysis. We analyzed the data by using the mixed technique of the Harvey model.

Results: The analysis revealed that the heritability for age at first calving (AFC) and gestation length (GL) was relatively low ($h^2 = 0.06, 0.15$) and moderate heritability for calving interval (CI) ($h^2 = 0.36$), and the lower estimates for lactation length (LL), lactation milk yield (LMY) ($h^2 = 0.140.078, 0.280.159$), higher estimates for heritability of standard milk yield (SMY), daily milk yield (DMY) ($h^2 = 0.44 \pm 0.266, 0.57 \pm 0.365$), and there was lower heritability of peak milk yield (PMY) ($h^2 = 0.060.031$). Productive traits showed positive genetic correlations, with lactation milk yield (LMY) at 0.31, standard milk yield (SMY) at 0.95, and daily milk yield (DMY) ranging from moderate to high positive correlations of 0.35 to 0.95. Conversely, negative genetic correlations ranged from -0.13 to -0.71. Similarly, genotypic correlations for daily milk yield were moderate to highly positive (0.35-0.95) and negatively correlated (-0.13 to -0.71), as well as for peak milk yield (0.24-0.93) with negative correlations (-0.19 to -0.74).

Conclusion: The research findings underscore the genetic potential for enhancing milk yield traits in crossbred Murrah Buffalo, with positive correlations indicating opportunities for improvement. However, the negative correlations with reproductive traits suggest the need careful selection strategies to optimize both productivity and reproductive efficiency, with further research needed to optimize genetic potential in Nepal.

Keywords: Crossbred Murrah buffalo, Correlation, Heritability, Productive traits, Reproductive traits

1 Introduction

Nepal is a landlocked country in South Asia that is primarily dependent on agriculture for its income (WBG, 2016). The agricultural sector contributes 32% to the country's GDP and employs 65% of the working-age population. The buffalo population is about 52.5 million in Nepal. They produce 1.4 million t of milk and 0.19 million t of meat every year (MoALD, 2021). The majority of buffalo breeds are indigenous breeds, whereas 36 percent of adult female buffaloes are being Murrah crossbred (Trivedi, K., & Paudel, K. 2019). This accounts for 57% of the country's milk and 36% of its meat production. Twenty-five percent of Nepal's agricultural GDP comes from the livestock subsector, which is a significant part of the country's agricultural industry (ADS, 2015).

Reproduction in dairy farming affects economics (Lopes et al. 2008), and thus several research works are carried out on reproductive qualities whereas annual genetic gain is crucial for breeding programs (Cassian et al. 2004). This information assists in estimating genetic parameters and implementing necessary changes in buffalo management. Because of the excellent adaptability of the Murrah buffalo to different climates, breeders are actively looking for ways to increase the genetic characteristics of the buffalo. Financial performance of dairy operations is significantly influenced by the environment, health, productivity, and reproduction of animals (Singh et al. 2020). The availability of high-quality animals with high genetic value is critical to herd success.

Genetic modification is a method to boost buffalo productivity by breeding superior buffaloes with superior traits, such as increased milk production and fertility. This improves agricultural productivity, food security, and

rural living standards (Agarwal and Apadhai, 2013). As demand for meat and milk increases, buffaloes are now preferred for their milk production, thereby improving farmers' quality of life (Nasr, 2016). Genetic analysts use heritability to predict genetic evolution and estimate the link between physical and reproductive traits (Falconer & McKay, 1996). This knowledge is important for breeding techniques and economic growth. Understanding genetic and phenotypic correlations and heritability is crucial for improving the genetics of crossbred Murrah buffaloes in Nepal. The information regarding pedigree record, importance of recording for genetic improvement information is still scarce in terms of scientific information in Nepal. The collected data can enhance farm management and productivity in the crossbred Murrah herd in Nepal, but challenges include estimating genetic traits due to environmental variability, data quality issues, and technical constraints. Genetic improvement programs are essential in enhancing the productivity of crossbred Murrah buffaloes, thus promoting more effective and sustainable agricultural practices that benefit farmers and consumers alike. Therefore, the objective of this research was set to estimate the genetic parameters of reproductive and productive traits of crossbred Murrah buffalo in Nepal.

2 Materials and methods

2.1 Sources of data

This research was done in Terai of Dhanusha and the Hill of Kaski districts, Nepal. The district lies at an altitude ranging from 78 meters of terai and 450 to 3937 meters of mid-hill above sea level of Dhanusha and Kaski, respectively. Dhanusa District belongs to the Madhesh Province, Nepal at latitude 26°50'31.56" North, longitude 86°02'09.60" E and Kaski of mid-hill at latitude 28.2622° N, longitude 84.0167° E.

The study, conducted on crossbred Murrah buffalo between 2017 and 2020, included a total of 16,912 milking buffaloes. Of these, 10,987 were located in the Terai region of Dhanusha, and 5,925 were in the Mid-hill region of Kaski. Data were collected from artificial insemination records, livestock service sections, milk collection centers, and livestock farms. This information was analyzed to assess reproductive and productive traits

2.2 Description and quality of traits management

The study year is divided into four seasons: summer (June-August), autumn (September-November), winter (December-February), and spring (March-May). All seasons presented year-round, with early parity being first and second lactation, mid parity being third and fourth lactation, and late parity being five or more. The collected reproductive traits were age of conception (ACO), age at first calving (AFC), calving interval (CI), and gestation length (GL), while productive traits were lactation length (LL), lactation milk yield (LMD), standard milk yield (SMY), daily milk yield (DMY), peak milk yield (PMY), percentage of fat (%F), percentage of protein (%P), and percentage of lactose (%L).

2.3 Feeding and Management of the Farm

In rural farms, the common practices for raising buffaloes include limited grazing, tethering, and cut-and-carry feeding. Buffaloes, with the exception of pregnant ones, are allowed to graze for about 4 to 7 hours daily on local pasture lands. The government farm provides berseem, oats, and silage as feed for the buffaloes from February to May, while green teosinte and sudan grass are given from June to September. In the winter months, when fodder crops are scarce, rice straw and concentrates are used to sustain the buffaloes. The breeding process of the buffaloes involves artificial insemination, where buffaloes in standing estrus are inseminated with semen from genetically superior Murrah bulls (Smith & Patel, 2021).

2.4 Statistical analysis

The analysis of genetic factors provided valuable insights into heritability, genetic, and phenotypic correlation coefficients. The paternal half-sib correlation method and Harvey's least-squares and maximum likelihood computer program were effective in obtaining these parameters. The statistical random model was applied to gain a comprehensive understanding of genetic constituents influencing reproductive and productive traits, enhancing outcomes accuracy (Harvey, 1990).

$$Y_{ij} = \mu + s_i + \varepsilon_{ij} \quad (1)$$

- Y_{ij} = Adjusted observation on the j -th daughter from the i -th sire.
- s_i = The effect of the i -th sire.
- ε_{ij} = The uncontrolled environment and genetic deviation attributed to the individuals in sire groups.

3 Results

3.1 Reproductive and productive traits

Findings of this research well revealed that average age at conception, age of at first calving, gestation length, and calving interval overall of crossbred Murrah buffaloes was 1006.41 ± 64.48 days, 1318.76 ± 64.23 days, 312.33 ± 2.48 and 419.69 ± 21.53 days (Table 1). Regarding the productive traits of crossbred Murrah buffaloes it was revealed that lactation length, standard lactation milk yield, standard milk yield, daily milk yield, and peak milk yield was 280.28 ± 14.27 days, 2207.59 ± 244.61 lit, 2401.58 ± 227.10 lit, 7.87 ± 0.096 lit, and 10.10 ± 0.096 lit, respectively. The mean values of milk fat, protein, and lactose are $7.30 \pm 0.056\%$, $3.63 \pm 0.011\%$, and lactose $4.77 \pm 0.10\%$ (Table 1).

3.2 Heritability's estimates

The h^2 of reproductive traits ACO, AFC, and GL was relatively low (0.06, 0.06, 0.15), and CI was moderate (0.36). The h^2 values of lactation length was low (0.14 ± 0.078), moderate h^2 value was obtained for lactation milk yield (0.28 ± 0.159). Likewise, high h^2 of standard milk yield (0.44 ± 0.267), daily milk yield (0.44 ± 0.266), and peak milk yield (0.57 ± 0.365) were achieved. There were low h^2 of fat, protein, and lactose (0.06 ± 0.031 , 0.12 ± 0.064 , and 0.05 ± 0.028 , respectively (Table 1). According to the findings as revealed in the analysis of variance (Table 2 & 3), both sire and season have a significant impact on all the examined buffalo reproductive traits. The data suggests that these effects are statistically significant $p < 0.01$, with the sire having a slightly more pronounced influence than the season. Such analyses are crucial for understanding the genetic and environmental factors that affect buffalo reproductive traits. This understanding can help develop effective breeding strategies to achieve desirable outcomes.

3.3 Genotypic Correlations of Economic Traits

Genetic correlation coefficients (r^G) of various reproductive and productive traits of crossbred Murrah buffaloes are performed. There were a strong positive genetic correlation between the age at first calving (ACO) and age at first conception (AFC). Additionally, there was a negative correlation between ACO and gestation length (GL), and ACO and calving interval (CI), which were found to be -0.39 and -0.26, respectively. Furthermore, GL and AFC had a higher negative correlation of -0.34, while AFC and CI had a correlation of -0.23. On the other hand, CI and GL had a higher positive correlation of 0.55 (Table 4). The lactation milk yield was positively correlated (0.03-0.31) with overall standard milk yield, which was highly positive (0.35-0.95) and negatively correlated (-0.13 to -0.71). Daily milk yield also had a moderate to high positive genotypic correlation (0.35-0.95) and was negatively correlated (-0.13 to -0.71) with peak milk yield (0.24-0.93) and lactation length (Table 4). Similarly, highly positive genetic correlation was observed between ($r^G=0.64-0.65$) fat and AFC, low positive genetic correlation was observed between fat and CI, LMY, SMY ($r^G=0.10-0.18$) and near to the 0 of (0.001) PMY. It was negatively associated with LL and GL ($r^G=-0.34$ to -0.39), and fat (Table 4). The major milk constituents protein moderately positive genetic correlation was observed GP, LL, and fat (0.34, 0.36, 0.12) and negatively associated with ACO, AFC, CI, LMY, SMY, DMY, PMY -0.14, -0.12, -0.43, -0.44, -0.44, -0.23, and -0.37, respectively.

3.4 Phenotypic correlation of productive and reproductive traits

The findings suggest that the correlation between ACO and AFC, ACO and GL, and ACO and CI was very weak ($r^P=0.09$), and they were negatively correlated ($r^P=-0.14$) and ($r^P=-0.03$), respectively. Similarly, the correlation of AFC with GP and AFC and CI was negatively associated ($r^P=-0.10$ and -0.04), whereas the correlation between GP and CI and GP and LL was phenotypically (Table 4) low and positively correlated ($r^P=0.11$ and 0.13), respectively.

There was a weak positive correlation between lactation length and CI ($r^P=0.04$). CI has a medium positive relationship with LMY ($r^P=0.30$), and a weak positive relationship between them ($r^P=0.03$, 0.03 , 0.02 , 0.25). LMY has a strong positive relationship with SMY ($r^P=0.91$). The standard milk yield had a strong positive phenotypic correlation with daily milk yield ($r^P=1$; 0.90), weak positive correlation with peak milk yield ($r^P=0.24$, 0.05 , 0.05). Daily milk yield had a strong positive phenotypic correlation with milk yield ($r^P=0.95$; 0.95 , 0.85), weak positive correlation with peak milk yield ($r^P=0.24$, 0.04 , 0.04), and similarly negative phenotypic correlation with the latter ($r^P=-0.04$, -0.15). Peak milk yield had a weak positive phenotypic correlation with fat percentage ($r^P=0.03$; 0.02 , 0.01 , 0.05 , 0.06), and similarly highly negative phenotypic correlation with the same ($r^P=-0.007$, -0.05 , -0.01 , -0.03 , -0.05 , -0.06), respectively. Fat percentage had a weak positive phenotypic correlation with protein percentage ($r^P=0.05$, 0.07) and highly negative phenotypic correlation with the latter ($r^P=-0.04$, -0.07 , -0.06 , -0.11 , -0.08 , -0.07 , -0.01 , -0.01), respectively (Table 4).

Table 1: Productive and reproductive traits of crossbred Murrah buffaloes (means, standard deviations (SD), and coefficient of variations (CV %)) with heritability estimates (h^2) and standard errors (SE) for these traits.

Traits	Mean \pm SD	CV (%)	$h^2 \pm$ SE
ACO	1006.41 \pm 64.48	6.41	0.06 \pm 0.032
AFC	1318.76 \pm 64.23	4.87	0.06 \pm 0.031
GP	312.33 \pm 2.48	0.81	0.15 \pm 0.083
CI	419.69 \pm 21.53	5.26	0.36 \pm 0.212
LL	280.28 \pm 14.27	5.08	0.14 \pm 0.078
LMY	2207.59 \pm 244.61	11.05	0.28 \pm 0.159
SMY	2401.58 \pm 227.10	9.50	0.44 \pm 0.267
DMY	7.87 \pm 0.096	9.51	0.44 \pm 0.266
PMY	10.10 \pm 0.096	9.68	0.57 \pm 0.365
FAT	7.30 \pm 0.056	7.67	0.06 \pm 0.031
PROTEIN	3.63 \pm 0.011	3.13	0.12 \pm 0.064
LACTOSE	4.77 \pm 0.10	2.28	0.05 \pm 0.028

Table 2: Analysis of variance for various productive and reproductive traits

Source of variation	Mean square						
	D.F.	ACO	AFC	GL	CI	LL	LMY
Sire	8	124556.26**	4138.29**	503.42**	113068.52**	15280.92**	10080968.80**
Season	3	113936.43**	108916.89**	122.54**	62423.73**	26782.51**	8410261.86**
Error	16900	4138.29	4107.14	6.16	452.86	199.02	58355.05

Table 3: Analysis of variance for various productive and reproductive traits

Source of variation	Mean square						
	D.F.	SMY	DMY	PMY	Fat	Protein	Lactose
Sire	8	17459928.62**	18701.36**	53787.48**	909.53**	78.99**	3070.99**
Season	3	6213603.26**	6683.11**	11348.23**	207.43**	114.60**	4917.67**
Error	16900	50482.32	54.37	90.62	31.37	1.28	117.62

Table 4: Genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for productive and reproductive traits in crossbred Murrah buffaloes

Traits	ACO	AFC	GP	LL	CI	LMY	SMY	DMY	PMY	%F	%P	%L
ACO	-	0.998	-0.396	-0.351	-0.267	0.303	0.350	0.350	0.247	0.656	-0.142	-0.14
AFC	0.099	-	-0.340	-0.316	-0.238	0.313	0.350	0.350	0.240	0.646	-0.123	0.64
GL	-0.147	-0.107	-	0.670	0.550	0.038	-0.133	-0.133	-0.192	-0.392	0.343	0.16
LL	-0.107	-0.041	0.113	-	0.149	-0.557	-0.714	-0.714	-0.740	-0.347	0.369	0.04
CI	-0.031	-0.025	0.136	0.045	-	0.285	0.979	0.979	0.898	0.105	-0.431	-0.05
LMY	0.034	0.036	0.025	0.307	0.253	-	0.444	1.00	0.939	0.185	-0.447	-0.040
SMY	0.056	0.056	-0.020	-0.114	0.244	0.910	-	0.443	0.939	0.186	-0.448	-0.040
DMY	0.056	0.056	-0.020	-0.114	0.244	0.909	1.000	-	0.579	-0.033	-0.235	-0.010
PMY	0.043	0.041	-0.043	-0.158	0.242	0.851	0.958	0.958	-	0.061	-0.378	0.292
%F	0.060	0.059	-0.038	-0.016	-0.051	0.019	0.029	0.030	-0.007	-	0.123	0.462
%P	-0.017	-0.014	0.077	0.050	-0.071	-0.087	-0.111	-0.111	-0.068	-0.04	-	0.055
%L	0.041	0.043	0.028	-0.003	-0.052	-0.010	-0.007	-0.007	-0.004	0.01	0.05	-

Age of conception (ACO), age of first calving (AFC), gestation length (GL), calving interval (CI), lactation length (LL), lactation milk yield (LMY), standard milk yield (SMY), daily milk yield (DMY), peak milk yield (PMY), percentage of fat (% F), percentage of protein(% P), percentage of lactose (% L)

4 Discussion

The h^2 value estimated for AFC in the present study (Table 1) was similar to those from reported by Seno *et al.* (2010) where heritability was 0.07. In contrast, higher estimates of 0.20, 0.24, and 0.41 were reported by Malhado (2009). Cassiano *et al.* (2004) achieved, to the breeds Carabao, Murrah, Mediterranean, and Jafarabadi, in the Brazilian Amazonia, h^2 from 0.12 to 0.38 and 0.04 to 0.05 for the same traits, respectively. CI was found



moderately (Table 1) heritable trait which was similar to those reported by Jakhar et al. (2016). These traits were moderately heritable which had a lower value in the present study in comparison with the findings of Kumar et al. (2005). These traits are mainly influenced by environment and management factors and can be improved by providing better management and feeding as well as selection based on progeny testing coupled with collateral relatives. Findings of our research revealed that the h^2 of lactation milk yield (Table 1) was similar with the findings of Malhado et al. (2013) and Sharma et al. (2023) and Thevamanoharan et al. (2002). Furthermore, the heritability estimates of standard milk yield and daily milk yield were (Table 1) similar to the results reported by Syed et al. (2009). The present study also revealed that the h^2 of peak milk yield was high which agrees with the findings of Tamboli et al. (2022).

Barros et al. (2016) revealed that Murrah buffaloes first calved at 37.6 months, while in our study they found a longer calving period. However, Helmy and Somida (2021) found the age at first calving in Egyptian buffalo to be 45.16 months. The mean lactation milk yield in our study was similar to the reported by Easa et al. (2022) for Egyptian buffaloes. Our findings were consistent with the findings of Barros et al. (2014) as authors had documented a 270-day lactation length in Brazilian buffalo (Table 2 & 3). Discrepancies in studies regarding major performance of buffalo may be due to biological differences in herd management practices, genetic diversity, herd size, environmental and management conditions, forage quality, and differences in calving season as advocated by Bhutkar et al. (2014). Selective breeding programs enhance these traits, resulting in a positive correlation between AFC and LMY (Singh, et al. 2017). A positive genetic correlation was observed between LL and TMY (Table 4). The crossbred Murrah buffalo have revealed a significant genetic correlation of 0.3 between LL and LMY (Smith et al. 2020). This positive correlation suggests with longer lactation periods tend to produce higher milk yields, indicating a potential genetic basis for milk production traits in this breed. The crossbred Murrah buffalo have revealed a positive genetic correlation (Table 4) between CI and LMY (Singh et al. 2011). This indicates a moderate relationship between calving interval and milk yield, signifying that buffalo with shorter calving intervals tend to have slightly higher milk yields. Crossbreeding programs aim to improve specific traits such as milk production, growth rate, and disease resistance (Kumar et al. 2021).

Gupta (2009) reported medium positive genetic and phenotypic correlations between AFC and SMY-305. The study revealed stronger relationship among PY, LMY and SMY-305. The PY had high significant and positive genetic correlation with LMY and SMY (Table 4). In affirmative the present findings of Chakraborty et al. (2010) estimated high and positive genetic and phenotypic correlations between LMY and PY. These findings indicate that selecting for lactation milk yield will increase the average daily milk yield and therefore increase the daily earnings of breeders.

The phenotypic correlation between LMY and milk constituents were low positive phenotypic correlation %F, %P and %L (Table 4), a finding approving that selection for increased MY will have a negative effect on the percentage of fat and protein in milk. The finding of our study in accordance with the Tonhati et al. (2000) reported much lower phenotypic correlations between MY and the percentage of fat and protein, respectively.

5 Conclusion

The high heritability of milk yield traits, such as SMY, DMY, and PMY, underscores the significant genetic influence on these traits for buffaloes. This suggests that selective breeding can lead to considerable improvements in milk production. However, the strong genetic correlations between these milk yield traits and CI highlight the potential impact of selective breeding on reproductive efficiency. Hence, a balanced approach is necessary to prevent any negative consequences on the herd's reproductive health. Furthermore, the high genetic correlation observed between LMY and both SMY and DMY indicates that targeted breeding programs can synergistically enhance these traits, thereby benefiting farmers who aim to boost milk production efficiency for buffaloes. Lastly, the positive phenotypic correlations between GL and LL with CI suggest that longer gestation and lactation may contribute to increased intervals between calving. This insight is essential for farmers to strategize their breeding and calving schedules to optimize herd productivity without compromising reproductive cycles. Overall, these findings offer a strong framework for developing breeding strategies that can elevate both milk yield and reproductive efficiency in crossbred Murrah buffaloes.

Author Contributions

DN contributed to data collection, curation, and manuscript drafting. NB was involved in designing the experiment and performing statistical analysis. ND assisted with interpreting the results and revising the manuscript. MP also contributed to manuscript revision. All authors contributed to the article and approved the submitted version.

Conflict of interest

There are no known conflicts of interest associated with this publication and there has been no significant financial support for this work that could have influenced its outcome.

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