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Genetic analysis of biometric traits in Murrah buffaloes using Bayesian approach

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Abstract: The body conformation traits, which support higher production and longer productive life are very important to breed future dairy buffaloes. Bayesian multiple-trait analysis was performed in biometric traits of Murrah buffaloes to estimate the (co)variance components using an animal model and Gibbs sampling. The model included the fixed effects of parity, season of calving, period of calving, and age group at the time of recording of traits. Random effects included were additive genetic and residual effects. Posterior means of heritability distribution for body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL) and average skin thickness (AST) were 0.45, 0.56, 0.56, 0.60, 0.48, 0.44, 0.53, and 0.53, respectively. Genetic correlation estimates ranged from –0.64 (RS and NFL) to 0.53 (HDB and HW) and residual correlation estimates ranged from –0.35 (RS and BL) to 0.57 (RS and HW). Results of the current study indicated that all considered linear type traits have a lot of genetic variabilities, which can be used for selection and genetic improvement of Murrah buffaloes in future.

Key words: Bayesian approach, genetic parameters, linear type traits, Murrah buffaloes

1. Introduction

The genetic resources of Indian buffaloes are comprised of 19 recognised breeds that have been adapted to a variety of environmental conditions [1][1]. Murrah is considered to be the best breed of Indian buffaloes and is native to Haryana state; however, graded Murrah buffaloes can be found throughout the country because of their higher production performance and adaptability to a variety of climatic conditions and better feed conversion efficiency. Murrah buffaloes have the maximum population among all the buffalo breeds in India, indicating their importance in the dairy sector [2]. Murrah buffaloes are also known as "black gold" or "Holstein-Friesian" of the buffalo world.

Linear type traits are of utmost importance, as their superiority usually helps to sustain a longer productive life. Animal breeders give importance to linear type features because of their impact on production and reproduction, as well as the lifetime of dairy animals and, ultimately, the enterprise's total profitability [3–7]. Dairy farmers can detect functional and structural weaknesses that are genetic and possible issues that will arise from incorrect breeding practices by measuring and analyzing specific parts of each animal. Dairymen and livestock breeders are often on the lookout for the best type of animals and are ready to pay extra for these beautiful animals [8-9]. Consideration of milk yield and body conformation together with selection for improved milk yield can lead to greater genetic progress [10]. Milk yield is influenced by linear type characteristics [11–12]. Dairy animals' strength, stamina, and survival will improve as a result of improved type traits selection [13]. For herd life, conformation traits have been utilized as an indirect selection criterion [14–15]. Animals with attractive looks and high production potential are not only a source of pride for farmers but are also associated with better lifetime profitability. As a result, conformation of the dairy animals must be considered in selection programs. A longer stay of animals in the herd will enhance profitability owing to lower replacement costs [9].

Animal breeding programs require knowledge of genetic parameters not only for the best linear unbiased prediction but also for predicting genetic gain, indirect selection response, and constructing and updating selection indices. Several researchers [16–18] have used REML and Bayesian approaches to estimate genetic parameters and covariance components in animal breeding. Bayesian approach provides a solution to the problem of limited

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sample size because each large or small data set has a precise posteriori distribution from which interpretations can be drawn. To the best of our knowledge, negligible work has been done on the estimation of genetic parameters in Murrah buffaloes using a Bayesian methodology. The aim of the current study was to use the Bayesian approach to estimate heritability and genetic correlations of body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL) and average skin thickness (AST) in Murrah buffaloes.

2. Materials and Methods

2.1 Data

Eighty-one lactating Murrah buffaloes maintained at Buffalo Farm of Lala Lajpat Rai University of Veterinary and Animal Sciences (LUVAS), Hisar, India were recorded for eight body morphometric traits. The Institutional Animal Ethics Committee of LUVAS, Hisar (Registration No. 1669/GO/ReBiBt/S/12/CPCSEA) gave their approval to conduct this research.

To ensure the normal distribution, the outliers were removed, and the data set was standardized using mean and standard deviation. Influence of nongenetic factors viz., parity, period of calving, the season of calving, and age group at the time of recording was studied on biometric traits viz; body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL), and average skin thickness (AST) in Murrah buffaloes. Pedigree viewer software was used to evaluate the reliability of pedigree information [19][2]. Seasons were classified as summer (April to June), rainy (July to August), autumn (September to November), and winter (December to March) based on the existing meteorological conditions. Lactations were divided into six parities, as well as calving periods and age groups at the time of recording, which were divided into three-year intervals.

2.2 Traits

Type traits refer to an animal's physical appearance in terms of body features that are linked to production and fertility in animals. Different linear type traits considered in the present study were body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL) and average skin thickness (AST) measured directly on the lactating Murrah buffaloes. These were measured according to the National Dairy Development Boards (NDDB) criteria for cattle and buffalo type classifications [20][3], as shown in Table 1. Data structure summary of the considered biometric traits are presented in Table 2.

2.3 Statistical analyses

Bayesian approach in multitrait analyses with the GIBBS3F90 software was applied for estimation of (co) variance components of considered traits [21]. The model of analysis included fixed effects of parity, season of calving, period of calving, and age group at the time of recording and random effects were additive genetic and residual effects. The following model was applied for analysis

$$y = X\beta + Za + e$$

where **y:** vector of observed traits (BL, HW, RW, HBD, RS, BD, NFL, AST); X: incidence matrix of fixed effects; β: vector of fixed effects; Z: incidence matrix of additive genetic random effects; a: vector of additive genetic random effects; and e: vector of random error effects. Inverted Wishart distribution was assumed for the fully conditional posterior distributions of additive matrices [22]. Using BLUPF90 family of programs, data were subjected to genetic analysis [21]. RENUMF90 was used to renumber and process the data. To estimate posterior densities of (co)variance components, the Gibbs sampler was employed. For all parameters, the marginal posterior distribution was calculated by assuming a single long chain with 10 lakhs iterations. Burn-in was applied to the first 1 lakh data points, after which one out of every 100 iterations was retained for further analysis. Following the verification of the graphics, we discovered that the burn-in period was adequate to achieve convergence in all parameter estimations. POSTGIBBSF90 [21] was used to test the convergence diagnostic of the Gibbs sampler chain, and the highest posterior density (HPD) region or confidence interval, which provides the interval that includes 95 percent of samples as a measure of reliability and standard error of parameters, was also obtained. The programs GIBBS3F90 and POSTGIBBSF90 [21] were used to compute variance components, heritability, and correlation.

3. Results and Discussion

The burn-in period considered was adequate to achieve convergence in all parameter estimations, as shown in Figure 1. For each parameter, the number of effective samples (9000) was adequate to measures estimates of central tendency and the HPD region. Mean, median and mode were similar for most of the trait estimates representing that the posterior distribution of the parameter estimates was close to normal distribution. Table 3 shows the 95% highest posterior density estimates of variance components for body length, height at wither, rump width, hip bone distance, rump slope, brisket distance, navel flap length, and average skin thickness in a multi-trait study. The additive genetic variance for rump width, hip bone

[2] http:// bking hor.une.edu.au/pedigree. htm

[3] https://www. dairyknowledge.in/sites/default /files/animal_type_classification_ guidelines_version_ii.pdf

Table 1. Abbreviations (unit), trait names, and their description in Murrah buffaloes [20].

S.No.	Abbreviation (Unit)	Trait name	Description
1	BL (cm)	Body length	Body length was taken as the distance from the point of shoulder to the point of pin bone
2	HW (cm)	Height at wither	Vertical distance from withers to ground
3	RW (cm)	Rump width	Rump width included the distance between the most posterior point of pin bones measured with the help of measuring tape
4	HBD (cm)	Hip bone distance	Hip bone distance was taken as the distance between two hip bones measured with the help of measuring tape
5	RS (degree)	Rump slope	Rump slope was taken as the angle of the rump structure from hips to pins
6	BD (cm)	Brisket distance	Brisket distance was measured as the distance between forelegs with help of measuring tape
7	NFL (cm)	Navel flap length	Length from the nearest body to end of naval measured with the help of scale
8	AST(cm)	Average skin thickness	Skin thickness was recorded at three sites with the help of Vernier caliper over the side skin of the buffalo's neck region, chest, and flank region, and the reading of Vernier calliper for skin fold thickness at each site was halved to know the exact skin thickness value. Finally, the average of skin thickness at three sites was considered for analysis

Table 2. Data structure statistics for biometric traits in Murrah buffaloes.

Description	BL (cm)	HW (cm)	RW (cm)	HBD (cm)	RS (degree)	BD (cm)	NFL (cm)	AST (cm)
Number of records	81	81	81	81	81	81	81	81
Mean	148.93	138.52	17.72	47.02	13.04	24.33	1.79	19.51
Minimum	127	129	13	36	0	15	0.20	13.75
Maximum	161	149	27.50	55	23	34	5.50	26.57
Standard deviation	6.89	3.97	2.41	3.70	5.16	4.10	1.25	2.80
CV (%)	4.63	2.87	13.61	7.87	40.10	16.83	69.70	14.35

Body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL), average skin thickness (AST), and coefficient of variation (CV).

distance, navel flap length, height at wither, average skin thickness was higher than a residual variance. However, residual variances for rump slope, brisket distance, and body length were higher than an additive genetic variance.

The potential response of a trait to selection is defined by its heritability and variance. To determine the relevance of type trait selection, the heritability of these traits must be estimated. In the present study, heritability of rump slope/rump angle was observed as 0.47 in Murrah buffaloes. On the other hand, lower heritability estimates of rump slope were reported by Nemcova et al. [23] in Holstein cattle (0.34) and Junior et al. [24] in Canadian Holstein cattle (0.36) by using the same methodology. Heritability estimates for rump width (pin bone distance) was 0.56 and hip bone distance was 0.59 in this study. Higher heritability estimates for rump width were reported as 0.81 ± 0.29, 0.79 ± 0.49, 0.91 ± 0.41, 0.78 ± 0.02, and 0.80 ± 0.02 by Khan and Khan [11], Vinayak [25], Dahiya and Rathi [26], Dahiya [27] and Khan et al. [28] respectively, in different breeds of cattle. On contrary, Vinayak [25] and Dubey et al. [29] reported lower heritability of rump width in Hariana (0.05 ± 0.14) and Sahiwal (0.44 ± 0.43) cattle. Nemcova et al. [23] and Junior et al. [24] also reported lower heritability estimates of rump width as 0.40 and 0.32, respectively in Holstein cattle by Bayesian approach. It is evident from Table 3 that the heritability estimates for navel flap length (NFL) were high (0.53). Khan et al. [28] also reported high heritability (0.95 ± 0.01) of navel flap length in Sahiwal cattle.

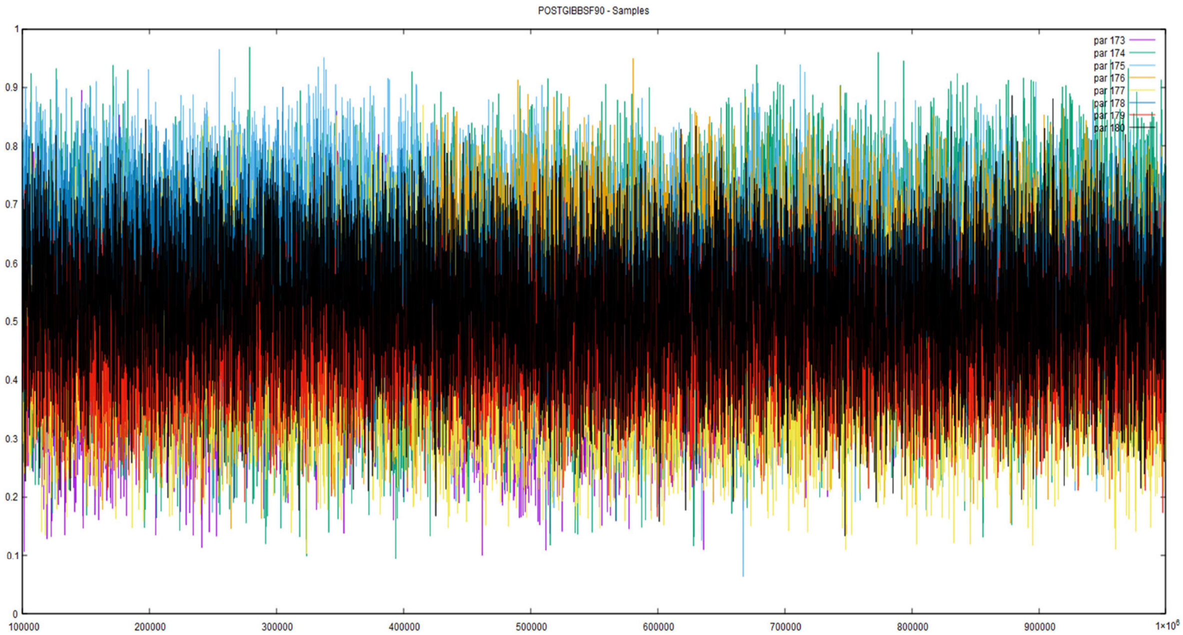

Figure 1. Trace plot depicting the convergence of heritability of body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL) and average skin thickness (AST) from parameters 173 to 180, respectively (shown in right upper corner of figure) in Murrah buffaloes.

Present study revealed medium heritability estimates (0.44) for brisket distance (BD). Junior et al. [24] reported lower (0.20) heritability estimates for the same trait in Canadian Holstein cattle by using Bayesian approach. The present study revealed high (0.56) heritability estimates for height at wither (Table 3). Similar estimates of heritability findings were reported by Vinayak [25], Dahiya [27] and Vij et al. [30] (0.63 ± 0.28, 0.54 ± 0.23, and 0.55 ± 0.22, respectively) in Hariana and Tharparkar cattle while higher heritability estimates were reported by Khan and Khan [11], Vinayak [25], Dahiya and Rathi [26] and Khan et al. [28] in Sahiwal and Tharparkar cattle as 0.81 ± 0.02, 0.81 ± 0.35, 0.73 ± 0.35 and 0.86 ± 0.01, respectively. On the other hand, by using Bayesian approach, Nemcova et al. [23] in Holstein cattle (0.45) and Junior et al. [24] in Canadian Holstein cattle (0.47) reported lower heritability estimates for height at withers. Heritability of body length (BL) was 0.45 in the present study, although, comparatively higher heritability estimates were reported by Khan et al. [28] in Sahiwal cattle (0.81±0.02) and Novotny et al. [31] in Czech Fleckvieh (0.58 ± 0.014), and lower estimates were reported by Mirza et al. [32] in Nili Ravi buffaloes (0.05 ± 0.09). Present study revealed high (0.53) heritability estimate for average skin thickness (AST) however, using the same method, Maiorano et al. [33] reported lower (0.12 ± 0.02) heritability of skin thickness in Nellore cattle. The present study revealed higher heritability estimates for most of the considered type traits in Murrah buffaloes as compared to other breeds. This may be due to limited data size and there is a need to revalidate the results on bigger data set.

Genetic correlation describes the magnitude and direction in which two traits are genetically linked and it can be due to linkage disequilibrium of genes or pleiotropy. Table 4 shows the genetic correlation estimates for considered traits. Genetic correlation estimates were obtained between rump slope (RS), rump width (RW), hip bone distance (HBD), navel flap length (NFL), brisket distance (BD), height at wither (HW), body length (BL), average skin thickness (AST). Genetic correlation estimates ranged from –0.64 (RS and NFL) to 0.53 (HDB and HW) in Murrah buffaloes. Genetic correlation between rump slope and rump width was found to be 0.415 in the present study but lower estimates were reported by Hakim et al. [34] and Berry et al. [35] in dairy cattle. In this study, genetic correlations of brisket distance with rump width and rump slope were –0.035 and –0.496; however, Hakim et al. [34] and Berry et al. [35] observed higher genetic correlations among the same traits. The present study revealed genetic correlations among height at wither and rump width as 0.184, though, Hakim et al. [34] reported higher (0.68) estimates and Berry et al. [35] observed lower (0.013) estimates in cattle. In present study, residual correlation estimates ranged from –0.35 (RS and BL) to 0.57 (RS and HW) in Murrah buffaloes as shown in Table 5.

In conclusion, from the results of present study it is concluded that linear type traits have sufficient genetic variation for selecting Murrah buffaloes based on these

Table 3. Posterior means and highest posterior density (HDP) region of variance components and genetic parameters for body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL), and average skin thickness (AST) in Murrah buffaloes.

Traits	Parameters	Mean	PSD	HPD interval (95%)	
				Low limit	High limit
Body length	σ_a^2	40.530	12.181	21.210	66.260
	σ_r^2	49.493	14.411	25.110	77.530
	σ_p^2	90.024	21.012	55.460	133.710
	h^2	0.451	0.085	0.278	0.611
Height at whither	σ_a^2	16.258	4.366	8.639	24.790
	σ_r^2	12.714	3.739	6.051	20.280
	σ_p^2	28.972	5.888	18.653	40.750
	h^2	0.561	0.091	0.377	0.734
Rump Width	σ_a^2	4.525	1.692	1.436	7.802
	σ_r^2	3.464	1.389	1.052	6.242
	σ_p^2	7.989	1.796	4.945	11.585
	h^2	0.563	0.152	0.267	0.842
Hip bone distance	σ_a^2	12.903	4.187	5.330	21.180
	σ_r^2	8.766	3.453	2.730	15.670
	σ_p^2	21.668	5.070	12.734	31.650
	h^2	0.595	0.128	0.355	0.843
Rump slope	σ_a^2	17.872	5.466	8.249	29.130
	σ_r^2	19.937	6.302	9.907	32.890
	σ_p^2	37.809	7.361	25.060	52.390
	h^2	0.475	0.115	0.250	0.687
Brisket distance	σ_a^2	12.584	4.695	4.453	21.910
	σ_r^2	16.076	5.232	6.780	26.460
	σ_p^2	28.660	7.020	16.535	42.230
	h^2	0.439	0.118	0.224	0.678
Navel flap length	σ_a^2	1.586	0.588	0.615	2.772
	σ_r^2	1.399	0.490	0.526	2.346
	σ_p^2	2.985	0.745	1.759	4.442
	h^2	0.527	0.126	0.280	0.762
Average skin thickness	σ_a^2	2.397	0.953	0.799	4.201
	σ_r^2	2.113	0.812	0.795	3.724
	σ_p^2	4.510	1.437	2.157	7.301
	h^2	0.529	0.109	0.312	0.734

σ_a^2 = additive genetic variance estimates; σ_r^2 = residual variance estimates; σ_p^2 = phenotypic variance estimates; h^2 = heritability estimates; PSD = posterior standard deviation; HPD = highest posterior density.

Table 4. Posterior means and highest posterior density (HPD) region of genetic correlation estimates between body length (BL), height at wither (HW), rumpwidth (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL), and average skin thickness (AST) in Murrah buffaloes.

Traits	Mean	PSD	HPD interval (95%)	
			Low limit	Low limit
RS/RW	0.415	0.236	–0.060	0.817
RS/HBD	–0.305	0.235	–0.742	0.155
RS/NFL	–0.640	0.221	–0.962	–0.238
RS/BD	–0.496	0.256	–0.891	0.029
RS/HW	–0.038	0.211	–0.434	0.380
RS/BL	0.370	0.211	–0.070	0.743
RS/AST	0.066	0.288	–0.459	0.640
RW/HBD	0.184	0.260	–0.323	0.675
RW/NFL	–0.045	0.284	–0.569	0.508
RW/BD	–0.035	0.300	–0.604	0.552
RW/HW	0.278	0.232	–0.180	0.719
RW/BL	0.285	0.246	–0.197	0.747
RW/AST	0.068	0.322	–0.539	0.686
HBD/NFL	0.220	0.232	–0.237	0.672
HBD/BD	0.183	0.250	–0.305	0.658
HDB/HW	0.526	0.171	0.176	0.826
HBD/BL	0.418	0.193	0.050	0.776
HBD/AST	0.161	0.266	–0.349	0.671
NFL/BD	0.084	0.273	–0.458	0.588
NFL/HW	0.192	0.212	–0.223	0.588
NFL/BL	–0.004	0.236	–0.475	0.430
NFL/AST	0.153	0.271	–0.371	0.670
BD/HW	–0.045	0.216	–0.454	0.384
BD/BL	–0.267	0.213	–0.664	0.157
BD/AST	0.081	0.276	–0.454	0.594
HW/BL	0.185	0.190	–0.188	0.541
HW/AST	0.043	0.231	–0.398	0.480
BL/AST	0.282	0.225	–0.144	0.710

PSD = posterior standard deviation; HPD = highest posterior density

Table 5. Posterior means and highest posterior density (HPD) region of residual correlation estimates between body length (BL), height at wither (HW), rump width (RW), hip bone distance (HBD), rump slope (RS), brisket distance (BD), navel flap length (NFL) and average skin thickness (AST) in Murrah buffaloes.

Traits	Mean	PSD	HPD interval (95%)	
			Low limit	Low limit
RS/RW	0.462	0.249	–0.025	0.860
RS/HBD	0.277	0.265	–0.238	0.755
RS/NFL	0.274	0.217	–0.158	0.689
RS/BD	0.375	0.224	–0.071	0.766
RS/HW	0.569	0.160	0.237	0.834
RS/BL	–0.346	0.187	–0.687	0.023
RS/AST	–0.216	0.272	–0.717	0.307
RW/HBD	0.138	0.300	–0.452	0.697
RW/NFL	0.005	0.290	–0.521	0.587
RW/BD	0.209	0.280	–0.330	0.742
RW/HW	0.163	0.266	–0.352	0.670
RW/BL	0.111	0.252	–0.402	0.573
RW/AST	–0.074	0.326	–0.703	0.547
HBD/NFL	0.241	0.245	–0.243	0.691
HBD/BD	0.187	0.254	–0.316	0.662
HDB/HW	0.261	0.236	–0.217	0.697
HBD/BL	0.023	0.238	–0.442	0.479
HBD/AST	–0.005	0.297	–0.585	0.551
NFL/BD	0.056	0.229	–0.394	0.494
NFL/HW	0.081	0.216	–0.350	0.484
NFL/BL	0.027	0.219	–0.402	0.450
NFL/AST	0.165	0.256	–0.342	0.642
BD/HW	0.210	0.215	–0.212	0.612
BD/BL	–0.031	0.443	–0.921	0.819
BD/AST	0.003	0.110	–0.222	0.215
HW/BL	0.278	0.188	–0.091	0.625
HW/AST	–0.081	0.237	–0.539	0.373
BL/AST	0.107	0.232	–0.349	0.549

PSD = posterior standard deviation; HPD = highest posterior density

traits. Heritability estimates indicated that linear type traits are under genetic control and genetic improvement can be achieved by selection in the desired direction. At organized farms, morphological measures should be recorded and may be used to select superior dairy animals in the future.

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