Estimation of Genetic Parameters and Breeding Values for Body weight and Linear Body Measurements of Mixed Flock of Cattle Breeds

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Abstract

The aim of this study was to estimate the genetic parameters and breeding values for body weight and linear body measurements namely body length, heart girth, height at withers, hip height and tail length of cattle. The number of animals used for the study was 176 and fixed factors such as breed, sex and age contemporary group were included in the mixed model equations. Estimation of genetic parameters was performed using restricted maximum likelihood (REML) procedure in univariate and multivariate animal models. Estimates of heritability (h^2) for body weight, body length, heart girth, height at withers, hip height and tail length was 0.31±0.11, 0.26±0.10, 0.54±0.11, 0.19±0.08, 0.22±0.09 and 0.02±0.12 respectively. The genetic correlations among body weight and linear body measurements ranged from -0.99 to 0.99. The mean estimated breeding value (EBV) for body weight, body length, heart girth, height at withers, hip height and tail length was 2.31kg, 0.23cm, 1.36cm, 0.66cm, 0.57cm and 0.03cm respectively. The low to high heritability estimates for body weight and linear body measurements implies rapid improvement of these traits via mass selection. High EBV for each trait implies high transmitting ability.

Keywords: Cattle, fixed factors, genetic correlations, heritability, REML

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1. Introduction

Cattle play important role in Nigerian agriculture as source of meat, hide, milk, traction and status symbol. Cattle trade involves millions of people engaged in various aspect of the enterprise from trade in live cattle and transportation to meat retailing. Cattle production in Nigeria is predominantly under extensive system as practice by Fulani herdsmen. Body weight and weight gains are the most important indicators of growth and development of animals and they are related to meat yield [1]. Body dimensions or linear body measurements have been a recurring interest in beef cattle industry either to supplement body weight as a measure of productivity or as predictors of some less visible characteristics [2]. Improvement of growth performance traits such as body weight and linear body measurements is one of the most important breeding goals in livestock production [3]. Knowledge of the genetic parameters of traits in the breeding objectives is a prerequisite for optimizing breeding programs and to predict selection response [4]. Genetic parameter for growth traits in Nigerian breed of cattle is scant in literature. Therefore, the aim of this study was to estimate heritability, genetic correlations and breeding values of body weight and linear body measurements of a mixed population of cattle.

2. Materials and methods

Location of the study: The study was carried out in the cattle unit of the teaching and research farm of the Department of Animal Science, Delta State University, Asaba Campus. The study area lies between latitude 6º 14′ N and longitude 6º 49′ E.

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Experimental Animals and their management: One hundred and seventy six (176) cattle consisting of Red bororo, Muturu, White Fulani and their crosses were used for the study. The animals were managed under a semi-intensive system of animal husbandry. They were allowed to graze available pasture consisting of grasses and legume from 8 am to 3 pm daily. Concentrates was also fed to the animals and *ad libitum* water provided.

Data Collection: Herd pedigree was collected from the farm records. Data collected were classified on the basis of age, breed and sex. The animals were classified into four age contemporary groups (CG) as follows: CG1= 11-13 years, CG2= 8-10 years, CG3= 1-4 years and CG4= less than 1 year. There were four breeds namely White Fulani (breed1), Red bororo (breed2), Muturu (breed3) and crosses between white Fulani and Muturu (breed4). The sexes were two namely male (sex1) and female (sex2). The linear body measurements (LBMs) of the animals were taken in the morning prior to grazing. Each animal was restrained with aid of a crush and allowed to calm down before measurements to avoid measurement errors. The LBMs were measured using a measuring tape and recorded in centimeters while body weight (BWT) was in kilograms (kg). The following measurements were taken on each animal. Body weight of each animal was estimated from the heart girth (HGT) using the metric chart that convert the HGT (cm) into bodyweight (kg). Heart girth: this was the body circumference immediately posterior to the fore limbs. Body length (BL): was measured from the joint of the scapular to the pin bone. Hip height (HH): The distance from the platform on which the animal stands to the point of its shoulder. Height at wither (HWT): The distance from the surface of the platform to the dorsal point of the withers. Tail length (TL): The distance from the base to the end of the tail.

Data Analysis: A univariate and multivariate animal models based on restricted maximum likelihood (REML) were used for the genetic analysis of the data. Univariate model was used to estimate variance components and heritability while multivariate animal model was used to provide the genetic correlations among BWT and LBMs. The univariate animal model in matrix notation is stated as follows: Y=Xb + Za + e, where Y = the vector of observation, b = vector of fixed effects (breed, sex and age contemporary group), a = vector of random animal effects, e = vector of random residuals. X, Z is design matrices relating the observations to fixed and random animal effects respectively. It is assumed that the expectation (E) of the variables are E(Y) = Xb, E(a)= E(e) = 0. It is also assumed that the residual variance was independently distributed with variance σ_e^2. The multivariate model in matrix notation is stated as follows:

$$\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

Where for trait i (i=1, 2), Yi=vector of observations, bi=solution vector of fixed effects, ai=solution vector of random direct additive effect, ei=vector of random residual effect, Xi and Zi are design matrices relating observations to fixed and direct additive genetic effects. The WOMBAT software [5] was used to run the analysis.

3. Results and discussion

Table 1 presents the descriptive statistics of body weight (kg) and linear body measurements (cm) of cattle. Body weight was the most variable trait while the linear body measurements were almost uniform as judged by their standard deviations.

Table 1. Descriptive statistics of body weight (kg) and linear body measurements (cm) of cattle

Trait	Mean	Sdev	min	max	Nrec
Body weight	220.07	123.80	56.00	428.00	176
Body length	117.32	22.58	67.00	148.00	176
Heart girth	139.85	25.70	103.00	185.00	176
Height at withers	104.91	25.63	50.00	141.00	176
Hip height	103.98	24.77	48.00	137.00	176
Tail length	57.00	24.43	30.00	92.00	176

Note: sdev = Standard deviation, nrec – number of records, min = minimum, max = maximum.

Table 2 shows the generalized least square solutions for fixed effect of breed, sex and CG together with their raw means and the number of observations for fixed effect subclasses of the body weight and LBMs of cattle. The GLS solution of fixed effect of breed indicates that breed 4 had the highest body weight, body length, heart girth, height at withers and tail length compared to the rest of the breeds (1-3). This is inconsistent with the raw mean of the breeds which show that breed 2 with only eight records had the highest value of the afore mentioned traits followed by breed 1 with seventy-two records. The fixed effects of sex1 and CG1 were set to zero during the mixed model analysis to take care of dependences among matrix of fixed effect. WOMBAT by default zero out the first level of each cross classified effect other than the first for each trait to account for dependences [6]. Consequent upon this, sex2 had a higher GLS solution than sex1 in body weight only. This is consistent with the raw mean of the sex effect. The raw mean of sex 2 was slightly higher than sex1 in the rest of the traits. This is in line with the observations of various workers that female cattle (sex2) were significantly superior to male cattle (sex1) in all body measurements [7, 8]. The GLS solution of CG1 though constrained to zero had higher body weight and other body measurements compared to other groups. This is consistent with the raw mean where CG1 had the highest value of body weight, body length and other body parameters compared with the rest of the CG groups.

Table2: Generalised least square solutions for fixed effects of breed, sex and CG on body weight and linear body measurements of cattle

		BWT		BL		HGT		HWT		HH		TL	
Breed	Nrec	Raw M	Sol	Raw M	Sol	Raw M	Sol	Raw M	Sol	Raw M	Sol	Raw M	Sol
1	72	272.23	148.74	122.33	32.35	147.44	36.30	110.56	28.30	108.67	26.15	70.22	26.80
2	8	356.00	92.15	136.00	24.57	165.00	31.73	122.00	22.53	118.00	18.04	87.00	27.66
3	56	173.86	145.83	104.71	24.26	127.00	32.50	92.71	20.33	91.39	20.16	47.51	14.40
4	40	177.20	213.00	116.00	45.46	122.40	42.30	18.40	46.36	106.40	45.85	58.00	36.22
Sex													
1	80	212.25**	0.00	115.38**	0.00	135.00**	0.00	104.50**	0.00	101.38**	0.00	60.50**	0.00
2	96	229.43	11.45	116.21	4.48	13.64	-2.39	105.14	-5.44	104.00	-3.24	61.29	-1.36
CG													
1	40	378.20**	0.00	142.40**	0.00	169.60**	0.00	127.20**	0.00	124.60**	0.00	88.20**	0.00
2	32	324.75	-51.94	126.00	-16.88	158.50	-11.36	119.25	-7.89	119.75	-5.50	82.75	4.30
3	56	159.71	-245.1	118.43	-28.79	124.14	-47.72	108.43	-25.22	105.43	-27.1	52.57	-34.9
4	48	100.33	-304.3	84.17	-63.53	107.00	-65.26	72.67	-61.19	71.17	-60.9	33.67	-53.6

Note: Nrec: Number of records. Raw M: Raw mean. Sol: Solution
***Mark effects which have been set to zero for the analysis*

Table 3 presents the additive genetic variance, residual variance and heritability of body weight and LBMs of cattle. Body weight recorded moderate h^2 estimate of 0.31±0.11. This is much lower than an h^2 estimate of 0.74 for live weight of Holstein cattle of South Africa reported by Ramatsoma *et al* [9]. Magnabosco *et al* [10] reported h^2 estimate of 0.66 for body weight of Brahman cattle in Mexico which is higher than the estimate obtained in this study. Boligon *et al* [11] reported direct h^2 estimates of 0.35 and 0.38 for mature weight in Nelore cattle using multitrait and random regression model respectively which are slightly higher than the estimate obtained in this study. The high h^2 estimate of 0.54±0.11 obtained for HGT is lower than a similar estimate of 0.62 in Bunaji cattle reported by Alphonsus *et al* [12]. Khan and Khan [13] reported a higher h^2 estimate of 0.82 for HGT in Sahiwal cattle of Pakistan. BL and HWT recorded h^2 estimates of 0.26±0.10 and 0.19±0.08 respectively. These are much lower than the h^2 estimates of 0.81±0.02 and 0.86±0.01 for BL and HWT respectively reported by Khan *et al* [14] in Sahiwal cattle in Pakistan. The h^2 of TL obtained in this study was 0.02±0.12 which is much lower than the h^2 estimate of 0.95±0.01 for the same trait reported in Sahiwal cattle by Khan *et al* [14]. A low h^2 estimate of 0.22±0.09 was obtained for HH. Riley *et al* [15] reported h^2 estimates that range from 0.37 to 0.53 for HH in Brahman cattle using random regression model. Heritability estimates vary according to estimation method, environmental effects and sampling error due to sampling size [16]. The moderate to high h^2

estimate for body weight, HGT and other body measurements of cattle implies that these traits can respond rapidly to individual selection. On the other hand, TL with low h^2 estimate implies that mass selection will not be applicable but information from relatives should be incorporated in the estimation of breeding value (EBV) of the cattle for the trait.

Table 3. Variance components and heritability of body weight and linear body measurements in cattle.

Trait	Additive variance	Residual variance	Phenotypic variance	Heritability
BWT	253.25	552.23	805.48	0.31±0.11
BL	21.88	60.96	82.85	0.26±0.10
HGT	40.74	34.39	75.12	0.54±0.11
HWT	22.59	99.05	121.64	0.19±0.08
HH	27.14	93.95	121.09	0.22±0.09
TL	1.31	61.16	62.47	0.02±0.12

Table 4 presents the statistics for estimated breeding value (EBV) of body weight, body length, heart girth, height at withers and hip height of cattle. The mean of estimated breeding value for body weight of cattle was 2.31kg. This implies that individual animal on average transmits 1.168kg of its EBV to its progeny. The mean EBV for the linear body measurements ranged from 0.03cm (TL) to 1.36 (HGT). The range of the EBV was highest in BWT (35.24), followed by HGT (15.85), HH (11.04), HWT (8.97) and BDL (8.81) and TL (0.79) in that order. The variability of the EBV as measured by the standard deviation of the mean shows that BWT was the most variable, followed by HGT. The least variable trait was TL. The variability implies wider scope for selection of individuals for each trait based on their estimated BV.

Table 4. Statistics for estimated breeding values for body weight and linear body measurements of cattle

	BWT	BL	HGT	HWT	HH	TL
Minimum	-18.87	-4.02	-7.76	-2.73	-3.63	-0.14
First quarter	-2.23	-1.29	-1.10	-0.76	-1.35	-0.03
Median	3.53	0.20	1.38	0.68	0.30	0.02
Mean	2.31	0.23	1.36	0.66	0.57	0.03
Third quarter	8.50	2.00	4.38	1.89	1.90	0.06
Maximum	16.37	4.80	8.09	6.24	7.41	0.66
Range	35.54	8.81	15.85	8.97	11.04	0.79
Std.Dev.	7.97	2.17	3.78	2.05	2.51	0.11

The genetic correction (rG) among BWT and LBMs are presented in Table 5. The rG were mostly positive and ranged from -0.99 to 0.99. High positive rG were obtained between BWT and all LBMs (range: 0.57 to 0.99) thus implying that the same set of genes control BWT and LBMs in cattle. Similarly, the rG between HGT and other LBMs were all positive (range: 0.47 to 0.99). This also implies pleiotrophic effect of genes on HGT and LBMs. Alphonsus *et al* [17] reported rGs among body conformation traits that ranged from 0.179 to 0.854. Positive rGs were obtained between BL and all the LBMs excepting HGT (range: 0.27 to 0.95), TL and all the LBMs excepting HGT (range: 0.27 to 0.99). The rG between HH and all the LBMs was positive (range: 0.88 to 0.99). These imply that improvement of any of the LBMs by selection will result to correlated improvement in others.

Table 5. Genetic (lower matrix) and phenotypic correlation (upper matrix) among body weight and linear body measurements of cattle

	BWT	BL	HGT	HWT	HH	TL
BWT	-	0.48(0.17)	0.15(0.10)	0.57(0.13)	0.51(0.14)	0.94(0.06)
BL	0.80 (0.36)	-	0.27(0.21)	0.13(0,19)	0.55(0.12)	0.28(0.19)
HGT	0.99 (0.38)	0.91 (0.41)	-	0.65(0.11)	0.57(0.13)	0.32(0.25)
HWT	0.57(0.29)	-0.99(0.37)	0.99 (0.25)	-	0.97(0.01)	0.24(0.26)
HH	0.88 (0.25)	0.95(0.28)	0.99 (0.25)	0.52 (0.08)	-	0.05(0.20)
TL	0.99(0.03)	0.27(0.31)	0.47 (7.17)	-0.64(4.61)	0.99(0.28)	-

Similar observation was reported by Supriyantono *et al* [2] who recorded low positive rG among body measurements of Bali cattle. The phenotypic correlations (rPs) among body weight and LBMs were all positive and ranged from 0.05±0.20 to 0.97±0.01 implying predictability among the body measurements.

4. Conclusions

The h^2 of BWT was 0.31±0.11 while the h^2 of LBMs were BL (0.26±0.10), HGT (0.54±0.11), HWT (0.19±0.08), HH (0.22±0.09) and TL (0.02±0.12). The rG ranged from -0.99 to 0.99 while the rPs ranged from 0.05 to 0.97. The mean EBV for BWT was 2.31kg while the mean EBV for LBMs ranged from 0.03cm (TL) to 1.38cm (HGT). The results of the study suggest that improvement of BWT and LBMs in the mixed flock of cattle breeds is possible through mass selection.

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