



Estimation of Genetic Parameters for Growth Traits in Nigerian N'dama and Muturu Cattle Crosses

Ifemma J. Ohagenyi ^{*1}, Valentine C. Udeh ¹, Chukwuemeka C. Okolo ², Gabriel A. Ezekwe¹, and Boniface M. Anene ²

¹ Department of Animal Science, University of Nigeria, Nsukka, Nigeria.

² Department of Veterinary Medicine, University of Nigeria, Nsukka.



CrossMark

THE rural communities in Nigeria and other developing countries, hitherto suffer protein malnutrition, early child mortality and poverty. Animal breeders have addressed similar challenges with the aid of genetic parameters, efficient breeding decisions, genetic improvements in milk, beef and cheese production of the exotic cattle, which ranks first in the gross domestic product of the agricultural sector of most civilized countries. These breeding tools were employed to develop the world breeds of cattle, which is estimated to be about 100 breeds. Nevertheless, estimates of genetic parameters of traits of the Nigerian N'dama and Muturu crosses is porous. A total of 300 records of the closed population of the Nigerian cattle herd, comprising of crosses of Muturu and N'dama cattle, were used for this research. This study was conducted from December 2018 to June 2019 to estimate the variance components and heritability for birth weight (BW) and weaning weight (WW), and the genetic and phenotypic correlations between these traits in N'dama and Muturu crosses at the University of Nigeria Nsukka (UNN) cattle herd. The study lasted for six months, and the heritability and genetic correlation of the traits were estimated using the Restricted Maximum Likelihood (REML) method of the SAS mixed model. The result revealed high estimates of direct heritability (0.39 and 0.62) for birth weight and weaning weight, respectively. High and positive (0.84) direct genetic correlation existed among both traits.

Keywords: Genetics, Heritability, N'dama, Muturu, Growth, Traits and Correlation.

Introduction

The Nigerian cattle subsector plays a substantial role in the generation of income for the rural communities in Africa; however, it has minimal influence on protein malnutrition, early child mortality [1] and far behind the European cattle (worth \$70 billion), which ranks first in GDP of the agricultural sector [2]. The reason is due to the poor genetic composition of the majority, which is characterized by small body size, slow growth and low reproductive performance.

Grain de Sel [3] reported that Nigeria remains the top beef cattle producer in Central and West

Africa owning over 16 million heads of cattle, which supersedes Niger, Mali and Chad whose cattle heads are 8.7, 8.2 and 7 million, respectively.

Nigeria's rapidly growing population, which is expected to reach 250+ million persons by 2030 [4], elicits rising earnings, civilization, as well as enhanced demand for livestock commodities [5].

Africa holds enormous potential for agriculture and is expected to support global food security by 2050. Nigeria has a strategic place in global food security, since it is the largest and most favoured nation in Africa. Africa's population, which represents one of continents with the highest

human growth rate, will grow from 1.3 billion people today to 2.5 billion by 2050, consequently, stupendous demand for more animal protein is anticipated [5]. Therefore, further corroborating recent prognosis that beef, poultry meat and milk consumption will increase by 117, 253 and 577 per cent, respectively between 2010 and 2050. Hence, there is a need to genetically upgrade the performance of our indigenous cattle species to raise their potential for higher meat yield.

Esté and Carina [6] opined that the genetic improvement of beef production systems is hinged principally on two procedures encompassing selection within/among breeds for enhanced performance of critical characters to produce individuals that possess better fitness. N'dama and muturu, predominant in southeastern Nigeria, produce minimally and are usually referred to as unimproved. However, they have good adaptive traits that make them hardy and resistant to certain environmental factors and diseases. Hence, they can be used in advanced beef cattle improvement programmes. Moreover, birth weight and weaning weight traits are recognized as important traits in determining the economic efficiency of beef cattle [7]. They constitute crucial element of breeding decision, because they can be evaluated with ease.

The efficiency of breeding decision depends on the accuracy of the estimated genetic and phenotypic parameters, comprising heritability and repeatability [8]. However, since the inception of breed improvement programs in Nigeria, no adept feat has been given to the comprehensive analysis of the data generated, estimation of genetic parameters or genetic progress among its cattle herds. Such estimates are rudimentary to the predictive accuracy, as well as the success of future breeding strategies. Although information abounds in the genetic parameter estimates of numerous breeds, estimates of genetic and phenotypic parameters for indigenous cattle populations are scarce.

The objective of this study was to estimate the variance components and heritability for birth weight and weaning weight, as well as the genetic and phenotypic correlations between these traits in N'dama and Muturu crosses reared at the University of Nigeria, Nsukka (UNN) cattle herd.

Material and Methods

The study area

Data were obtained from the breeding and

production records of a closed population of Nigerian N'dama and Muturu cattle crosses beginning from the month of December 2018 to June 2019 at the University of Nigeria Nsukka Animal Science Farm. Nsukka lies within longitude 7°20'E and 7°29'E and latitude 6°54'N and 7°00'N [9]. It's locate on above the sea level is at altitude 447m. Nsukka has a climate that is commonly tropical. It's relative humidity ranges from 65 – 80% and a mean daily temperature of 26.8°C [10]. The months of April to October witness rainy season, while November to March the dry season. The annual rainfall of the area lies in range of 1680 – 1700mm [11]. The experiment lasted for six months.

Management of the herd

A total of 150 cows and 5 sires were used for the experiment. They were bred and managed properly through calving till weaning. Calving occurs all year round, since there was no concrete breeding program. Calves were weighed within 24 h of birth and subsequently calves body weights were recorded at monthly intervals using a 100Kg capacity weighing scale. Calves' identity was done with rings at birth and branded before weaning. Cows breast milk were supplemented with powdered milk. About 10g of milk dissolved in water was given to each calf from birth to 8 weeks of age. Calves were weaned at about 4 months of age. Routine prophylaxis was administered to all animals against ecto- and endoparasites, trypanosomiasis and babesiosis. The vegetation of the research station is defined as guinea savannah type. The predominant grass species on UNN pasture are *Panicum maximum*, *Cynodon dactylon* and *Pennisetum purpureum* incorporated with leguminous crop such as the *Centrosema pubesence*, *Mimosa sp.*, *Mucuna sp.* and others.

Statistical analysis

Data cleaning was done to enable only animals with complete records on sire, dam and all fixed effects to be used. The data of animals was analysed by the MIXED model procedure of SAS [12]. The model incorporated the sex (male and female) as fixed effect and sire as random effect. The Restricted Maximum Likelihood (REML) method of SAS mixed model was used to estimate the observable variance components due to sire (σ_s^2) and error (σ_w^2). A single-trait model analysis was fitted to determine the variance components of BW and WW. The general animal model was

$$y = X_b + Z_a + e$$

where y is the vector of observations for each trait; b is the vector of all fixed effects; a is the vector of random direct additive genetic effects of the animals and e is the vector of random residual errors associated with the observations. Meanwhile, X , and Z , are incidence matrices related to fixed and additive genetic effects, respectively.

The genetic correlation of BW and WW was determined using two-trait analysis of similar model. Estimates of genetic correlations were measured through varcomp procedure of Harvey [13]. In addition, the programme computed the genetic correlations and the standard errors of heritabilities.

$$h^2 = \frac{4\delta_s^2}{\delta_s^2 + \delta_w^2}$$

Where, h^2 is the sire heritability; δ_s^2 is the sire variance component and δ_w^2 is the error variance component.

$$rG = \frac{\text{Cov}(x,y)}{\sqrt{\delta_s^2(x)\delta_s^2(y)}}$$

Where, rG is the genetic correlation; $\text{Cov}(x,y)$ is the genetic covariance of x and y components; $\delta_s^2(x)$ is the sire variance of x trait and $\delta_s^2(y)$ is the sire variance of y trait.

The detailed description of animals at UNN population is presented in Table 1.

Results

The descriptive statistics for BW and WW of calves of the crosses between N'dama and Muturu are presented in Table 1. Sex had significant effect ($P>0.05$) on calves weights at birth and weaning. The BW of male and female calves were 11.80 ± 0.19 and 10.05 ± 2.12 , while the WW of the male and female calves were 61.19 ± 5.90 and 53 ± 5.58 , respectively. The phenotypic standard deviation of BW and WW were 2.29kg and 6.64kg, respectively in Eastern Nigeria calves.

Variance components and heritability in UNN cattle population

The (co)variance and heritability estimates for BW and WW of Indigenous calves reared in Nigerian environment are presented in Table 2. The direct genetic variance for BW and WW were 1.89kg^2 and 22.21kg^2 . The phenotypic variances obtained for BW and WW were 4.85kg^2 and 35.33kg^2 , respectively (Table 2).

Direct heritability estimates were 0.39 and 0.62 for the BW and WW. The highest direct heritability (0.62) was found in WW. The estimated direct heritability for BW was medium, but high for WW.

TABLE 1. Descriptive statistics for birth weight (kg) and weaning weight (kg)

Sex		Male	Female
Birth weight (kg BW)	n	150	150
	Mean±SD	11.80±0.19	10.05±2.12
Weaning weight (WW) Kg	n	150	150
	Mean±SD	61.19±5.90	53±5.58

SD: Standard deviation

TABLE 2. Variance covariance components and estimates for heritability (\pm SD) for birth and weaning weights

Traits	Covariance components	Estimates	SE	Direct Heritability \pm S.E
Birth Weight	Sire	1.8909	1.44	0.39±0.72
	Error variance	2.9608	0.57	
	Phenotypic variance	4.8517		
Weaning weight	Sire	22.2115	1.43	0.62±0.69
	Error variance	13.1201	2.86	
	Phenotypic variance	35.3316		

S.E = Standard error

Correlation

The coefficients of phenotypic and additive direct genetic correlation that existed between BW and WW are presented in Table 3. The genetic, phenotypic and environmental correlation estimates among body weights and weaning weights were 0.84, 0.60 and 0.4, respectively. The measure obtained for genetic and phenotypic coefficients between birth weight and weaning weight were high.

Discussion

The weight of male and female calves found in this study is lower than the value (17.7 and 17.2) reported by Ahunu *et al.* [14] in N'dama, Muturu and Santa Gertrudis crosses. Male calves weighed 1.75kg (16.1%) heavier. The result is in line with the work of Bryan *et al.* [7], who observed increased sex differences with increasing growth rate, signifying that sires are more responsive to improvement in the environment. The degrees of weight gain of male calves recorded in this study are comparable to the values reported in Gudali by Tawah *et al.* [15], but did not concur with values recorded in Charolais cattle by Mujibi *et al.* [16]. The observed decrease in body weight of the UNN cattle herd could be attributed to the effect of inbreeding in a closed population, which enabled mating of related muturu and N'dama cattle for several generations in the experimental population.

The value reported in this study is lower than the phenotypic standard deviation (5.69 kg²), (4.92 kg²) and (4.90 kg²) reported by Cepon *et al.* [17], Řiha *et al.* [27] and Jakubec *et al.* [28], respectively in the Czech Republic for Charolais calves.

The works of Cepon *et al.* [17] and Bennett and Gregory [18] found higher values (13.12 kg²), 4.66kg, 12.09kg, 9.93kg, 12.22 and 13.92kg in Charolais, Angus, Gelbvieh, Hereford, Limousine and Red Poll cattle for direct genetic variances for BW. Phocas and Laloë [19] measured higher phenotypic variances (20.0 kg², 7.5 kg², 22.49

kg² and 15.41 kg²) for the BW of Charolais, Limousine, Blonde d'Aquitaine and Maine-Anjou, respectively.

The estimated direct heritability for BW in this study was medium and in conformity with the value recorded by Tawah *et al.* [15] in Gudali. The estimate of heritability, 0.39 ± 0.72 obtained in the course of this research for BW was higher than 0.149 reported by Peters *et al.* [20] for the indigenous calves in Nigeria; and values (0.32, 0.34, 0.21 ± 0.024 and 0.22) reported by Bosso *et al.* [21], Bennett and Gregory [18], Nesar *et al.* [22] and Bryan *et al.* [7] in N'dama and Hanwoo calves. Donoghue and Bertrand [26] similarly reported lower direct heritabilities for BW of American Charolais calves (0.21) and Australian calves (0.34).

However, higher values (0.41, 0.68, 0.59 and 0.65) were recorded by Kars *et al.* [23], Mujibi *et al.* [16], Martínez-González *et al.* [24] and Tawah *et al.* [15] among Nguni cattle stud, Charolais, Nellore and Wakwa cattles. Other researchers such as Cepon *et al.* [17] (0.74 Charolais); Phocas and Laloë [19] and Crews *et al.* [25] equally obtained higher values (0.74; 0.43 and 0.53), respectively among Charolais calves.

The measure of direct additive heritability obtained for weaning weight (0.62 ± 0.69) was high, however it was lower than the value (0.45) reported by Gutierrez *et al.* [29] in beef cattle reared in Asturiana de Los Valley, (0.51 ± 0.03) in Hanwoo cattle by Bryan *et al.* [7], (0.23 ± 0.021) by Nesar *et al.* [22], (0.01) by Choi *et al.* [30] in Hanwoo calves, and (0.37 ± 0.14) by Bosso *et al.* [21] in pure N'dama cattle. The increase in heritability estimates with increase in age obtained in this study follows the same trend noted by Bryan *et al.* [7].

Bosso *et al.* [21] reported 0.26, as coefficient of phenotypic correlation between birth weight and weaning weight. This is lower than 0.60 found in this study, however the genetic correlation

TABLE 3. Phenotypic and additive direct genetic correlation coefficients between birth weight and weaning weight

Traits	BW	WW
BW		0.60
WW	$rG = 0.84$; $rE = 0.40$	

Phenotypic correlations above the diagonal.

Genetic correlations (rG) and Environmental correlation (rE) below the diagonal.

coefficient (0.84) obtained in this study was greater than the values (0.32) reported by Ahunu et al. [14] in N'dama and Muturu crosses with Santa Gertrudis, (0.51) reported by Bryan et al. [7], (0.26) by Bosso et al. [21] and (0.78) reported by Naser et al. [22]. A review by Koots *et al.* [31] of all previous studies on correlations between birth and weaning weights reported 0.36 and 0.46; and 0.47 and 0.55 for phenotypic correlations and genetic correlations, respectively. The results of the present research reveal a lower measure of the phenotypic correlation relative to genetic correlation and is in agreement with the trend reported in the reviews by Koots et al. [31]. The high and positive genetic correlation between birth and weaning weights implicates pleiotropy, a condition in which two traits are under the control of same gene. This further indicates that animals with higher birth weights will have a faster postnatal growth.

Conclusion

Estimates of covariance indicate that additive genetic variance exists for these traits. Therefore, selection for these traits is likely to result in a genetic gain for growth in the Nigerian cattle population under tsetse infection pressure in south-eastern Nigeria and the humid zone of Africa in general. The high genetic correlations between birth weight and weaning weight indicate that birth weight could be a cost-effective means for selecting cattle with high post-weaning weight. The high estimates of direct heritability obtained in this study suggest that if genetic improvement through selection for birth and/or weaning weight of indigenous cattle and their crosses is desired, there is a high possibility for high genetic progress to be achieved.

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Ethical consideration

This research was conducted in compliance with the ethical and welfare policies guide for animal research of University of Nigeria, Nsukka.

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Conflict of interest

Authors declare that they had no conflict of interest.

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