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Heritability of docility and correlation with body weight and linear body measurements in cattle

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ABSTRACT

This study aimed to estimate heritability of docility and its correlations with body weight and linear body measurements in cattle. The number of animals tested for docility was 132. Fixed factors such as breed, sex, hump status and age contemporary group were fitted in the models. The body parameters measured were body weight, body length, heart girth and height at withers. Docility was scored on a scale of 1 to 5. The data was analysed using restricted maximum likelihood method. The results indicate mean docility score of 2.82 ± 1.51. The heritability of docility was 0.23 ± 0.05 which implies that docility in the cattle population can respond to selection. The heritability of body weight (0.013 ± 0.004) and the linear body measurements (range: 0.001 ± 0.15 to 0.02 ± 0.20) were very low. The genetic and phenotypic correlation between docility and body weight was 0.48 ± 0.07 and 0.60 ± 0.04 respectively. The genetic and phenotypic correlations between docility and the linear body measurements ranged from -0.99 ± 0.18 to -0.14 ± 0.25 and from 0.09 ± 0.20 to 0.60 ± 0.04 respectively. It was concluded that improvement of docility in the cattle population is possible through mass selection.

Keywords: docility, genetic correlation, heritability, REML, selection

INTRODUCTION

Docility in cattle is defined as the behavioural response of the animal when handled by human (Walkom et al. 2016). It is believed that the temperament of cattle affects the profitability of the herd through impacting production costs, meat quality, reproduction, maternal behaviour, the welfare of the animals and their handlers (Walkom et al. 2016). Several methods have been used to measure docility in cattle ranging from visual observation to computerized technique (Norris et al. 2014). Docile cattle are referred to as good while the opposite is referred to as aggressive animals or animal with poor temperament (Patherick et al. 2002). Walkom et al. 2016 described docility score as a subjective score of the animal's response to being restrained and isolated within a crush, at weaning and is scored on a scale of 1 to 5. In traditional small scale cattle production system as we have in some African countries, the relationship between docility and production traits has not been studied. Therefore, it is the objective of this study to estimate the heritability of docility and its correlation with body weight and LBMS in cattle.

MATERIALS AND METHODS

The experimental site and location: The study was conducted at the Department of Animal Science cattle research farm of Delta State University, Abraka, Nigeria. The study area lies between latitude 6o 14'N and longitude 6o 49'N. It is located in the rainforest agro ecological zone.

The experimental animals and their management

The animals used for the study were 132 cattle comprising of 16 muturu, 64 white Fulani and 52 red bororo. The animal was classified into 5 contemporary age groups as was done by Udeh et al. (2020) namely, age 1: 11-13 years, age 2: 8-10 years, age 3: 5-7 years, age 4: 1-4 years and age 5: less than 1 year. There were 43 males and 89 females in the cattle population. Semi intensive system was adopted in the management of the animals. The animals were allowed to graze on pastures (grasses and legumes) usually from 8am to 3 pm daily. Thereafter, they were fed on concentrates. Water was also provided for them throughout the day.

Measurements of docility

This involves restraining each animal in a crush and scoring relative to behaviour. Docility of each animal was scored using a 5-point scoring system described by the British Limousin cattle society. In this system, 1 represents docile or calm, 2 indicates restless or quieter than average, 3 indicates nervous or squirming, 4 indicates flighty or wild and 5 aggressive and very aggressive (Torres Vazquez and Spangler, 2016).

Body weight and Linear body measurements

Body weight (BWT) in pounds (Ibs) was calculated with a cattle weight calculator using the following formula: BWT = (heart girth x heart girth x body length)/300. The BWT in Ibs was multiply by 0.453592 in order to convert to kg. Body length (BL) in cm was measured with a tape from the point of shoulder to the point of rump or pin bone. Heart girth (HGT): This is the body circumference immediately posterior of the front legs or the body circumference on the fore ribs (Onowhakpor, 2017). The HGT in cm was measured using a measuring tape. Height at withers (HWT) in cm: This was measured in cm using a tape as the distance from the surface of a platform to the dorsal point of the withers (Udeh et al, 2020).

Statistical Analyses

In this study, docility was treated as a quantitative trait with normal distribution. The data obtained were analysed using restricted maximum likelihood methods in a single trait and bivariate animal models. The two models are presented in matrix notation accordingly.

$$Y = Xb + Za + e \quad (1)$$

$$\begin{bmatrix} Y_1 \\ Y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} \quad (2)$$

Where, $y_{1,2}$ represent vector of observations, $b_{1,2}$ = vectors of fixed effect, $a_{1,2}$ = vectors of additive genetic effects and $e_{1,2}$ = vectors of residual effects. The x and z represent design matrices which relate the observations to fixed and random genetic effects. The software employed for the analysis was WOMBAT (Meyer, 2007).

RESULTS AND DISCUSSION

A summary of the pedigree information of the animals used for the study is presented in Table 1.

Table 1. Pedigree information of the animal used for the study

No of animal identities in pedigree file = 132
Number of additional animal identities in data file = 0
Number of animal identities in total = 132
Number of sires = 5
Number of sires with progeny in the data = 5
Number of sires with records and progeny in the data = 5
Number of dams = 11
Number of dams with progeny in the data = 11
Number of dams with records and progeny in the data = 11
The number of animals without offspring = 116
The number of animals with offspring = 16

Shown in Table 2 are the statistics that describe the docility, body weight and some linear body measurements of cattle. The table shows that docility (scores) has a mean of 2.82 and a standard deviation of 1.51. This is similar to the results of Nesamvuni et al (2002) who reported a mean docility score of

2.57 with a standard deviation of 1.39 in beef cattle reared under communal system. Similarly, Halloway and Johnston (2003) reported a crush docility score of 2.38 to 2.41 in Angus breed of cattle which was slightly lower than the average docility obtained in this study. The implication of this result is that the animals were slightly restless to nervous when evaluated for docility. The average body weight of the animals evaluated for docility was 584.75 kg with a standard deviation of 237.14. The high standard deviation implies high variability among the mixed flock of cattle breed. Body length has a mean of 55.09 cm with a standard deviation of 9.56 which makes it the most variable linear body measurements. The highest mean value of 55.15cm was recorded by HGT with a standard deviation of 8.29. Mean HWT in the cattle population was 45.00 cm with a standard deviation of 6.00 cm.

Table 2. The statistics that describe docility (scores) and linear body measurements of cattle

Traits	Mean	Sdeviation	Minimum	Maximum	Nrecords
Docility	2.82	1.51	1.00	5.00	132
Body weight	584.75	237.14	103.53	1028.00	132
Body length	55.09	9.58	31.00	73.00	132
Height at withers	45.00	6.00	29.00	55.00	132
Heart girth	55.15	8.29	31.50	65.00	132

Note: Sdeviation = standard deviation, Nrecords = number of records

The heritability of docility, body weight and some linear body measurements of cattle is presented in table 3. Docility recorded an h2 estimate of 0.23 ± 0.05, thus implying that significant progress can be made in improving the docility of this animal population through mass selection. Mass selection involves ranking the animals according to their estimated breeding values (EBV) for the trait. Otterman et al, (2013) reported an h2 estimate of 0.22 for docility in Angus heifers which is very close to the h2 estimate obtained in this study. Similarly, Walkom et al, (2016) estimated the heritability of docility (measured on the scale of 1 to 5) to be 0.21 and 0 39 in Angus and Limousine cattle respectively while Torres-Vazquez and Spangler, (2016) reported direct heritability estimate of 0.27 ± 0.02 for docility in Hereford cattle. Direct h2 estimates for all measures of docility ranged from 0.03 to 0.67 implying that the trait can respond to selection (Norris et al, 2014)

Table 3. Heritability of docility, body weight and some linear body measurements of cattle

Trait	$h^2 \pm se$
Docility	0.23 ± 0.05
Body weight	0.013 ± 0.004
Body length	0.01 ± 0.15
Height at withers	0.02 ± 0.20
Heart girth	0.02 ± 0.10

Table 4 presents the genetic and phenotypic correlations between docility and body weight and some linear body measurements of cattle. The genetic correlation between docility and body weight was high and positive (0.48 ± 0.07) indicating that improvement of docility through selection would lead to correlated improvement in body weight of the animal. This is in agreement with the report of Torres-Vazquez and Spangler (2016) that selection for higher weaning weight would result in selecting animals with calmer temperament. However, the genetic correlations between docility and linear body measurements (range: -0.92 to -0.14) would imply that improvement of any of the LBMs would not result to animals with improved docility.

Table 4. Genetic (rG) and phenotypic (rP) correlations between docility and body measurements of cattle

Trait	rG	rP
Body weight	0.48 ± 0.07	0.60 ± 0.04
Body length	-0.14 ± 0.25	0.16 ± 0.24
Height at withers	-0.92 ± 0.25	0.09 ± 0.20
Heart girth	-0.64 ± 0.22	0.22 ± 0.23

The phenotypic correlation between docility and body weight was high and positive. This would imply that it is possible to predict the weight of cattle through docility score and vice versa. Similarly, the phenotypic correlation between docility and LBMs were low in size (range: 0.09 to 0.22) implying that any of the LBMs could be used to predict docility in cattle.

CONCLUSION

The heritability estimate obtained from this population of cattle suggests that docility would respond favorably to mass selection. The genetic correlation between docility and LBMs suggests that improvement of any of the LBMs would result to correlated improvement in docility and vice versa.

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