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2 **GENETIC PARAMETER ESTIMATES FOR MILK YIELD, UDDER AND BODY**
3 **CONFORMATION TRAITS OF JERSEY CATTLE IN THE NEW DERIVED**
4 **GUINEA SAVANNAH ZONE OF NIGERIA**

5 **Abstract**

6 In order to estimate the genetic parameters of milk, udder and conformation traits for Jersey
7 cattle in the derived guinea savannah zone of Nigeria, a total of 4200 lactation records for
8 milk yield and udder traits of Jersey cows were analysed by fitting and solving a multiple trait
9 animal model solutions using average information restricted maximum likelihood algorithm.
10 The heritability estimates was 0.35 for milk yield, 0.34 through 0.52 for udder traits and 0.20
11 through 0.72 for conformation traits. The genetic trend were higher than the environmental
12 correlations between milk yield and linear type traits and were less than unity which showed
13 the likelihood of developing a selection index scheme targeted towards genetic improve of
14 milk yield in adapted Jersey cattle in Nigeria.

15 **Keywords: Jersey, Udder, Aireml, Milk Yield**

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17 **1. INTRODUCTION**

18 The improvement of cattle for milk production in Africa through selective breeding had been
19 successful through the exploitation of additive genetic variance in the population. Jersey
20 cattle had been extensively used for crossbreeding in Africa due to their high level of
21 adaptability and robust coping strategy to the tropical climate. In Africa, milk volume has
22 been the most important breeding objective, with minimal emphasis on functional traits [1].
23 The functional plan for genetic improvement of milk had relied solely on the use of imported
24 semen from high merit sires and the importation of pregnant heifers from the United States
25 and European countries such as Germany and the Netherlands [2]. In response to the quest for
26 protein sufficiency in Nigeria due to population explosion, there is a need to establishing an
27 effective and robust breeding program for improvement of milk yield from adapted temperate
28 and tropical dairy cattle. [3] found genetic correlation of the range near zero in the first
29 lactation to moderate negative in the second lactation between BW and milk production traits.
30 Several researchers [3, 4, 5] had reported low to high genetic trends for milk yield in Jersey
31 cattle in tropical and temperate countries. [6] reported heritability estimate for milk yield in
32 Jersey cattle to range from 0.17 to 0.36 while permanent environmental effect was between

0.13 and 0.17. Therefore, the aim of this study was to estimate the genetic parameters for milk yield and biometric traits in Jersey cattle.

2.0 Materials and Methods

Data was obtained from Shonga dairy farm, Kwara State. The farm is situated at Edu Local Government. The farm is situated in the hot humid climate of Nigeria, with pronounced wet and dry seasons and steady high temperatures. Its geographical coordinates are 9° 1' north, 5° 9' East at an altitude 305m above the sea level. The rainy season with a duration of about 218 days, starts in April and ends in October [7].

2.1 Experimental animals

The records of purebred Jersey cattle of Farm 10 in Shonga dairy farm were used for the estimation of genetic parameters. The mating system adopted on the farm was artificial insemination technique using random doses of frozen purebred semen with a restriction to avoid inbreeding by mating related animals. Incomplete lactations records were yanked off from the original data before the statistical analyses.

2.2 Milk yield

Lactation records (4200) for milk yield and udder traits of Jersey cows were analysed by fitting multiple trait animal model using average information restricted maximum likelihood algorithm. The number of Jersey cows with records was 1080 with 3047 animals in the genetic relationship matrix. Milk yield was adjusted for lactation length of 305th days by multiplicative correction factors. Test day milk yield were calculated using the test interval method following the computational expression below [8]

$$MY_{305} = (P_1 \times D_1) + \sum_{i=2}^k \left[\left(\frac{P_i + P_{i-1}}{2} \right) \times (D_i - D_{i-1}) \right] + (P_{k+1} \times D_{k+1})$$

Where MY₃₀₅ is the milk yield, P₁ is the test-day first month milk output after calving, D₁ is differential between five days after calving and first day of the first month sampled, P_i is the test-day milk yield in month i (i = 2, ..., k), P_{k+1} is the test-day milk yield in the month when 305 days in lactation was achieved, and D_{k+1} is the difference between the 305th day of lactation and the last day of the month.

2.3 Type traits measurement

Body weight was measured by strict positioning of the animal on the Avery weigh bridge scale without agitation and was expressed in kilogram (kg). The body conformation (chest ligament, chest width, body depth, stature, rump width and heart girth) and udder (udder clearance, rear udder height, rear udder width and teat length) traits were all measured in centimeters using flexible tape calibrated for cattle measurement [9].

2.4 Statistical model and analysis

Data extracted from cattle herd books regarding conformation traits, milk yield and udder traits was fed into VAMMP Software, version 1.0. Data was cross examined for outliers before analysis. Covariance components were solved using the algorithm of Derivative free Restricted Maximum Likelihood Method using the MTDFREML software [10], which estimates fixed and random effect solutions by estimating the mixed models equations. The computations of variance components for the traits were estimated using multi-traits animal model.

The model used [10] can be described as:

$$y = Xb + Wpe + Za + e$$

in which y = vector of observations; b = vector of fixed effects (herd, number of calving, and season). pe = vector of random permanent environmental effects; a = vector of random animal effects; e = vector of random residual effects; X , W , and Z = incidence matrices that establish relationships between the records and the effects.

Heritability estimate was computed as the ratio of the additive genetic variance to total phenotypic variance while repeatability was estimated as ratio of the sum of the additive genetic variance plus permanent environmental variance to phenotypic variance, as described by [11]

The genetic and environmental relationship matrix were solved using a bivariate animal model. The matrix model is described as:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

in which y_i = vector of N observations; b_i = vector of fixed effects (herd, number of calving, contemporary group); pe_i = vector of random permanent environmental effects; a_i = vector of random animal effects; e_i = vector of random residual effects; X , W , and Z = incidence matrices establishing relationships between the records and the fixed and random effects,

92 respectively. It is assumed that random permanent environmental, animal and error effects are
 93 independently distributed with mean of zero and variance:

$$94 \quad Y \begin{bmatrix} \alpha \\ \mu \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

95 in which $\otimes$ = direct or Kronecker product; I = identity matrix equal to number of
 96 observations; A = relationship matrix among all animals in the pedigree; G_0 = variance and
 97 covariance matrix of random animal effects; $\sigma_{a_{ii}}^2$ = animal additive genetic variance for trait
 98 i ; $\sigma_{a_{jj}}^2$ = animal additive genetic variance for trait j ; $\sigma_{a_{ij}} = \sigma_{a_{ji}}$ = animal additive genetic
 99 covariance between traits i and j ; Q_0 = variance and covariance matrix of random permanent
 100 environmental effects; $\sigma_{pe_{ii}}^2$ = permanent environmental variance for trait i ; $\sigma_{pe_{jj}}^2$ = permanent
 101 environmental variance for trait j ; $\sigma_{pe_{ij}} = \sigma_{pe_{ji}}$ = permanent environmental covariance between
 102 traits i and j ; R_0 = variance and covariance matrix of residual effects; $\sigma_{e_{ii}}^2$ = residual variance
 103 for trait i ; $\sigma_{e_{jj}}^2$ = residual variance for trait j ; and $\sigma_{e_{ij}} = \sigma_{e_{ji}}$ = residual covariance between
 104 traits i and j .

105 3.0 Results and Discussion

106 The fat corrected milk yield of Jersey cattle had a moderate (0.35) heritability with high
 107 repeatability estimates of 57% (Table 2). The estimate of heritability (35 %) in milk yield
 108 obtained for Jersey cows was within the range of 30-35 % under low and high input
 109 production system [12] but higher than the 30 % reported by [13] when the parity were
 110 pooled for genetic parameter estimation in Zimbabwe but lower to heritability and
 111 repeatability estimates of 0.54, 0.56 and 0.36, 0.38 for milk yield in Zimbabwean Jersey
 112 cows, respectively as reported by [14] and [15]. Variations in estimates could be attributed to
 113 method of estimation and sample size. However, our heritability estimates were slightly
 114 higher than those reported by [15] working with Jersey cattle population in a subtropical
 115 environment. However, the most heritable type trait was CL (0.72) while BW (0.02) had the
 116 least heritability estimate. The repeatability estimate of linear type traits varied between 0.03
 117 (BW) to 0.75 (CL) for body conformation traits. The low to high heritability estimates (2-72

118 %) of conformation traits were within the range reported by several researchers [16, 17] in
 119 dairy cattle. Body conformation traits had positive, significant ($P<0.05$) correlations with 305
 120 d fat corrected milk yield. The environmental correlations was recorded between CL and BD
 121 (0.90) which implies that both chest ligament and body depth are driven by similar
 122 environmental factors.

Table 2: Heritability (h^2), repeatability (R), genetic and environmental correlations of fat corrected milk yield and body conformation traits in Jersey cattle

Traits	Milk yield	BW	BCS	CL	CW	BD	ST	Rump	HG
Milk yield	0.35	0.86**	0.21*	0.42**	0.70**	0.67**	0.65**	0.69**	0.52**
BW (kg)	0.01	0.02	0.04	0.36*	-0.33*	-0.68**	0.71**	0.43**	-0.39*
BCS (cm)	0.05	-0.09	0.25	-0.34*	0.79**	0.23*	0.99**	-0.39*	0.53**
CL (cm)	-0.02	0.48*	0.64**	0.72	0.67**	0.64**	0.48**	0.37*	0.14
CW (cm)	-0.03	-0.05	-0.03	0.77**	0.23	0.10	-0.36*	-0.37*	-0.14
BD (cm)	0.38*	0.53*	0.56**	0.90*	0.81**	0.61	0.98**	0.87**	0.96**
ST(cm)	0.35*	0.27*	0.83**	0.73*	-0.17	-0.37*	0.12	0.95**	0.77**
Rump(cm)	0.01	0.05	0.77*	0.68**	-0.25*	-0.38*	0.08	0.04	0.02
HG(cm)	0.25*	0.26*	0.54**	-0.16	0.74**	0.65**	0.06	0.08	0.09
R	0.57	0.03	0.31	0.75	0.28	0.65	0.18	0.05	0.14

123

124 Table 3 shows that udder conformation traits had positive and significant correlations with fat
 125 corrected milk yield. Udder conformation traits showed positive, significant ($P<0.05$)
 126 moderate to high correlation with fat corrected milk yield. This implies that improvement of
 127 udder conformation will cause a corresponding increase in milk production which agreed
 128 with the report of [16]. The strongest and positive genetic correlations for within udder
 129 conformation traits was between TL and RUH (0.93). Environmental correlations among
 130 udder conformation traits were weak with the exception of TL and RUH (0.22) and TL and

RUW (-0.22) which were positive, negative, with moderate associations. Moderate to high repeatability estimates for milk yield, body condition score, chest length, chest width, body depth, hearth girth, rear udder height and width were implicated with low variability within lactations; implying that all the measurements taken on the body conformation traits were closely related to bone structure of the cows. The positive genetic correlation between milk yield and TL suggest that correlated responses from selection on milk yield would result in longer teat length probably due to the prolonged effect of milking.

Table-3

Heritability (h^2), repeatability (R), genetic and environmental correlations of fat corrected milk yield and udder conformation traits in Jersey cattle

Traits	Milk yield	UC	RUH	RUW	TL
Milk yield	0.35	0.29*	0.42*	0.10	0.34
UC (cm)	0.56**	0.44	-0.03	0.34*	0.42*
RUH(cm)	0.64**	-0.03	0.38	-0.28*	-0.81**
RUW(cm)	0.94**	-0.09	-0.14	0.52	0.93**
TL (cm)	0.34*	0.14	0.22*	-0.20*	0.34
R	0.57	0.45	0.41	0.63	0.40

4.0 CONCLUSIONS

The study is a response to confirmation of the response of body and udder confirmation traits to increased milk yield which suggest the need for genetic improvement for milk yield of Jersey cattle through selection index for simultaneous improvement of these traits in the new derived guinea savannah zone of Nigeria.