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GENETIC PARAMETER ESTIMATES FOR MILK AND CONFORMATION TRAITS OF JERSEY CATTLE IN THE NEW DERIVED GUINEA SAVANNAH ZONE OF NIGERIA

Abstract

The objectives of this research were to estimate the genetic parameters of milk and conformation traits under environmental sensitivity of multi-genotype cattle. The data from the study came from two genotypes of cows (Jersey). Milk yield, five body traits (stature, ST; chest width, CW; body depth, BD; heart girth, HG; rump width, RW) and five udder traits (chest ligament, CL; rear udder height, RUH; rear udder width, RUW; udder clearance, UC; teat length, TL). Multi-trait animal models were used to estimate the (co)variance components based on average information restricted maximum likelihood method (AIREML) using R 3.0.3 software. Heritability estimates for milk production and conformation traits were low to high (h^2=7 to 44%, Holstein; 16 to 42%). Genetic and environmental correlation between 305 day fat corrected milk yield and conformation traits were less than unity across different genotypes. It was concluded that considerable exploitable genetic variation exists for milk production and conformation traits which suggest potential for improvement of economic traits.

KEYWORDS: 3/4HolsteinX1/4Bunaji, GENETIC, AIREML, MILK YIELD

1. INTRODUCTION

Breeding programs in cattle are primarily focused on milk yield. It is then obvious that accurate measurement and prediction of milk yield is also essential for the economy of the dairy industry. Genetic architecture refers to the composition or organization of the whole genome and its connection to the expression of complex phenotypes rather than single locus traits [7]. It is synonymous with the “genotype-phenotype map” for a trait. [11] provided a contemporary definition of genetic architecture as “the pattern of genetic effects that build and control a given phenotypic character and its variational properties”. Dissecting the genetic architecture and accurate statistical modeling has the propensity to increase genetic gain by increasing the estimate of heritability. Taking account of this variation by fitting herd as a fixed effect when

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modeling milk yield will decrease the residual variance, therefore decreasing phenotypic variance and increasing heritability estimate. This will lead to an increase in accuracy of the predicted breeding value which directly increases genetic gain.

In a population, heritability, additive genetic variance and genetic correlation, are the base knowledge of selection in quantitative genetics [10]. Although managerial factors significantly affect the level of reproductive performance achieved within a dairy herd [21]. The relationship between yield traits and body weight is complex largely dependent on both the frame size of a cow and body condition score. Some studies found unfavorable genetic relationship between weight at first calving and milk, fat and protein yields. They indicated that genetically heavier cows after calving produce less milk, fat and protein but conceive earlier than smaller cows [1]. [5] found genetic correlation of the range near zero in the first lactation to moderate negative in the second lactation between BW and milk production traits. Selection for milk yield has a negligible progress on the BW of animal [5] However, there are still potential exists to select animals with less BW loss at high levels of milk production, which is expected to improve cow health and reproductive performance [5]
Increasing emphasis on the need for policy formulation for dairy cattle in Nigeria under a National genetic evaluation program is highly desirable due to loss of our valuable genetic resources [3] suggested that the genetic and environmental relationship among breeds should be determined on different environmental scales, so that the breed could be grouped into sets that are genetically similar in terms of products delivery. Thus an objective quantification of the magnitude of the genetic architecture among a set of dairy breeds can be obtained from quantitative, qualitative, and computational measures under different production environment. The role or potential of this approach in dairy value chain should not be underplayed.

Genetic evaluation programmes have been used in the dairy industry for many years [22] in the developed countries. Estimation of the heritabilities of production traits is required for the genetic evaluation of breeds. These parameters for individual herds are compared with those of the national dairy herds. From this, the genetic and environmental trends for production parameters can be determined for each herd and compared with those of the national herd [18]. No such information is presently available for the dairy cattle industry in Nigeria. There is currently a growing interest in the keeping of dairy cows in Nigeria due to quest for protein sufficiency. A genetic

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evaluation of the national dairy herd in Nigeria has not been done and with the small number of records available, it was considered necessary to include all available records of all dairy cattle over all lactations in the analysis. This will provide a basis for a breeding and selection programme for dairy cattle farmers with the aim of improving the milk yield and conformation traits of dairy cattle in Nigeria.

Therefore, the objective of this study was to estimate the genetic (heritability, repeatability and genetic correlations) and environmental relationships among milk production, conformational (body and udder) in genetic groups of in multi-breed dairy cattle.

2.0 MATERIALS AND METHODS

2.1 Location of the Study

This study was carried out in some selected states with large commercial dairy facilities.

Kwara State

Shonga dairy farm is situated in Edu Local Government (Kwara State, Nigeria). The farm is located in the tropical 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. The nearest meteorological station showed maximum rainfall in month of September which drops to zero in December. The rainy season with a duration of about 218 days, starts in April and ends in October [8].

2.1.1 Experimental animals

Jersey cattle belonging to different dairy herd which were used for the study. Females were imported as pregnant heifers. Artificial insemination technique was randomly performed for heifers in the temperate country before importation and for cows after parturition (in Nigeria) using random doses of frozen purebred bull semen (imported from the U.S.A.) with a restriction to avoid full-sib and sire-daughter inseminations. The breeding plan in the farms of the study permitted practicing pure and crossbreeding through artificial insemination. Lactations without breeding dates and those of aborted cows or those affected by mastitis or other udder disorders were considered as abnormal lactations and their records were excluded from the

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original data before the statistical analyses. Also, records of cows sold for production purposes and data that was not normally distributed were excluded.

2.1 Milk yield

Milk yield was adjusted for lactation length at 305th days by multiplicative correction factors. Monthly test day milk yields of individual cows were used to calculate the accumulated 305-d MY using the test interval method following the computational expression below [15]

$$MY305 = \left(P_i XD_i\right) + \sum_{i=2}^{k}\left[\left(\frac{P_i + P_i - 1}{2}\right)\right] + \left(P_{K+1} XD_{K+1}\right)$$

Where MY305 is the milk yield of a cow adjusted to 305 d of lactation, P_1 is the milk yield of the test-day in the first month after calving, D_1 is the interval between five days after calving and the 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 interval between the 305th d of lactation and the last day of the month prior to achieving 305 d of lactation.

2.1 Body weight measurement

This was measured by firmly positioning of the animal on the Avery weigh bridge scale without agitation. The weight was expressed in kilogram (kg). Weight of the animals were recorded at monthly intervals.

Table A: Conformation traits definition of dairy cattle

No	Measurements	Units	Description	Instruments
1	Chest ligament	cm	Measured as the depth of cleft at the base of the rear udder	Flexible tape
2	Chest width	cm	Measured as the inside surface distance between the top of the front legs	Flexible tape
3	Body depth	cm	Measured as the distance between the top of spine and the bottom floor of the abdomen at last rib	Flexible tape
4	Stature	cm	Measured from the top of the spine in between hips to ground	Flexible tape
5	Rump width	cm	Measured between the inner walls of the two ischial tuberosities (i.e. pin bones)	Flexible tape
6	Heart girth	cm	Measured behind the front legs and shoulder blades	Flexible tape
7	Udder clearance	cm	Measured from the ground to the bottom of the udder	Measuring stick

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8	Rear Udder height	cm	Measured as the distance from the bottom of the vulva to the top of the rear udder	Flexible tape
9	Rear Udder width	cm	Measured as the udder width at the point where the rear udder is attached to the body.	Flexible tape
10	Teat length	cm	Measured as the distance from base to tip of the front teat.	Flexible tape

[13].

2. Statistical model and analysis

All herd information regarding conformation, bodyweight or health-calving dates, cow entry/exit, were obtained from historical records, notebooks and cattle management software. This information was entered, analyzed and saved using the VAMMP Software, version 1.0. Data selection was based upon reliability: information whose validity could not be guaranteed was deleted from the final data set before analysis, as well as extreme values that were considered physiologically abnormal or erroneously coded. Covariance components were estimated by Derivative free Restricted Maximum Likelihood Method using the MTDFREML software [6], which estimates fixed and random effect solutions by solving the mixed models equations. Variance components for milk and conformation were estimated through univariate analysis using an animal model considering the effects of herd, number of calving and contemporary group as fixed, and the permanent environmental, animal additive genetic and residual effects as random. The contemporary group included herd, year of calving and calving season.

The model used [17] 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. It is assumed that permanent environmental, animal, and residual effects are independently distributed with mean zero and constant variance:

$$V\begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

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Considering that A = relationship matrix, $I\sigma^2 e = R$, then $V(y) = ZAZ'\sigma^2_a + WI\sigma^2_{pe}W' + R$. Thus, the mixed model equations for the best linear unbiased estimator (BLUE) of estimable functions of b and for the best linear unbiased prediction (BLUP) of p_e and a are:

$$\begin{bmatrix} b \\ a \\ pe \end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A^{-1}_{\alpha 1} & Z'W \\ W'X & W'Z & W'W + I_{\alpha 2} \end{bmatrix}^{-1} = \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

in which A = relationship matrix; and $a1 = \sigma^2_e / \sigma^2_a$ and $a2 = \sigma^2_e / \sigma^2_{pe}$. Heritability was estimated as the ratio of the additive genetic variance to total phenotypic variance; and repeatability, as the ratio of the sum of the additive genetic variance plus permanent environmental variance to phenotypic variance, as described by Falconer and Mackay (2001):

$$h^2 = \frac{\sigma_a^{\ 2}}{\sigma_a^{\ 2} + \sigma_p^{\ 2} + \sigma_e^{\ 2}}$$

$$w^2 = \frac{\sigma_a^{\ 2} + \sigma_p^{\ 2}}{\sigma_a^{\ 2} + \sigma_p^{\ 2} + \sigma_e^{\ 2}}$$

To estimate genetic, environmental and residual correlations, a bivariate model was used which included herd, number of calving and contemporary group (which included year of calving and calving season) as the fixed effects, and the permanent environmental and additive genetic direct effects as random. The matrix model used was:

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

in which y_i= vector of N observations; b_i= vector of fixed effects (herd, number of calving, contemporary group); p_{ei} = 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, respectively. It is assumed that random permanent environmental, animal and error effects are independently distributed with mean of zero and variance:

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$$V\begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

in which ⊗ = direct or Kronecker product; I = identity matrix equal to number of observations; A = relationship matrix among all animals in the pedigree; G_0 = variance and covariance matrix of random animal effects; σ^2_{aii} = animal additive genetic variance for trait i; σ^2_{ajj} = animal additive genetic variance for trait j; $\sigma_{aij} = \sigma_{aji}$ = animal additive genetic covariance between traits i and j; Q_0= variance and covariance matrix of random permanent environmental effects; σ^2_{peii} = permanent environmental variance for trait i; σ^2_{pejj} = permanent environmental variance for trait j; $\sigma_{peij} = \sigma_{peji}$ = permanent environmental covariance between traits i and j; R_0 = variance and covariance matrix of residual effects; σ^2_{eii} = residual variance for trait i; σ^2_{ejj} = residual variance for trait j; and $\sigma_{eij} = \sigma_{eji}$ = residual covariance between traits i and j. The mixed model equations for the best linear unbiased estimator (BLUE) of estimable functions of b and for the best linear unbiased prediction (BLUP) of a and ap are:

$$G_0 = \begin{bmatrix} \sigma^2_{aii} & \sigma^2_{aij} \\ \sigma_{aji} & \sigma_{ajj} \end{bmatrix}, Q_0 = \begin{bmatrix} \sigma^2_{peii} & \sigma_{peij} \\ \sigma_{peji} & \sigma^2_{pejj} \end{bmatrix}, R_0 = \begin{bmatrix} \sigma^2_{eii} & \sigma_{eij} \\ \sigma_{eji} & \sigma^2_{ejj} \end{bmatrix}$$

$$\begin{bmatrix} \hat{b} \\ \hat{a} \\ \hat{pe} \end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z & X'R^{-1}W \\ Z'R^{-1}X & Z'R^{-1}Z + k_1 & Z'R^{-1}W \\ W'R^{-1}X & W'R^{-1}Z & W'R^{-1}W + I * Q^{-1} \end{bmatrix}^{-1} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ W'R^{-1}y \end{bmatrix}$$

$$in\ which\ k_1 = G_0 * A^{-1}, \hat{b} = \begin{bmatrix} \hat{b} \\ \hat{b}_2 \end{bmatrix}, \hat{a} = \begin{bmatrix} \hat{a}_1 \\ \hat{a}_2 \end{bmatrix} and\ \hat{pe} = \begin{bmatrix} \hat{pe}_1 \\ \hat{pe}_2 \end{bmatrix}$$

The estimates of genetic (r_g) and environmental correlations (r_e) were obtained from the estimation of covariance components using the following equations:

$$r_g = \frac{\sigma_{aij}}{\sqrt{\sigma^2_{aii}\sigma^2_{aij}}} \qquad r_e = \frac{\sigma_{eij}}{\sqrt{\sigma^2_{eii}\sigma^2_{eij}}}$$

in which σ_{aij} = additive genetic covariance between traits i and j; σ^2_{aii} = additive genetic variance for trait i; and σ^2_{ajj} = additive genetic variance for trait j were used for genetic correlation while for environmental correlations, σ_{eij} = environmental covariance between traits i and j; σ^2_{eii} = environmental variance for trait i; and σ^2_{ejj} = environmental variance for trait j.

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3.0 RESULTS AND DISCUSSION

The 305 d fat corrected milk yield had a moderate (0.35) heritability (Table 1). Regarding the linear type traits, the h^2 was between 0.02 (BW) and 0.72 (CL). However, the most heritable body measurement was CL (0.72) while rear udder width was the most heritable udder trait (0.52). BW (0.02) had the least heritability for body conformation traits while the least heritable udder conformation trait was RUH (0.38). Generally, the h^2 estimates for udder conformation traits were higher than those for body type traits with the exception of BD and CL. The 305 d fat corrected milk yield had high repeatability (0.57) estimates. The repeatability of the measurements of linear conformation traits varied between 0.03 (BW) to 0.75 (CL) for body conformation traits and from 0.40 (TL) to 0.63 (RUH) for udder measurements. The most repeatable udder and body conformation traits were CL (0.75) and RUH (0.63), respectively.

Body conformation traits had positive, significant ($P<0.05$) correlations which ranged from moderate to high with 305 d fat corrected milk yield. Udder conformation traits were positive, significant ($P<0.05$) and ranged from moderate to high with 305 d fat corrected milk yield but with the exception of TL (-0.13) which was low with negative correlations. The strongest and positive genetic correlations for body and udder conformation traits were between ST and BCS (0.99) and TL and RUH (0.93), respectively. The strongest and negative genetic correlation for

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body and udder conformation traits were between BD and BW (-0.68) and UC and CW (-0.93), respectively. The highest, significant (P<0.05) and positive environmental correlations for body and udder conformation traits with 305 d fat corrected milk yield were BD (0.38) and RUW (0.94).

All the udder conformation traits had positive and significant correlations with 305 d fat corrected milk yield (Table 2). Environmental correlations between BW and BCS had positive and near zero correlations while CL and CW recorded negative and near zero correlations with 305 d fat corrected milk yield. The highest and positive environmental correlations among the body type traits was between CL and BD (0.90) while correlation between BCS and ST (-0.83) was negative and highest. Environmental correlations among udder conformation traits were positive and negatively weak with the exception of the correlation between TL and RUH (0.22) with RUW (-0.22) which were positive, negative, moderate and significant (P<0.05).

4.0 CONCLUSIONS

Moderate to high heritability for 305 day fat corrected milk yield in suggests the possibility of genetic improvement through direct selection while low heritability estimates among some conformation traits implies that genetic improvement through selection will be slow.

Heritability (h^2), repeatability (*R*), genetic and environmental correlations of 305dFCM and body conformation traits in Jersey cattle

Traits	305Dfcm	BW	BCS	CL	CW	BD	ST	Rump	HG
305dFCM	**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*	**0.16**	0.95**	0.77**
Rump(cm)	0.01	0.05	-0.77**	0.68**	-0.25*	-0.38*	0.08	**0.04**	0.02

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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***

Table-1

Heritability (h^2), repeatability (***R***), genetic and environmental correlations of 305dFCM and udder conformation traits in Jersey cattle

Traits	305dFCM	UC	RUH	RUW	TL
305dFCM	**0.35**				
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***

Table-2

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