Genetic Parameter Estimates for Milk and Conformation Traits of Multi-genotype Cattle

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Authors' contributions

This work was carried out in collaboration between all authors. Author OMA designed the study. Author IBA performed the statistical analysis. Author AOA wrote the protocol. Author LU wrote the first draft of the manuscript. Author DSB managed the literature searches. Authors DJJ and MOB managed the analyses of the study. All authors read and approved the final manuscript.

Original Research Article

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 (Holstein and 3/4HolsteinX1/4Bunaji). Milk yield, six body traits (stature, ST; chest width, CW; body depth, BD; heart girth, HG; rump width, RW, chest ligament, CL) and four udder traits (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.

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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 a potential for improvement of economic characteristics.

1. INTRODUCTION

Breeding programs in cattle are primarily focused on milk yield. It is then evident 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 organisation of the whole genome and its connection to the expression of complex phenotypes rather than single locus traits [1]. It is synonymous with the "genotype-phenotype map" for a trait. [2] 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 modelling 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 modelling milk yield will decrease the residual variance, therefore reducing 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 [3] Although managerial factors significantly affect the level of reproductive performance achieved within a dairy herd [4,5]. The relationship between yield traits and body weight is complex and largely dependent on both the frame size of a cow and body condition score. Some studies [6,7] found an unfavourable 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 [6] 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 [8] 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 [9,10] 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 [11,12] 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 a quest for protein sufficiency. Genetic 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 in Nigeria.

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

2. MATERIALS AND METHODS

2.1 Location of the Study

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

Adamawa State: Sebore farm in Adamawa State is located at an altitude of 200 to 300 metres, between latitude $9°20'$ and $9°33'N$ and longitude $12°30'$ and $12°50'E$. It is bordered by Borno State to the North West, Gombe to the West and Taraba to the South West and has an Eastern border with Cameroun Republic. It has average daily minimum and maximum temperatures of 23.2°C and 35.2°C respectively. The average annual rainfall is 718.1 millimetres and relative humidity, 44.2%. It occupies an area of 39,742.12 square kilometres. Many rivers characterise the; the major one being the Benue whose source is from the highlands of the Cameroun and flows southwards to join the River Niger [13].

Plateau State: West Africa Milk Company Integrated Dairies Farm (WAMCOIDF) is located on the plateau at an altitude of 1280 m above sea level. The farm is situated on longitude $9°43'$ east of the Greenwich and latitude $8°45'43''$ north of the equator. The area is characterized by about seven months of rainfall beginning from April and terminating in October. The dry season occurs between November and March and rain peak with very low temperature occurs in July and August. The mean annual rainfall ranges from 1300 mm to 1500 mm. The ambient temperature ranges from 21.8°C to 22.8 °C. The harmattan usually prevails between late December and January while relative humidity is highest in August (82.28%) and lowest (43.78%) in November [13].

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 305 m. The nearest meteorological station showed maximum rainfall in the 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 [13].

2.1.1 Experimental animals

Holstein and 3/4HolsteinX1/4Bunaji cattle belonging to the 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 practising 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 original data before the statistical analyses. Also, records of cows sold for production purposes and data that were not normally distributed were excluded.

2.1.2 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 utilizing the test interval method following the computational expression below [14]

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

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.

2.1.3 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 was recorded at monthly intervals.

2.1.4 Statistical model and analysis

All herd information regarding conformation (Holstein, n=1201 and 3/4Holstein, and 1/4HosteinXBunaji, n=1604) and lactation records (Holstein, n=6605 and 3/4Holstein, and 1/4HosteinXBunaji, n=5001) were extracted from cattle management software over a period of 8 years (2008-2016). 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

Table 1. 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
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

[15]

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 [16], 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, the number of calving and the 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:

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

Considering that A = relationship matrix, $I\sigma^2 e = R$, then $V(y) = ZAZ'\sigma_a^2 + WI\sigma_{pe}^2 W' + R$. 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:

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

In which A = relationship matrix; and $a1 = \sigma_e^2 / \sigma_a^2$ and $a2 = \sigma_e^2 / \sigma_{pe}^2$. 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 and environmental correlations, a bivariate model was used which included herd, number of calving and contemporary group (which included a 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 a mean of zero and variance:

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

in which $\otimes$ = 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_{aij} = 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 the best linear unbiased prediction (BLUP) of a and ap are:

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

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

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

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.

3. RESULTS AND DISCUSSION

Table 2 shows the heritability, repeatability, genetic and environmental correlations of 305FCM and conformation traits in Holstein dairy cows. Heritability estimates for 305dFCM (44%) was high and was within the moderate to high range reported for 305d heritability estimates used by the majority of countries in their genetic evaluations [18,19] The heritability estimates of the conformation traits which varied between 0.07 (body condition score) to 0.41(bodyweight) were within the range reported in the several publications for Holstein cattle [20,5]. The positive and significant genetic correlation between 305 day fat corrected milk yield with some selected body and udder conformation traits (CL, HG, RUH, BCS, and BW) implied that taller, deeper, wider and longer cow in a positive energy balance with a longer teat length would produce more milk [13,21]. High and negative correlated estimate observed between 305 day fat corrected milk yield and udder clearance suggest that under genetic selection to improve milk yield would lead to udder that were not bulgy.

In 3/4HolsteinX1/4Bunaji cows (Table 3), the heritability of 305dFCM (h^2=30%) was similar to the estimates reported by several researchers [22,23]. This shows that 70% of the variations in the fat corrected milk yield could be attributed to management and environmental factors [24]. Heritability estimates for conformation traits ranged from 16-42% which was lower than the ranged of 19-58% reported by [7,25] in 3/4HolsteinX1/4Bunaji cows at National Animal Production Research Institute, Shika. Differences in estimates obtained may be linked to management and the estimation method used for computation of the variance component for genetic parameters (Restricted maximum

Table 2. Heritability (h^2), repeatability (w^2), genetic and environmental correlations of 305FCM and conformation traits in Holstein cows

Traits	305FCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305FCM	**0.44**	0.72**	0.44**	0.35*	0.09	0.01	0.18	0.03	0.44**	-0.47**	0.80**	-0.35*	0.32*
BW (kg)	0.25*	**0.41**	0.49**	-0.60**	0.08	0.12	0.21*	0.08	0.88**	0.63**	0.96**	0.25*	-0.88**
BCS	0.41**	-0.13	**0.07**	0.97**	0.52**	0.39*	0.47**	0.52**	0.47**	-0.39*	0.18	-0.04	0.05
CL (cm)	0.32*	0.19	0.64**	**0.12**	0.80**	0.45**	0.91**	-0.33*	0.39*	-0.93**	0.06	-0.35*	-0.64**
CW (cm)	0.05	0.49**	-0.36*	0.49**	**0.33**	-0.79**	0.88**	0.80**	0.45**	-0.54**	0.08	-0.09	-0.14
BD (cm)	-0.44**	0.39	-0.67**	-0.83**	-0.25*	**0.17**	-0.90**	0.62**	-0.30*	0.34*	0.18	-0.04	0.05
ST (cm)	0.37*	-0.03	0.82**	0.57**	-0.25*	-0.15	**0.06**	0.97**	0.83**	-0.48*	0.93**	0.70**	-0.67**
RW(cm)	0.46**	0.44**	0.63**	0.76**	0.20*	-0.96**	0.16	**0.32**	0.89**	0.93**	0.88**	0.78**	-0.63**
HG(cm)	0.51**	0.19	0.95**	0.44**	0.54**	0.12	0.24*	0.49**	**0.18**	0.99**	0.56**	0.97**	-0.81**
UC (cm)	-0.13	0.06	-0.85**	-0.32*	0.58**	0.34*	-0.79**	-0.35*	-0.15	**0.30**	-0.33*	0.95**	-0.26*
RUH(cm)	0.47**	0.30*	0.34*	0.38*	0.07	-0.19	0.60**	0.19	0.34*	-0.44**	**0.11**	0.38*	0.48**
RUW(cm)	0.19	-0.17	0.87**	0.53**	-0.35*	-0.59**	0.44**	0.52**	0.82**	-0.67**	0.02	**0.38**	0.12
TL (cm)	-0.07	-0.68*	-0.63**	0.50**	-0.04	-0.09	0.03	-0.04	0.28*	-0.24*	0.01	0.22*	**0.25**
W²	*0.61*	*0.46*	*0.11*	*0.18*	*0.35*	*0.26*	*0.08*	*0.36*	*0.22*	*0.33*	*0.15*	*0.44*	*0.28*

** = P<0.05; h^2 = Heritability estimates (along the diagonal).Genetic correlation (above diagonal) and environmental correlation (below diagonal); **W^2** – Repeatability; FCM305-Fat corrected 305day milk yield; BW-Bodyweight; BCS-Body condition score; CL-Chest ligament; CW-Chest width; BD-Body depth; HG-Heart girth; UC-Udder clearance; RUH-Rear udder height; RUW-Rear udder width; TL-Teat length; ST-Stature; RW-Rump width*

Table 3. Heritability (h^2), repeatability (w^2), genetic and environmental correlations of 305 FCM and conformation traits in Holstein x Bunaji cows

Traits	305 FCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305FCM	**0.30**	0.29*	0.48**	0.58**	-0.23*	0.50**	0.14	-0.35*	0.61**	-0.40**	0.52**	0.21*	0.13
BW (kg)	0.45**	**0.42**	0.40**	0.62**	0.49**	0.47**	0.20*	0.28*	0.22*	0.34*	-0.22*	0.47**	0.07
BCS	0.07	0.31*	**0.38**	0.49**	0.45**	0.34*	0.89**	-0.06	-0.03	-0.21*	-0.31*	-0.29*	0.56**
CL (cm)	0.43**	0.44**	0.17	**0.22**	0.57**	0.29*	0.08	0.35*	0.38*	0.38*	0.44**	0.45**	0.30*
CW (cm)	0.05	0.47**	0.42**	0.04	**0.31**	0.43**	0.15	0.19	0.21*	0.33*	0.27*	0.48**	0.61**
BD (cm)	0.31*	0.33*	0.06	0.01	0.28*	**0.37**	-0.26*	0.37*	0.08	0.28*	0.37*	-0.36*	0.20*
ST (cm)	0.14	0.25*	-0.72**	0.22*	0.03	-0.15	**0.32**	0.54**	0.05	0.77**	0.11	0.66**	0.01
Rump(cm)	0.04	0.15	-0.09	-0.07	0.22*	0.13	0.09	**0.28**	-0.29*	0.15	-0.08	0.39*	-0.33*
HG(cm)	0.42**	0.17	0.14	0.33*	0.25*	0.05	0.51**	0.33*	**0.16**	-0.31*	0.25*	-0.28*	0.46**
UC (cm)	0.30*	0.05	-0.02	0.26*	0.61**	0.11	-0.21*	-0.31*	0.05	**0.20**	0.77**	0.40**	0.38*
RUH(cm)	0.18	0.02	-0.13	0.09	0.06	0.44**	0.49**	-0.13	0.09	0.08	**0.29**	-0.11	-0.39*
RUW(cm)	0.26*	0.08	0.16	-0.22*	-0.33*	0.38*	0.28*	-0.02	-0.11	0.30*	-0.12	**0.23**	-0.55**
TL (cm)	0.01	0.13	0.26*	0.28*	-0.23*	0.23*	0.17	0.04	0.22*	0.36*	0.38*	0.50**	**0.41**
W²	*0.35*	*0.56*	*0.39*	*0.29*	*0.40*	*0.39*	*0.48*	*0.40*	*0.27*	*0.26*	*0.49*	*0.28*	*0.60*

** = P<0.05; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal); **W^2** – Repeatability*

likelihood vs Expected mean square computations). High repeatability estimate for 305 fat corrected milk yield and all the conformation traits signified that single measurement per lactation would be sufficient for each trait. The antagonistic genetic relationship between 305dFCM and CW, rump and udder clearance implied that genetic selection for 305dFCM would cause a reduction in the stability of the cow. Thus, selection for 305dFCM should be done with caution so as not to increase the risk of involuntary culling of dairy cows. Positive genetic correlation between 305dFCM yield and conformation traits implied that increase in 305dFCM would cause a corresponding increase in conformation traits under selection.

4. CONCLUSIONS

Moderate to high heritability for 305 day fat corrected milk yield 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.

ETHICAL APPROVAL

As per international standard or university standard written ethical approval has been collected and preserved by the authors.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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