

GENETIC PARAMETERS ANALYSIS OF BROWNSWISS CATTLE FOR MILK AND CONFORMATION TRAITS IN HIGH ARID CLIMATE

ABSTRACT

The aim of the current research was to estimate the genetic parameters for milk and conformation traits in Brown Swiss cattle breed. Heritability estimates was 0.22 for milk yield while body type traits ranged from 0.10 in central ligament through 0.48 in chest width. Repeatability estimates were low to high between milk yield and conformational traits. The data comprised 2,059 daily milk yield records of 404 Brown swiss cattle that calved between 2001 and 2015. The total numbers of sires, dams and animal in the pedigree file were 98, 356 and 809 respectively. Overall the heritabilities of all traits were moderate to high except body condition score and chest ligament, these indicated that most traits in this herd can be improved by selective breeding in Brownswiss cattle.

INTRODUCTION

The accurate estimation of genetic parameters for biometric traits are of importance in genetic improvement programs targeted towards economic sustainability [1]. Statistical and computational developments make it possible to separate the additive and maternal components, while determining the relationship between these two components, which is mostly negative. This is of utmost importance, since negative genetic correlations between traits would have consequences for the breeding program,

22 eventually leading to the development of specialized sire and dam lines [2]. Good estimates of variances for milk yield and
23 conformation traits in Nigeria are not available for Brown Swiss in Nigeria due to low sample size [3]. To estimate variance
24 components, use of the model for prediction, or of a similar model as used for the prediction of breeding values, seems desirable.
25 The objective of this study was to estimate genetic correlations, phenotypic correlations, heritabilities and repeatabilities for milk
26 and conformation traits of Brown Swiss cattle in Nigeria by the REML (restricted maximum likelihood) algorithm using the animal
27 model with repeated records.

28

29 **MATERIALS AND METHODS**

30 **Location of the Study**

31 This study was carried out in Sebore dairy facility in Mayo Belwa, Adamawa State.

32 **Adamawa State**

33 Sebore farm in Adamawa State is located at an altitude of 200 to 300 metres, between latitude $9^{\circ} 20'$ and $9^{\circ} 33'N$ and longitude 12°
34 $30'$ and $12^{\circ} 50' E$. It is bordered by Borno State to the North West, Gombe to the West and Taraba to the South West and has an
35 Eastern border with Cameroun Republic. It has average daily minimum and maximum temperatures of $23.2^{\circ}C$ and $35.2^{\circ}C$
36 respectively. The average annual rainfall is 718.1 millimetres and relative humidity, 44.2 %. It occupies an area of 39,742.12 square
37 kilometres. The is generally characterized by many rivers; the major one being the Benue whose source is from the highlands of
38 the Cameroun and flows southwards to join the River Niger [4].

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41 2.1.2 Milk yield

42 Milk yield was adjusted for lactation length at 305th days by multiplicative correction factors. Monthly test day milk yields of
43 individual cows were used to calculate the accumulated 305-d MY using the test interval method following the computational
44 expression below [5]

$$45 \quad MY_{305} = (P_1 X D_1) + \sum_{i=2}^k \left[\left(\frac{P_i + P_{i-1}}{2} \right) (D_i - D_{i-1}) \right] + (P_{k+1} X D_{k+1})$$

46 Where MY₃₀₅ is the milk yield of a cow adjusted to 305 d of lactation, P₁ is the milk yield of the test-day in the first month after
47 calving, D₁ 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
48 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
49 between the 305th d of lactation and the last day of the month prior to achieving 305 d of lactation.

50 2.1.3 Body weight measurement

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

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	Flexible tape

			between hips to ground	
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

[6].

53 2.1.4 Statistical model and analysis

54 All herd information regarding conformation, bodyweight or health-calving dates, cow entry/exit, were obtained from historical
55 records, notebooks and cattle management software. The data comprised 2,059 daily milk yield records of 404 Brown swiss cattle
56 that calved between 2001 and 2015. The total numbers of sires, dams and animal in the pedigree file were 98, 356 and 809
57 respectively. This information was entered, analyzed and saved using the VAMMP Software, version 1.0. Data selection was based
58 upon reliability: information whose validity could not be guaranteed was deleted from the final data set before analysis, as well as
59 extreme values that were considered physiologically abnormal or erroneously coded. Covariance components were estimated by
60 Derivative free Restricted Maximum Likelihood Method using the MTDFREML software [7], which estimates fixed and random
61 effect solutions by solving the mixed models equations. Variance components for milk and conformation were estimated through
62 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 [8] 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, $I\sigma_e^2 = R$, then $V(y) = ZAZ'\sigma_a^2 + W\sigma_{pe}^2W' + R$. V =Variance of the response y . 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 pe and a are:

$$\begin{bmatrix} b \\ a \\ pe \end{bmatrix} = \begin{bmatrix} X'X & X'Z & X'W \\ Z'X & Z'Z + A_{a1}^{-1} & Z'W \\ W'X & W'Z & W'W + I_{a2} \end{bmatrix}^{-1} \begin{bmatrix} X'y \\ Z'y \\ W'y \end{bmatrix}$$

in which A = relationship matrix; and $a_1 = \sigma_e^2 / \sigma_a^2$ and $a_2 = \sigma_e^2 / \sigma_{pe}^2$. 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 [8]:

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); 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, respectively. It is assumed that random permanent environmental, animal and error effects are independently distributed with 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; $\sigma_{a_{ii}}^2$ = animal additive genetic variance for trait i ; $\sigma_{a_{jj}}^2$ = animal additive genetic variance for trait j ; $\sigma_{a_{ij}} = \sigma_{a_{ji}}$ = animal additive genetic covariance between traits i and j ; Q_0 = variance and covariance matrix of random permanent environmental effects; $\sigma_{pe_{ii}}^2$ = permanent environmental variance for trait i ; $\sigma_{pe_{jj}}^2$ = permanent environmental variance for trait j ; $\sigma_{pe_{ij}} = \sigma_{pe_{ji}}$ = permanent environmental covariance between traits i and j ; R_0 = variance and covariance matrix of residual effects; $\sigma_{e_{ii}}^2$ = residual variance for trait i ; $\sigma_{e_{jj}}^2$ = residual variance for trait j ; and $\sigma_{e_{ij}} = \sigma_{e_{ji}}$ = 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:

$$G_0 = \begin{bmatrix} \sigma_{a_{ii}}^2 & \sigma_{a_{ij}}^2 \\ \sigma_{a_{ji}} & \sigma_{a_{jj}}^2 \end{bmatrix}, Q_0 = \begin{bmatrix} \sigma_{pe_{ii}}^2 & \sigma_{pe_{ij}}^2 \\ \sigma_{pe_{ji}} & \sigma_{pe_{jj}}^2 \end{bmatrix}, R_0 = \begin{bmatrix} \sigma_{e_{ii}}^2 & \sigma_{e_{ij}}^2 \\ \sigma_{e_{ji}} & \sigma_{e_{jj}}^2 \end{bmatrix}$$

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

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

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

$$101 \quad r_g = \frac{\sigma_{aij}}{\sqrt{\sigma_{aii}^2 \sigma_{ajj}^2}} \quad r_e = \frac{\sigma_{eij}}{\sqrt{\sigma_{eii}^2 \sigma_{ejj}^2}}$$

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

105

106 DATA ANALYSIS

107 Heritabilities and repeatabilities were estimated by univariate models and genetic and phenotypic correlations were estimated by a
108 series of pairwise bivariate models using the same term of fixed and random effects as univariate models.

109

110 3.0 RESULT AND DISCUSSION

111 Table 2 shows the descriptive statistics of milk and conformation traits of Simmental cows. The average milk yield was
112 1780.4±54.61litres. The confidence interval for bodyweight is 396.1-644.72kg with average of 580.7±22.8kg. Body condition score
113 was 3.3±0.16 on a threshold scale. Central ligament, chest width and body depth were 4.2±0.07cm, 42.2±0.04cm and 214.7±1.48
114 cm. Udder clearance, rear udder height, rear udder width and teat length were 43.8±0.64cm, 39.3±0.10cm, 12.5±0.12cm and
115 3.1±0.01 cm. The body weight of Brown swiss cattle was 580.7±22.8 kg which was within the limits of the breed's standard of 550-
116 650 kg [9]. This is indicated that Brown swiss cattle will have higher propensity for milk yield.

117

Table 2: Descriptive statistics of milk yield and conformation traits

Traits	N	Mean±SD	95%CI
Milk yield (litres)	404	1786.4±50.61	1589.1-2201.61
Body weight (kg)	404	580.7±22.8	396.1-644.72
BCS (1-5)	404	3.3±0.16	2.6-3.7
Central ligament (cm)	404	4.2±0.07	3.8-4.2
Chest width (cm)	404	42.2±0.04	39.7-47.6
Body depth(cm)	404	214.7±1.48	186.8-209.83
Stature (cm)	404	154.7±2.48	145.32-152.19
Rump width (cm)	404	12.5±0.12	8.9-14.2
Heart girth (cm)	404	233.0±1.76	200.8-269.18
Udder clearance (cm)	404	43.8±0.64	39.7-47.8
Rear Udder height	404		36.5-43.3
(cm)		39.3±0.10	
Rear Udder width	404		10.8-16.7
(cm)		12.5±0.12	
Teat length (cm)	404	3.1±0.01	2.7-3.3

SD-Standard deviation; CI-Confidence intervals

Genetic parameters of conformation traits and 305d FCM yields in Brown Swiss cows.

The estimates of heritabilities, repeatabilities, environmental and genetic correlations of the 305d FCM and conformational traits in Brown Swiss are shown in Table 3. In Brown Swiss cows, moderate heritability estimates obtained was lower than the 37 % reported by [10] in Turkey. This implied that improvement of milk yield via individual selection will be possible. The low to high heritability estimates for conformation traits implied that traits were under the influence of additive and non-additive gene action. High repeatability estimates for all the quantitative traits signifies less variability within the body and udder conformations of the

128 cows. Since the linear measurement were taken on mature milking cows, it is presumed that the bone structure of a mature cows
129 may not change significantly within lactations. This might be attributed to physiological changes that may occur during lactation,
130 indicating that high genetic merit for BCS is correlated with less severe negative energy balance [12]. The antagonistic genetic
131 correlations between 305dFCM yield and CW had also been reported by many authors [13]. This showed that genetic selection for
132 305dFCM yield alone would reduce the chest width. The positive and moderate correlations between 305dFCM yield and RUH
133 implied that increase in udder length would lead to a major increase in 305dFCM milk volume.

134 Repeatability estimates for milk production traits were lower and higher than some of the estimates in the literatures for Brown
135 Swiss [14]. The highest repeatability was obtained by lactation length, thus it is possible that it is sufficiently reliable to using
136 lactation length for early selection in Brown Swiss cows. Highest heritability for body type traits was recorded for CW (0.48) while
137 the least was CL while RUH was highest for udder traits. TL and UC had the lowest estimates (20 %) for udder conformation traits.
138 Repeatability estimates was moderate to high for udder conformation traits but low to high for body conformation traits.

139 Repeatability estimates for 305 d FCM was 37 %. The BD had the strongest and significance genetic correlation with 305 d FCM
140 yield for body type traits while RUH had similar trend for udder conformation traits. BW, BCS, ST and RW had moderate and
141 significant genetic correlations with 305d FCM yield in body type traits while UC and RUW were the only traits that revealed similar
142 trend in udder conformation traits. Strong, positive and significant genetic correlation was observed between HG and BD in body
143 type traits while TL and RUW had very strong, positive and significant genetic correlation for udder conformation traits. In this case,

cows with longer teats had genetics for wider rear udder attachment. Most of the environmental correlations between 305 d FCM and conformational were taped toward zero, with the exception of rear udder height with moderate, positive and significant correlation. Highest environmental correlation existed between BD and HG (0.81) for body type traits while UC and TL recorded the highest environmental correlation in a negative direction (-0.46).

Table 3: Heritability (h^2), repeatability (R), genetic and environmental correlations of 305d FCM and conformation traits in Brownswiss cows

Traits+	305d FCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305dFCM	0.22	0.29*	0.34*	0.18	-0.16	0.49**	0.20*	0.23*	0.11	0.26*	0.45**	0.30*	0.16
BW (kg)	-0.08	0.25	0.01	-0.24*	-0.28*	0.07	-0.11	0.39*	0.29*	0.21*	0.33*	-0.15	0.12
BCS	0.10	0.05	0.15	-0.19	0.31*	0.32*	0.34*	0.34*	0.33*	0.29*	0.10	0.62**	-0.04
CL (cm)	0.16	0.11	-0.04	0.10	0.11	0.25*	0.18	0.32*	0.44**	0.31**	0.06	-0.36*	0.32*
CW (cm)	-0.02	0.16	0.18	0.14	0.48	0.33*	0.24*	0.21	0.12	0.29*	0.47*	0.34*	0.15
BD (cm)	0.04	-0.27	-0.05	0.06	-0.04	0.29	0.35*	0.47**	0.49**	0.31**	0.42*	0.45**	0.09
ST(cm)	-0.09	0.04	-0.05	0.07	-0.03	0.38*	0.35	0.44**	0.37*	0.11	0.12	0.42**	0.19
Rump(cm)	0.02	0.10	0.32*	0.12	0.30*	0.22*	0.22*	0.37	0.46**	0.30*	0.51**	-0.32*	0.14
HG(cm)	0.17	-0.28	0.08	-0.03	-0.11	0.81**	-0.10	-0.13	0.28	0.39*	0.39*	0.10	-0.33*
UC (cm)	0.08	0.37*	0.07	0.06	0.03	-0.26*	-0.12	0.31*	-0.32*	0.20	0.35*	0.31*	0.12
RUH(cm)	0.29*	0.20	-0.02	-0.04	-0.13	-0.16	0.08	0.03	-0.33*	0.06	0.39	0.19	0.26*

RUW(cm)	0.04	-0.02	-0.10	-0.08	0.23*	-0.31*	-0.17	-0.24*	-0.22*	-0.02	0.19	0.26	0.60**
TL (cm)	-0.04	-0.40*	0.04	-0.09	-0.05	0.62**	-0.27*	-0.20*	0.78**	-0.46**	-0.33*	-0.14	0.20
R	0.37	0.50	0.18	0.26	0.61	0.35	0.44	0.46	0.43	0.49	0.45	0.38	0.34

151 * = P<0.05; h² = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation
 152 (below diagonal); d=day, FCM-Fat corrected milk yield, R= Repeatability
 153

154 **4.0 CONCLUSIONS**

155 Overall the heritabilities of all traits were moderate to high except body condition score and chest ligament, these indicated that
 156 most traits in this herd can be improved by using an appropriate mating program and genetic selection. However, breeders should
 157 take into consideration the negative genetic correlations between traits. However, the heritability estimate of milk yield is slightly
 158 moderate. The selection based on an index of milk production traits and milk yield can provide maximum genetic gain in overall
 159 productivity in these herds.

160 **ETHICAL APPROVAL**

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

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