



Analysis of Milk and Biometric Traits of Brown Swiss Cattle in High Arid Climate

**Oludayo Michael Akinsola^{1*}, Dorcas John Jirgi², Amos Adedamola Ogundeji³,
Madaki Omammeh Shuaib⁴, Adebayo Waheed Ismail⁵ and Louis Ugwu⁶**

¹*Department of Theriogenology and Production, Faculty of Veterinary Medicine, University of Jos, Nigeria.*

²*Federal Ministry of Agriculture and Rural Development, P.M.B 135, Garki, Abuja, Nigeria.*

³*Military HIV Research Program, Walter Reed Army Institute of Research-Nigeria, U.S. Embassy, Abuja, Nigeria.*

⁴*School of Environmental Studies, Department of Urban and Regional Planning, Federal Polytechnic Nasarawa, Nigeria.*

⁵*Department of Urban and Regional Planning, School of Environmental Studies, Federal Polytechnic Bida, Nigeria.*

⁶*Department of Biology, School of Science, Federal College of Education, Katsina, Nigeria.*

Authors' contributions

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

Article Information

DOI: 10.9734/CJAST/2018/42150

Editor(s):

(1) Dr. Seham Mohammed Elkassas, Department of Animal Wealth Development, Faculty of Veterinary Medicine, Kafrelsheikh University, Kafrelsheikh, Egypt.

Reviewers:

(1) Ayse Deniz Cardak, Aydin Adnan Menderes University, Turkey.

(2) D. S. Pushparani, SRM Dental College, India.

Complete Peer review History: <http://www.sciencedomain.org/review-history/25466>

Original Research Article

Received 26th April 2018

Accepted 2nd July 2018

Published 9th July 2018

ABSTRACT

The aim of the research was to estimate the genetic parameters for milk and conformation traits in Brown Swiss cattle breed. The data comprised 2,059 daily milk yield records of 404 Brown Swiss cattle that calved between 2001 and 2015. The total number of sires, dams and animal record extracted from the pedigree file were 98, 356 and 809 respectively. 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.

*Corresponding author: E-mail: dayoakinsola@gmail.com;

Repeatability estimates were low to high between milk yield and conformational traits. 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.

Keywords: Arid climate; milk; heritability estimate; Brown Swiss.

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

2. MATERIALS AND METHODS

2.1 Location of the Study

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

2.2 Adamawa State

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 $12^{\circ} 30'$ 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 Eastern border with Cameroun Republic. It has average daily minimum and maximum temperatures of $23.2^{\circ} C$ and $35.2^{\circ} C$ respectively. The average annual rainfall is 718.1 millimetres and relative humidity, 44.2%. It occupies an area of 39,742.12 square kilometres. The is generally characterized by many rivers; the major one being the Benue

whose source is from the highlands of the Cameroun and flows southwards to join the River Niger [4].

2.2.1 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 [5].

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

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 ($i = 2, \dots, k$), 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.

2.2.2 Body weight measurement

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

2.2.3 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. The data comprised 2,059 daily milk yield records of 404 Brown swiss herds that calved between 2001 and 2015. The total numbers of sires, dams and animal in the pedigree file were 98, 356 and 809 respectively. This information was entered, analysed 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 [7], which evaluates 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 modern 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 the 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 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; $\sigma_{a_{ij}}^2$ = 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 the best linear unbiased prediction (BLUP) of a and ap are:

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

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

in which $k_1 = G_0 * A^{-1}$, $\hat{b} = \begin{bmatrix} \hat{b}_1 \\ \hat{b}_2 \end{bmatrix}$, $\hat{a} = \begin{bmatrix} \hat{a}_1 \\ \hat{a}_2 \end{bmatrix}$ and $\hat{p}e = \begin{bmatrix} \hat{p}e_1 \\ \hat{p}e_2 \end{bmatrix}$

Table 1. Biometric 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 under	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

[6].

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

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

in which σ_{ajj} = 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_{eij} = environmental variance for trait j .

2.3 Data Analysis

Heritabilities and repeatabilities were estimated by univariate models and genetic and phenotypic

correlations were estimated by a series of pairwise bivariate models using the same term of fixed and random effects as univariate models.

3. RESULTS AND DISCUSSION

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

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 circumference (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 (cm)	404	39.3±0.10	36.5-43.3
Rear Udder width (cm)	404	12.5±0.12	10.8-16.7
Teat length (cm)	404	3.1±0.01	2.7-3.3

SD-Standard deviation; CI-Confidence intervals

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

* = $P < 0.05$; h^2 = Heritability estimates (along the diagonal). Genetic correlation (above diagonal) and environmental correlation (below diagonal); d=day, FCM-Fat corrected milk yield.

3.1 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 would be possible. The moderate to high heritability estimates for conformation traits suggested 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 cows. Since the linear measurement were taken on mature milking cows, it is presumed that the bone structure of mature cows may not change significantly within lactations [11]. This might be attributed to physiological changes that may occur during lactation, indicating that high genetic merit for BCS is correlated with less severe negative energy balance [12]. The antagonistic genetic correlations between 305dFCM yield and CW had also been reported by many authors [13]. This showed that genetic selection for 305dFCM yield alone would reduce the chest width. The positive and moderate correlations between 305dFCM yield and RUH implied that increase in udder length would lead to a significant increase in 305dFCM milk volume.

Repeatability estimates for milk production traits were lower and higher than some of the forecast in the kinds of literature for Brown Swiss [14]. Lactation length obtained the highest repeatability, thus it is possible that it is sufficiently reliable to using lactation length for early selection in Brown Swiss cows. Highest heritability for body type traits was recorded for CW (0.48) while the least was CL while RUH was highest for udder traits. TL and UC had the lowest estimates (20%) for udder conformation traits. Repeatability estimates were moderate to high for udder conformation traits but low to top for body conformation traits. Repeatability estimates for 305 d FCM was 37%. The BD had the strongest and significant genetic correlation with 305 d FCM yield for body type traits while RUH had similar trend for udder conformation traits. BW, BCS, ST and RW had moderate and significant genetic correlations with 305d FCM yield in body type traits while UC and RUW were

the only traits that revealed the similar trend in udder conformation traits. Energetic, confident and significant genetic correlation was observed between HG and BD in body type traits while TL and RUW had robust, confident and significant genetic association for udder conformation traits. In this case, cows with longer teats had the genetics for more extensive rear udder attachment. Most of the environmental correlations between 305 d FCM and conformational were taped toward zero, except rear udder height with moderate, positive and significant relationship. A highest ecological correlation existed between BD and HG (0.81) for body type traits while UC and TL recorded the highest ecological correlation in a negative direction (-0.46).

4. CONCLUSIONS

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

CONSENT

It is not applicable.

ETHICAL APPROVAL

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

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Akinsola. Estimation of genetic capacity of Simmental dual purpose cattle for milk and conformation traits in high arid climate. Asian Journal of Research in Animal and Veterinary Sciences. 2018; 1(2):1-8.

2. Swalve HH. Test day model in the analysis of dairy production data-a review. *Archive Tierz.* 1993;38:591-612.
3. Akinsola. Estimation of phenotypic and genetic parameters of milk yield, conformation and fertility traits in dairy cattle: A multi-genotype and multi-localational study. A PhD thesis submitted to the Department of Animal Science, Ahmadu Bello University, Zaria. 2017;280.
4. Climate-Data. *Climate-Data.org*; 2015. (Retrieved December 12, 2015) Available:<http://en.climatedata.org/location/402824>
5. Koonawootrittriron S, Elzo MA, Tumwasorn S. Multibreed genetic parameters and predicted genetic values for first lactation 305-d milk yield, fat yield, and fat percentage in a *Bos taurus*×*Bos indicus* multibreed dairy population in Thailand. *Thai Journal of Agricultural Science.* 2002;36:339–360.
6. ICAR. International committee for animal recording guidelines. Approved by the general assembly held in Koupio, Finland in June 2006; 2007.
7. Boldman KG, Kriese LA, Van Vleck LD, Van Tassell CP, Kachman SD. A manual for use of MTDFREML. A Set of programs to obtain estimates of variances and covariances [DRAFT]. USDA-ARS, Lincoln, NE, USA; 1995
8. Falconer DS, Mackay TFC. Introduction to quantitative genetics (4st ed.). Zaragoza, ES: Acribia; 2001.
9. Galip B, Kaygisiz A, Ulker H. Estimates of Genetic Parameters of Milk Yield in Brown Swiss and Holstein Friesian Cattle. *Pakistan Journal of Biological Science.* 2004;7(7):70-74.
10. Atkins G, Shannon J, Muir B. Using conformational anatomy to identify functionality and economics of dairy cows. *Advance Dairy Technology.* 2008;20:279-295.
11. Dechow CD, Rogers GW, Clay JS. Heritability and correlations among body condition score loss, body condition score, production and reproductive performance. *Journal of Dairy Science.* 2002;85:3062-3070.
12. Ojango JMK, Pollot GE. Genetics of milk yield and fertility traits in Holstein-Friesian cattle on large-scale Kenyan farms. *Journal of Dairy Science.* 2001;79:1742-1750.
13. Cassandro M, Ghiroldi S, Bagnato A, Gallo, Carnier P, Santus E. Genetic evaluation of longevity in Italian Brown Cattle *Breed Proc. Int. Workshop on EU Concerted Action Genetic Improvement of Functional Traits (GIFT) Jouy-en Josas, France.* 1999;21(73):81.
14. DeHaas Y, Hanss LLG, Kadarmideen HN. Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds *J. Anim. Breed. Genet.* 2007;124(12):19.

© 2018 Akinsola et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<http://www.sciencedomain.org/review-history/25466>