



Estimation of Genetic Capacity of Simmental Dual Purpose Cattle for Milk and Conformation Traits in High Arid Climate

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Authors' contributions

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

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ABSTRACT

The aim of the current research was to estimate the genetic parameters for milk and conformation traits in Simmental dual-purpose cattle breed. Heritability estimates were 21% for milk yield while body type traits were 26, 13, 10, 28, 20, 35, 6 and 33% for BW, BCS, CL, CW, BD, ST, rump and HG, respectively. Repeatability estimates were all moderate and high for FCM 305 day milk yields, body and udder conformational traits. The BW and HG had positive, high and significant genetic

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correlation with 305 d FCM. The genetic correlation between 305 d FCM and CL was positive, moderate and significant. The Rump and BD had the highest and significant genetic correlation between body type traits. All the udder conformation traits had positive, high and significant genetic correlation with 305 d FCM except of udder clearance. Current results suggest that selection for conformation traits will translate into increased milk in Simmental cattle.

Keywords: Simmental; genetic gain; arid climate; milk; conformation.

1. INTRODUCTION

Traditional breeding schemes are often fraught with the cost of measuring traits and maintaining accurate pedigree in developing countries like Nigeria where database for record keeping are lacking. Quantitative traits such as conformation have not been routinely measured in our farms and research institute in Nigeria. In particular, conformation traits are being selected to acclimatize livestock to unfavorable environmental conditions. Hence, they are as important as other economic traits [1]. In high-arid zones, animal economic traits are closely correlated with several traits, including body height, depth, and size; croup angle and width; and leg conditions among others. These characteristics are used as informative features that could facilitate improvement in milk yield and longevity through selective breeding [2]. The utmost genetic progress in Simmental populations in several countries was attained for milk production traits [3] though is a dual purpose breed (meat and milk). This was expected because milk production have great heritability and economical weight in total selection as compared to conformation traits. Improvement of milk production is a central goal of dairy cattle breeding systems across the world [4]. In recent times, Simmental cattle is gaining strong recognition in its milk production but, currently its productivity is declined under harsh environmental conditions because of different problems like shift of production system, genetic admixture with uncharacterized local breeds, inbreeding, absence of well-defined breeding programs, poor selection strategy and genetic gain. Therefore, the objective of this study was to estimate the genetic capacity of Simmental cattle for milk and conformation traits in high arid climate of Nigeria.

2. MATERIALS AND METHODS

2.1 Location of the Study

This study was carried out in Sebore farm in 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 [5]. 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 [6].

2.2 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 using the test interval method following the computational expression below [7]

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

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 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 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.

2.3 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 [8].

2.4 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 [7] 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 [7] 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:

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



Fig. 1. Map of Nigeria showing Adamawa state

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

[8]

Considering that $A =$ relationship matrix, $1\sigma^2e = R$, then $V(y) = ZAZ'\sigma_a^2 + W1\sigma_{pe}^2W' + R$. $V =$ 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 p_e and a are:

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

in which $A =$ relationship matrix; and $a1 = \sigma_e^2 / \sigma_a^2$ 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 [7]

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 $y =$ vector of N observations; $b =$ 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:

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

in which $\otimes =$ director 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; $\sigma_{aj}^2 =$ animal additive genetic variance for trait i ; $\sigma_{aj}^2 =$ animal additive genetic variance for trait j ; $\sigma_{aj} = \sigma_{aji} =$ animal additive genetic covariance between traits i and j ; $Q_0 =$ variance and covariance matrix of random

permanent environmental effects; σ_{peii}^2 = permanent environmental variance for trait i ; σ_{pejj}^2 = 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_{eii}^2 = residual variance for trait i ; σ_{ejj}^2 = 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:

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

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

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 $\hat{p}e = \begin{bmatrix} \hat{p}e_1 \\ \hat{p}e_2 \end{bmatrix}$

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

$$r_g = \frac{\sigma_{a_{ij}}}{\sqrt{\sigma_{a_{ii}}^2 \sigma_{a_{jj}}^2}} \quad r_e = \frac{\sigma_{e_{ij}}}{\sqrt{\sigma_{e_{ii}}^2 \sigma_{e_{jj}}^2}}$$

in which $\sigma_{a_{ij}}$ = additive genetic covariance between traits i and j ; $\sigma_{a_{ii}}^2$ = additive genetic variance for trait i ; and $\sigma_{a_{jj}}^2$ = additive genetic variance for trait j were used for genetic correlation while for environmental correlations, $\sigma_{e_{ij}}$ = environmental covariance between traits i and j ; $\sigma_{e_{ii}}^2$ = environmental variance for trait i ; and $\sigma_{e_{jj}}^2$ = environmental variance for trait j .

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 492.3-601.22 kg with average of 578.6±22.7 kg. Body condition score was 3.2±0.20 on a threshold scale. Central ligament, chest width and body depth were 4.3±0.06, 47.6±0.22 and 190.6±1.04 cm. Udder clearance, rear udder height, rear udder width and teat length were 43.7±0.71,

39.0±0.21, 15.2±0.09 and 3.8±0.03 cm. The body weight of Simmental cattle was within the limits of the breed's standard of 550-650 kg [9]; however, at the lower limit, taking into consideration that the Simmental is a dual-purpose breed, with the selection in Romania being mainly orientated for milk traits with 60%, followed by meat with 35% and fitness traits 5% [4].

Table 3 shows the heritability, repeatability, environmental and genetic correlations of the conformation type traits and fat corrected 305 day milk yield in Simmental dairy cows. Heritability estimate was 21% for fat corrected 305 day milk yield and the repeatability estimate was 27%. Heritability estimates for body type traits were 26, 13, 10, 28, 20, 35, 6 and 33% for BW, BCS, CL, CW, BD, ST, rump and HG, respectively. Repeatability estimates were all moderate and high for FCM305 day milk yields, body and udder conformational traits. Genetic correlations between body weight and milk production were moderate and negative, as a result, focusing the selection scheme on milk yield would have a reduced effect on body weight gain within a breed. This was antagonistic to the previous report by [10]. The variation in the strength of relationship could be linked to genotype x environment interactions.

Environmental and genetic correlations varied both in magnitude and directions. The BW and HG had positive, high and significant genetic correlation with 305 d FCM. The genetic correlation between 305 d FCM and CL was positive, moderate and significant. The Rump and BD had the highest and significant genetic correlation between body type traits. All the udder conformation traits had positive, high and significant genetic correlation with 305 d FCM except of udder clearance. Estimates of genetic correlations were higher than the values recorded for environmental correlations. The BD and HG had positive, strong and significant environmental correlation with 305 d FCM for body type traits while RUW and TL showed similar trend for udder conformation traits. The BW and RUH had negative, moderate and significant environmental correlation with fat corrected 305 day milk yield. The BCS, CW, rump and UC had near zero environmental correlations with fat corrected 305 day milk yield. The RUW and TL had the strongest, positive and significant environmental correlations.

Table 2. Descriptive statistics of milk yield and conformation traits

Traits	N	Mean \pm SD	95%CI
Milk yield (litres)	560	1780.4 \pm 54.61	1677.5-1980.4
Body weight (kg)	560	578.6 \pm 22.7	492.3-601.22
BCS (1-5)	560	3.2 \pm 0.20	2.9-3.8
Central ligament (cm)	560	4.3 \pm 0.06	4.1-4.6
Chest width (cm)	560	47.6 \pm 0.22	42.2-51.8
Body depth(cm)	560	190.6 \pm 1.04	180.8-201.7
Stature (cm)	560	155.5 \pm 1.86	148.75-158.92
Rump width (cm)	560	10.5 \pm 0.11	9.4-10.8
Heart girth (cm)	560	208.5 \pm 0.96	199.8-214.5
Udder clearance (cm)	560	43.7 \pm 0.71	40.1-46.2
Rear Udder height (cm)	560	39.0 \pm 0.21	37.8-42.9
Rear Udder width (cm)	560	15.2 \pm 0.09	14.4-15.9
Teat length (cm)	560	3.8 \pm 0.03	3.6-3.9

SD-Standard deviation; CI-Confidence intervals

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

Traits	305dFCM	BW	BCS	CL	CW	BD	ST	Rump	HG	UC	RUH	RUW	TL
305dFCM	0.21	0.54**	0.11	0.25*	0.11	0.61**	0.17	-0.10	0.62*	0.10	0.42*	0.60**	0.74**
BW (kg)	-0.29*	0.26	0.26*	-0.30*	0.18	0.14	0.48**	0.45**	0.41**	0.18	0.29*	0.50*	0.61**
BCS	0.02	-0.15	0.13	0.16	0.14	0.40**	0.49**	0.19	0.38*	0.73**	0.06	0.27*	0.11
CL (cm)	0.17	0.20*	-0.08	0.10	0.25*	0.17	0.25*	0.13	0.22*	0.74**	0.12	0.38*	0.58**
CW (cm)	0.04	-0.11	0.31*	-0.30*	0.28	0.10	0.18	0.45**	0.56**	0.67**	-0.22*	-0.31*	0.19
BD (cm)	0.45**	0.09	-0.23*	-0.08	-0.17	0.20	0.63**	0.94**	0.23*	0.18	0.95**	0.91**	0.37*
ST(cm)	-0.06	0.06	-0.09	-0.12	-0.03	0.44**	0.35	0.20*	0.15	-0.10	0.16	0.20*	0.38*
Rump(cm)	0.03	-0.34*	0.07	0.10	-0.08	0.85**	-0.17	0.06	0.18	0.33*	0.29*	0.10	0.29**
HG(cm)	0.53**	-0.38*	-0.15	0.05	-0.14	-0.13	-0.14	-0.12	0.33	-0.40**	-0.15	0.91**	0.90**
UC (cm)	0.04	-0.05	0.02	0.16	0.07	-0.15	0.07	0.15	-0.20*	0.31	-0.30*	0.15	0.25*
RUH(cm)	-0.33*	0.05	-0.01	-0.15	-0.03	0.91**	-0.03	0.26*	-0.05	-0.18	0.20	-0.23*	0.49**
RUW(cm)	0.54**	-0.43**	-0.26*	-0.04	-0.13	0.88**	-0.13	-0.05	0.89**	-0.11	-0.15	0.18	-0.10
TL (cm)	0.46**	-0.42**	-0.24*	-0.02	-0.10	-0.30*	-0.10	-0.06	0.86**	-0.10	-0.12	0.96**	0.59
W^2	0.27	0.43	0.20	0.20	0.62	0.35	0.70	0.07	0.38	0.35	0.28	0.52	0.64

* = $P < 0.05$; ** = $p < 0.01$; NS = Not Significant, h^2 = Heritability estimates (between the diagonal). Genetic correlation above and environmental correlation below the diagonal
 W^2 – Repeatability, 305d FCM-305 day fat corrected milk yield

Lastly, moderate heritability estimates of 21% for milk yield was lower than 49% reported by [6] in Simmental cows from Serbia. However, it was lower when compared to the results reported by [11] but significantly higher than the results established by [12]. The heritability values were relatively moderate which can be explained to some extent through moderate variation within the group of daughters of one bull-sire and between groups of bulls. Heritability estimates range of 6% in rump and 59% in teat length was higher than the values used in October national evaluation of breeding values for classified conformation traits [13,14]. In this study, better estimates of heritability were obtained using continuous linear body measurement rather than the scale classification system. The low repeatability estimates obtained in this study suggested that rump was strongly influenced by temporary environmental effects. The antagonistic genetic relationship between 305dFCM yield and rump implied that genetic improvement of milk volume would lead to extreme sloped rump. Cows with extreme slope to the hock or are awkward in their hind leg movement which might lead to high risk of calving difficulty and reduced longevity. The positive genetic correlation between 305dFCM yield and the other body and udder conformation traits could be due to pleiotropic effects. The negative correlation between 305dFCM yield with BW, ST and RUH was an indication that selection to increase 305dFCM yield would lead to a decreased body size and length of udder in Simmental cows.

4. CONCLUSIONS

Milk yield and some selected conformation traits of Simmental cattle in high arid climate were moderately heritable and reliable, although this could be improved in the future with the collection of big data records. The majority of the correlations estimated between milk yield and conformation traits were positive; therefore, future breeding programs for milk improvement would benefit from including these traits to ensure that selection for increased productivity is not accompanied by the unwanted deterioration of functional fitness.

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.

REFERENCES

1. Wu X, Fang M, Liu L, Wang S, et al. Genome wide association studies for body conformation traits in the Chinese Holstein cattle population. *BMC Genomics*. 2013;14:897. Available:<http://dx.doi.org/10.1186/1471-2164-14-897>
2. Avendaño-Reyes L, Álvarez-Valenzuela FD, Correa-Calderón A, Algándar-Sandoval A, et al. Comparison of three cooling management systems to reduce heat stress in lactating Holstein cows during hot and dry ambient conditions. *Livest. Sci*. 2010;132:48-52. Available:<http://dx.doi.org/10.1016/j.livsci.2010.04.020>
3. Egger-Danner C, et al. Registration of direct health traits in Austria – Experience review with emphasis on aspects of availability for breeding purposes. Manuscript in preparation; 2011.
4. Perisic P, Skalicki Z, Petrovic MM, Bogdanovic VD. Ruzic-muslic simmental cattle breed in different production systems, *Biotechnol. Anim. Husb.* 2009; 25(5-6):315-326.
5. Climate-Data. *Climate-Data.org*; 2015. (Retrieved December 12, 2015) Available:<http://en.climate-data.org/location/402824>
6. Vlada P, Sretenovic OD, Snezana T, Milan M, Petrovic SA, Dragana RM. Heritability and genetic correlation of production and reproduction traits of Simmental cows. *African Journal of Biotechnology*. 2011; 10(36):7117-7121.
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. ICAR. International committee for animal recording guidelines. Approved by the general assembly held in Koupio, Finland in June 2006; 2007.
9. Acatincai S. Acatincai tehnologia cresterii bovinelor agroprint. Timisoara, Romania. 2010;167-170.
10. Berry DP, Buckley F, Dillon P, Evans RD, Rath M, Veerkamp RF. Genetic

- relationships among body condition score, body weight, milk yield and fertility in dairy cows. *Journal of Dairy Science*. 2003;86: 2193–2204.
11. König S, Chang YM, Borstel UUv, Gianola D, Simianer H. Genetic and phenotypic relationships among milk urea nitrogen, fertility, and milk yield in Holstein cows. *J. Dairy Science*. 2008;91:4372–4382.
 12. Silvestre AM, Petim-Batista F, Colaco J. Genetic parameter estimates of Portuguese dairy cows for milk, fat and protein using a spline test-day model. *Journal of Dairy Science*. 2005;88(3): 1225-1230.
 13. Center za strokovno delo. Redni obračun PV za Oceno telet; 2011. Available:http://www.bfro-uni-lj.si/zoo/org/centre/gov/zunanjost/oct/1102/_main.html
 14. 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.

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