



Genetic Analysis of Milk and Health Traits in Divergently Classified Holstein Friesian Cows

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Authors' contributions

This work was carried out in collaboration among all authors. Author OTO managed the data cleaning. Author ORO designed the study. Author OMA performed the statistical analysis. Author SIO wrote the protocol. Author AOG wrote the first draft of the manuscript. Author MN managed the literature searches. Author IBA managed the analyses of the study. Author AO managed the data collection. All authors read and approved the final manuscript.

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ABSTRACT

Genetic parameters for milk and health related traits in low and high milk producing Holstein Friesian cows were estimated using farm collected information on the Jos, Plateau, Nigeria. Milk yield and health related records were extracted from database of the West Africa Milk Company Integrated Dairies Limited. An innovative statistical modeling in this study was the application of repeatability animal models to estimate the genetic parameters. The resulting dataset consisted of

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5043 lactations from 608 dams and 39 sires. Genetic correlations were obtained by bivariate analyses of all pair-wise combinations between two traits. In high milk yield Holstein, heritabilities estimate recorded for milk yield (0.43), mastitis (0.26) and lameness (0.33) was high while NIS (0.56), PR (0.22), RR (0.67) and PR (0.22) recorded high estimate in low milk yield Holstein cows. Highest genetic correlation was observed between rectal temperature and vaginal temperature (0.91). Lameness had significant ($p < 0.05$), positive and highest environmental correlation with mastitis (0.95). The heritability estimates of health related traits were low to high; therefore, genetic gain through direct selection alone would be slow, yet still positive and cumulative in the divergently classified Holstein Friesian cows on the Plateau.

Keywords: Repeatability animal models; mastitis; lameness; respiratory rate; milk yield.

1. INTRODUCTION

Heat stress (HS) is of significant importance in global studies as it relates to animal production due to increasing number of hot days and mean earth temperatures of 1.5°C in Africa [1]. These climatic changes are forecasted to influence dairy production systems in numerous ways, ranging from fodder properties to breeding/genetic priorities. Cattle as homeothermic animals, require to keep their core body temperature in a relatively steady state, when the external temperature changes. The antagonistic genetic association between milk production traits and cattle resistance to heat stress had resulted in the impairment of cattle immune system due to quest to improve milk yield by geneticist/breeders. The genetic background is a key factor to infer antagonistic effects of heat stress on cattle vitality. In lactating and non-lactating cattle, the genetic components of heat stress have been extensively studied including production, health and welfare traits [2]. Moreover, genetic parameters of heat stress were also discussed for health and physiological traits of dairy cattle in US [2] and Spain [2].

Buch et al. [3] estimated genetic parameters for mastitis and lameness in Holstein–Friesians in the United Kingdom; however, until recent years sufficient data were lacking. Different results on genetic scales for identical traits recorded in different climatic zones furthermore address the topic of genotype by environment (GxE) interactions [4]. Physiological traits including rectal temperature (RT), skin temperature (ST), vaginal temperature (VT), respiration rate (RR), and pulse rate (PR), were already used as an indicator for HS in studies addressing feeding strategies and feeding efficiency [5]. Most of these studies also analyzed associations between physiological traits with production, health and animal welfare. Hence, these physiological traits play an important role in

thermoregulation in mammalian, but their genetic background and their value for genetic selection towards improved heat stress resistance is widely unknown. Studies proved that regulation of body temperature in dairy cattle is heritable [6], with moderate heritability (0.17) for rectal temperature during heat stress [6].

Genetic parameter estimation for physiological and health traits only considered one single record per animal [7]. However, physiological traits showed substantial fluctuations on phenotypic scales with an animals aging, and with environmental changes [7]. Hence, it might be imperative also for genetic studies to consider repeated measurements for physiological and health traits via a longitudinal data structure. Therefore, this study is designed to explore the genetic background of milk and health related traits in low and high yield Holstein cows reared under harsh environmental conditions in warm and temperate climate of Jos Plateau State, Nigeria.

2. MATERIALS AND METHODS

2.1 Location of the Study

This study was carried out in West Africa Milk Company Integrated Dairies Limited (WAMCOIDL). West Africa Milk Company Integrated Dairies Limited (WAMCOIDL) is located on the Plateau at an altitude of 1,280 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 through 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.

2.2 Data Recording

Data on the first six lactations were used from Holstein–Friesian dairy cattle across different herds. Dataset extracted consisted of 5043 lactations from 608 dams and 39 sires Holstein Friesian sires. Data were used from cows that had 100% Holstein–Friesian genes born from 1996 to 2016. The first daughters born of a bull were selected to ensure that the first crop daughters of proven bulls were used in the analysis. This implies that the data are not dominated by daughters of a few widely used proven bulls, which will tend alter the genetic variance. The recording of health events used in this study was undertaken by farmers on a voluntary basis as part of routine milk recording and the data were made available by Integrated Dairies Limited.

2.3 Divergent Classification of Milk Yield

Animals with daily average milk production less than 10 kg were classified as low milk yield Holstein Friesian cows while those that produce above 10 kg were classified as high milk yield Holstein Friesian cows. The milk yield was measured in kilograms over a lactation period of 305 days.

2.4 Data Collection on Health Related/ Vital Traits Records

Health data consisted of the health event code (e.g. mastitis) and the health event/treatment date for the affected animal. A health event (either mastitis or lameness in this study) was taken as an event or treatment taking place from 0 to 305 days from calving.

Mastitis and lameness were each defined as two separate traits for analysis. Mastitis (MAS) and lameness (LAM) were treated as a binary trait; thus, affected animals were classed as 1 and non-affected animals were classed as 0. Repeated events within the same lactation were not considered, that is, one record per cow per lactation.

Physiological traits such as rectal temperature (RT), vaginal temperature (VT), respiration rate (RR), and pulse rate (PR) are widely used as indicators for on the spot assessment of health

status in dairy cattle. A digital veterinary thermometer (Scala SC 12) was used to measure RT and VT by inserting the thermometer into the rectum and into the vagina, respectively.

Pulse rate and respiratory rate were recorded during a time period of 30 seconds with a stopwatch, and converted to a per minute basis.

Pulse rate was defined as the number of beats per minute, and manual determined by pressing hand fingertips at the caudal artery.

Respiration rate was defined as the number of flank movements per minute. It was expressed in breaths per minutes.

2.5 Statistical Model and Analysis

All herd information regarding 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, which estimates fixed and random effect solutions by solving the mixed models equations. Data across different farms were pooled together to have larger sample size for genetic analysis. 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 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 [8]:

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

Considering that A = relationship matrix, $I\sigma_e^2 = R$, then $V(y) = ZAZ'\sigma_a^2 + W\sigma_{pe}^2W' + R$. 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 $a_1 = \sigma_e^2 / \sigma_a^2$ 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]:

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

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

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

in which y_i = vector of N observations; b_i = vector of fixed effects (herd, number of calving, contemporary group); 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; σ_{aij}^2 = animal additive genetic variance for trait i ; σ_{ajj}^2 = animal additive genetic variance for trait j ; σ_{aij} = 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 pe are:

$$G_0 = \begin{bmatrix} \sigma_{a11}^2 & \sigma_{a12}^2 \\ \sigma_{a21}^2 & \sigma_{a22}^2 \end{bmatrix}, Q_0 = \begin{bmatrix} \sigma_{pe11}^2 & \sigma_{pe12} \\ \sigma_{pe21} & \sigma_{pe22}^2 \end{bmatrix}, R_0 = \begin{bmatrix} \sigma_{e11}^2 & \sigma_{e12} \\ \sigma_{e21} & \sigma_{e22}^2 \end{bmatrix}$$

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

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 $\hat{pe} = \begin{bmatrix} \hat{pe}_1 \\ \hat{pe}_2 \end{bmatrix}$

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

$$r_g = \frac{\sigma_{aij}}{\sqrt{\sigma_{a11}^2 \sigma_{a22}^2}} \quad r_e = \frac{\sigma_{eij}}{\sqrt{\sigma_{e11}^2 \sigma_{e22}^2}}$$

in which σ_{aij} = additive genetic covariance between traits i and j ; σ_{a11}^2 = additive genetic variance for trait i ; and σ_{a22}^2 = 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_{e11}^2 = environmental variance for trait i ; and σ_{e22}^2 = environmental variance for trait j .

3. RESULTS AND DISCUSSION

The descriptive statistics of milk yield, number of insemination, mastitis, lameness, rectal temperature, vaginal temperature, pulse rate and respiratory rate are presented in Table 1. There were significant differences ($P < 0.05$) in milk

yield, number of insemination per service and rectal temperature between high and low yield Holstein cattle. High yield Holstein cattle had significantly ($P<0.05$) higher milk yield and increase number of insemination per service. Low yield Holstein cattle had significantly ($P<0.05$) higher rectal temperature than High yield Holstein cattle. The coefficient of variation ranged from 10.31 (Mastitis) - 46.30 (Respiratory rate).

High heritabilities estimate was recorded for milk yield (0.43), mastitis (0.26) and lameness (0.33) (Table 2). Low heritability estimates was recorded in NIS (0.11), RT (0.14), VT (0.10), PR (0.18) and RR (0.06). Milk yield was negative, significant and had moderate environmental correlations with rectal temperature (-0.23). LAM, RT and RR were positive, significant and had moderate environmental correlations with NIS, though high and positive (0.43) association was recorded with NIS. Mastitis was negative, significant and had moderate environmental correlations with pulse rate. LAM was positive, significant and had moderate environmental correlations with rectal temperature. VT LAM was positive, significant and had high environmental correlations with rectal temperature (0.74). Milk yield had moderate, significant and positive genetic correlations with vagina (0.26) and rectal temperature (0.30). Highest genetic correlations was observed between MAS and PR (0.55) while NIS and LAM had the least genetic correlations (0.02).

High heritabilities estimate was recorded for NIS (0.56), PR (0.22), RR (0.67) and PR (0.22) in low milk yield Holstein cows (Table 3). Low heritability estimates was recorded in MY (0.04), NIS (0.13), MAS (0.05), LAM (0.16), RT (0.10) and VT (0.12). Milk yield was positive, moderate

(0.20) and significant ($p<0.05$) genetic correlations lameness and strongly associated with respiratory rate (0.45). Highest genetic correlation was observed between rectal temperature and vaginal temperature (0.91). Lameness had significant, positive and highest environmental correlation with mastitis (0.95).

The heritability estimates for mastitis were in the range reported in literature using a linear model [9] Heritability estimates were slightly higher using a multivariate model compared with a univariate model. In similar studies, the heritability estimates for lameness, using linear models, have been reported as low (1% to 2%; [10]). In general, low heritability is common for functional traits, such as vital traits. The low heritability estimates for cows with high and low milk yield can be explained by large environmental influences and as their classification as a qualitative trait, which results in a low variation among cows. The large environmental influences suggest that some improvements could be made by changes in herd management. The relationship between milk production and mastitis leads to a greater propensity to predict future costs associated with mastitis. Heritability estimates for RT (0.151) and RR (0.766) were also within the range compared to results from our study in high and low milk yield Holstein Friesian cows. The highest heritability was found for respiratory rate (0.67) in low milk yield Holstein-Friesian cows. This trait is quite simple to measure, without requiring installation of any recording technique. Traits with the highest heritability, i.e. RR, RT and PR, are already routinely recorded in large-scale dairy herds during the first week after calving to detect diseases and stress symptoms early in lactation. Genetic correlations between mastitis and lameness traits were positive in high yield

Table 1. Descriptive statistics of milk and health related traits in low and high yield Holstein cattle

Traits	LYH	HYH	CV
MY	1650.8±25.59 ^b	4840.0±74.92 ^a	16.82
NIS	2.2±0.08 ^b	2.9±0.09 ^a	27.37
MAS	0.22±0.06	0.28±0.02	10.31
LAM	0.31±0.12	0.39±0.07	22.72
RT	38.95±0.07 ^a	38.08±0.03 ^b	11.86
VT	39.88±0.19	39.01±0.36	37.86
PR	35.50±0.19	35.93±0.10	23.10
RR	77.04±0.21	77.65±0.17	46.30

^{ab}Means in the same trait between locations with different superscripts differ significantly ($P<0.05$). HYH-High Yielding Holstein, LYH-Low Yielding Holstein, CV-Coefficient of variation, MY-Milk yield, NIS-Number of Insemination, MAS-Mastitis, LAM-Lameness, RT-Rectal temperature, VT-Vaginal temperature, PR-Pulse rate, RR-Respiratory rate

Table 2. Estimates with standard errors (in parenthesis) from bivariate analyses with heritability (on diagonal), genetic correlations (below the diagonal) and environmental correlations (above the diagonal) using a repeatability model in high yield Holstein cows

Traits	MY	NIS	MAS	LAM	RT	VT	PR	RR
MY	0.43(0.11)	-0.07	0.16	0.02	-0.23*	0.11	0.19	-0.15
NIS	-0.15	0.11(0.03)	0.13	0.11	0.26*	0.43**	-0.17	0.23*
MAS	0.13	0.17	0.21(0.04)	0.08	0.09	0.10	-0.28*	0.05
LAM	0.05	0.02	0.17	0.13(0.05)	0.22*	0.17	0.13	0.11
RT	0.11	0.21*	-0.32*	0.09	0.14(0.04)	0.74*	0.05	0.04
VT	0.26*	0.18	0.30*	-0.02	-0.13	0.10(0.03)	0.03	0.09
PR	-0.10	0.31*	0.25*	-0.13	-0.02	0.07	0.18(0.05)	-0.11
RR	0.30*	0.05	-0.02	0.26*	0.04	0.03	0.15	0.06(0.02)

MY-Milk yield, NIS-Number of Insemination, MAS-Mastitis, LAM-Lameness, RT-Rectal temperature, VT-Vaginal temperature, PR-Pulse rate, RR-Respiratory rate. * = $p < 0.05$

Table 3. Estimates with standard errors (in parenthesis) from bivariate analyses with heritability (on diagonal), genetic correlations (below the diagonal) and environmental correlations (above the diagonal) using a repeatability model in low yield Holstein cows

Traits	MY	NIS	MAS	LAM	RT	VT	PR	RR
MY	0.17(0.04)	0.22*	0.56**	0.12	0.38*	0.13	0.22*	0.74**
NIS	0.05	0.56(0.13)	0.67**	-0.22*	-0.31*	0.45**	0.56**	0.83**
MAS	0.09	0.23*	0.18(0.01)	0.95**	0.91**	0.94**	0.23*	0.18
LAM	0.20*	0.15	-0.10	0.16(0.03)	0.20*	0.20*	0.15	-0.10
RT	0.06	0.18	0.33*	0.29*	0.10(0.01)	0.06	0.18	0.33*
VT	-0.12	0.33*	-0.40**	-0.15	0.91**	0.12(0.02)	0.33	-0.40**
PR	0.13	0.22*	0.74**	0.12	0.38*	0.13	0.22(0.07)	0.74**
RR	0.45**	0.56**	0.67**	-0.22*	-0.31*	0.45**	0.56**	0.67(0.11)

MY-Milk yield, NIS-Number of Insemination, MAS-Mastitis, LAM-Lameness, RT-Rectal temperature, VT-Vaginal temperature, PR-Pulse rate, RR-Respiratory rate. * = $p < 0.05$

cows, which suggest that animals that are genetically prone to mastitis are also more prone to lameness but a converse pattern was recorded in low yield cows. The economics, behind it is that for a low milk yield cows, improvement in one mastitis through selection may lead to decrease in lameness. Laursen et al. [12] reported moderate genetic correlations between mastitis with hoof diseases, sole ulcer and solehaemorrhage, in first-parity Swedish Red cows, which were 0.32 and 0.35, respectively, which were similar to estimates in this study (0.36 to 0.38). Onyiro and Brotherstone [13] suggested that a compact mammary system was well correlated with better locomotion, whereas cows with pendulous udders were more likely to suffer from lameness. The association between health and milk yield is well documented in the literature for both mastitis and lameness [14] for high and low milk producing cattle. Genetic correlations between both health traits (mastitis and lameness) with milk yield were all positive in low and high milk yield cows, indicating that animals genetically below and above average for yield traits will have high likelihood to have mastitis and lameness.

A high milk yield is predisposing to mastitis or lameness, although a case of either of these will decrease the yields for the remainder of the lactation [14] and particularly mastitis will affect milk yields of subsequent lactations because of impaired or destroyed secretory tissues of the udder [15]. Thus, the advantage of cows with higher yields is lost, or to benefit from much higher yields better management is required.

4. CONCLUSIONS

The high yield Holstein Friesian cows had high heritabilities for milk yield and mastitis indicating that selection for these traits would be expected to make reasonable progress. Genetic correlations between MY and VT and between MY and RR were low and positive. These genetic correlations indicated that progress for MY, VT and RR could be achieved by selecting for these traits directly. The low yield Holstein Friesian cows had high heritabilities for number of inseminations, pregnancy rate and respiratory rate. The genetic parameters estimated showed variations and it may be feasible to improve fertility, heat stress resistance and milk yield to help farmers optimize dairy improvement and mating programs.

ETHICAL APPROVAL

As per international standard informed written ethical approval has been collected and preserved by the author(s).

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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