



## **Analysis of Milk and Fertility Traits in Holstein Friesian Cattle on the Plateau, Jos Nigeria**

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### **Authors' contributions**

*This work was carried out in collaboration among all authors. Author ORO designed the study. Author OMA performed the statistical analysis. Author SIO wrote the protocol. Author SDO clean the data. Author MN wrote the first draft of the manuscript. Author LU managed the literature searches. Author OH managed the data extraction. Author IBA managed the data collection. All authors read and approved the final manuscript.*

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### **ABSTRACT**

The data set for the estimation of genetic parameters for milk and fertility traits of 650 cows calved between 1992 and 2015 was obtained from the database of Integrated Dairies Limited, Jos, Nigeria. The analytical model included the effects of herd-year-season, sire, cow and residual effects. Sire, cow, and residual effects were random while all other effects were fixed. Heritability estimates for calving interval (CI), conception rate (CR), number of services per conception (NSC) and no return rate at 56 days (NRR56 days) were low and ranged between 0.028 (CR) and 0.166 (NSC) in the

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third parity. Milk yield had high heritability and repeatability estimates across parities. The coefficient of variation was highly variable and ranged from 14.86-43.67%. Thus, there was no indication of an adverse genetic relationship between fertility and milk production in this population and overall genetic parameters imply a good practical management on the Plateau will be essential for improving milk without deteriorating the efficiency of fertility traits in Holstein Friesian cattle.

*Keywords: Milk traits; fertility traits; calved; dairy cattle.*

## 1. INTRODUCTION

Fertility is one of the non-yield traits of great economic importance in dairy herds. The quest to profiteer by improving milk yield over the last decades through the use of selective breeding and omics technology by dairy scientist had been a source of concern due to its snowballing effect on fertility traits. The genetic gain in milk production per cow on daily basis had extended fertility traits by 1% increment [1]. In Italy, the genetic gain in milk yield per cow on yearly basis is 112 kg in Holstein-Friesian with an extension in calving interval by 1.4 day per year [2]. Despite the huge variations in breeding practice across the countries under diverse production systems and divergent climatic conditions, all had synergistic effect on the extension of fertility traits [2]. This lack of a unique measure of fertility is due to the diverse type of information available to assess the reproductive success [3]. If results of artificial inseminations in each insemination cycle are available, traits such as days open (DO), interval from calving to first insemination, number of inseminations per conception, the interval between first and last insemination or conception rate have been used. When information of result of inseminations is not available, calving interval (or an approximate measure of days open obtained from calving interval and average pregnancy duration in the population) provide a measure of the overall reproductive efficiency in each parity and it is widely used because it can be easily obtained from milk recording schemes [4]. However, this measure is highly influenced by farmer interventions (mainly, voluntary waiting period) and by problems regarding to the low quality of fertility measurements such as censored records [5]. Therefore, a wide number of statistical models have been used in the genetic evaluations of fertility traits with no clear consensus as to what approach is best for each trait. One of the features shared by most fertility traits is that several measures are available along the cows productive life. Treatment of longitudinal traits in animal breeding has followed several approaches from the simplest repeatability model [3] to the most complex

multiple trait models [6]. Other studies have found evidence of differences in patterns of response to fertility traits along parities [7] in some fertility traits. However, none of the previous studies have dealt with the combined selection for fertility level and fertility persistency along lactation. In this study, relationships between fertility traits in different parities were quantified. Attention was paid to the effect of selection on the estimates of genetic parameters for milk and fertility traits.

## 2. MATERIALS AND METHODS

The Jos Plateau is a plateau located near the centre of Nigeria. It covers 8600 km<sup>2</sup> and is bounded by 300-600 m escarpments around much of its circumference. With an average altitude of 1280 m, it is the largest area over 1000 m in Nigeria, with a high point of 1829 m, in the Shere Hills.

A total of 4405 records from 650 cows collected from parity 1 to 3 during the period 1992 to 2015 were used in this study sired by 55 bulls on the Jos Plateau.

Milk yield was adjusted for lactation length at 305<sup>th</sup> days by multiplicative correction factors

$$\text{Fat corrected milk (FCM)} = [(0.4 * \text{milk yield (kg)} + [(15 * \text{fat yield (kg)})] [8].$$

Fertility traits were computed using fertility chart which was then preprocessed in VAMMP dairy management software interface. The traits were:

Calving Interval (CI) was defined as the period (in days) between the first and the next calving.

Number of service per conception (NSC) was defined as the number of service or matings to effect a pregnancy.

Conception rate was calculated by dividing the number of pregnant cows by the total number of inseminations.

Variance components for milk and fertility 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 and year of calving.

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  $V(y) = ZAZ'\sigma_a^2 + W\sigma_{pe}^2W' + R$ .

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 Ghiasi et al. [9]:

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

$$W^2 = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

To estimate genetic and environmental correlations, a multi-trait animal model was used which included herd, number of calving and contemporary group (which included year of calving) as the fixed effects, and the permanent environmental and additive genetic direct effects as random [10]. 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);  $pe_i$  = 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;  $\sigma_{aji}^2$  = animal additive genetic variance for trait  $i$ ;  $\sigma_{ajj}^2$  = animal additive genetic variance for trait  $j$ ;  $\sigma_{ajj} = \sigma_{aji}$  = animal additive genetic covariance between traits  $i$  and  $j$ ;  $Q_0$  = variance and covariance matrix of random permanent environmental effects;  $\sigma_{peii}^2$  = permanent environmental variance for trait  $i$ ;  $\sigma_{pejj}^2$  = 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;  $\sigma_{eij}^2$  = residual variance for trait  $i$ ;  $\sigma_{eij}^2$  = residual variance for trait  $j$ ; and  $\sigma_{eij} = \sigma_{eji}$  = residual covariance between traits  $i$  and  $j$  [11].

### 3. RESULTS

Table 1 shows the least squares means for milk and fertility traits at different parities. Milk yield and calving intervals differs significantly ( $p < 0.05$ ) between parities. The coefficient of variation was highly variable, which ranged from 14.86-43.67%. The phenotypic mean of milk yield and calving interval linearly increased at consecutive parities and this change only was statistically significant ( $p < 0.01$ ) between parities. An increasing trend for milk yield and calving interval has also been found in other studies [1,7]. The descriptive statistics for calving interval indicate that cows in earlier parities had more chances for good fertility performance than cows in later parities. The number of records decreased from parity 1 to 3 due to voluntary and involuntary culling of cows. This may reflect differences in management conditions for varied values reported at different parities.

Table 2 shows the genetic and environmental correlations for milk yield and fertility traits at different parities in Holstein Friesian cattle in the study area. This value (+0.40) is the genetic correlation value between calving rate (CR) and milk yield (MY) while +0.34 is the genetic correlation value between NRR56days and calving interval (CI) in parity 1. No significant genetic and phenotypic correlations were found between herd fertility and milk yield in the second parity. Milk yield showed significant genetic correlation between calving interval and number of services per conception in the third parity. Significant phenotypic positive correlation was found between milk yield and number of services per conception (+0.28). The highest negative

correlation was found between calving rate and non return rate at 56 days (-0.72) in parity 3.

Figs. 1, 2 and 3 shows the permanent environmental effect, heritability and repeatability for milk yield and herd fertility variable. The permanent environmental effect, heritability and repeatability had the highest values for milk yield in the second parity as compared to first and third parity.

#### 4. DISCUSSION

Genetic values for herd fertility variables were non linear and low from the first to the third parity. The changes were primarily due to the

**Table 1. Least squares means of milk and fertility traits at different parities**

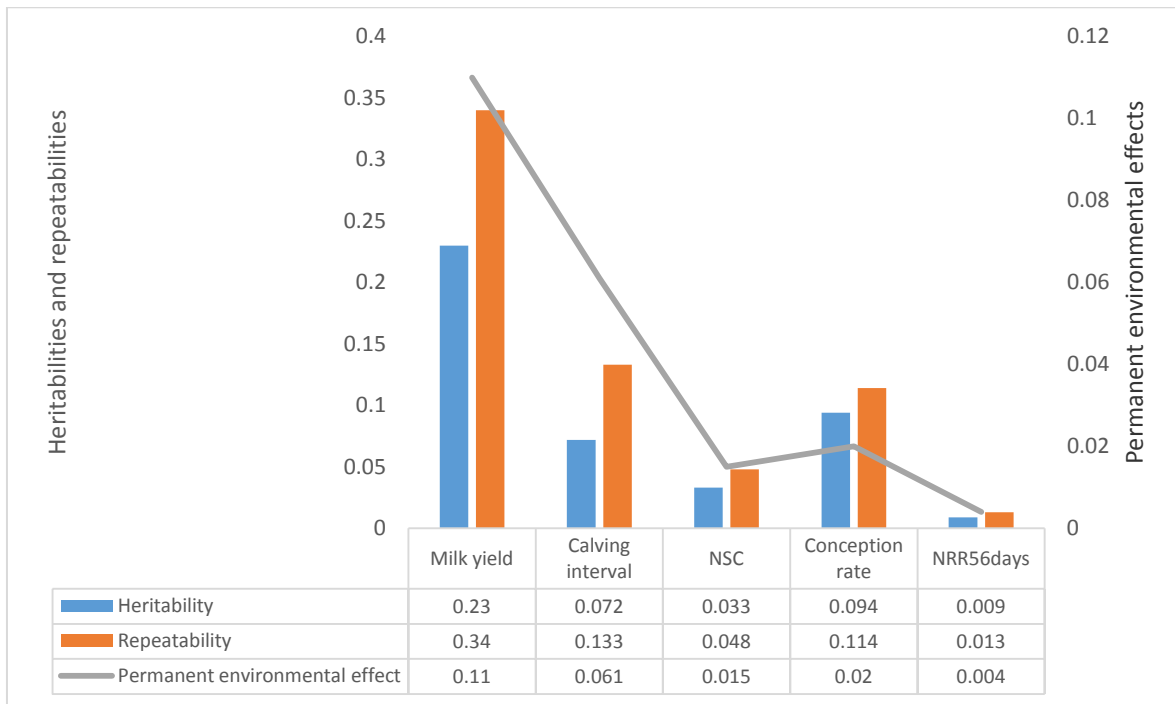
Parameters	Parities			CV
	1	2	3	
No of records	4500	2899	2006	
Milk yield (kg)	876.11(87.23) <sup>c</sup>	1288 (77.29) <sup>b</sup>	1602 (120.50) <sup>a</sup>	14.86
Calving interval (days)	138 (26.4) <sup>b</sup>	129 (22.4) <sup>a</sup>	128 (21.1) <sup>a</sup>	16.44
Number of services per conception	2.07	2.10	2.00	43.67
Conception rate	59.4	55.0	54.6	32.01
No return rate at 56 days	80.1	77.5	74.0	40.12

CV-Coefficient of variation; <sup>abc</sup>Means with different superscript are significantly different ( $P<0.05$ ); standard deviation is given in brackets

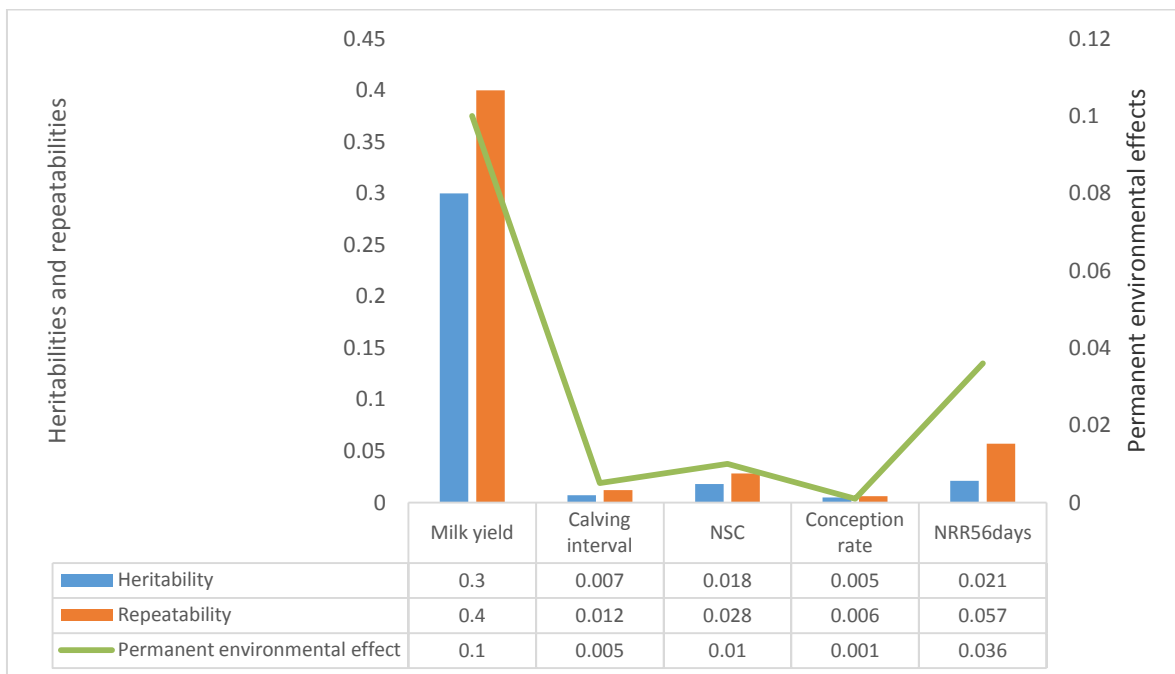
**Table 2. Genetic correlations (above diagonal) and environmental correlations (Below diagonal) for milk yield and herd fertility traits in Holstein Friesian cattle at different parities**

Traits	MY	Parity 1			NRR56days
		CI	NSC	CR	
MY	1	-0.19	0.08	0.40	0.09
CI	0.13	1	0.04	0.18	0.34
NSC	0.02	0.19	1	0.19	-0.13
CR	0.45	0.14	-0.12	1	0.10
NRR56days	-0.09	0.08	0.05	-0.10	1
<b>Parity 2</b>					
MY	1	-0.12	0.03	0.04	0.08
CI	0.19	1	0.19	0.10	0.12
NSC	0.03	0.12	1	0.03	-0.02
CR	0.04	0.18	-0.10	1	0.16
NRR56days	-0.08	0.15	0.03	0.05	1
<b>Parity 3</b>					
MY	1	0.48	0.20	0.12	0.06
CI	0.19	1	0.11	0.09	0.14
NSC	0.28	-0.11	1	0.07	-0.13
CR	0.07	0.16	-0.12	1	0.10
NRR56days	-0.02	-0.12	0.19	-0.72	1

CR-Conception rate, MY-Milk yield, CI-Calving interval, NSC-Number of services per conception, CR-Calving rate, NRR56days-No return rate at 56days



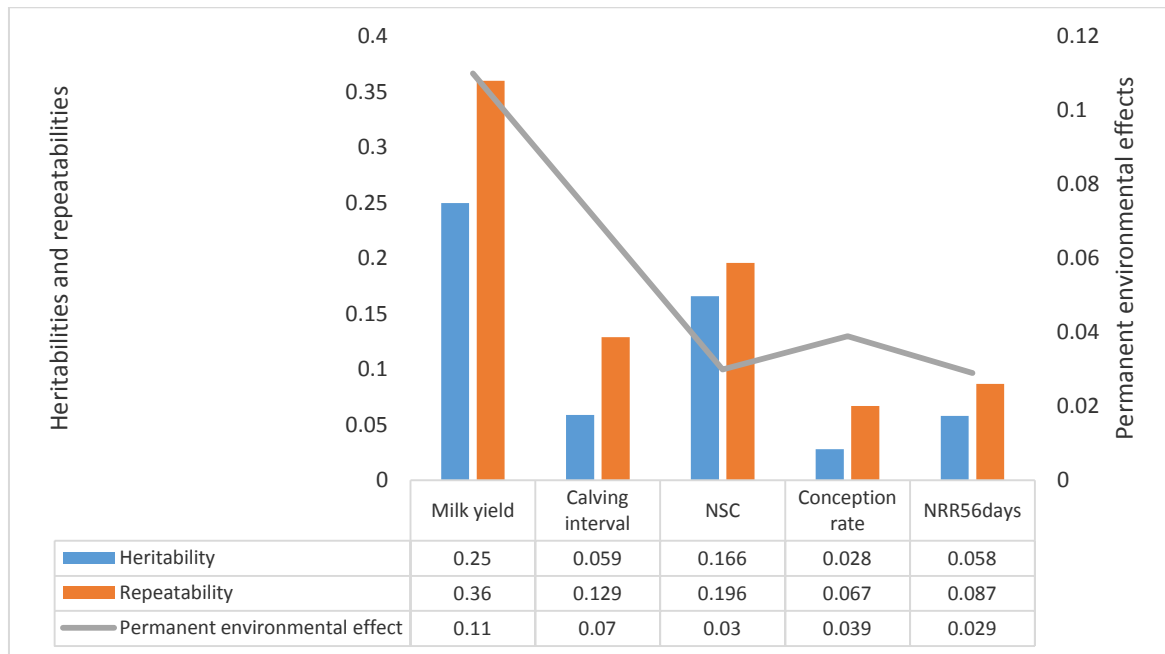
**Fig. 1. Genetic parameter estimates for milk and fertility traits in parity 1**



**Fig. 2. Genetic parameter estimates for milk and fertility traits in parity 2**

sire of cow component as a great deal of the inseminations in different parities comes from the same sires. These results confirm the findings of Jorjani [12], who found low genetic correlations for number of services per period for sire of cow in heifers and first parity cows (0.20). Genetic correlations between sire of

cow and sire of insemination for parity 2 and 3 were close to values found by Donoghue et al. [5] and Ghiasi et al. [9]. Although it would be tempting to improve fertility in cows via indirect selection on non-return rate of sires, the results indicate that this would not be effective for the improvement of conception rate in



**Fig. 3. Genetic parameter estimates for milk and fertility traits in parity 3**

heifers and first parity cows. Indirect selection on non-return rates of sires would have a moderately positive effect on conception rates of older cows. This change may be related to the increase in metabolic rate when the cows start producing milk. The differences in repeatability estimates obtained indicate that some herd fertility parameters are more useful for characterization of herd management than others. For milk production repeatability of herd yearly averages of 0.85 to 0.90 have been found [1] which is higher than the estimates reported in this study. The deviations observed may be caused by the variations in sample size, statistical model and location of the study.

## 5. CONCLUSION

The use of fertility traits in selection index programs can reduce genetic slippage caused by correlated selection response of milk production in Holstein Friesian cattle. Genetic correlations between milk yield and fertility traits were not robust and less than 0.6 across parities. However, these estimates are likely to be associated with large sampling variance because of the small data set and poor connectedness.

## COMPETING INTERESTS

Authors have declared that no competing interests exist.

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