

1 **ANALYSIS OF MILK AND FERTILITY TRAITS OF HOLSTEIN FRIESIAN CATTLE**
2 **IN WARM AND TEMPERATE CLIMATE OF JOS PLATEAU**

3 **ABSTRACT**

4 The edited data set for the estimation genetic parameters of milk and fertility traits of 4405
5 records from 650 cows calved between 1992 to 2015. The analytical model included the effects
6 of herd-year-season, group of sires, sire, cow, and residual. Sire, cow, and residual were random:
7 all other effects were fixed. Heritability estimates calving interval (CI), conception rate (CR),
8 number of services per conception (NSC) and no return rate at 56 days (NRR56 days) were low
9 and ranged between 0.028 (CR) and 0.166 (NSC) in the third parity. Milk yield had high
10 heritability and repeatability estimates across parity. The coefficient of variation was highly
11 variable, which range from 14.86-43.67%. Thus, there was no indication of an adverse genetic
12 relationship between fertility and milk production in this population and overall genetic
13 parameters imply a good practical management in warm and temperate conditions of Jos Plateau
14 will be essential for improving milk and fertility efficiency of dairy cattle

15 **INTRODUCTION**

16 Fertility is one of the non-yield traits which is of great economic importance in dairy herds. The
17 quest to profiteer by improving milk yield over the last decades through the use of selective
18 breeding and omics technology by dairy scientist had been a source of concern due to its
19 snowballing effect on fertility traits. The genetic gain in milk production per cow on daily basis
20 had extended fertility traits by 1% increment [1]. In Italy, the genetic gain in milk yield per cow
21 on yearly basis is 112 kg in Holstein-Friesian with an extension in calving interval of 1.4 day per
22 year [2]. Despite the huge variations in breeding practice across the countries under diverse
23 production systems and divergent climatic conditions, all had synergistic effect on the extension

24 of fertility traits [2]. This lack of a unique measure of fertility is due to the diverse type of
25 information available to assess the reproductive success [3]. If results of artificial inseminations
26 in each insemination cycle are available, traits such as days open (DO), interval from calving to
27 first insemination, number of inseminations per conception, the interval between first and last
28 insemination or conception rate have been used. When information of result of inseminations is
29 not available, calving interval (or an approximate measure of days open. obtained from calving
30 interval and average pregnancy duration in the population) provide a measure of the overall
31 reproductive efficiency in each parity and it is widely used because it can be easily obtained from
32 milk recording schemes. However, this measure is highly influenced by farmer interventions
33 (mainly, voluntary waiting period) and by problems regarding to the low quality of fertility
34 measurements such as censored records [5]. Therefore, a wide number of statistical models have
35 been used in the genetic evaluations of fertility traits with no clear consensus as to what approach
36 is best for each trait. One of the features shared by most fertility traits is that several measures
37 are available along the cow's productive life. Treatment of longitudinal traits in animal breeding
38 has followed several approaches from the simplest repeatability model [3] to the most complex
39 multiple trait models [7]. Other studies have found evidence of differences in patterns of
40 response to fertility traits along parities [6]. in some fertility traits. However, none of the
41 previous studies have dealt with the combined selection for fertility level and fertility persistency
42 along lactation. In this study relationships between fertility traits in different parities were
43 quantified. Attention was paid to the effect of selection on the estimates of genetic parameters.

44 **Materials and Methods**

45 A total of 4405 records from 650 cows collected from parity 1 to 3 during the period 1992 to
46 2015 were used in this study sired by 55 bulls on the Jos Plateau.

47 Milk yield was adjusted for lactation length at 305th days by multiplicative correction factors
 48 Fat corrected milk (FCM) = [(0.4*milk yield (kg) + [(15*fat yield (kg)] [10].
 49 Fertility traits were computed using fertility chart which was then preprocessed in VAMMP
 50 dairy management software interface. The traits were:
 51 Calving Interval (CI) was defined as the period (in days) between the first and the next calving.
 52 Number of service per conception (NSC) was defined as the number of service or matings to
 53 effect a pregnancy
 54 Conception rate was calculated by dividing the number of pregnant cows by the total number of
 55 inseminations.
 56 Variance components for milk and fertility were estimated through univariate analysis using an
 57 animal model considering the effects of herd, number of calving and contemporary group as
 58 fixed, and the permanent environmental, animal additive genetic and residual effects as random.
 59 The contemporary group included herd and year of calving

60 The model used [10] can be described as:

$$61 \quad y = Xb + Wpe + Za + e$$

62 in which y = vector of observations; b = vector of fixed effects (herd, number of calving, and
 63 season). pe = vector of random permanent environmental effects; a = vector of random animal
 64 effects; e = vector of random residual effects; X , W , and Z = incidence matrices that establish
 65 relationships between the records and the effects. It is assumed that permanent environmental,
 66 animal, and residual effects are independently distributed with mean zero and constant variance:

$$67 \quad V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

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

69 Heritability was estimated as the ratio of the additive genetic variance to total phenotypic
 70 variance; and repeatability, as the ratio of the sum of the additive genetic variance plus
 71 permanent environmental variance to phenotypic variance, as described by Falconer and Mackay
 72 (2001):

$$73 \quad h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

$$74 \quad W^2 = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

75 To estimate genetic and environmental correlations, a multi-traits animal model was used which
 76 included herd, number of calving and contemporary group (which included year of calving) as
 77 the fixed effects, and the permanent environmental and additive genetic direct effects as random.

78 The matrix model used was:

$$79 \quad \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

80 in which y_i = vector of N observations; b_i = vector of fixed effects (herd, number of calving,
 81 contemporary group); pe_i = vector of random permanent environmental effects; a_i = vector of
 82 random animal effects; e_i = vector of random residual effects; X , W , and Z = incidence matrices
 83 establishing relationships between the records and the fixed and random effects, respectively. It
 84 is assumed that random permanent environmental, animal and error effects are independently
 85 distributed with mean of zero and variance:

$$86 \quad V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

87 in which \otimes = direct or Kronecker product; I = identity matrix equal to number of observations; A
 88 = relationship matrix among all animals in the pedigree; G_0 = variance and covariance matrix of

89 random animal effects; $\sigma_{a_{ii}}^2$ = animal additive genetic variance for trait i ; $\sigma_{a_{jj}}^2$ = animal additive
90 genetic variance for trait j ; $\sigma_{a_{ij}} = \sigma_{a_{ji}}$ = animal additive genetic covariance between traits i and j ;
91 Q_0 = variance and covariance matrix of random permanent environmental effects; $\sigma_{pe_{ii}}^2$ =
92 permanent environmental variance for trait i ; $\sigma_{pe_{jj}}^2$ = permanent environmental variance for trait
93 j ; $\sigma_{pe_{ij}} = \sigma_{pe_{ji}}$ = permanent environmental covariance between traits i and j ; R_0 = variance and
94 covariance matrix of residual effects; $\sigma_{e_{ii}}^2$ = residual variance for trait i ; $\sigma_{e_{jj}}^2$ = residual variance
95 for trait j ; and $\sigma_{e_{ij}} = \sigma_{e_{ji}}$ = residual covariance between traits i and j .

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Table 1: Least squares means of milk and fertility traits at different parity; standard deviation is given in brackets.

| Parameters | Parities | | | CV |
|-------------------------|----------------------------|---------------------------|----------------------------|-------|
| | 1 | 2 | 3 | |
| No of records | 4500 | 2899 | 2006 | |
| Milk yield (kg) | 876.11(87.23) ^c | 1288 (77.29) ^b | 1602 (120.50) ^a | 14.86 |
| Calving interval (days) | 138 (26.4) ^b | 129 (22.4) ^a | 128 (21.1) ^a | 16.44 |
| NSC | 2.07 | 2.10 | 2.00 | 43.67 |
| Conception rate | 59.4 | 55.0 | 54.6 | 32.01 |
| NRR at 56 days | 80.1 | 77.5 | 74.0 | 40.12 |

CV-Coefficient of variation; NRR-no return rate; NSC-Number of services per conception

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98 Table 1 shows the least squares means for milk and fertility traits at different parity. Milk yield
99 and calving intervals differs significantly ($p < 0.05$) between parity. The coefficient of variation
100 was highly variable, which range from 14.86-43.67%. The phenotypic mean of milk yield and
101 calving interval linearly increased at consecutive parities and this change only was statistically
102 significant ($p < 0.01$) between parities. An increasing trend for milk yield and calving interval has
103 also been found in other studies [1, 6]. The descriptive statistics for calving interval indicate that
104 cows in earlier parities had more chances for good fertility performance than cows in later
105 parities. The number of records decreased from parity 1 to 3 due to voluntary and involuntary

106 culling of cows. This may reflect differences in management conditions for varied values
 107 reported at different parities.

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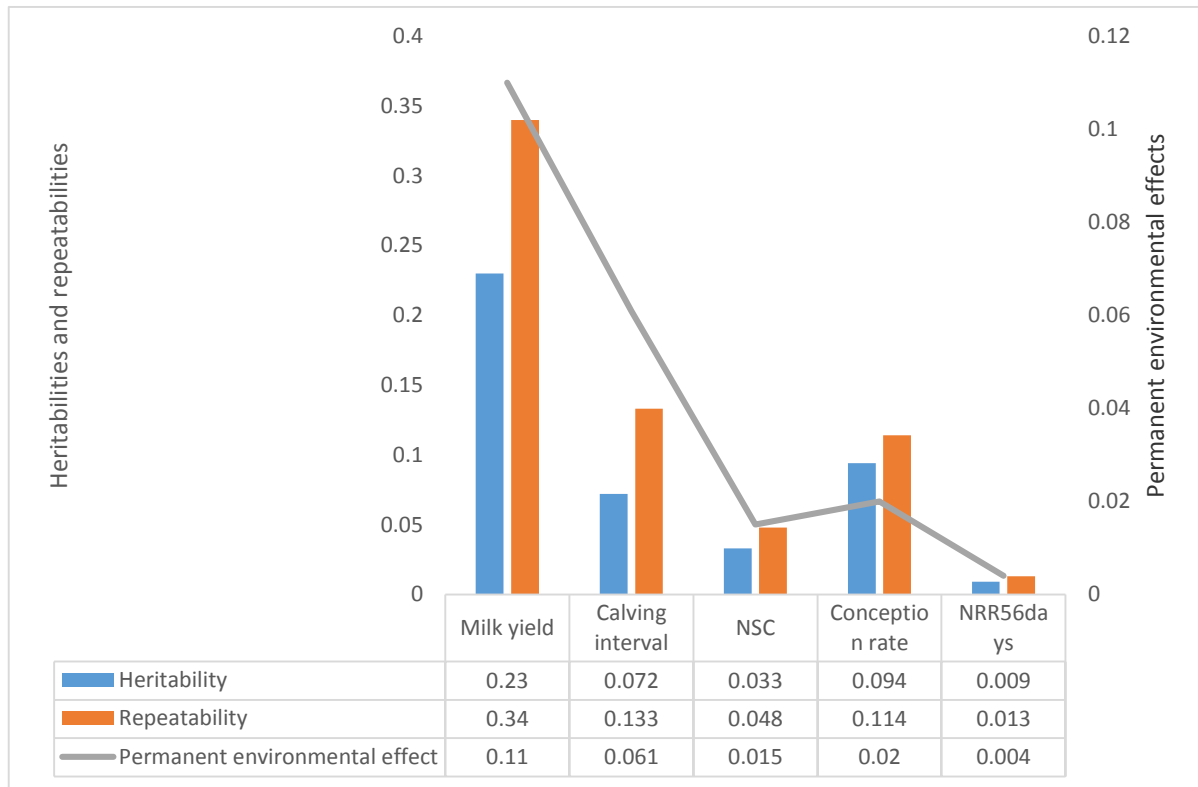
Table 2: Genetic correlations (above diagonal) and environmental correlations (below diagonal) for milk yield and herd fertility traits in Holstein Friesian cattle at different parities

| Parity 1 | | | | | |
|-----------------|-------|-------|-------|-------|-----------|
| Traits | MY | CI | NSC | CR | NRR56days |
| 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 |
| Parity 2 | | | | | |
| 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 |
| Parity 3 | | | | | |
| 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 |

109 CR-Conception rate, MY-Milk yield, CI-Calving interval, NSC-Number of services per conception, CR-Calving
 110 rate, NRR56days-No return rate at 56days
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112 Table 2 shows the genetic and environmental correlations for milk yield and fertility traits at
 113 different parity in Holstein Friesian cattle. Significant genetic correlations was found for calving
 114 rate (0.40) and non return rate at 56 days (0.34) while milk yield was phenotypically correlated
 115 with calving rate in the first parity. No significant genetic and phenotypic correlations were
 116 found between herd fertility and milk yield in the second parity. Milk yield showed significant
 117 genetic correlation between calving interval and number of services per conception in the third
 118 parity. Significant phenotypic positive correlation was found between milk yield and number of

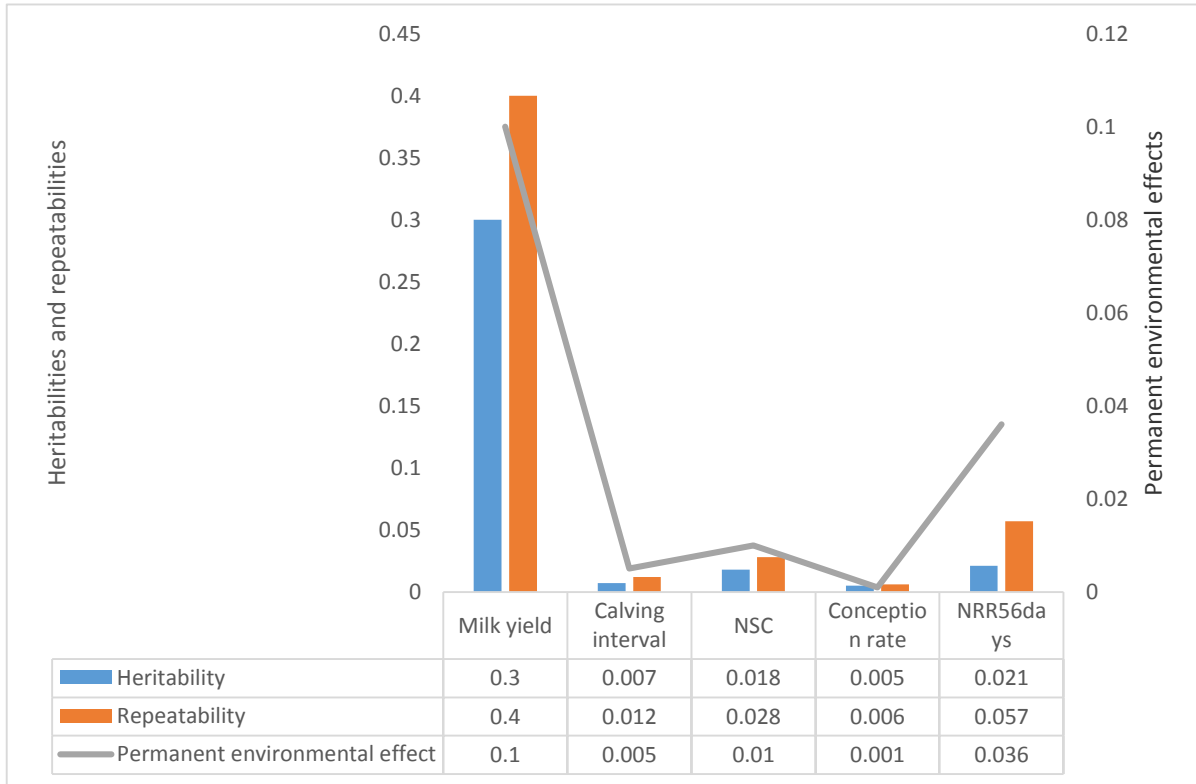
119 services per conception (0.28). The highest negative correlations was found between calving rate
 120 and non return rate at 56 days (-0.72).



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Figure 1: Genetic parameters of milk and fertility traits in parity 1

UNDER REVIEW



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Figure 2: Genetic parameters of milk and fertility traits in parity 2

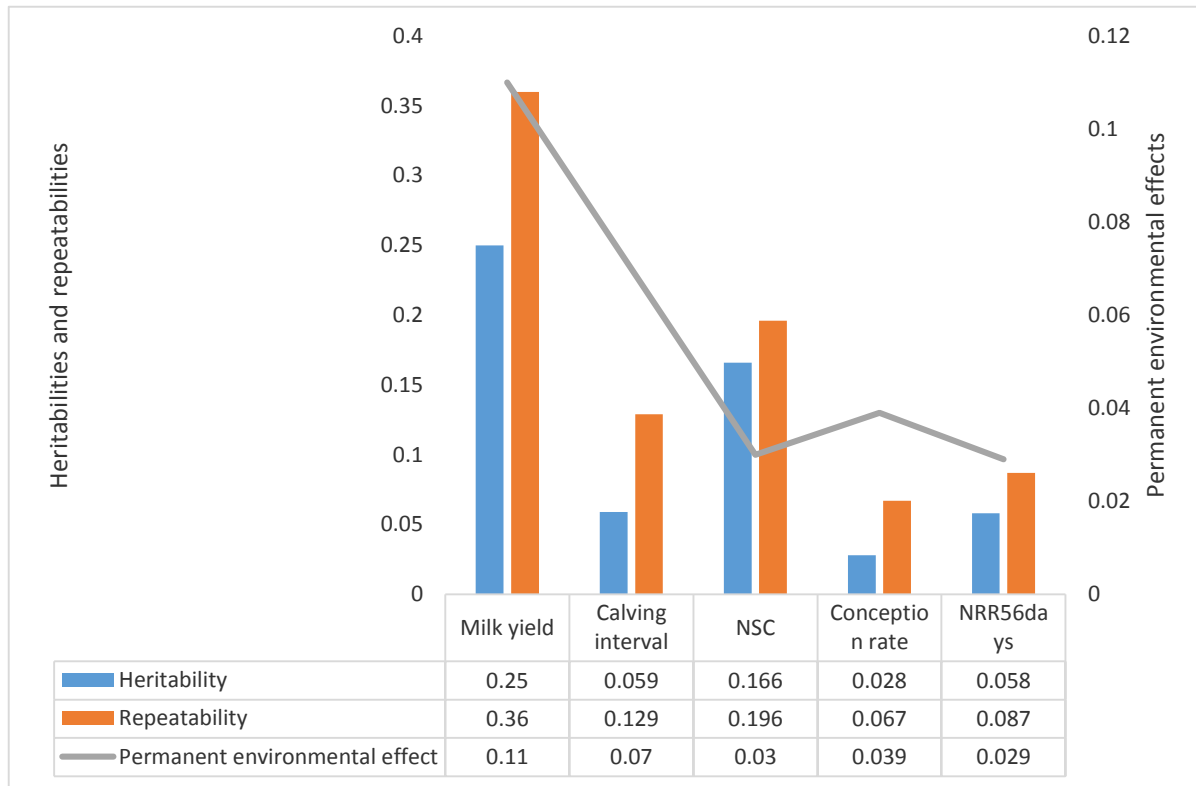


Figure 3: Genetic parameters of milk and fertility traits in parity 3

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Figure 1, 2 and 3 shows the permanent environmental effect, heritability and repeatability of 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. 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 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 [4], who found low genetic correlations for number of services per period for sire of cow in heifers and first parity cows (.20). [5] however, found correlations close to 1. Genetic correlations between sire of cow and sire of insemination for parity 2 and 3 were close to values found by [8]. 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

148 of conception rate in heifers and first parity cows. Indirect selection on non-return rates of sires
149 would have a moderately positive effect on conception rates of older cows. This change may be
150 related to the increase in metabolic rate when the cows start to produce milk. The differences in
151 repeatability estimate obtained indicate that some herd fertility parameters are more useful for
152 characterization of herdmanship than others. For milk production repeatability of herd yearly
153 averages of 0.85 to 0.90 have been found (Wilmink, personal communication, 1985) which
154 higher than the estimates reported in this study. The deviation observed may be caused by the
155 variations in sample size, statistical model and location of the study. **(PUT YOUR WORK IN**

156 **SUB HEADINGS FOR CLARITY)**

157 **CONCLUSION**

158
159 Selection of fertility traits in selection index program can reduce genetic slippage caused by
160 correlated selection response of milk production in dairy cattle. Genetic correlations between
161 milk yield and fertility traits were not robust and always less than 0.6 across parity. However,
162 these estimates are likely to be associated with large sampling variance because of the small data
163 set and poor connectedness **(PUT YOUR CONCLUSION IN ONE SENTENCE).**

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