

1 | ANALYSIS OF MILK AND FERTILITY TRAITS ~~OF IN~~ HOLSTEIN FRIESIAN
2 | CATTLE IN WARM AND TEMPERATE CLIMATES ~~S~~ OF JOS PLATEAU

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6 | **ABSTRACT**

7 | The ~~edited data~~ set for the estimation ~~of~~ genetic parameters ~~of~~ ~~for~~ milk and fertility traits of
8 | ~~4405 records from~~ 650 cows calved between 1992 ~~to~~ ~~and~~ 2015. The analytical model
9 | included the effects of herd-year-season, group of sires, sire, cow, and residual ~~effects~~. Sire, cow,
10 | and residual ~~effects~~ were random: ~~=~~ ~~while~~ all other effects were fixed. Heritability
11 | estimates, calving interval (CI), conception rate (CR), number of services per conception
12 | (NSC) and no return rate at 56 days (NRR56 days) were low and ranged between 0.028 (CR) and
13 | 0.166 (NSC) in the third parity. Milk yield had high heritability and repeatability estimates
14 | across parities ~~y~~. The coefficient of variation was highly variable, ~~which and~~ ranged ~~d~~ from 14.86-
15 | 43.67%. Thus, there was no indication of an adverse genetic relationship between fertility and
16 | milk production in this population and overall genetic parameters imply a good practical
17 | management in warm and temperate conditions of Jos Plateau will be essential for improving
18 | milk and fertility efficiency of dairy cattle

19 | **INTRODUCTION**

20 | Fertility is one of the non-yield traits which is of great economic importance in dairy herds. The
21 | quest to profiteer by improving milk yield over the last decades through the use of selective
22 | breeding and omics technology by dairy scientist had been a source of concern due to its
23 | snowballing effect on fertility traits. The genetic gain in milk production per cow on daily basis
24 | had extended fertility traits by 1% increment [1]. In Italy, the genetic gain in milk yield per cow

Comment [PE1]: Why edited data?

25 on yearly basis is 112 kg in Holstein-Friesian with an extension in calving interval of 1.4 day per
26 year [2]. Despite the huge variations in breeding practice across the countries under diverse
27 production systems and divergent climatic conditions, all had synergistic effect on the extension
28 of fertility traits [2]. This lack of a unique measure of fertility is due to the
29 diverse type of information available to assess the reproductive success [3].
30 If results of artificial inseminations in each insemination cycle are
31 available, traits such as days open (DO), interval from calving to first
32 insemination, number of inseminations per conception, the interval between
33 first and last insemination or conception rate have been used. When
34 information of result of inseminations is not available, calving interval (or
35 an approximate measure of days open, obtained from calving interval and
36 average pregnancy duration in the population) provide a measure of the overall
37 reproductive efficiency in each parity and it is widely used because it can be
38 easily obtained from milk recording schemes. However, this measure is highly
39 influenced by farmer interventions (mainly, voluntary waiting period) and by
40 problems regarding to the low quality of fertility measurements such as
41 censored records [5]. Therefore, a wide number of statistical models have been
42 used in the genetic evaluations of fertility traits with no clear consensus as
43 to what approach is best for each trait. One of the features shared by most
44 fertility traits is that several measures are available along the cow' s
45 productive life. Treatment of longitudinal traits in animal breeding has

46 followed several approaches from the simplest repeatability model [3] to the
47 most complex multiple trait models [7]. Other studies have found evidence of
48 differences in patterns of response to fertility traits along parities [6], in
49 some fertility traits. However, none of the previous studies have dealt with
50 the combined selection for fertility level and fertility persistency along
51 lactation. In this study, relationships between fertility traits in different parities were
52 quantified. Attention was paid to the effect of selection on the estimates of genetic parameters.

53 **Materials and Methods**

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

57 Milk yield was adjusted for lactation length at 305th days by multiplicative correction factors

58 Fat corrected milk (FCM) = $[(0.4 * \text{milk yield (kg)} + [(15 * \text{fat yield (kg)}])]$ [10].

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

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

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

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

66 Variance components for milk and fertility were estimated through univariate analysis using an
67 animal model considering the effects of herd, number of calving and contemporary group as

68 fixed, and the permanent environmental, animal additive genetic and residual effects as random.

69 The contemporary group included herd and year of calving

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

71
$$y = Xb + Wpe + Za + e$$

72 in which y = vector of observations; b = vector of fixed effects (herd, number of calving, and

73 season). pe = vector of random permanent environmental effects; a = vector of random animal

74 effects; e = vector of random residual effects; X , W , and Z = incidence matrices that establish

75 relationships between the records and the effects. It is assumed that permanent environmental,

76 animal, and residual effects are independently distributed with mean zero and constant variance:

77
$$V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

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

79 Heritability was estimated as the ratio of the additive genetic variance to total phenotypic

80 variance; and repeatability, as the ratio of the sum of the additive genetic variance plus

81 permanent environmental variance to phenotypic variance, as described by Falconer and Mackay

82 (2001):

83
$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

84
$$W^2 = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

85 To estimate genetic and environmental correlations, a multi-traits animal model was used which

86 included herd, number of calving and contemporary group (which included year of calving) as

87 the fixed effects, and the permanent environmental and additive genetic direct effects as random.

88 The matrix model used was:

Comment [PE2]: Define the items in the equation (e.g. where h^2 = heritability, etc.)

$$89 \quad \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

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

$$96 \quad V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

97 in which \otimes = direct or Kronecker product; I = identity matrix equal to number of observations; A
98 = relationship matrix among all animals in the pedigree; G_0 = variance and covariance matrix of
99 random animal effects; σ_{aii}^2 = animal additive genetic variance for trait i ; σ_{aij}^2 = animal additive
100 genetic variance for trait j ; $\sigma_{aij} = \sigma_{aji}$ = animal additive genetic covariance between traits i and j ;
101 Q_0 = variance and covariance matrix of random permanent environmental effects; σ_{peii}^2 =
102 permanent environmental variance for trait i ; σ_{peij}^2 = permanent environmental variance for trait
103 j ; $\sigma_{peij} = \sigma_{peji}$ = permanent environmental covariance between traits i and j ; R_0 = variance and
104 covariance matrix of residual effects; σ_{eii}^2 = residual variance for trait i ; σ_{eij}^2 = residual variance
105 for trait j ; and $\sigma_{eij} = \sigma_{eji}$ = residual covariance between traits i and j .

106

Table 1: Least squares means of milk and fertility traits at different parities y ; 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

Comment [PE3]: Give the full meaning of this abbreviation as a foot note to the Table.

Comment [PE4]: Give the full meaning of this abbreviation as a foot note to the Table.

107

108 Table 1 shows the least squares means for milk and fertility traits at different parities y . Milk
 109 yield and calving intervals differs significantly ($p < 0.05$) between parities y . The coefficient of
 110 variation was highly variable, which ranged from 14.86-43.67%. The phenotypic mean of milk
 111 yield and calving interval linearly increased at consecutive parities and this change only was
 112 statistically ~~signifeant~~ significant ($p < 0.01$) between parities. An increasing trend for milk yield
 113 and calving interval has also been found in other studies [1, 6]. The descriptive statistics for
 114 calving interval indicate that cows in earlier parities had more chances for good fertility
 115 performance than cows in later parities. The number of records decreased from parity 1 to 3 due
 116 to voluntary and involuntary culling of cows. This may reflect differences in management
 117 conditions for varied values 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

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

119 CR-Conception rate, MY-Milk yield, CI-Calving interval, NSC-Number of services per conception, CR-Calving
 120 rate, NRR56days-No return rate at 56days
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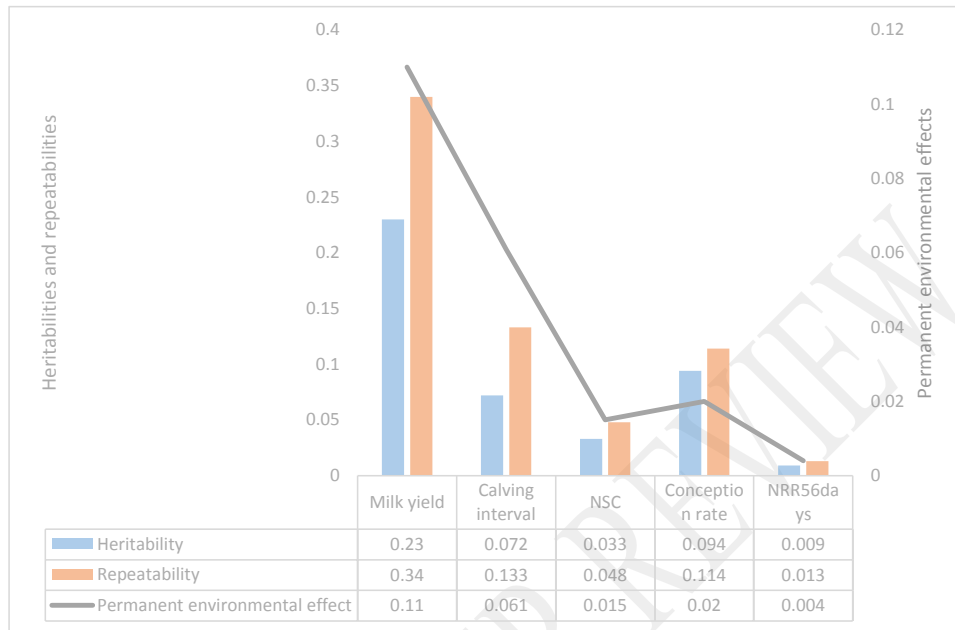
122 Table 2 shows the genetic and environmental correlations for milk yield and fertility traits at
 123 different parities y in Holstein Friesian cattle in the study area. Significant genetic correlations
 124 were as found for calving rate (0.40) and non-return rate at 56 days (0.34) while milk yield was
 125 phenotypically correlated with calving rate in the first parity. No significant genetic and
 126 phenotypic correlations were found between herd fertility and milk yield in the second parity.
 127 Milk yield showed significant genetic correlation between calving interval and number of
 128 services per conception in the third parity. Significant phenotypic positive correlation was found
 129 between milk yield and number of services per conception (0.28). The highest negative
 130 correlations was found between calving rate and non return rate at 56 days (-0.72) in parity 3.

Comment [PE5]: This value (0.40) is the genetic correlation value between calving rate (CR) and milk yield (MY) in parity 1. Please, present as such.

Comment [PE6]: This value (0.34) is the genetic correlation value between NRR56days and calving interval (CI) in parity 1. Please, present as such.

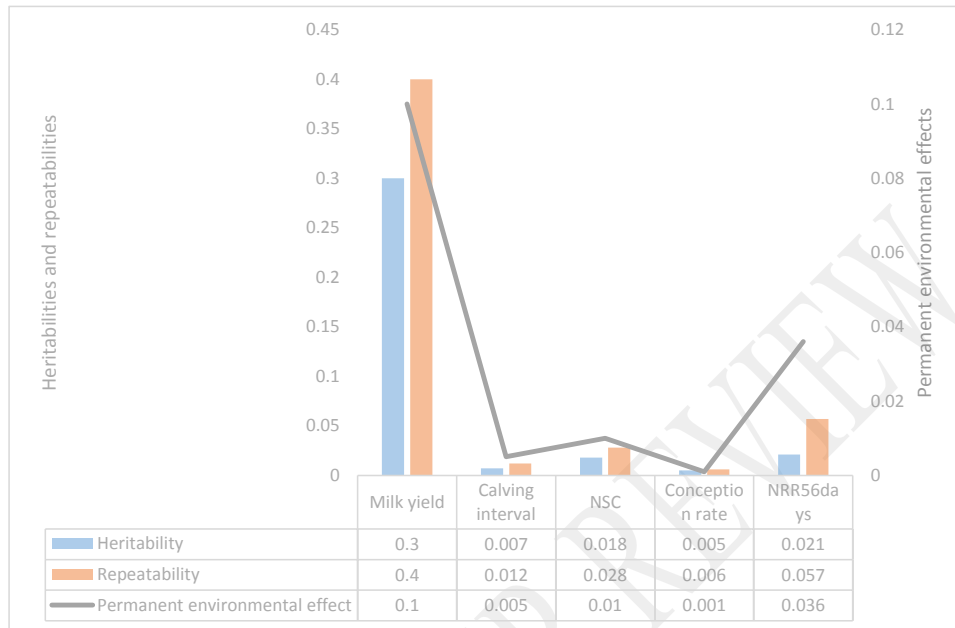
Comment [PE7]: In presenting correlation values, it is important to specify both the direction (positive or negative) and the variables been correlated.

UNDER PEER REVIEW

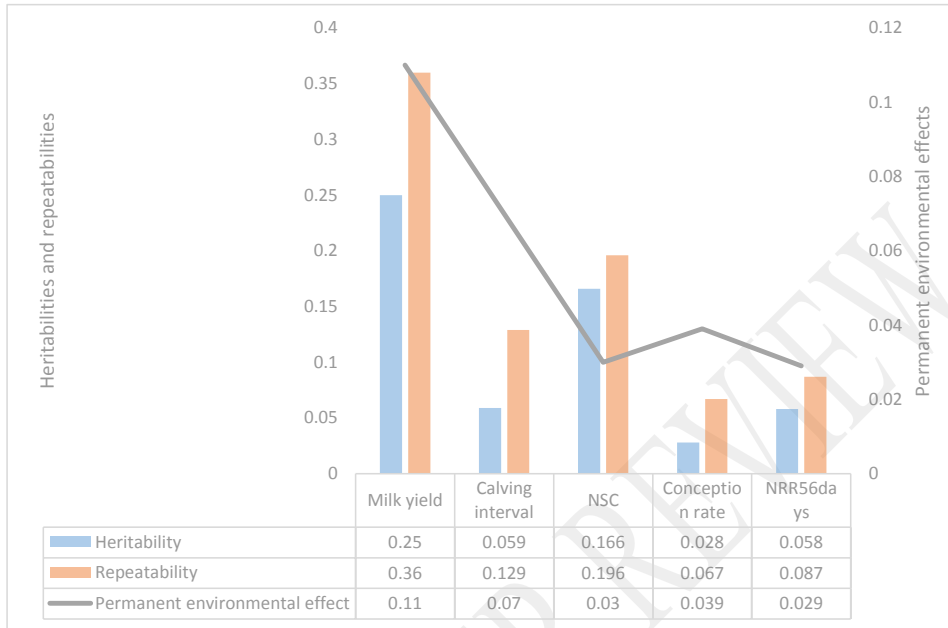


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 133 | Figure 1: Genetic parameters estimates of for milk and fertility traits in parity 1
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 139 | Figure 2: Genetic parameter estimates for milk and fertility traits in parity 2
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144 | Figure 3: Genetic parameter estimates for milk and fertility traits in parity 3

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147 | Figures 1,-2 and 3 shows the permanent environmental effect, heritability and repeatability for of
148 milk yield and herd fertility variable. The permanent environmental effect, heritability and
149 repeatability had the highest values for milk yield in the second parity as compared to first and
150 third parity. Genetic values for herd fertility variables were non linear and low from the first to
151 the third parity. The changes were primarily due to the sire of cow component as a great deal of
152 the inseminations in different parities comes from the same sires. These results confirm the
153 findings of [4], who found low genetic correlations for number of services per period for sire of
154 cow in heifers and first parity cows (.20). [5] however, found correlations close to 1. Genetic
155 correlations between sire of cow and sire of insemination for parity 2 and 3 were close to values
156 found by [8]. Although it would be tempting to improve fertility in cows via indirect selection on
157 non-return rate of sires, the results indicate that this would not be effective for the improvement

158 of conception rate in heifers and first parity cows. Indirect selection on non-return rates of sires
159 would have a moderately positive effect on conception rates of older cows. This change may be
160 related to the increase in metabolic rate when the cows start ~~to~~ producing milk. The differences
161 in repeatability estimates obtained indicate that some herd fertility parameters are more useful
162 for characterization of herdmanhood than others. For milk production repeatability of herd yearly
163 averages of 0.85 to 0.90 have been found (Wilmink, personal communication, 1985) which is
164 higher than the estimates reported in this study. The deviations observed may be caused by the
165 ~~variations~~ variations in sample size, statistical model and location of the study.

166 CONCLUSION

167
168 The use Selection of fertility traits in selection index programs can reduce genetic slippage
169 caused by correlated selection response of milk production in dairy cattle. Genetic correlations
170 between milk yield and fertility traits were not robust and always less than 0.6 across parities y.
171 However, these estimates are likely to be associated with large sampling variance because of the
172 small data set and poor connectedness.

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