

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

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6 **ABSTRACT**

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

18 **INTRODUCTION**

19 Fertility is one of the non-yield traits which is of great economic importance in dairy herds. The  
20 quest to profiteer by improving milk yield over the last decades through the use of selective  
21 breeding and omics technology by dairy scientist had been a source of concern due to its  
22 snowballing effect on fertility traits. The genetic gain in milk production per cow on daily basis  
23 had extended fertility traits by 1% increment [1]. In Italy, the genetic gain in milk yield per cow  
24 on yearly basis is 112 kg in Holstein-Friesian with an extension in calving interval of 1.4 day per

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

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

## 52 **Materials and Methods**

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

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

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

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

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

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

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

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

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

68 The contemporary group included herd and year of calving

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

70 
$$y = Xb + Wpe + Za + e$$

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

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

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

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

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

76 
$$V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & I\sigma_{pe}^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

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

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

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

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

81 (2001):

82 
$$h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{pe}^2 + \sigma_e^2}$$

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

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

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

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

87 The matrix model used was:

$$88 \quad \begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} pe_1 \\ pe_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

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

$$95 \quad V \begin{bmatrix} a \\ pe \\ e \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 & 0 \\ 0 & Q_0 \otimes I & 0 \\ 0 & 0 & R_0 \otimes I \end{bmatrix}$$

96 in which  $\otimes$  = direct or Kronecker product;  $I$  = identity matrix equal to number of observations;  $A$   
97 = relationship matrix among all animals in the pedigree;  $G_0$  = variance and covariance matrix of  
98 random animal effects;  $\sigma_{a_{ii}}^2$  = animal additive genetic variance for trait  $i$ ;  $\sigma_{a_{jj}}^2$  = animal additive  
99 genetic variance for trait  $j$ ;  $\sigma_{a_{ij}} = \sigma_{a_{ji}}$  = animal additive genetic covariance between traits  $i$  and  $j$ ;  
100  $Q_0$  = variance and covariance matrix of random permanent environmental effects;  $\sigma_{pe_{ii}}^2$  =  
101 permanent environmental variance for trait  $i$ ;  $\sigma_{pe_{jj}}^2$  = permanent environmental variance for trait  
102  $j$ ;  $\sigma_{pe_{ij}} = \sigma_{pe_{ji}}$  = permanent environmental covariance between traits  $i$  and  $j$ ;  $R_0$  = variance and  
103 covariance matrix of residual effects;  $\sigma_{e_{ii}}^2$  = residual variance for trait  $i$ ;  $\sigma_{e_{jj}}^2$  = residual variance  
104 for trait  $j$ ; and  $\sigma_{e_{ij}} = \sigma_{e_{ji}}$  = residual covariance between traits  $i$  and  $j$ .

105

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) <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

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

106

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

117

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

<b>Parity 1</b>					
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
<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

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

120

121 Table 2 shows the genetic and environmental correlations for milk yield and fertility traits at  
122 different parity in Holstein Friesian cattle. Significant genetic correlations was found for calving  
123 rate (0.40) and non return rate at 56 days (0.34) while milk yield was phenotypically correlated  
124 with calving rate in the first parity. No significant genetic and phenotypic correlations were  
125 found between herd fertility and milk yield in the second parity. Milk yield showed significant  
126 genetic correlation between calving interval and number of services per conception in the third  
127 parity. Significant phenotypic positive correlation was found between milk yield and number of  
128 services per conception (0.28). The highest negative correlations was found between calving rate  
129 and non return rate at 56 days (-0.72).

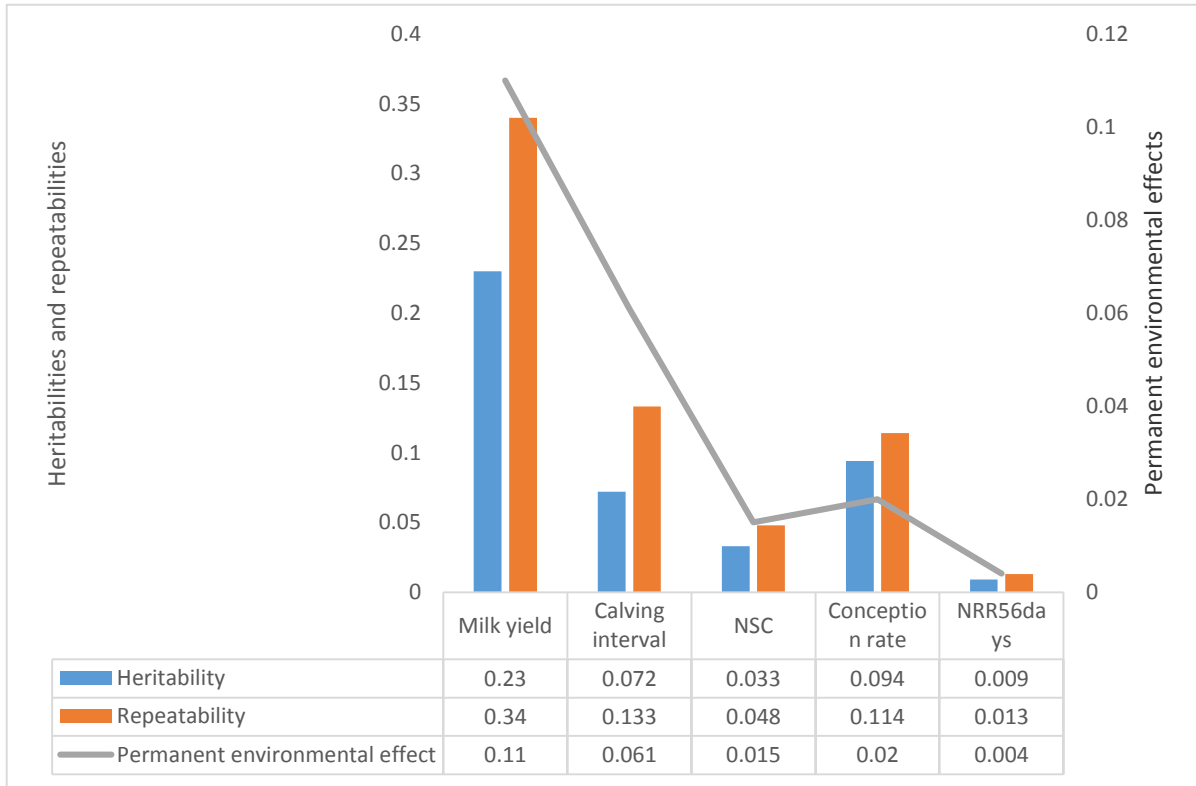
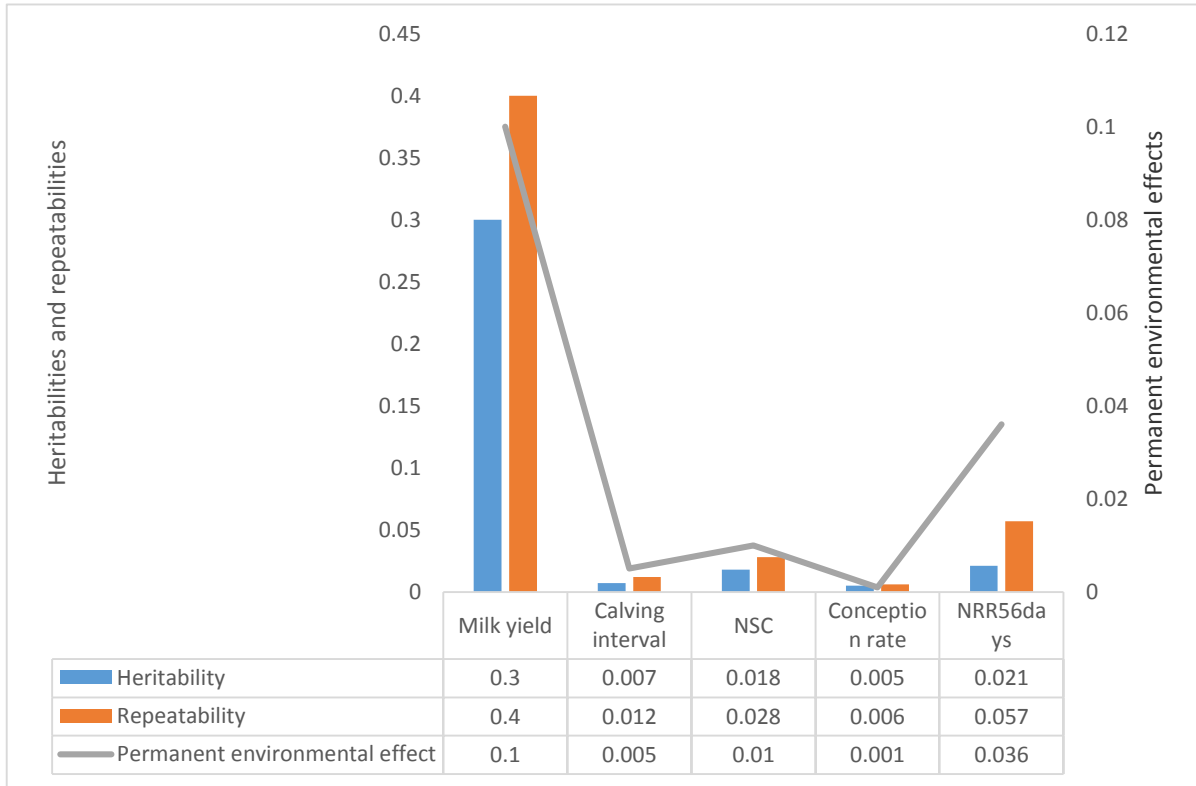


Figure 1: Genetic parameters of milk and fertility traits in parity 1

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UNDER PEER REVIEW





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

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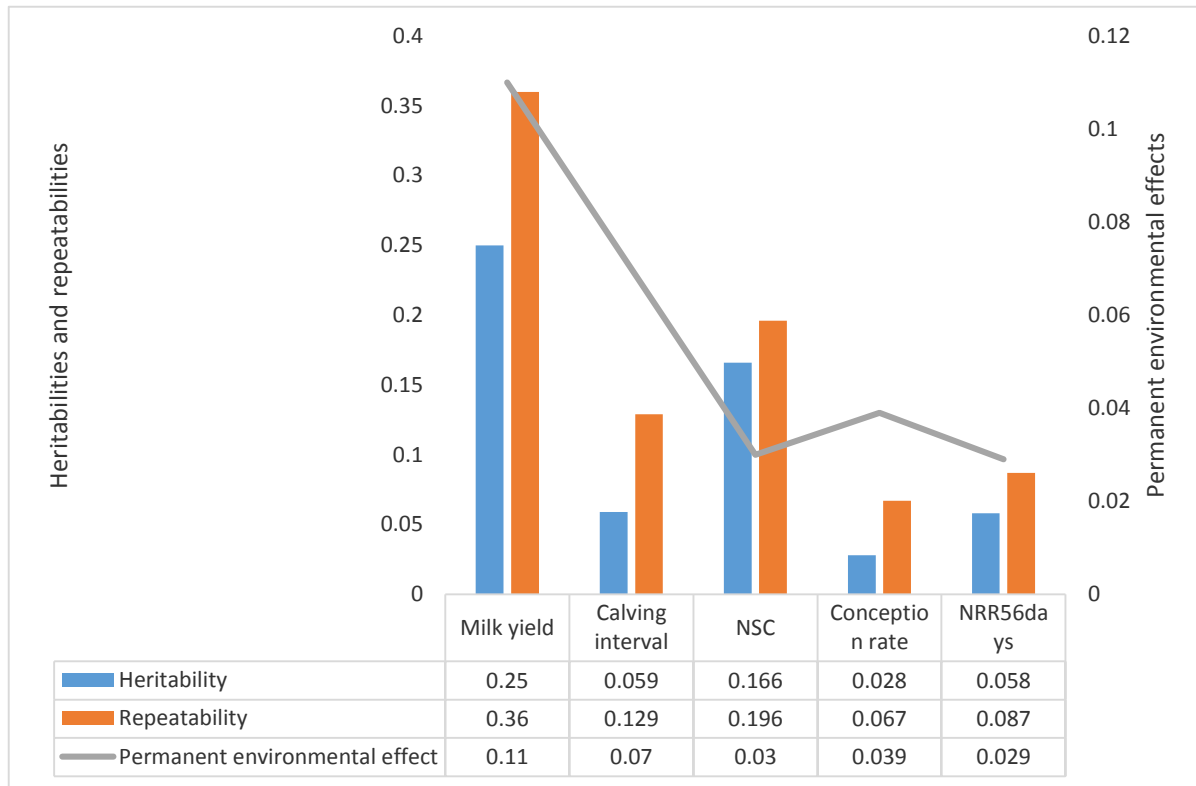


Figure 3: Genetic parameters of milk and fertility traits in parity 3

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

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

## 165 **CONCLUSION**

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