

# Genetic Analysis of Fertility Traits in Israeli Dairy Cattle

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## ABSTRACT

First through third parity lactation records of 91,770 Israeli Holsteins inseminated between 1980 and 1986 were evaluated by univariate mixed model methodology for fertility and production traits. The analytical model included the effects of herd-year-season, group of sires, sire, cow, and residual. Sire, cow, and residual were random; all other effects were fixed. Sires were assumed to be unrelated. Variance components were computed separately for first and second parity by Henderson's method 3. First parity heritabilities were .035 for conception status [1/number of inseminations to conception], .048 for days from calving to first breeding, and .135 for milk production. Corresponding second parity heritabilities were .022, .031, and .125. First parity genetic correlations were  $-.02$  between conception status and milk,  $.27$  between days to first breeding and milk, and  $-.03$  between the two fertility traits. All environmental correlations, and all second parity genetic correlations among these traits, were between  $-.2$  and  $.2$ . Genetic trends, estimated as twice the regression of the evaluation of the cow's sire on calving date, were 1% for conception status, .1 for days to first breeding, and 154 kg milk/yr. Thus, there was no indication of an adverse genetic relationship between fertility and milk production in this population.

## INTRODUCTION

Despite the economic importance of fertility in dairy cattle (5, 24), there has been little

emphasis on breeding for either male or female fertility since heritability for most measures of fertility is low (2, 4, 7, 8, 9, 11, 13, 14, 15, 16, 18, 20, 21, 23, 25, 27). Because the field data generally available consist of insemination dates, most studies have estimated female fertility by nonreturn rates, the number of times a cow is bred during a lactation, or by days open (2, 7, 8, 9, 11, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 25, 27). Several studies (4, 8, 11, 18, 23, 27) found negative genetic correlations on the economic scale between fertility and production traits, whereas others (2, 24, 26) found no significant relationships.

Fertility traits are problematic for genetic analysis. Cows that do not conceive do not have a value for days open. Therefore, studies that have analyzed days open have either deleted cows that did not conceive from the analysis (13, 14, 15, 20, 23, 27) or used a "pseudo" days open value, such as last insemination date (16, 17, 18, 19, 23) or some arbitrary high value (4, 8, 9, 11). All of these options will tend to bias resulting estimates. The first approach is undesirable, because cows with the most obvious fertility problems are eliminated from the analysis. Among cows that do not conceive readily, farmers will be more likely to reinseminate those with superior milk production or which are daughters of elite sires. Thus, cows with long open periods will not be a random sample with respect to either production or pedigree. Furthermore, because data on conception are not generally available, neither number of breedings nor nonreturn rate distinguishes whether or not the cow conceived on a given insemination. Thus, for cows that did not conceive, a low number of inseminations is not indicative of high fertility.

Field data collected in Israel are unique in that pregnancy is determined by veterinary examination for all cows that do not display estrus within 60 d of insemination (21). The goal of this study was to estimate genetic and

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TABLE 1. Frequency table for fertility traits of 91,770 first parity cows.

No. of inseminations to conception	Conception status		Days to first AI		Frequency	
	(%)	(no.)	(%)	(no.)	(%)	(%)
1	100	43,993	48	<50	1617	2
2	50	19,603	21	51-70	25,594	28
3	33	9999	11	71-90	34,570	38
4	25	5205	6	91-110	19,238	21
>4	20	6115	7	111-130	7155	8
No conception	0	6855	7	>130	3596	4

phenotypic parameters of fertility using these data and to estimate genetic and environmental trends for fertility and production traits in the Israeli Holstein population.

#### MATERIALS AND METHODS

Data were first through third parity insemination and production records of Israeli Holsteins inseminated between January 1, 1980 and July 31, 1986. Records were eliminated if: 1) no insemination was recorded prior to 153 d in milk; 2) days in milk were less than 34, or number of monthly tests was less than 2; 3) previous parity records of the cow were missing; 4) there were fewer than 20 daughters per sire; or 5) records were otherwise abnormal. The edited data set consisted of 91,770 cows, daughters of 296 sires. Because cows without first parity records were deleted, the number of first parity records was also 91,770. Of these cows, 1487 were daughters of 26 elite sires from the US, Canada, New Zealand, Sweden, and Israel. Evaluations of these test sires for various traits have been presented previously (1). Daughters of the test sires were included in the computation of sire evaluations but not in the other analyses.

Production traits analyzed were milk and fat annualized yields (AY) [365(total lactation yield)/days between calvings]. Prior to analysis, production records were adjusted for the effects of days open, calving season, calving age, and parity; incomplete records were extended, as described previously (3, 6, 30). Fertility traits analyzed were conception status (CS) [1/number of inseminations to conception], and days from calving to first breeding (DFB). Cows that were inseminated but did not conceive, as de-

termined by veterinary examination, were scored 0 for CS. Cows with more than five inseminations were given the same score as those with five inseminations. Fertility traits were adjusted for the effect of parity, using additive adjustment factors. Frequency tables of the fertility traits for first parity are given in Table 1. Results were similar for second and third parity, and therefore are not presented.

The following mixed model was used to compute sire evaluations:

$$Y_{ijklmn} = G_i + S_{ij} + HYS_{kl} + C_{km} + e_{ijklmn} \quad [1]$$

where  $Y_{ijklmn}$  is the production or fertility record for the  $n^{\text{th}}$  lactation of the  $m^{\text{th}}$  cow during the  $l^{\text{th}}$  year-season of the  $k^{\text{th}}$  herd, daughter of the  $j^{\text{th}}$  sire of the  $i^{\text{th}}$  group of sire;  $G_i$  is the fixed effect of the  $i^{\text{th}}$  group of sires;  $S_{ij}$  is the random effect of the  $j^{\text{th}}$  sire of the  $i^{\text{th}}$  group;  $HYS_{kl}$  is the fixed effect of the  $l^{\text{th}}$  year-season of the  $k^{\text{th}}$  herd;  $C_{km}$  is the random effect of the  $m^{\text{th}}$  cow of the  $k^{\text{th}}$  herd; and  $e_{ijklmn}$  is the random residual associated with each record. For sire evaluations, sire, cow, and residual variance components were assumed to be 1, 9, and 90% of the total variance for CS and DFB and 5, 45, and 50% of the variance for milk and fat production. Groups were determined biennially by year of birth for the general population and by country of origin for the 26 test sires. The HYS and cow effects were absorbed, whereas sire and group solutions were solved by iteration. Sires were assumed to be unrelated. Sire evaluations were computed as the sum of each sire's group and sire solutions. Repeatibilities of evaluations were computed as follows (1):

$$RPT_j = 1 - \frac{\text{Var } e}{D_j (\text{Var } S)} \quad [2]$$

where  $RPT_j$  is the repeatability for the  $j^{\text{th}}$  sire,  $D_j$  is the diagonal element for the  $j^{\text{th}}$  sire, and  $\text{Var } e$  and  $\text{Var } S$  are the residual and sire components of variance.

Phenotypic trends for all four traits were computed as the regression of each cow's first parity record on her first parity calving date. Genetic trends were estimated as twice the regression of the evaluation of each cow's sire on the cow's first parity calving date. Environmental trends were estimated as the difference between the phenotypic and genetic trends. The procedure of doubling sire evaluations, which assumes equal genetic progress on the dam side, although commonly used for production traits (29) may in fact be an overestimate. Because progress in the dam line tends to lag behind progress in the sire line (28).

Variance components were estimated separately for first and second parity by Henderson's method 3 (HM3) (10). The analysis model was the same as described in Equation [1], except that a cow effect was not included, because each parity was analyzed separately. In the first parity analyses, only cows with records on all four traits were included. Heritabilities for each trait and genetic correlations among the traits were estimated from the following equations:

$$h^2 = (4\text{Var } S_x) / (\text{Var } S_x + \text{Var } e_x) \quad [3]$$

$$r_g = \frac{(\text{Cov } S)}{[(\text{Var } S_x)(\text{Var } S_y)]^{1/2}} \quad [4]$$

where  $h^2$  is the heritability for trait  $x$ ,  $r_g$ , and  $\text{Cov } S$  are the genetic correlation and the sire covariance between traits  $x$  and  $y$ , and  $\text{Var } S_x$  and  $\text{Var } S_y$  are the sire components of variance for traits  $x$  and  $y$ . Genetic correlations between first and second parity performance for the same traits were estimated in a similar manner, with  $x$  and  $y$  representing first and second parity, respectively. Sire covariance components were estimated using the following equation (22):

$$\text{Cov } S = (\text{Var } S_c - \text{Var } S_x - \text{Var } S_y) / 2 \quad [5]$$

where  $\text{Var } S_c$  is the sire component of variance of the sum of traits  $x$  and  $y$ , and the other terms are as defined previously. Only cows with records for both parities were used to estimate between parity covariance components. Because only cows with second parity records were used to estimate variance and covariance components for second parity, these results may be biased due to selection on first parity. Environmental correlations were estimated in a similar manner, except that the sire variance and covariance components were replaced with the residual variance components in Equations [4] and [5].

The expected correlated responses to two generations of index selection for milk, fat, and CS were estimated as follows (11, 12):

$$CR_t = 2IS(h)r_t(\sigma_t) \quad [6]$$

where  $CR_t$  is the correlated response for the  $t^{\text{th}}$  trait,  $IS$  is the selection intensity,  $h$  is the accuracy of the index,  $r_t$  is the genetic correlation between the selection index and the  $t^{\text{th}}$  trait, and  $\sigma_t$  is the square root of the genetic variance for the  $t^{\text{th}}$  trait. The  $IS$  was assumed to be equal to 1.5, which is equivalent to selection of the best 17%. The  $h$  and  $r_t$  were estimated as follows:

$$h = \frac{[a'GRa]^{.5}}{[a'Ga]^{.5}} \quad [7]$$

$$r_t = \frac{a'Gb}{\{[a'Ga][b'Gb]\}^{.5}} \quad [8]$$

where  $a$  is the vector of economic weights;  $G$  is the genetic variance-covariance matrix, as estimated from the HM3 analysis;  $R$  is a matrix of order  $G$  with mean sire repeatabilities as on the diagonal and zero elsewhere; and  $b$  is a vector of the same order as  $a$  with an element of one for trait  $t$  and all other elements equal to zero. Mean repeatabilities were computed as follows:

$$MRPT_t = \frac{100}{(K_t) + 100} \quad [9]$$

where  $MRPT_t$  is the mean repeatability for trait  $t$ , and  $K_t$  is the ratio of residual to sire variance for trait  $t$ . The mean number of effective daughters was assumed to be equal to 100, which is similar to the actual situation for young sires in Israel (29).

It can be seen from Equation [6] that  $CR_t$  is dependent only on  $IS$ ,  $h$ ,  $a$ , and  $G$ , and  $IS$  and  $h$  will be constant for all traits. Thus, although  $IS$  was chosen arbitrarily, and  $h$  was computed for an arbitrary number of daughters, the relative values of  $CR_t$  will not differ. The following two indices were compared:

$$\text{Index 1} = .51 (\text{kg milk}) + 14 (\text{kg fat}) \quad [10]$$

$$\text{Index 2} = .51 (\text{kg milk}) + 14 (\text{kg fat}) + 20 (\%CS) \quad [11]$$

Index 1 is proportional to the US PD\$. With the coefficients given, a kilogram of 3.5% milk will have a value of unity. Therefore, if the profit from an additional kilogram of 3.5% milk is \$.1, then an increase of CS of 1% is assumed to have a value of \$.20.

## RESULTS AND DISCUSSION

First parity variance components for the four traits analyzed, as estimated by the HM3 analy-

ses, are listed in Table 2; and the corresponding heritabilities and the genetic and environmental correlations are listed in Table 3. All genetic and environmental correlations listed are within the range of .3 to  $-.3$ , except for the correlations between milk and fat production, which are similar to results found previously for these traits (29). The next highest correlation is the genetic correlation between milk production and DFB. All the remaining correlations are within the range of .2 to  $-.2$ . The genetic correlation between DFB and the production traits is similar to most previous reports on other populations (4, 8, 18, 27), except for Hermas et al. (11), who found an almost complete genetic correlation between DFB and production traits. The virtually nil genetic correlation between CS and production traits is probably not significantly different from the value of  $-.2$  found by Hermas et al. (11) on a small sample of Guernsey cows. However, the exact definition for this trait was different. Environmental correlations between fertility and production traits were also close to zero, similar to the results for annualized yields (8), and 305-d yields corrected for days open (27); but contrary to most previous studies (11, 13, 23) that did not correct production traits for the effect of days open. Heritabilities for fertility traits are similar to most previous studies on different populations, except for the study of

TABLE 2. First parity variance components for fertility and production traits.<sup>1</sup>

Variance component and trait	Conception status (%)	Days to first AI (d)	Milk (kg × 10 <sup>2</sup> )	Fat (kg)
Sire				
CS <sup>2</sup>	10.66	-.18	-.14	-.81
DFI <sup>3</sup>		4.38	1.32	2.29
Milk			5.32	10.57
Fat				32.03
Residual				
CS	1220.8	18.0	10.4	57.2
DFI		362.9	10.6	9.4
Milk			152.5	354.8
Fat				1116.0

<sup>1</sup>Variance components were estimated by Henderson's Method 3. The analysis model also included sire-group and herd-year-season as fixed effects. Units of the variance components are the square of the units given in parenthesis.

<sup>2</sup>Conception status.

<sup>3</sup>Days to first AI.

TABLE 3. Heritabilities and genetic and environmental correlations among first parity fertility and production traits.<sup>1</sup>

Traits	Conception status	Days to first AI	Milk	Fat
Conception status	.035	-.026	-.019	-.044
Days to first AI	.027	.048	.271	.194
Milk, kg	.024	.045	.135	.81
Fat, kg	.049	.015	.86	.112

<sup>1</sup>Heritabilities are on the diagonal, genetic correlations are above the diagonal, and environmental correlations are below the diagonal.

TABLE 4. Heritabilities and genetic and environmental correlations for first and second parity fertility traits.

Items	Conception status	Days to first AI
Heritability		
Parity 1	.035	.048
Parity 2	.022	.031
Correlation		
Genetic	.792	.732
Environmental	.090	.061

Hermas et al. (11) in which heritability for DFB was estimated to be .13. Heritabilities for yield traits are lower than most results for Holsteins, but consistent with results published for the Israeli population (29).

First and second parity heritabilities for the fertility traits, and the genetic and environmental correlations between first and second parities for these traits, are listed in Table 4. Comparable results for production traits in this and other populations are well documented (29) and are therefore not presented. Heritabilities were slightly lower in second parity. Similar to previously published results (15) genetic correla-

tions were  $>.7$  while environmental correlations were  $<.1$ . Although genetic control of different parities is not identical, it is similar, and the assumption of a common sire component of variance for all parities employed in equation [1] seems reasonable. Conversely, since the environmental correlation is so low, second parity results should not have been appreciably biased by selection.

The frequency tables of the sire evaluations for CS and DFB are given in Table 5. The 26 test sires are excluded from these frequencies. The range of RPT was from .22 to .98, with a mean of .56. Even though the heritability of CS was  $<.04$ , more than 10% of the sires were outside the range of -4 to 4% for CS. Of these sires, 16 (53%) had RPT  $>.5$ . Thus real genetic differences do exist for these traits, as previous studies have indicated (4, 8, 11, 15, 27).

The genetic, environmental, and phenotypic trends for all four traits are listed in Table 6. Although the numbers of cows and sires were relatively large, the number of progeny per sire vary greatly, and a few sires with many daughters could have had major effects on the values presented. Furthermore, as stated, the procedure of doubling sire evaluations may overestimate.

TABLE 5. Frequency table of 273 sire evaluation for fertility traits.

Range	Conception status		Range	Days to first AI	
	Frequency			Frequency	
	(no.)	(%)		(no.)	(%)
<-4	14	5	<-2	17	6
(-4)-(-2)	38	14	(-2)-(-1)	57	21
(-2)-0	91	33	(-1)-0	71	26
0-2	76	28	0-1	58	21
2-4	38	14	1-2	54	20
>4	16	6	>2	16	6

TABLE 6. Genetic (G), environmental (E), and phenotypic (P) trends in the Israeli dairy population from 1980 through 1986.

Traits	Trends		
	G	E	P
Conception status, %/yr	.96	-1.01	-.05
Days to first AI, d/yr	.09	-.72	-.63
Milk, kg/yr	154	-38	116
Fat, kg/yr	3.03	-.45	2.58

Nevertheless, it is significant that all genetic trends were positive on the scales measured, which are associated with increased profitability for all traits, except for DFB. When the genetic correlation between production and CS was negative and the genetic trend for production was positive, then the genetic trend for CS should have been negative. These results are at variance with the only other known report on genetic trends for fertility traits (11), which found negative genetic trends on the economic scale, but those results were based on only two experimental herds. All environmental trends were negative, but phenotypic trends were positive for production and slightly negative for fertility traits.

Expected correlated responses of milk, and CS to selection by Index 1 and Index 2 are presented in Table 7. Accuracy is slightly lower for Index 2, due to the lower mean repeatability for CS than for production traits. Although response for milk and fat are lower by 8% and 9% in Index 2, which gives an economic weight for CS, progress for CS will be 5.1%. If an economic value of zero is assumed for CS,

TABLE 7. Expected correlated responses of component traits and accuracies of sire evaluations for two selection indices.

Traits	Index 1	Index 2
<b>Economic weights</b>		
Milk, kg	.51	.51
Fat, kg	14.00	14.00
Conception status, %	0	20.00
<b>Response to index</b>		
Milk, kg	1175.29	1090.92
Fat, kg	27.69	25.46
Conception status, %	-.52	5.10
<b>Accuracy of index</b>	.88	.86

TABLE 8. Holstein strain differences for production and fertility traits.<sup>1</sup>

Traits	Strains		
	Israel	US	Sweden
Conception status, %	3.32	-2.24	9.44
Days to first AI, d	1.24	-.60	-1.25
Milk, kg	817.9	432.1	-103.4
Fat, kg	16.5	6.8	2.4

<sup>1</sup>Each strain is represented by five or six sires, each of which had between 36 and 82 daughters in Israel. The evaluations were based on first through third parity daughter lactations.

then the genetic decline for this trait will be .52. However, even if fertility is not included in the selection index, there may still be positive selection for fertility, due to culling of cows for nonconception. The correlated responses listed in this table were computed for two generations of sire selection, which is roughly equal to twelve years. Although less than the values presented in Table 6, the expected responses are similar to estimates of genetic trends for this population computed previously for 9 yr (29).

The group effects for the elite test sires from Israel, the US and Sweden are given in Table 8. Canadian and New Zealand sires were intermediate for fertility, and are therefore not presented. The Swedish sires were highest for CS, but lowest for the other traits. The US sires were lowest for CS but intermediate for the other three traits. Although the number of daughters of each strain was about 300, only 5 to 6 sires are represented. Even though these sires were selected based on milk production, they may be considered a random but small sample of the host populations with respect to fertility traits.

## CONCLUSIONS

Heritability for both CS and DFB was <.05. The genetic correlation between DFB and production traits was between .2 and .3, but there was no genetic correlation between CS and production traits. Genetic trends in the Israeli-Holstein population were economically positive for production traits and for CS but negative for DFB. There are significant genetic differences for fertility among national Holstein Strains; Swedish sires are favorable for CS, and US sires unfavorable.

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