

Genetic Analysis of Female Fertility of Israeli Holsteins by the Individual Animal Model

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Introduction

Numerous studies have estimated genetic correlations between female fertility and milk production, and most studies have found that the genetic correlation was economically negative (1, 2, 4, 6). There are only a few reports of realized long-term genetic trends for fertility (1, 6).

Analysis of female fertility is further complicated by the fact that there is no consensus on the trait definition, and numerous definitions have been suggested, all of which are problematic (1, 2, 5, 6). Fertility data in Israel is unique in that all cows that do not display estrous within 60 days of the last insemination are checked for pregnancy by a veterinarian (5, 6, 7). Thus, unless the cow is culled prior to 60 days, the result of each insemination is known. Two models have been used in Israel for genetic analysis of fertility, an "insemination" model, in which each insemination was considered a separate record; and a "lactation" model, in which the fertility trait was defined as the inverse of the number of inseminations to conception (5, 6, 7). This trait has been denoted previously as "conception index" (CI). Analysis of CI has the technical advantage that it can be readily adapted to analysis via the Individual Animal Model (IAM), similar to the analysis model for production traits and somatic cell score (SCS). In IAM analyses, genetic evaluations are derived for all animals included in the analysis. Thus, accurate estimates of genetic trends can be readily estimated.

The objectives of this study were to estimate the genetic and phenotypic parameters for CI, SCS, and production traits; to estimate genetic and phenotypic trends for

fertility via an IAM analysis; and to compare these trends to the trends predicted from the genetic and phenotypic variance matrices, and selection on the Israeli breeding index.

Materials and Methods

For cow that conceived, uncorrected CI was computed as $100/\text{con}$, where con = number of inseminations to conception. For cows that were inseminated at least once, but culled prior to conception, con was replaced with its expectation, $E(\text{con}_j)$, where j = number of recorded inseminations. $E(\text{con}_j)$ was estimated using 1,196,686 first through sixth inseminations in parities one through five that occurred between January 1, 1985, and August 31, 1995, for which conception status was known. We computed mean conception rate for each combination of insemination number and parity. For cows with $j < 6$, $E(\text{con}_j)$, was computed separately for each parity as follows:

$$E(\text{con}_j) = \sum_{i=j+1}^{i=13} i(p_i)pc_i \quad [1]$$

where

- i = the number of the insemination beginning with insemination $j+1$
- p_i = the probability the cow did not conceive until the i^{th} insemination, given that the cow did not conceive until the j^{th} insemination, and
- pc_i = the probability of conception at the i^{th} insemination, computed from the mean conception rate for the i^{th} insemination, computed from the data set described above.

For insemination $j+1$, $p_i = 1$. For inseminations $j+2$ to sixth, p_i was computed as follows:

$$p_i = \prod_{k=j+2}^{k=i} (1 - pc_k) \quad [2]$$

where

Π denotes multiplicative sum
 k = insemination number from $j+2$ to i , and the other terms are as defined previously.

For $k \leq 6$, pc_k was set to the appropriate mean conception rate. For $i > 6$, pc_k was set equal to pc_6 for the corresponding parity. The summation up to $i = 13$ in equation [1] was arbitrary, but preliminary studies showed that increasing i did not significantly effect $E(\text{con}_j)$, because p_i tended to zero for high values of i . $E(\text{con}_j)$ values are approximately equal to $j+3$, but increase slightly with increase in parity. This is due to a decrease in p_j with increasing parity. For cows with six or more inseminations per parity, $E(\text{con}_j)$ was arbitrary set to $E(\text{con}_5)+1$ for each parity.

Previous results showed a strong seasonal effect on conception rate of Israeli Holsteins (5, 7). Since it was not possible in a lactation model to correct for season of each insemination, we decided to correct CI for freshening month. In order to derive correction factors, uncorrected CI was computed from 518,730 lactation records from parities one through five with at least one valid insemination record. As expected from previous results, uncorrected CI was lowest for cows calving in June, which tended to have their first insemination in August, and highest for cows calving in November, which tended to have all inseminations in winter. Corrected conception index, was then computed as follows:

$$CI = CI_u - M_{ij} + M_{1-4} \quad [3]$$

where

CI = corrected conception index
 CI_u = uncorrected CI

M_{ij} = mean of CI_u for parity i and freshening month j , and

M_{1-4} = mean of CI_u for first parity cows freshening in April

Records were included only of cows with valid first parity records. Records of parities up to fifth were included, provided that there were valid record for all previous parities. All known parents and grandparents of cows with records, and the paternal grandsire and granddam of sires of cows with records were included in the analysis. CI, SCS, and milk, fat, and protein production were analyzed by the following animal model:

$$Y_{ijkl} = HYS_i + A_j + G_k + PE_j + P_l + e_{ijkl} \quad [4]$$

where

Y_{ijkl} = CI or SCS record for parity l of cow j in herd-year-season i

HYS_i = fixed effect of herd-year-season i

A_j = random portion of additive genetic merit for cow j

G_k = effect of unknown parent group k

PE_j = random permanent environmental effect of cow j

P_l = fixed effect of parity l , and

e_{ijkl} = random residual associated with each record.

Two seasons, beginning in April and October, were determined for each herd-year. Only animals with valid records for milk, fat, and protein, and freshening dates between January 1, 1985 and September 30, 1995 were included in the analysis of production traits. The numbers of animals, records, genetic groups, and HYS included in the three IAM analyses are included in Table 1.

Variance components for the additive genetic, permanent environmental, and residual variance components as a fraction of the total phenotypic variance for the three analyses are given in Table 2. These values are based on previous studies (2, 3, 6). Values for SCS and CI were validated as described below. Reliabilities were estimated as described previously. The genetic base for all evaluations was set to the mean of cows born in 1990. Genetic trends were computed as the

regression of cows' genetic evaluations on their birth dates beginning with cows born in 1981. Phenotypic trends were estimated as the regression of first parity corrected records on birth dates of the cows beginning with cows born in 1983.

Genetic and phenotypic variance-covariance matrices for first parity milk, fat, and protein production, CI, SCS, and cow culling were estimated with a sire model by multivariate REML. Cow culling was scored dichotomously. Cows that were culled during first parity were scored as one, and zero otherwise. The model included the effects of sire, HYS, sire group by year of birth, and residual. Only the sire and residual effects were considered random. HYS were determined as described above. Only records of cows with valid first parity records for all five traits, and freshening dates between January 1, 1985, and August 31, 1995, were included in the analysis. Records of cows whose sires had less than ten daughters were also deleted. Relationships other than sire and daughter were not considered in this analysis.

In addition, the genetic and phenotypic variance-covariance matrices between first and second parity CI was estimated separately by the same model. Only cows with valid records for both parities, and first parity freshening dates between January 1, 1985, and August 31, 1995, were included in the analyses. HYS was determined relative to first parity. Cows that changed herds between parities were deleted. Otherwise edits were the same.

Heritabilities were estimated as four times the sire component of variance divided by the sum of the sire and residual variances. Genetic correlations were estimated as correlations among sire variance components. Phenotypic correlations were estimated as the correlation of the sum of the sire and residual covariances.

Results and Discussion

The first parity heritabilities of milk, fat, protein, CI, SCS, and culling rate, and the genetic and phenotypic correlations among

these traits are given in Table 3. Heritabilities were 0.035, 0.158, and 0.021 for CI, SCS, and culling rate, respectively. Heritabilities for the production traits were similar to most previous studies. Genetic correlations were negative between CI and milk production traits, and positive between SCS and milk production traits. Both of these relationships are economically unfavorable, but similar to most previous studies. Weller (6) found no genetic correlation between CI and either milk or fat on a previous analysis of this population using Henderson's method 3. Hermas et al. (1) found a negative genetic correlation between milk and CI, but positive correlations between CI, and fat and protein. Reheja et al. (4) found no genetic correlations between milk production and three fertility traits. As expected, the genetic correlations between culling rate on one hand and milk production traits and CI on the other were all negative. The positive genetic correlation between culling rate and SCS is also as expected. The genetic correlation between CI and SCS was -0.37. Thus selection for either milk or protein should lead to an increase in SCS and a decrease in CI. The genetic and environmental correlations between first and second parity CI were 0.9 and 0.08, respectively. Thus, the evaluation model used, which assumes a common genetic effect over all parities is a reasonable approximation.

Annual genetic and first parity phenotypic means by birth year are plotted for CI in Figure 1. Realized genetic trends after ten years of selection on the current breeding index, the predicted genetic trends based on selection index theory, and the phenotypic trends are given in Table 4. The realized genetic trends were computed as the annual genetic trends times 10. Realized genetic gains were greater than the predicted gain for milk, and less for fat and protein. This was expected, considering that selection until 1990 was chiefly for milk. The realized genetic trends for both SCS and CI are not at all similar to the predicted values by either selection on the breeding index, or direct selection on milk production. The realized genetic trend for CI was slightly positive, despite the predicted negative trend, and the realized genetic trend for SCS, although

positive, as predicted, was four-fold the predicted value.

Weller (6) in a previous analysis of this population found a positive genetic trend of nearly 1%/yr for CI, based on a sire model without inclusion of a parity effect in the model. However, selection during the period considered was for the previous Israeli index based chiefly on milk quantity. Furthermore, recent studies have shown that in a multiparity analysis, estimates of genetic trends can be severely biased if a parity effect is not included in the analysis model.

The discrepancies between the realized and predicted genetic trends for SCS and CI cannot be explained by random variation among cows. The standard error for the ten year genetic trend for CI was 0.017. The standard errors of all other genetic trends were less than 1% of the trends. However, the regression standard errors do not reflect random variation among sires. About 50 sires are progeny tested annually in the Israeli Holstein population, and only 4-5 of these sires are returned to general service. Thus, random variation among sires for CI could be a significant factor. The positive trend for CI may also be due to positive selection for fertility at the farm level, as indicated by the negative genetic and phenotypic correlation between cow culling and CI. Other possible explanations could be selection on criteria other than the recommended breeding index, for example conformation traits which are not included in the index.

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Table 1. The numbers of animals, records, genetic groups, and HYS included in the animal model analyses of conception index and somatic cells

Factor	Conception index	Somatic cell score	Milk, fat, and protein production
Sires	903	876	1033
Total cows	229,631	217,198	301,870
Cows born since 1980	214,102	209,328	285,812
Cows with records	185,613	120,904	221,542
Total records	440,558	224,869	500,151
Genetic groups	48	48	48
HYS	4,842	8,821	11,782

Table 2. Variance components for animal model analyses as a fraction of the total phenotypic variance

Variance component	Conception index	Somatic cell score	Milk, fat, and protein production
Additive genetic	0.025	0.100	0.250
Permanent environmental	0.075	0.250	0.250
Residual	0.900	0.650	0.500

Table 3. The first parity heritabilities, and the genetic and phenotypic correlations for milk, fat, protein, conception index (CI), mean lactation somatic cell score (SCS), and culling rate. Genetic correlations are above the diagonal, phenotypic correlations are below the diagonal, and heritabilities are on the diagonal

	Milk	Fat	Protein	CI	SCS	Culling
Milk	0.251	0.445	0.743	-0.286	0.116	-0.510
Fat	0.597	0.354	0.608	-0.301	0.054	-0.270
Protein	0.873	0.663	0.238	-0.419	0.172	-0.400
CI	0.037	0.023	0.023	0.035	-0.366	-0.469
SCS	-0.067	-0.045	-0.029	-0.024	0.158	0.203
Culling	-0.144	-0.100	-0.133	-0.344	0.080	0.020

Table 4. The predicted and realized genetic trends and the first parity phenotypic trends after ten years of selection on the Israeli breeding index¹

Trait ²	Genetic trends		Phenotypic trends
	predicted	realized	
Milk (kg)	718.7	1039.5	1372.2
Fat (kg)	37.0	22.3	41.1
Protein (kg)	31.1	26.8	32.3
CI (%)	-5.50	0.40	-2.39
SCS	0.13	0.53	0.28
Culling rate (%) ³	-3.4	-	-

¹ The breeding index = -0.274 (kg milk) + 6.41 (kg fat) + 34.85 (kg protein).

² Trait units are given in parenthesis.

³ Genetic evaluations, and realized trends were not computed for culling rate.

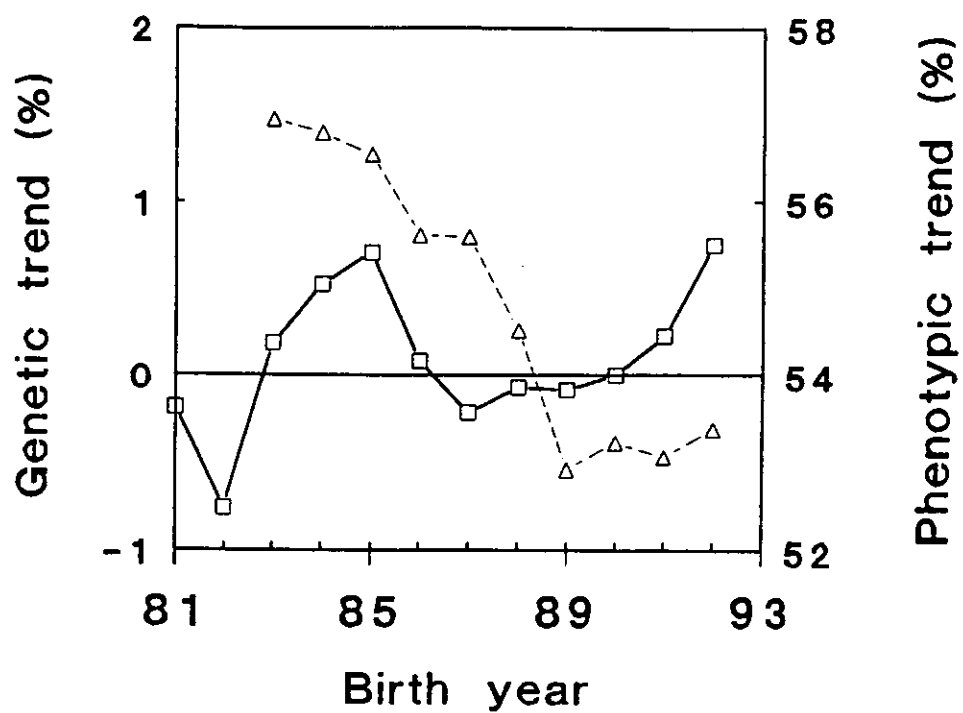


Figure 1. Annual genetic and first parity phenotypic means by birth year for conception index. (□- □), genetic trend; (Δ- -Δ) phenotypic trend.