

# Models for Genetic Analysis of Dystocia and Calf Mortality

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## ABSTRACT

Calvings of 106,750 Israeli Holstein heifers were analyzed for dystocia and calf mortality, which were scored dichotomously. Models fitted included herd-year-season, sex of calf, calving age, calving month, sire of cow, sire of calf, and groups of sire of cow and calf. Herd-year-season, sire of cow and of calf, and residuals were random with diagonal variance-covariance matrices. Traits were analyzed with and without a herd-year-season effect, and dystocia was analyzed separately for male and female calvings and with both sexes combined. Variance components were estimated by REML for linear models and by the counterpart of REML for threshold models. Heritability estimates were two to four times larger in threshold than in linear models, but correlations between corresponding sire evaluations were all greater than .9. Correlations between evaluations computed with and without herd-year-season effects were .9 for sire of calf evaluations for dystocia and greater than .97 for all other evaluations. Correlations between sire evaluations computed separately for male and female calvings were between .3 and .7. Thus, calving difficulty is expressed differently in male and female calvings. Genetic trends were unfavorable for dystocia but favorable for calf mortality. Phenotypic trends were curvilinear with maxima in 1982 and 1983 for calf mortality and dystocia.

## INTRODUCTION

Dystocia and calf mortality are of economic importance to dairy farmers (13). These traits have low heritability, a high genetic correlation, and a sizable residual correlation (1, 2, 4, 12, 13, 14, 17, 18, 19, 20, 21, 22). Several studies have suggested that the threshold model, which assumes the existence of an underlying normal variable, is theoretically appealing for genetic analysis of many categorical traits (3, 4, 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 22), and several studies have applied this model to analysis of field data (4, 14, 22). Because a threshold model analysis is nonlinear and involves normal probability functions, computational complexity and computing resources required are greater than in a linear model analysis. However, recent developments in computers and programming techniques have made large-scale threshold model analyses feasible (16).

A number of studies indicate the effect of sire of calf is greater than that of the sire of the cow (1, 13, 17, 18, 19, 21, 22), that the incidence of dystocia and calf mortality is higher for male calves (1, 2, 4, 13, 14, 17, 18, 19, 20, 21, 22), and that heritabilities for these traits are several times larger for first than for later parities (1, 13, 17, 21, 22). Van Vleck and Edlin (20) suggested a four-trait analysis for dystocia consisting of the four combinations of first and later parity, and male and female calvings. Weller et al. (22) concluded that the usefulness of analysis of later parity calving traits was doubtful due to their minuscule heritability and to the apparently low genetic correlations between first and later parities.

Most studies have assumed a fixed herd-year-season (HYS) effect (1, 2, 12, 14, 17, 18, 20), but a few studies have either assumed this effect to be random (4, 22) or did not include it in the model (19, 21). Justifications for deletion of this effect are: 1) inclusion of a factor with many levels complicates the analysis; 2) in order to create sufficient ties between different HYS, it is necessary to include large quantities of relatively old data on sires no longer of

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Received June 22, 1988.

Accepted April 6, 1989.

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interest; 3) the HYS variance component apparently accounts for only a small fraction of the total variance; 4) because calving traits are only of secondary economic importance, relative to production traits, associations among sires and HYS effects for these traits are likely to be random; and 5) if the HYS variance component is small, relative to the residual variance, and the distribution of sires across HYS is random, as suggested, then the increase in accuracy due to inclusion of this effect in the model will be negligible. Djemali (personal communication) found that sire evaluations computed with fixed and random HYS effects were appreciably different. No comparison has been made between sire evaluations computed with and without HYS effects in the model. Because fixed HYS and elimination of HYS effects can be considered to be opposite extremes of analysis with random HYS, the comparison of most interest would be between random versus no HYS effect.

The objectives of this study were: 1) to examine the effect of alternative model specifications for threshold and linear model analyses of calving traits, with emphasis on the role of HYS and sex effects; and 2) to estimate genetic parameters and genetic and environmental trends for these traits under the models studied.

#### MATERIALS AND METHODS

Data were 106,750 first parity calving records of milk-recorded Israeli-Holsteins, calving between January 1978 and June 1985. Dystocia (DC) was scored as 0 if the calving was normal, or as 1 if it was difficult; calf mortality (CM) was scored 0 for a live birth or 1 if the calf died within 48 h of birth. These records were the first-parity subset of the data set described by Weller et al. (22). Basic statistics are presented in Table 1. The edits performed on the original data set prior to analysis have been described previously (22). The ratio of male to female calves was 1.077, which is consistent with the general situation in the Israeli-Holstein population.

All analyses were by both threshold (TM) and linear models (LM). The following basic model was used for both DC and CM:

$$Y_{ijklmnopq} = \text{HYS}_i + \text{GS}_j + \text{SIRE}_{jk} + \text{GSC}_l + \text{SC}_{lm} + \text{S}_n + \text{A}_o + \text{M}_p + e_{ijklmnopq} \quad [1]$$

TABLE 1. Basic statistics of the data set analyzed.

	Sex		
	Both	Males	Females
Incidence (%) of			
Dystocia	8.05	10.89	5.00
Calf mortality	7.66	10.19	4.93
Dystocia + calf mortality	4.17	5.88	2.33
Number of			
Records	106,750	55,360	51,390
Herd-year-seasons	5882	5365	5252
Sires of cow	377	362	360
Sires of calf	329	322	313

where:

- $Y_{ijklmnopq}$  = record on cow  $q$ ;
- $\text{HYS}_i$  = random effect of herd-year-season  $i$ ;
- $\text{GS}_j$  = fixed effect of group  $j$  of sires of cows;
- $\text{SIRE}_{jk}$  = random effect of sire of cow  $k$  in group  $j$ ;
- $\text{GSC}_l$  = fixed effect of group  $l$  of sires of calves;
- $\text{SC}_{lm}$  = random effect of sire of calf  $m$  in group  $l$ ;
- $\text{S}_n$  = fixed effect of sex  $n$ ;
- $\text{A}_o$  = fixed effect of calving age  $o$ ;
- $\text{M}_p$  = fixed effect of calving month  $p$ ;
- and
- $e_{ijklmnopq}$  = random residual.

Calving seasons were October to March, and April to September. Sires were grouped by year of birth, with all sires born prior to 1972 in group 1. Groups 2 to 7 included all sires born during each subsequent 2-yr interval. Values for calving month correspond to the 12 calendar mo. Because HYS was random, there was no "confounding" between HYS and calving month. There were 10 calving ages, which were grouped by month from 21 to 30 mo. The 1st also included cows calving prior to 21 mo of age, and the 10th included cows that calved after 30 mo. The distribution of records by fixed effects is presented in Table 2. The mode of calving age was 24 mo. Calvings were less frequent in the early summer, because fertility is lowest in late summer.

The data were also analyzed without a HYS effect in model [1] for both traits and for DC

TABLE 2. Distribution of records by level of fixed effects.

	Sex		
	Both	Males	Females
<b>Group of sires of cow</b>			
1	35,295	18,720	16,575
2	14,749	7511	7238
3	24,755	12,766	11,989
4	19,152	9871	9281
5	8241	4254	3987
6	4558	2238	2320
<b>Group of sires of calf</b>			
1	18,640	9722	8918
2	14,271	7508	6763
3	22,282	11,606	10,676
4	45,705	23,535	22,170
5	3414	1717	1697
6	1576	831	745
7	862	441	421
<b>Calving age (mo)</b>			
<22	963	491	472
22	6609	3381	3228
23	27,704	14,029	13,675
24	31,896	16,718	15,178
25	18,386	9560	8826
26	10,017	5315	4702
27	5536	2915	2621
28	3126	1616	1510
29	1816	967	849
>29	697	368	329
<b>Calving month</b>			
Jan	11,233	5829	5404
Feb	9491	5015	4476
Mar	9233	4750	4483
Apr	8026	4108	3918
May	6921	3584	3337
Jun	4966	2645	2321
Jul	5242	2697	2545
Aug	6380	3283	3097
Sep	10,335	5372	4963
Oct	11,159	5848	5311
Nov	11,470	5854	5616
Dec	12,294	6375	5919
<b>Calving year</b>			
1978	7766	4118	3648
1979	9693	5385	4308
1980	5053	2598	2455
1981	15,470	7955	7515
1982	17,993	9310	8683
1983	19,840	10,324	9516
1984	22,414	11,331	11,083
1985	8521	4339	4182

for male and female calvings separately. In the analyses without HYS effect, the model included the effects of calving year and no sex effects were included in the separate analyses of male and female calvings. Otherwise the

models for all analyses were the same. Analysis was facilitated by assuming that all random effects were mutually uncorrelated with diagonal dispersion matrices. For analyses that included a HYS effect, variance of this effect was

assumed known and equal to 10% of the residual variance, which is similar to estimates calculated from US data (4). These assumptions allowed absorption of HYS, which had many levels in all analyses. The assumption of diagonal dispersion matrices was inaccurate for SIRE and SC effects because sires were related. The assumption of a null correlation between these effects was also an approximation, because several studies have found nonnegligible correlations between SIRE and SC effects (13, 17, 18, 21, 22).

A program based on principles described by Misztal et al. (16) and adapted to the CRAY XMP-48 supercomputer was used for analysis. The SIRE, SC, and residual variance components were estimated by REML for linear model analyses and by the counterpart of REML for threshold models (5, 9, 10). Details of the specific strategy used have been described previously (22).

Sire evaluations were computed as the sum of the sire and sire group effects. Heritability ( $h^2$ ) as a trait of the cow was calculated as:

$$h^2 = \frac{4\text{VAR}(\text{SIRE})}{\text{VAR}(\text{SIRE}) + \text{VAR}(\text{SC}) + \text{VAR}(\text{HYS}) + \text{VAR}(\text{e})} \quad [2]$$

where VAR(-) denotes the variance component for the corresponding effect. Assuming that the SIRE effect includes half of the maternal genetic effect and one-quarter of the direct genetic effect, the numerator of this estimate of "heritability" includes one-quarter of the direct genetic variance for this trait plus all of the maternal genetic variance and the covariance between these effects. As stated previously, VAR(HYS) was assumed to be 10% of the residual in the analyses that included this factor and zero in the analyses that did not. Heritability as a trait of the calf was computed in a similar manner except that VAR(SC) replaced VAR(SIRE) in the numerator. Because the SC effect includes one-half of the direct effect, the numerator of this estimate of heritability includes only the direct genetic variance for these traits.

The unit of measurement of estimates and predictions in threshold models is the residual standard deviation on the underlying scale. To facilitate comparison between LM and TM results, the TM solutions were multiplied by the square root of the corresponding LM residual variance component so that the units of the two

models would be equivalent. Results obtained with the two different methods of analysis were compared in terms of ratios of variance components (heritability) and correlations between solutions or evaluations. Correlations between sire evaluations were also computed for all sires and for sires with at least 20 and at least 50 records in both analyses.

Phenotypic trends were estimated as the regression of mean monthly DC and CM values on calving month, weighted by the number of observations, and corrected for the effect of calving month, so as to remove seasonal influences. Direct and maternal genetic trends were estimated from the analyses, which included both sexes and the HYS effect. Direct genetic trends were estimated as twice the regression of the transmitting abilities of each calf's sire on freshening date. The maternal genetic trend was estimated as twice the regression of the transmitting ability of each cow's sire on freshening date, minus the SC regression as computed above. These estimates assume that the SC effect includes half of the direct genetic effect and that the SIRE effect includes half of the maternal genetic effect and one-quarter of the direct genetic effect.

Environmental trends were estimated by two methods: 1) the difference of the phenotypic and genetic trends, and 2) the regressions of year effects on freshening year from the analyses without HYS effects weighted by the number of observations per year. Although genetic and phenotypic trends were estimated from the analyses computed with HYS effects, environmental trends by the second method were estimated from the analyses without HYS effects, because only these analyses included year effects. Inspection of monthly mean incidence for DC and CM indicated that the phenotypic trends for these traits were curvilinear. Therefore, quadratic regressions of DC and CM on calving month were also computed. All trends were expressed on a per year basis.

## RESULTS

Central processing unit (CPU) times and number of rounds of iteration for the DC analyses are given in Table 3. Results of the CM analyses were similar and are therefore not presented. The LM analyses required 8 to 9 rounds of REML iteration, and the TM analy-

TABLE 3. Central processing unit (CPU) times and number of iterations for the dystocia analyses.<sup>1</sup>

Sexes	HYS Effect <sup>2</sup>	Total CPU minutes		No. of iterations <sup>3</sup>	
		TM	LM	TM	LM
Both	-	4.0	1.7	8	9
Both	+	9.0	3.0	7	8
Males	+	7.3	2.8	8	9
Females	+	7.2	2.7	8	9

<sup>1</sup>TM = Threshold model; LM = linear model.

<sup>2</sup>- = Herd-year-season (HYS) not in the model; + herd-year-season included in the model.

<sup>3</sup>Number of Fisher scoring rounds for TM and number of REML rounds for LM analyses. For TM analyses, three rounds of expectation maximization iteration were performed within each Fisher scoring round.

ses required 7 to 8 rounds of Fisher scoring iteration to converge. However, computing times for LM analyses were less than half of those in the corresponding TM analyses. Similarly, computing times for models without HYS effects were about half as large as for the complete model. Computing times for standard mainframe computers would probably be considerably greater than for the CRAY XMP-48 supercomputer.

Variance component and heritability estimates for all analyses are presented in Table 4. In agreement with previous studies (12, 21, 22), heritability was higher for DC than for CM. Heritability for CM, on the linear scale, was fourfold the estimate of Martinez et al. (12), who analyzed all parities jointly, and TM estimates were even larger. In the LM analyses, heritability of DC was higher for male than for female calvings. Heritability estimates from LM analyses of dichotomous traits will be dependent on incidence (7). Therefore, this result is not an indication that heritability for male calves is greater on the underlying scale. In the TM analyses, in which estimates of heritability should not be affected by the mean frequency, heritability was higher in male than in female calvings as a trait of the calf but lower as a trait of the cow. Heritability and variance component estimates, as a fraction of residual variance, were similar in analyses with and without HYS effects. For all LM analyses, the SC component of variance was greater than the SIRE component. In the TM analyses, the SIRE component of variance was greater than the SC component for DC of female calvings and for CM.

Solutions for fixed effects are presented in Table 5 for the combined sex analyses of DC

and CM without HYS in the model, and in Table 6 for the analyses of DC by sex. Seasonal and age effects on CM and DC, for the combined sex analyses with inclusion of a HYS effect, have been reported previously (22). In the combined sex analyses without HYS effects (Table 5), trends were similar for fixed effects for TM and LM. Solutions generally followed similar trends for both traits, except for the group of sire of calf solutions. For example, group 4 had the highest TM solution for DC but was intermediate for CM. Fixed effect solutions were dissimilar for the separate male and female DC analyses (Table 6).

Correlations between fixed effect solutions for DC and CM have been presented previously (22). All correlations between first parity TM and LM fixed effect solutions were greater than .96, similar to the results found in the previous study. Correlations between fixed effect solutions for analyses with and without HYS in the model and for separate male and female calving analyses are presented in Table 7. The correlations between fixed effects with and without HYS effects in the model were all greater than .95, except for the SC group effect in the DC analyses, which was less than .3. All correlations between fixed effect solutions for male and female calvings were less than .5, except for calving month.

Correlations between SIRE and SC evaluations with and without HYS effects are presented in Table 8 for sires with at least 20 progeny. All correlations were greater than .96, except for SC evaluations for DC, which were about .9. Correlations of evaluations of all sires were marginally lower, whereas those computed only on sires with at least 50 daughters were slightly higher. Correlations between solu-

TABLE 4. Variance component and heritability estimates obtained with the threshold and liner model analyses.

Trait	Sexes	HYS Effects <sup>1</sup>	Model <sup>2</sup>	Variance components <sup>3</sup>		Heritability <sup>4</sup>	
				SIRE	SC	SIRE	SC
Dystocia	Both	-	TM	.0274	.0368	.103	.138
			LM	.0086	.0167	.034	.065
	Both	+	TM	.0287	.0406	.098	.139
			LM	.0088	.0181	.031	.063
	Males	+	TM	.0300	.0439	.102	.150
			LM	.0114	.0229	.040	.081
Females	+	TM	.0355	.0330	.122	.113	
		LM	.0090	.0147	.031	.051	
Calf mortality	Both	-	TM	.0235	.0212	.090	.081
			LM	.0071	.0096	.028	.038
Calf mortality	Both	+	TM	.0241	.0202	.084	.071
			LM	.0076	.0088	.027	.031

<sup>1</sup>- = Herd-year-season (HYS) not in the model; + = herd-year-season included in the model.

<sup>2</sup>TM = threshold model; LM = linear model.

<sup>3</sup>As a fraction of residual variance. SIRE = Sire of cow, SC = sire of calf.

<sup>4</sup>Herd-year-season component was assumed to be .1 of the residual variance.

tions were very similar to the corresponding evaluation correlations except for SC solutions for DC. In this case, correlations between solutions were slightly greater than between evaluations. This is not surprising, because the SC group solutions were nearly uncorrelated for DC.

Correlations among male, female, and combined (both sexes) DC evaluations are presented in Table 9 for sires with at least 20 records in each comparison. Although all correlations differed from zero ( $P < .001$ ), SIRE correlations between male and female calvings were as low as .35 and .40 for LM and TM, respectively. The SC correlations were also under .7. Correlations between male or female calving evaluations and evaluations based on both sexes were higher than those between male and female calvings, due to a part-whole relationship. Correlations between male and combined evaluations were higher than those between female and combined evaluations. Two factors may account for this: there were more male than female calvings, and heritability for male calvings was generally higher than for female calvings.

Genetic, environmental, and phenotypic trends are presented in Table 10 for combined DC and CM analyses for both TM and LM.

The estimates of environmental trends presented are the differences between the phenotypic and genetic trends. Estimates of environmental trends computed from the regressions of year solutions on years are not presented, because none differed significantly from zero ( $P > .01$ ). (There were only eight values for the year effects.) Phenotypic trends are slightly different for TM and LM because each was calculated using the seasonal effects as estimated from the corresponding analysis. Phenotypic trends were negative (favorable) for CM and positive (unfavorable) for DC, but none of these trends was different from 0 ( $P < .01$ ). There was, however, a significant curvilinear phenotypic trend for both traits ( $P < .001$ ) with maximum dystocia near the end of 1981 and maximum calf mortality at the beginning of 1981 for CM. Genetic trends estimated by TM and LM were in the same direction except for the direct genetic trend for DC. Genetic trends for DC were generally unfavorable, whereas both maternal and direct trends for CM were favorable. Genetic trends for milk production in Israel during this period were about 100 kg/yr. Most estimates of genetic correlations between calving and production traits have not differed from 0 (13), and this is also the case for the Israeli population (unpublished data).

TABLE 5. Solutions for fixed effects for the analyses of dystocia and calf mortality without herd-year-season effects.<sup>1</sup>

	Dystocia		Calf mortality	
	Threshold model	Linear model	Threshold model	Linear model
	(%)			
Group of sires of cow				
1	-.74	-.36	.38	.28
2	-.62	-.27	1.08	.71
3	-2.85	-1.41	-1.74	-.90
4	.31	.33	.51	.31
5	-.11	.04	-.26	-.09
6	0	0	0	0
Group of sires of calf				
1	1.04	1.09	-.96	-.18
2	.05	.74	-2.07	-.80
3	1.64	1.52	.18	.67
4	1.79	1.43	-1.22	-.28
5	-.70	.02	-4.58	-2.31
6	-1.69	-.68	-2.77	-1.36
7	0	0	0	0
Sex				
Male	11.41	5.92	10.07	5.22
Female	0	0	0	0
Calving age, mo				
>22	2.64	1.66	2.62	1.75
22	1.15	.72	.98	.78
23	-.28	-.06	-.30	.07
24	-.73	-.32	-.54	-.11
25	-1.40	-.63	-.60	-.12
26	-1.63	-.78	-.92	-.32
27	-1.26	-.63	-.25	.04
28	-.81	-.36	-.75	-.24
29	-1.52	-.87	-1.18	-.54
>29	0	0	0	0
Calving month				
Jan	1.60	.92	1.14	.64
Feb	3.42	2.05	1.38	.80
Mar	3.22	2.05	.90	.50
Apr	.03	-.03	-.26	-1.28
May	-2.29	-1.12	-3.50	-1.69
Jun	-3.91	-1.95	-2.43	-1.23
Jul	-1.66	-.88	-.55	-.32
Aug	.61	.25	.04	.02
Sep	-.52	-.27	-1.06	-.53
Oct	-1.10	-.56	-1.26	-.64
Nov	-.80	-.37	-.97	-.48
Dec	0	0	0	0
Calving year				
1978	-7.97	-3.64	-.05	-.04
1979	-10.24	-5.18	.34	-.13
1980	-1.94	-1.37	-.39	-.36
1981	-.09	-.32	1.17	.47
1982	2.35	1.24	2.18	1.09
1983	2.62	1.45	1.75	.82
1984	.64	.40	.54	.26
1985	0	0	0	0

<sup>1</sup>Threshold model solutions were multiplied by the square root of the residual variance component from the linear model analyses.

TABLE 6. Solutions for fixed effects for the separate sex analyses of dystocia with herd-year-season effects.<sup>1</sup>

	Solutions			
	Males		Females	
	Threshold model	Linear model	Threshold model	Linear model
<b>Group of sires of cow</b>				
1	-2.32	-.12	-.58	-.31
2	-.50	-.60	-.01	-.10
3	-4.56	-2.32	-1.79	-.88
4	.89	.44	.52	.21
5	.25	1.37	-1.24	-.81
6	0	0	0	0
<b>Group of sires of calf</b>				
1	-.36	.06	-3.38	-1.88
2	-1.84	-.18	-4.57	-2.22
3	1.72	1.56	-1.48	-.84
4	.68	.67	-1.83	-1.11
5	.37	.18	-4.43	-2.35
6	1.54	.98	-3.43	-1.99
7	0	0	0	0
<b>Calving age, mo</b>				
<22	6.15	3.85	-.21	-.28
22	4.57	2.70	-2.47	-1.37
23	1.97	1.35	-2.43	-1.24
24	1.24	.91	-2.60	-1.34
25	.72	.61	-3.53	-1.79
26	-.17	.03	-3.46	-1.81
27	-.21	-.09	-2.88	-1.66
28	.17	.07	-2.79	-1.51
29	-1.65	-1.04	-1.76	-1.10
>29	0	0	0	0
<b>Calving month</b>				
Jan	.83	.39	3.39	1.65
Feb	3.76	2.19	2.40	.96
Mar	2.52	1.43	4.11	1.86
Apr	-.04	-.11	.48	.04
May	-2.69	-1.61	-1.40	-.61
Jun	-4.96	-2.78	-1.33	-.54
Jul	-3.02	-1.64	1.01	.45
Aug	-.30	-.34	2.31	1.08
Sep	.27	.35	.28	.12
Oct	-.82	-.34	-.73	-.44
Nov	-1.17	-.59	-.27	-.12
Dec	0	0	0	0

<sup>1</sup>Threshold model solutions were multiplied by the square root of the residual variance component from the linear model analyses.

## DISCUSSION

Although CPU times were lower for the analyses without HYS effects, these results may not extrapolate to other situations. In the present study, variance components were estimated using time-consuming techniques. In routine evaluations, it is generally assumed that good estimates are available a priori. Furthermore, with the recent developments in computers,

CPU time per se has become a less important factor. Thus, the main computational reason for disregarding HYS effects would be reduced programming time, which is still a significant factor in computing costs.

Except for SC evaluations for DC, evaluations with and without HYS effects were quite similar. In Israel, sires of calves found unfavorable for calving traits are generally not mated



TABLE 7. Correlations between solutions for fixed effects obtained in different analyses.

Comparison	Model <sup>1</sup>	Effects			
		Group of sires of		Calving	
		Cow	Calf	Age	Month
<b>Dystocia</b>					
With vs. without HYS <sup>2</sup>	TM	.97	.25	.98	.99
	LM	.98	.28	.97	.98
Male vs. female	TM	.45	.38	.34	.73
	LM	.25	.22	.31	.66
<b>Calf mortality</b>					
with vs. without HYS <sup>2</sup>	TM	.97	.99	.99	.99
	LM	.98	.99	.99	.98

<sup>1</sup>TM = Threshold model; LM = linear model.

<sup>2</sup>Fixed effect solutions for the combined sex analyses with a HYS effect in the model are presented by Weller et al. (22).

to heifers. However, calving traits are not important when choosing sires as mates of older cows. Therefore, the distribution of heifer mates across herds may not be random, and SC evaluations that disregard HYS may be biased. Although computing costs can be considerably reduced by excluding HYS from the model, it would appear that for dystocia it may not be advisable to do so, even if differences among herds for this trait merely reflect subjectivity in recording rather than biological effects.

Heritabilities as a trait of the calf were higher for male than for female calvings by both TM and LM. As a trait of the cow, heritability was higher for males by LM but lower for TM. This is not surprising, because LM heritability estimates are affected by the incidence of DC (7), which was higher for males. Although calving traits are generally

considered to have low heritability, the SC heritability for the TM male analysis was 15%. Estimates of heritability for production traits in dairy cattle are generally in the range of 20 to 30%.

A possible explanation for the differences between results from male and female calvings with respect to SIRE and SC components of variance can be obtained from the biology of dystocia. Difficult births are more common for male calves because these calves tend to be larger (13). Thus, for male calves the main factor causing dystocia may be the size of the calf, which is partially determined by the direct genetic effect. For female calves, calf size may be less important than pelvic conformation of the dam. Part of the genetic component of this

TABLE 8. Correlations between sire evaluations obtained with and without herd-year-season effects.<sup>1</sup>

Trait	Model	Evaluation	
		Sire of cow	Sire of calf
Dystocia	Threshold	.97	.87
	Linear	.97	.90
Calf mortality	Threshold	.99	.99
	Linear	.98	.98

<sup>1</sup>Correlations were computed using sires with at least 20 progeny. There were 313 sires of cow and 171 sires of calf that met this criterion.

TABLE 9. Correlations between male, female, and combined (both sexes) sire evaluation for dystocia.<sup>1</sup>

Comparison	Model	Evaluations	
		Sire of cow	Sire of calf
Male vs. female	Threshold	.40	.68
	Linear	.35	.67
Combined vs. male	Threshold	.89	.94
	Linear	.89	.94
Combined vs. female	Threshold	.74	.84
	Linear	.71	.86

<sup>1</sup>Correlations were computed using sires with at least 20 progeny in both the male and female calving analyses. There were 290 sires of cow and 113 sires of calf that met this criterion.

TABLE 10. Genetic, environmental, and phenotypic trends (%/yr) for first parity dystocia and calf mortality.

Trait and model	Trends			
	Genetic		Environmental	Phenotypic
	Direct	Maternal		
Dystocia				
Threshold	.314*	.409*	-.418	.305
Linear	-.064	.213*	.178	.327
Calf mortality				
Threshold	-.475*	-.196	.498	-.173
Linear	-.224*	-.059	.126	-.157

\* $P < .01$ .

trait is expected to be expressed in the SIRE variance component. The solutions for the effect of calving age also support this hypothesis. An indication that male and female calvings are under different physiological control is that the incidence of dystocia decreased with calving age for male but not for female calvings (Table 6).

If the genetic correlation between male and female calvings is less than unity, then the mean of separate sex heritabilities would be expected to be higher than heritability for a combined analysis, assuming equal representation of sexes (23). This was true in all cases except for the SC effect in the TM analyses. For SIRE effects, both male and female heritabilities were higher than the combined analysis values. Also, correlations between the separate sex evaluations were relatively low, even when restricted to sires with large number of daughters. Furthermore, correlations between solutions for corresponding fixed effects were also low. These results cannot be ascribed to the effect of random sampling, because there were more than 300 observations for each fixed effect.

The evidence presented indicates that male and female calvings should be analyzed separately or possibly by a multitrait analysis. However, the gain from separate sex evaluations may be slight if the separate sex evaluations are combined into an index with equal economic weight for male and female calvings. The correlations between the combined analyses evaluations and the means of the separate sex evaluations were greater than .98 for both LM and TM. Nevertheless, separate sex evaluations may have intrinsic economic importance, especially for CM, due to fluctuations in the relative prices of milk and meat.

Results for genetic and phenotypic trends were not easy to interpret. Different results were found for TM and LM analyses and for the two traits. In fact, genetic trends for DC and CM were generally in the opposite direction. These results are surprising in view of the very high correlations between the TM and LM evaluations and the relatively high genetic correlation between DC and CM (12, 22). However, estimates of genetic trends under .2%/yr were not different from zero ( $P > .01$ ) for this data set. Furthermore, the time period analyzed was only 7.5 yr, which is near the mean generation interval in Israel. The significant curvilinear phenotypic trends found for both traits may in fact represent trends in recording rather than physiological effects. It is possible that in the early years some herd managers may have listed all calvings as "normal". It would seem important to monitor genetic and environmental trends as the breeding program develops further.

#### ACKNOWLEDGMENTS

We thank I. Misztal for providing computer programs used in this analysis. This research was supported by the US-Israel Binational Agricultural Research and Development Fund, Project No. US-805-84, and by the National Center for Supercomputing Applications, Champaign, IL.

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