

University of Nebraska - Lincoln

DigitalCommons@University of Nebraska - Lincoln

---

Faculty Papers and Publications in Animal  
Science

Animal Science Department

---

January 1985

## Trends in Genetic and Phenotypic Variances for Milk Production

S. L. Mirande  
*Cornell University*

L. Dale Van Vleck  
*University of Nebraska-Lincoln*, [dvan-vleck1@unl.edu](mailto:dvan-vleck1@unl.edu)

Follow this and additional works at: <https://digitalcommons.unl.edu/animalscifacpub>



Part of the [Animal Sciences Commons](#)

---

Mirande, S. L. and Van Vleck, L. Dale, "Trends in Genetic and Phenotypic Variances for Milk Production" (1985). *Faculty Papers and Publications in Animal Science*. 293.  
<https://digitalcommons.unl.edu/animalscifacpub/293>

This Article is brought to you for free and open access by the Animal Science Department at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Faculty Papers and Publications in Animal Science by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

# Trends in Genetic and Phenotypic Variances for Milk Production

S. L. MIRANDE and L. D. VAN VLECK

Department of Animal Science  
Cornell University  
Ithaca, NY 14853

## ABSTRACT

Residual standard deviations estimated separately for each year of first freshening from first lactation milk records of artificially sired Holstein cows increased from 1960 to 1982, especially after 1976. The pattern on the square root scale was similar. On the logarithmic scale, residual standard deviations were smallest in the middle of the time period. Heritabilities estimated from paternal half-sib correlations were greater than .30 on all scales until about 1976 when estimates began to go below .20. Estimates were similar for untransformed and transformed records. When records were divided into four herd production groups within each year, the same patterns over time for residual standard deviations were observed as for the combined data for each year. On the untransformed scale, the largest standard deviations were associated with high herd production and the smallest with low herd production. On the square root scale, standard deviations were similar for all herd production groups. On the log scale, residual standard deviations were smallest with high production and largest with low production—the reverse of the untransformed scale, although differences were smaller. Heritability was highest with middle-production groups and smallest with low-production groups. Data available for each year ranged from 1,400 and 2,849 to 6,821 and 58,082 records, respectively, of daughters of sampling and proved bulls with from 115 to 513 sampling bulls.

## INTRODUCTION

Everett et al. (3) estimated residual variances for individual herds by summing squared

residuals from a model used to estimate transmitting ability of cows for milk yield (6). They reported that herds on test for a longer time and herds using more artificial insemination (AI) had smaller residual variances than herds on test a short time and using little AI. Previous analyses, however, suggested that variance increases as production increases (7,15,20,21), which might explain results of Everett et al. (3); herds on test for a long time would furnish records when production was lower as well as when production was higher, whereas herds still on test and for a short time would furnish records only when production likely would be higher. Powell et al. (16,17) found more "elite" cows in high-production herds than in low ones and suggested that increase in variation with increasing production might be the explanation. That also might be the explanation for the similar results of Everett et al. (3). Previous reports (2,11,14,15,20) with some exceptions (9,19,23) also indicate that heritability may be different in herds with different production. These analyses often were for completely random models which are subject to biases from association of management and sire effects. Herdmate deviations also have been used and seem to provide estimates different from those used with mature equivalent (ME) records (14,21).

A usual method of equalizing variances is to transform data. Logarithmic transformation is most frequently used (1,4,7). The consequence of such transformations for milk records has not been studied in depth except for Hill et al. (7).

Data for this study were milk records from first lactation from an AI-sired population of Holstein cows stratified by year of freshening and herd production; the model eliminated bias because of confounding of herd-year-season and sire effects. The objectives were to: 1) estimate differences in residual components of variance due to time and yield, 2) estimate heritability from paternal half-sib correlations for different time periods and yield, and 3) compare esti-

---

Received December 26, 1984.

mates of variances and heritabilities from logarithmic and square root transformations with estimates from untransformed (linear) records.

#### MATERIALS AND METHODS

Robertson (18), in memorable style, warned against using records of daughters of proved bulls to estimate heritability from an among-sires analysis. However, if only records of first crop daughters (those used to obtain first progeny proof) freshening in a single year are used, the number of degrees of freedom to estimate residual variance is reduced, and, in addition, absorption of herd-year-season effects may result in the effective loss of more records and perhaps even the loss of sires for analysis (22). Therefore, records of daughters of both sampling and proved bulls were included as suggested by Meyer (12) and Hill et al. (7) after this study began. Sire and residual components of variance were estimated by Method 3 of Henderson (5) as described by Van Vleck (22) for the model:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 \\ X_2 \end{bmatrix} h + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} s_1 \\ s_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where  $y_1$  and  $y_2$  are the vectors of records of proved and sampling daughters;  $h$  is the vector of herd-year-season effects;  $s_1$  and  $s_2$  are the vectors of effects of proved and sampling bulls;  $e_1$  and  $e_2$  are corresponding vectors of random, uncorrelated residual effects; and  $X_1$ ,  $X_2$ ,  $Z_1$ , and  $Z_2$  are matrices associating effects with records.

Residual variance is estimated as:

$$V_e = [y'y - R(h, s_1, s_2)] / [N - r(X, Z)]$$

where  $R(h, s_1, s_2)$  is reduction in sum of squares due to fitting the complete model;  $N$  is the number of records; and  $r(X, Z)$  is the rank of the coefficient matrix for ordinary least squares equations for the full model.

Sire component of variance is estimated as:

$$V_s = [R(s_2 | h, s_1) - r(Z_2' W Z_2) V_e] / \text{tr}(Z_2' W Z_2)$$

where  $Z_2' W Z_2$  is the coefficient matrix after absorbing equations for  $h$  and  $s_1$ . Thus only

effects of sampling sires contribute to the estimate of the sire component of variance.

First-lactation records (adjusted to ME, two times-a-day milking, and 305-d length by standard procedures in use at the Northeastern Dairy Records Processing Laboratory (DRPL)) of AI-sired daughters of Holstein sires were obtained from DRPL. Age at freshening was required to be in the range of 19 to 34.5 mo. Seasons of freshening were December through April and May through November with the computational year beginning in December of the preceding calendar year. Daughters of sampling bulls were required to be born within 45 mo of when the sire's semen was first distributed. Records of the first 80 daughters of a sampling bull freshening in the specified year were included in the analysis for that year. Records of daughters of proved bulls also were included for a year. A bull was defined as proved if he had more than 100 daughters born more than 45 mo after his semen was first distributed. Records of other cows freshening in that year were excluded from the analysis. A bull could be defined as a sampling bull in one year and as a proved bull in a later year. The final data set was limited to freshenings from 1960 through 1982 (see Table 1).

Herd production was categorized by the rolling herd average for milk yield as of May of that computational year. Although not completely independent of the data being analyzed, as would be ideal, rolling herd average consists of actual yearly milk yield of all cows in the herd, not just first-lactation ME records of AI-sired cows. Records were divided into four groups with three dividing points for each: average rolling herd average associated with cows in the data set freshening in that year, average rolling herd average plus or minus the standard deviation of the associated rolling herd averages. Thus, the lowest production group contained about one-sixth, the two middle groups about one-third each, and the highest group about one-sixth of the records. For more detail see Mirande (13).

Milk, fat, and fat test records were analyzed for variance and covariance components as were the natural logarithms and square roots of these traits. Heritability was estimated as four times the paternal half-sib correlation, genetic correlations were estimated from the sire components of variance and covariance, and pheno-

TABLE 1. Means and distribution of data by year of freshening.

Year	Records	Sampling daughters	Sires	Sampling sires	(kg)		(%)
					Milk	Fat	Test
1960	4,249	1,400	127	115	6,049	222	3.68
1961	6,397	2,215	192	172	6,085	224	3.69
1962	8,074	2,718	209	187	6,349	233	3.69
1963	9,460	2,461	205	174	6,467	237	3.68
1964	13,232	2,734	208	171	6,674	244	3.67
1965	14,378	2,729	223	180	6,850	249	3.66
1966	17,469	2,483	218	167	6,864	251	3.67
1967	18,101	2,655	245	197	6,845	250	3.67
1968	20,152	3,313	324	274	6,840	249	3.66
1969	27,013	3,555	359	293	6,882	250	3.65
1970	29,994	4,114	354	300	6,962	253	3.64
1971	30,724	4,541	350	299	6,995	254	3.64
1972	30,536	4,702	343	297	6,903	249	3.63
1973	30,682	3,805	345	296	6,799	242	3.60
1974	33,852	4,052	352	284	6,973	252	3.62
1975	36,453	4,568	409	338	7,160	259	3.63
1976	39,148	5,043	441	368	7,244	266	3.69
1977	41,029	5,658	496	433	7,407	273	3.70
1978	42,519	5,729	553	486	7,680	281	3.67
1979	50,596	6,108	562	487	7,885	283	3.61
1980	55,990	6,121	554	475	8,063	287	3.60
1981	64,903	6,821	606	513	8,097	291	3.61
1982	37,903	4,415	456	398	8,041	290	3.63

typic correlations were estimated from the sums of sire and residual components of variance and covariance.

### RESULTS AND DISCUSSION

Heritability estimated from milk records when effects of both proved and sampling sires are assumed random as compared with heritability estimates from the procedure described in the previous section are in Figure 1. As predicted by Robertson (18), until about 1976, estimates when effects of all sires are considered random were smaller than when using the reduction in sum of squares after eliminating herd-year-season and proved sire effects. After 1976, estimates are similar and are smaller than usually assumed for milk production (10). These estimates suggest selection of parents of sampling bulls with daughters freshening prior to 1976 was not effective enough to reduce apparent genetic variability.

After 1976, the reduction is larger than could be expected even from intense selection of parents of sampling bulls (18). For example,

selection of the top 1% based on 100 daughters of the sire and three records of the dam would reduce heritability to about 73% of that prior to selection, whereas the actual decrease was

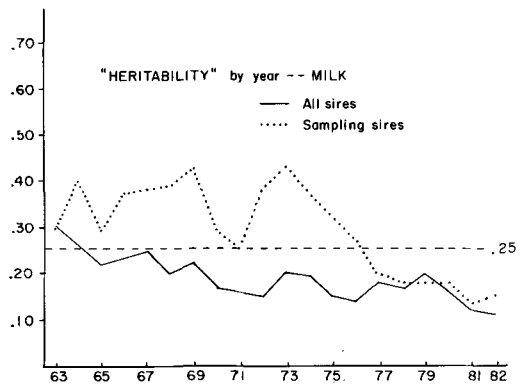


Figure 1. Heritability for milk yield estimated from among sire variation by year of first freshening from a model considering all bulls to have random effects and from a model considering only sampling bulls to have random effects.

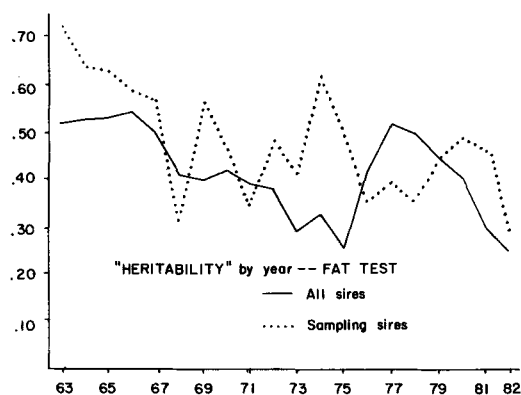


Figure 2. Heritability for fat test estimated from among sire variation by year of first freshening from a model considering all bulls to have random effects and from a model considering only sampling bulls to have random effects.

about 50%. Selection of proved bulls, however, can explain much of the reduction in sire variance when effects of both proved and sampling bulls are considered random from a common distribution with zero mean.

Patterns of heritability estimates for fat test are more variable than for milk yield (Figure 2)

and appear to be influenced by short-term changes in emphasis on fat test in selection of sampling bulls and in selection of proved bulls. The pattern for fat yield follows that for milk yield.

#### Correlations

Phenotypic correlations among milk, fat, and test are in Table 2. Estimates show little change over time except for decreases in correlations between milk and fat or milk and test and an increase in correlation between fat and test.

Genetic correlations are in Figure 3. An explanation for this pattern of genetic correlations between milk and fat yields and between test and fat is not obvious. The first few years contained relatively few records for estimation of genetic correlations. However, beginning about 1977 the correlations between milk and fat decreased and between test and fat increased comparably. This time period corresponds to a decrease in heritability of milk yield and a substantial increase in milk yield. The pattern may represent an unexplained biological relationship between milk yield and synthesis of fat. Correlations between milk and test

TABLE 2. Estimates of phenotypic correlations between milk, fat, and fat test.

Year	Milk, fat	Milk, test	Fat, test
1960	.87	-.29	.18
1961	.88	-.27	.18
1962	.88	-.25	.21
1963	.87	-.31	.17
1964	.88	-.29	.17
1965	.86	-.28	.22
1966	.86	-.28	.22
1967	.86	-.29	.21
1968	.86	-.31	.18
1969	.86	-.33	.17
1970	.86	-.32	.18
1971	.86	-.30	.19
1972	.83	-.31	.23
1973	.84	-.31	.22
1974	.83	-.35	.19
1975	.83	-.33	.22
1976	.81	-.35	.25
1977	.80	-.34	.25
1978	.79	-.34	.26
1979	.80	-.34	.26
1980	.80	-.35	.25
1981	.78	-.35	.27
1982	.77	-.34	.30

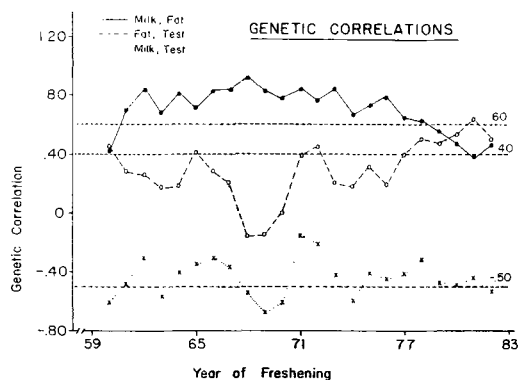


Figure 3. Estimates of genetic correlations between milk, fat, and fat test by year of first freshening.

fluctuate but do not follow a pattern of decrease or increase. Milk with fat correlations before 1976 are similar to those in the literature (8,10), but correlations after 1976 are smaller.

#### Transformations

**Residual Standard Deviations.** Comparison of standard deviations of transformed and nontransformed variables is made difficult by differences in magnitude. For example, on a linear scale, the residual standard deviations range from 960 to 1350 kg. On a natural logarithmic scale the range is .1680 to .1920, whereas on the square root scale the range is 6.4 to 7.7  $\text{kg}^{.5}$  for milk records by year for freshenings from 1960 to 1982. Therefore, to compare trends in residual standard deviations, estimates for each year were divided by 1980 estimates and expressed as percentages in Figure 4. The 1980 estimates were 1353 kg and .1847 and 7.77  $\text{kg}^{.5}$  for linear, logarithmic, and square root scales.

The lower line in Figure 4 shows the increase on the linear scale from 76% in 1961 to 100% in 1980. Little trend is evident until about 1976. From 1976 to 1980 the increase in residual standard deviation is dramatic. The pattern on the square root scale is similar to that on the linear scale, except the smallest standard deviation (1973) is 85% of the 1980 standard deviation. The pattern on the square root scale is intermediate between the patterns on the linear and logarithmic scales. The pattern on the log scale is somewhat unexpected, although standard deviations over time

are more uniform than on the other scales with a range from 106 (1961) to 91 (1973) to 100% (1980). The unexpected pattern consists of larger standard deviations early and late and smaller standard deviations in the middle period. Except for whatever occurred from 1976 on that apparently caused variability to increase greatly, the trend on the log scale would have been predicted to continue to decrease with increasing production over time. The log transformation more nearly equalizes variation over time than the linear or square root scales, but an explanation for lower variability in the middle years of the period is not apparent.

Estimates of residual standard deviations by year and herd production groups are quite variable. Therefore, trends were smoothed by selecting the median from the estimate for the year and the estimates for the 2 yr preceding and 2 yr succeeding. The smoothed estimates then were expressed as a percentage of the largest estimate for all year and herd production combinations. Smoothed percentages are in Figure 5. The linear scale shows the expected pattern of larger standard deviations as production increases. Although means increased over time for all production groups, there is little evidence for much of an increase in standard deviation until 1976 and later when the standard deviations increased for all groups. Patterns for all groups, in general, are similar to the pattern when data are combined by year.

On the square root scale the pattern is similar over time to the pattern on the linear scale, but the differences between groups are

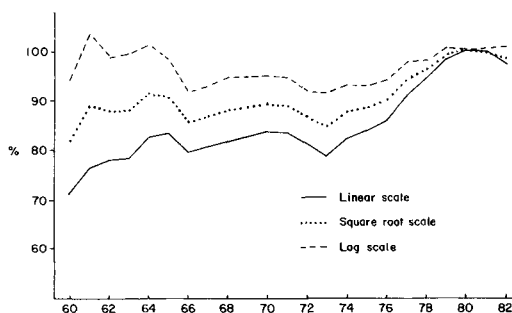


Figure 4. Residual standard deviations by year as a percentage of the residual standard deviations for milk records of cows freshening in 1980. These were 1,353 kg and .1847 and 7.77  $\text{kg}^{.5}$  on the linear, natural log, and square root scales.

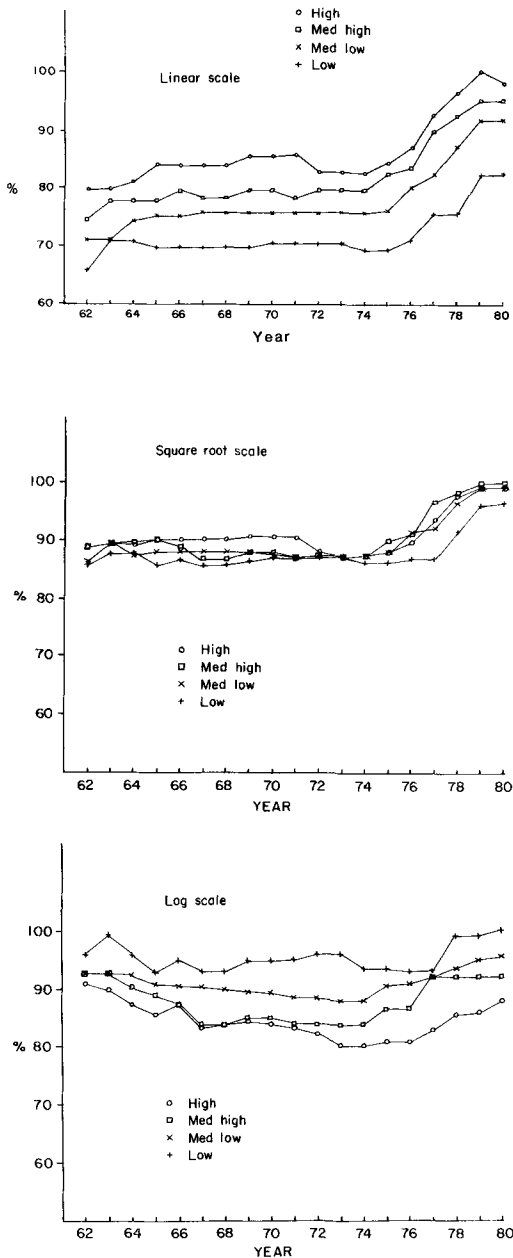


Figure 5. Smoothed residual standard deviations for first milk records by year of freshening and management level as a percentage of the largest residual standard deviation: a) linear scale, largest standard deviation was 1,430 kg for cows freshening in 1979 in the high-production group; b) square root scale, largest standard deviation was 7.76 kg<sup>•5</sup> for cows freshening in 1979 and 1980 in the medium-high-production group; c) logarithmic scale, largest standard deviation was .198 for cows freshening in 1980 in the low-production group.

slight, usually 4 to 5% from low to high production groups. Except for the upward trend after 1976, the square root transformation seems to equalize variation over time and production groups.

The pattern in Figure 5c for standard deviations by group over time for log-transformed records is different from patterns for linear and square root-transformed records. For all groups the pattern is similar: larger standard deviations at the beginning and end of the period and smaller standard deviations in the middle of the period. Differences among standard deviations for the same year are larger than on the square root scale and somewhat smaller than on the linear scale. The range from the smallest to largest standard deviations across groups and time is smallest for the square root scale (86 to 100%) as compared with the linear scale (70 to 100% after excluding the low group for 1962) and the logarithmic scale (80 to 100%).

The most surprising feature about the standard deviations on the log scale is the ranking of standard deviations across groups: low-production herds had the largest standard deviations. A concern expressed by Everett et al. (3) and Powell et al. (16,17) was that with a larger standard deviation, a higher fraction of cows would be overevaluated and thus designated as "elite" cows than should be expected. Powell et al. (16,17) linked this frequency to production, whereas Everett et al. (3) implicated herds on Dairy Herd Improvement (DHI) recording for a short time and with a low percentage of AI. Results of this study, however, suggest that with a logarithmic transformation, cows in low-production herds would be overevaluated and cows in high-production herds would be underevaluated. If heritability is actually lower in low-production herds than in herds with medium and high production, then use of a common heritability for all production groups would lead to even greater overevaluation for cows in low-production herds by logarithmic transformation.

**Heritability Estimates.** Heritability estimates on linear, log, and square root scales were essentially the same for each year of freshening, as illustrated in Figure 6 for linear and log scales. In nearly all cases these estimates bounded estimates for the square root scale. Hill et al. (7) not only found higher heritability for

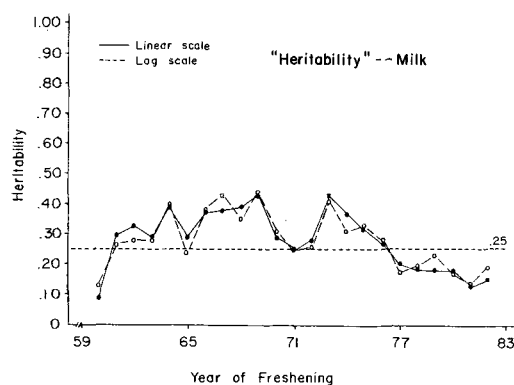


Figure 6. Heritability estimates for first milk records by year of freshening on the linear and logarithmic scales. Estimates on the square root scale generally are bounded by these estimates.

records in herds producing above average but also found slightly higher heritability on the log scale. Heritability estimates for year and production group combinations were quite variable, especially for high- and low-production groups in the early years of the study. Table 3 contains heritability estimates by herd production averaged over time by weighting the number of sampling daughters associated with each estimate. Heritability of test shows no association with production in contrast to heritability of milk and fat. Figure 7 shows smoothed estimates of heritability of milk by production over time. Except for the early years, heritability for the low-production group was very low. In contrast to averages in Table 3,

heritability for the high-production group is larger for the smoothed estimates for most of the period than heritability for the low-production group until the last part of the period. Smoothed estimates for the middle production groups do not fluctuate much over time and are similar for both middle production groups with a marked decrease in the last few years. Heritability, as estimated from variation among sampling sires, decreased over time in all herd production groups and is distinctly higher in middle than in lower production groups. In contrast to many reports (11,14,15,23)-heritability for high-production herds appears smaller than in middle-production herds for milk yield but not for fat yield nor test.

### Correlations

Genetic and phenotypic correlations by production groups averaged over time are also in Table 3. No trend is apparent for genetic correlations although, the phenotypic correlation between milk and fat appears smaller in herds with high than low production. Genetic correlations for production and year combinations were extremely variable. Smoothing did not aid in determining any patterns.

### CONCLUSIONS

Many questions arise from the results of these analyses. In agreement with earlier reports, residual variation has increased with time. The pattern of increase is similar for records divided into four production groups,

TABLE 3. Estimates of heritability and genetic and phenotypic correlations for milk (M), fat (F), and test (T) by production groups averaged over years by weighting by number of sampling records in each year.

Production group	Heritability			Genetic correlations			Phenotypic correlations		
	Milk	Fat	Test	M,F	M,T	F,T	M,F	M,T	F,T
Low	.21	.18	.59	.73	-.22	.12	.86	-.28	.20
Medium low	.28	.33	.44	.77	-.20	.38	.85	-.29	.21
Medium high	.33	.28	.57	.60	-.53	.26	.83	-.32	.21
High	.22	.27	.55	.76	-.26	.48	.81	-.33	.23
Combined data	.25	.27	.56	.69	-.44	.28	.84	-.30	.20



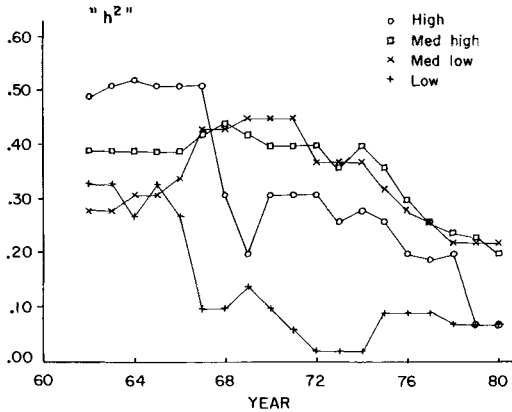


Figure 7. Smoothed heritability ( $h^2$ ) estimates for first milk records by year of freshening and production group.

although variation is greater in the higher production groups on the linear scale. On the square root scale, variation is similar for any year in all production groups. On the linear and square root scales, the question is, what caused the large increase in residual variation beginning about 1976? On the log scale, two questions arise. Why is variation the smallest in the middle of the time period and greatest at the beginning and end? The second question may be more important. Why is variation greatest in herds with low production and least in herds with high production? The implications of this result for sire and cow evaluation are not clear but need investigation, especially because heritability seems distinctly lower in herds with lower production. These two results argue for continued investigation of what is an appropriate transformation, which is in agreement with Falconer (4), who cautioned that scaling procedures should be chosen carefully and only when there is enough justification.

Heritability estimates are nearly the same whether records are expressed on linear, log, or square root scales. Two questions, however, seem to require further research. Has genetic variation in the population decreased over time, as suggested by analyses of variation among sampling sires, or can the decrease be explained by selection of parents of the sampling bulls? A daughter-dam analysis within sire should determine whether genetic variation has been maintained. There is a second question. Is

heritability in herds with low production really as small as appears from these data, particularly in the past 15 yr? If so, does low heritability imply that bulls should be sampled only in herds in middle production? There is some indication that heritability as estimated from among-sire variation is also smaller in high-production herds than in middle-production herds. Previous studies suggest only that heritability may be only a little smaller in high-production herds than in middle-production management conditions.

These analyses suggest that correlations among milk, fat, and test are essentially the same for the herd production groups included in these data. Although phenotypic correlations seem to have changed only slightly over time, the genetic correlation between milk and fat seems to have decreased markedly and between fat and fat test seems to have increased comparably. No linear trend is evident over time in the genetic correlation between milk and fat test.

#### ACKNOWLEDGMENT

This research was supported in part by a grant from Eastern Artificial Insemination Cooperative, Ithaca, NY.

#### REFERENCES

- 1 Bartlett, M. S. 1947. The use of transformations. *Biometrics* 3:39.
- 2 Danell, B. 1981. Evaluation of sires on first-lactation yield of Swedish dairy cattle. Thesis, Swedish Univ. of Agric. Sci., Uppsala, Sweden.
- 3 Everett, R. W., J. F. Keown, and J. F. Taylor. 1982. The problem of heterogeneity within herd error variances when identifying elite cows. *J. Dairy Sci.* 65(Suppl. 1):100.
- 4 Falconer, D. S. 1981. Introduction to quantitative genetics. Longman, NY.
- 5 Henderson, C. R. 1953. Estimation of variance and covariance components. *Biometrics* 9:226.
- 6 Henderson, C. R. 1975. Use of all relatives in intraherd prediction of breeding values and real producing abilities. *J. Dairy Sci.* 58:1910.
- 7 Hill, W. G., M. R. Edwards, M.K.A. Ahmed, and R. Thompson. 1983. Heritability of milk yield and composition at different levels of variability of production. *Anim. Prod.* 36:59.
- 8 Hudson, G.F.S., and L. D. Van Vleck. 1981. Relationship between production and stayability in Holstein cattle. *J. Dairy Sci.* 64:2246.
- 9 Legates, J. E. 1962. Heritability of fat yields in herds with different production levels. *J. Dairy Sci.* 45:990.

- 10 Majjala, K., and M. Hanna. 1974. Reliable phenotypic and genetic parameters in dairy cattle. Page 541 in 1st World Congr. Genet. Appl. Livest. Prod., Madrid.
- 11 Mason, I. L., and A. Robertson. 1956. The progeny test of dairy sires on different levels of production. *J. Agric. Sci.* 47:357.
- 12 Meyer, K. 1982. Estimation of genetic parameters for later lactation in dairy cattle. Proc. 2nd World Congr. Genet. Appl. Livest. Prod., Madrid, Spain.
- 13 Mirande, S. L. 1984. Trends in genetic and phenotypic variances in milk, fat and fat test production in Holstein cattle. M. S. Thesis, Cornell Univ., Ithaca, NY.
- 14 Norman, H. D., B. T. McDaniel, and F. N. Dickinson. 1972. Conflicts between heritability estimates of mature equivalent and herd-mate-deviation milk and fat. *J. Dairy Sci.* 55:507.
- 15 Powell, R. L., and H. D. Norman. 1983. Heritabilities of milk and fat yields according to herd-average yield. *J. Dairy Sci.* 66(Suppl. 1):123.
- 16 Powell, R. L., H. D. Norman, and B. T. Weinland. 1981. Effects of herd phenotypic and genetic classes on cow evaluation for production. *J. Dairy Sci.* 64(Suppl. 1):72.
- 17 Powell, R. L., H. D. Norman, and B. T. Weinland. 1983. Cow evaluation at different milk yields of herds. *J. Dairy Sci.* 66:148.
- 18 Robertson, A. 1977. The effect of selection on estimation of genetic parameters. *Z. Tierz. Zuchtungsbiol.* 94:131.
- 19 Robertson, A., L. K. O'Connor, and J. Edwards. 1960. Progeny testing dairy bulls at different management levels. *Anim. Prod.* 2:141.
- 20 Van Vleck, L. D. 1963. Genotype and environment in sire evaluation. *J. Dairy Sci.* 46:983.
- 21 Van Vleck, L. D. 1966. Change in variance components associated with milk records with time and increase in mean production. *J. Dairy Sci.* 49:36.
- 22 Van Vleck, L. D. 1983. Including records of daughters of selected bulls in estimation of the sire component of variance. *J. Dairy Sci.* 66(Suppl. 1):123.
- 23 Van Vleck, L. D., and G. E. Bradford. 1964. Heritability of milk yield at different environment levels. *Anim. Prod.* 6:285.