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Variation of Milk Records Within Paternal-Sib Groups

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Abstract

Differences between daughter-dam and paternal sib estimates of heritability of first lactation milk yield have not been explained for New York data. Deviations of first lactation records from herd-mate means of 155,070 artificially sired Holsteins were analyzed to examine the effect of unequal within group variances on the paternal sib estimate of heritability. The statistical model used to describe the data was $y_{ij} = \mu + s_i + e_{ij}$ with $\sigma_{y_i}^2 = \sigma_s^2 + \sigma_{e_i}^2$. Estimates of the within sire-group variances, $\sigma_{e_i}^2$, were heterogeneous ($P < .05$) for each year of freshening, 1951-64. Average heritability estimates were .24, for both the usual analysis which assumes $\sigma_{e_i}^2 = \sigma_e^2$ for all i and the method which estimates σ_s^2 as σ_{1^2} , each $\sigma_{e_i}^2$ as σ_{i^2} and heritability as $4\sigma_{1^2}/(\sigma_{1^2} + \sigma_{e^2})$. Similar results were obtained for other breeds. Repeatability of $\sigma_{e_i}^2$ from year to year was estimated as .39 if yearly $\sigma_{e_i}^2$ was expressed as a fraction of the average within group variance for that year and as .58 if yearly changes in average variance were ignored. Estimates of genetic value changed little when using $\sigma_{e_i}^2$ in the regression of the group mean on true daughter superiority as compared to using the pooled within group variance in the regression coefficient.

Bradford and Van Vleck (2) reported a large difference between estimates of heritability of first lactation milk production from daughter-dam regression, .40, and paternal half-sib correlations, .25. Further reports have not satisfactorily resolved the difference but have apparently eliminated maternal effects and the interaction of additive by additive genetic effects as possible causes of the difference. Small fractions of the difference have been attributed to environmental correlations between daughter and dam records and to changes in variance associated with an increase in mean production. Johnson (3), Wadell, Van Vleck, and Henderson (8), and Van Vleck and Barr

(7) have, however, reported heterogeneity of variances within groups of paternal half-sisters. The present study was initiated to determine if such heterogeneous variances are responsible for the differences in heritability estimates.

Data

First lactation (2×, 305-day, mature equivalent) milk records of artificially sired (AI) cows of the Ayrshire, Brown Swiss, Jersey, Holstein, and Guernsey breeds were available from the AI sire file of the New York Dairy Records Processing Laboratory. Records begun after 35 months of age were not included nor were records initiated or ended by abortion. The records were expressed as deviations from their adjusted herd-mate averages (4). The number of records and number of sires for each year from 1950 through 1964 are shown in Tables 1, 2, 3, 4, and 5. Each year began April 1 and ended March 31 of the following calendar year.

Methods

The statistical model used to describe a record of the j^{th} daughter of the i^{th} sire was:

$$y_{ij} = \mu + s_i + e_{ij}, \text{ where}$$

μ is a population constant;

s_i is a random effect common to daughters of the i^{th} sire with mean, zero, and variance, σ_s^2 ;

e_{ij} is a random effect common to the record of the j^{th} daughter of the i^{th} sire with mean, zero, and variance, $\sigma_{e_i}^2$, which is equivalent to $k_i\sigma_e^2$ (k_i being a constant associated with the i^{th} sire). The s_i and e_{ij} are assumed to be independent for all i and j .

If $k_i = 1$ for all i , then this is the usual random effects, one-way classification model. σ_s^2 and σ_e^2 were estimated for the usual model which assumes k_i equals one for all i by equating the total sum of squares, the sire sum of squares and the correction factor to their expectations.

σ_s^2 and $\sigma_{e_i}^2$ were estimated by equating the total sum of squares, the individual sire contributions to the sire sum of squares and the correction factor to their expectations. The

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TABLE 1. Summary statistics for analysis of Ayrshire milk records (kg) for heterogeneity of within sire variances.

Year Apr-Mar	No. sires	No. records	Hetero. Chi-square	Estimated variance components					Heritability estimates		
				Usual analysis ($k_i = 1$)					h_1^a	h_2	h_3
				$\hat{\sigma}_e^2$	$\hat{\sigma}_s^2$	σ_{1s}^2	$\overline{\sigma_{1s}^2}$	σ_{2e}^2			
1951	10	133	5.96	62,777	516,542	67,582	512,417	461,678	.43	.47	.51
1952	13	167	5.51	42,622	609,397	46,834	605,660	561,402	.26	.29	.31
1953	14	244	24.07 ^b	15,306	573,572	11,753	576,811	630,023	.10	.08	.07
1954	11	356	7.48	12,721	438,609	12,288	438,997	451,193	.11	.11	.11
1955	11	316	12.93	2,366	494,562	2,937	494,079	480,698	.02	.02	.02
1956	12	300	9.79	16,237	518,630	15,623	519,158	531,824	.12	.12	.11
1957	12	291	23.76 ^b	28,964	560,049	24,826	563,714	648,942	.20	.17	.15
1958	10	410	17.60 ^b	60,435	623,135	62,974	623,180	536,993	.35	.37	.42
1959	15	498	12.76	27,615	581,002	27,416	581,174	586,731	.18	.18	.18
1960	19	666	37.47 ^b	61,883	829,128	62,117	828,917	821,745	.28	.28	.28
1961	27	909	55.66 ^b	122,011	779,988	122,731	779,314	757,323	.54	.54	.56
1962	25	908	28.89	75,743	828,434	77,467	826,839	770,514	.34	.34	.37
1963	24	806	39.91 ^b	64,164	771,786	65,379	770,711	735,696	.31	.31	.33
1964	25	992	56.52 ^b	191,229	886,368	191,252	886,347	885,403	.71	.71	.71
Overall	76	7,215	301.12 ^b	75,950	716,590	76,152	716,395	698,166	.38	.38	.39

^a $h_1 = 4\hat{\sigma}_s^2/(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$; $h_2 = 4\sigma_{1s}^2/(\sigma_{1s}^2 + \overline{\sigma_{1s}^2})$; $h_3 = 4\sigma_{1s}^2/(\sigma_{1s}^2 + \sigma_{2e}^2)$.
^b $P < .05$.

TABLE 2. Summary statistics for analysis of Guernsey milk records (kg) for heterogeneity of within sire variances.

Year Apr-Mar	No. sires	No. records	Hetero. Chi-square	Estimated variance components					Heritability estimates		
				Usual analysis ($k_i = 1$)					h_1^a	h_2	h_3
				$\hat{\sigma}_e^2$	$\hat{\sigma}_s^2$	σ_{1s}^2	$\overline{\sigma_{1s}^2}$	σ_{2e}^2			
1951	15	204	10.12	73,658	528,464	74,720	527,478	515,052	.49	.50	.51
1952	23	323	35.02 ^b	15,310	509,121	18,503	506,117	466,942	.12	.14	.15
1953	20	461	23.13	37,972	412,466	38,150	412,299	408,612	.34	.34	.34
1954	25	622	19.55	25,848	411,128	25,617	411,346	416,564	.24	.23	.23
1955	24	581	19.09	33,873	432,503	34,987	431,452	407,061	.29	.30	.32
1956	24	629	55.06 ^b	32,351	437,827	34,070	436,217	395,719	.28	.29	.32
1957	25	605	37.78 ^b	39,810	541,979	36,905	544,679	607,323	.27	.25	.23
1958	28	696	47.59 ^b	34,871	513,428	34,978	513,329	510,982	.25	.26	.26
1959	32	827	37.76	22,453	534,998	20,441	536,899	584,126	.16	.15	.14
1960	33	952	43.08	27,395	634,195	29,046	632,677	590,419	.17	.18	.19
1961	71	1,896	104.88 ^b	62,090	616,827	61,902	616,809	621,463	.37	.36	.36
1962	75	1,982	100.31 ^b	36,440	664,596	39,747	661,402	580,136	.21	.23	.26
1963	84	1,990	92.34	55,860	732,202	56,688	731,399	713,145	.28	.29	.29
1964	78	1,999	111.96 ^b	50,379	758,476	53,253	755,688	687,096	.25	.26	.29
Overall	234	14,529	551.56 ^b	39,307	618,031	39,458	617,882	608,794	.24	.24	.24

^a $h_1 = 4\hat{\sigma}_s^2/(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$; $h_2 = 4\sigma_{1s}^2/(\sigma_{1s}^2 + \sigma_{1e}^2)$; $h_3 = 4\sigma_{1s}^2/(\sigma_{1s}^2 + \sigma_{2e}^2)$.
^b $P < .05$.

TABLE 3. Summary statistics for analysis of Holstein milk records (kg) for heterogeneity of within sire variances.

Year Apr-Mar	No. sires	No. records	Hetero. Chi-square	Estimated variance components					Heritability estimates		
				Usual analysis ($k_i = 1$)		$k_i \neq 1$ and average σ_e^2			h_1^a	h_2	h_3
				$\hat{\sigma}_s^2$	$\hat{\sigma}_e^2$	σ_{is}^2	$\overline{\sigma_{is}^2}$	σ_{se}^2			
1951	43	1,732	69.25 ^b	51,940	959,338	53,187	958,129	910,979	.21	.21	.22
1952	47	3,021	57.56	56,989	982,589	57,018	982,561	980,847	.22	.22	.22
1953	39	4,036	63.94 ^b	48,327	910,132	48,020	910,132	883,094	.20	.20	.21
1954	47	5,058	74.06 ^b	67,210	870,106	67,084	870,227	883,160	.29	.29	.28
1955	70	5,452	120.75 ^b	49,379	924,131	49,476	924,038	916,886	.20	.20	.20
1956	77	5,688	125.81 ^b	61,648	865,297	61,297	865,682	893,824	.27	.26	.26
1957	90	6,415	136.88 ^b	45,666	954,677	45,310	955,022	979,228	.18	.18	.18
1958	114	7,275	163.69 ^b	69,812	985,940	69,521	986,224	1,003,924	.26	.26	.26
1959	139	9,394	195.00 ^b	78,081	1,031,477	78,105	1,031,455	1,029,912	.28	.28	.28
1960	174	11,751	261.12 ^b	83,310	1,147,008	83,616	1,146,710	1,126,806	.27	.28	.28
1961	250	18,276	451.31 ^b	68,704	1,241,873	68,725	1,241,853	1,240,540	.21	.21	.21
1962	270	21,829	486.44 ^b	76,615	1,322,673	76,473	1,322,813	1,334,463	.22	.22	.22
1963	281	25,832	660.81 ^b	98,748	1,350,307	98,261	1,350,785	1,394,153	.27	.27	.26
1964	289	27,761	614.12 ^b	105,264	1,458,522	105,441	1,458,349	1,442,095	.27	.27	.27
Overall	642	155,070	3,719.00 ^b	77,164	1,216,561	77,011	1,216,712	1,253,405	.24	.24	.23

^a $h_1 = 4\hat{\sigma}_s^2/(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$; $h_2 = 4\sigma_{is}^2/(\sigma_{is}^2 + \sigma_e^2)$; $h_3 = 4\sigma_{is}^2/(\sigma_{is}^2 + \sigma_{se}^2)$.

^b $P < .05$.

TABLE 4. Summary statistics for analysis of Jersey milk records (kg) for heterogeneity of within sire variances.

Year Apr-Mar	No. sires	No. records	Hetero. Chi-square	Estimated variance components					Heritability estimates		
				Usual analysis ($k_i = 1$)		$k_i \neq 1$ and average σ_e^2			h_1^a	h_2	h_3
				$\hat{\sigma}_s^2$	$\hat{\sigma}_e^2$	σ_{is}^2	$\overline{\sigma_{is}^2}$	σ_{se}^2			
1951	9	132	14.09	152,103	455,846	150,626	457,118	474,484	1.00	.99	.96
1952	13	212	15.85	41,000	414,032	40,614	414,381	419,732	.36	.36	.35
1953	18	281	36.21 ^b	19,203	417,245	21,652	414,978	381,859	.18	.20	.21
1954	17	347	23.93	-1,109	494,182	-613	493,723	484,810	-.01	-.00	-.01
1955	17	332	12.88	25,830	468,928	24,267	470,379	497,259	.21	.20	.19
1956	11	296	10.76	16,213	462,739	16,927	462,104	445,638	.14	.14	.15
1957	13	304	24.78 ^b	-5,274	573,688	-3,290	571,907	532,034	-.04	-.02	-.02
1958	17	344	11.76	35,952	561,878	36,506	561,378	551,760	.24	.24	.25
1959	22	434	17.62	16,896	503,662	18,581	502,107	472,994	.13	.14	.15
1960	28	506	33.00	11,847	602,806	9,495	605,021	642,842	.08	.06	.06
1961	70	1,359	75.32	33,672	659,281	35,257	657,728	629,159	.19	.20	.21
1962	69	1,434	87.52 ^b	65,033	643,316	66,250	642,127	618,581	.37	.37	.39
1963	70	1,579	109.86 ^b	47,701	666,018	47,240	667,069	676,805	.27	.26	.26
1964	71	1,598	91.05 ^b	50,249	696,914	52,083	695,126	656,662	.27	.28	.29
Overall	170	9,730	360.69 ^b	38,377	615,994	38,389	615,982	615,318	.23	.23	.23

^a $h_1 = 4\hat{\sigma}_s^2/(\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$; $h_2 = 4\sigma_{is}^2/(\sigma_{is}^2 + \sigma_e^2)$; $h_3 = 4\sigma_{is}^2/(\sigma_{is}^2 + \sigma_{se}^2)$.

^b $P < .05$.

TABLE 5. Summary statistics for analysis of Brown Swiss milk records (kg) for heterogeneity of within sire variances.

Year Apr-Mar	No. sires	No. records	Hetero. Chi-square	Estimated variance components					Heritability estimates		
				Usual analysis ($k_i = 1$)	$k_i \neq 1$ and average σ_e^2		σ_e^2		h_1^a	h_2	h_3
				$\hat{\sigma}_s^2$	$\hat{\sigma}_e^2$	σ_{1s}^2	σ_{2e}^2	σ_{3e}^2	h_1^a	h_2	h_3
1953	7	76	11.67	85,655	856,445	89,989	852,862	817,538	.36	.38	.40
1954	9	88	4.15	86,253	926,381	89,235	923,797	901,111	.34	.35	.36
1955	7	103	7.27	123,065	1,060,386	124,536	1,059,135	1,041,977	.42	.42	.43
1956	9	90	11.52	3,599	871,528	5,761	869,609	852,343	.02	.03	.03
1957	8	119	2.36	-6,356	959,189	-675	954,346	887,156	-.02	-.00	-.00
1958	10	163	16.26	71,045	1,339,669	68,220	1,342,130	1,379,785	.20	.19	.19
1959	14	252	9.45	3,430	1,240,752	5,780	1,238,638	1,202,701	.01	.02	.02
1960	14	262	14.40	140,801	1,308,804	141,494	1,308,196	1,297,411	.39	.39	.39
1961	18	328	14.31	72,447	1,445,112	67,914	1,449,264	1,520,764	.19	.18	.17
1962	19	358	33.81 ^b	60,720	1,405,738	44,366	1,420,732	1,688,262	.17	.12	.10
1963	20	383	25.90	109,248	1,411,330	108,718	1,411,822	1,420,772	.29	.29	.28
1964	25	388	25.22	191,376	1,690,991	176,500	1,705,008	1,908,536	.41	.38	.34
Overall	62	2,839	83.32 ^b	78,646	1,329,852	78,870	1,329,636	1,319,897	.22	.22	.23

^a $h_1 = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_e^2}$; $h_2 = \frac{4\sigma_{1s}^2}{\sigma_{1s}^2 + \sigma_{2e}^2}$; $h_3 = \frac{4\sigma_{1s}^2}{\sigma_{1s}^2 + \sigma_{3e}^2}$.

^b $P < .05$.

expectations, as are well known, are given below where n_i is the number of daughters of the i^{th} sire, $n. = \sum_i n_i$, and s is the number of sires.

The symbol $E[]$ is used to indicate expectation.

$$E \left[\sum_i \sum_j \frac{n_i n_j}{i j} Y_{ij}^2 \right] = n. \mu^2 + n. \sigma_s^2 + \sum_i n_i \sigma_{ei}^2$$

$$E \left[\frac{n_i}{j} \left(\sum_j Y_{ij} \right)^2 / n_i \right] = n_i \mu^2 + n_i \sigma_s^2 + \sigma_{e1}^2$$

$$E \left[\frac{n_s}{j} \left(\sum_j Y_{sj} \right)^2 / n_s \right] = n_s \mu^2 + n_s \sigma_s^2 + \sigma_{es}^2, \text{ and}$$

$$E \left[\frac{s n_i}{i j} \left(\sum_j Y_{ij} \right)^2 / n. \right] = n. \mu^2 + \frac{1}{n.} \sum_i n_i^2 \sigma_s^2 + \frac{1}{n.} \sum_i n_i \sigma_{ei}^2.$$

The easiest computing procedure is to estimate each σ_{ei}^2 from the corresponding within sire sum of squares as

$$\sigma_{ei}^2 = \left[\sum_j Y_{ij}^2 - \frac{n_i}{j} \left(\sum_j Y_{ij} \right)^2 / n_i \right] / (n_i - 1)$$

and σ_s^2 as

$$\sigma_s^2 = \left[\sum_i \sum_j \frac{n_i n_j}{i j} Y_{ij}^2 - \frac{s n_i}{i j} \left(\sum_j Y_{ij} \right)^2 / n. - \frac{(n. - 1)}{n.} \sum_i n_i \sigma_{ei}^2 \right] / \left(n. - \frac{1}{n.} \sum_i n_i^2 \right).$$

The σ_{ei}^2 were tested for heterogeneity with Bartlett's (1) test.

The comparison of most interest was between the estimates of σ_s^2 under the two different assumptions: $k_i = 1$ and $k_i \neq k_i$.

Heritability was estimated in three ways:

1) $h_1 = 4\hat{\sigma}_s^2 / (\hat{\sigma}_s^2 + \hat{\sigma}_e^2)$ where $\hat{\sigma}_s^2$ and $\hat{\sigma}_e^2$ were estimates from the usual analysis ($k_i = 1$). Note that $\hat{\sigma}_e^2$ is equivalent to

$$\sum_i (n_i - 1) \sigma_{ei}^2 / (n. - s);$$

2) $h_2 = 4\sigma_{1s}^2 / (\sigma_{1s}^2 + \sigma_{2e}^2)$ where σ_{1s}^2 and σ_{2e}^2 were estimated from the other analysis ($k_i \neq k_i$) where

$$\sigma_{2e}^2 = \sum_i n_i \sigma_{ei}^2 / n.; \text{ and}$$

3) $h_3 = 4\sigma_{1s}^2 / (\sigma_{1s}^2 + \sigma_{3e}^2)$ where $\sigma_{3e}^2 = \sum_i \sigma_{ei}^2 / s$.

These analyses were done for data from each year of freshening beginning April 1950 and for data over all years. The minimum number of daughter records per sire for calculation of a variance was five.

Repeatability of $\sigma^2_{e_i}$ was estimated by doing an among and within sire analysis using the $\sigma^2_{e_i}$ as the units of observation. For example, sire i with daughters in four years would have four observations: $\sigma^2_{e_i}$ for year 1, $\sigma^2_{e_i}$ for year 2, etc. Various adjustments in the $\sigma^2_{e_i}$ were made in an attempt to remove the effect of increasing variance in the later years: 1) each $\sigma^2_{e_i}$ was expressed as a fraction of the unweighted average $\sigma^2_{e_i}$ for the corresponding year, 2) procedure 1 was repeated except that standard deviations were used, 3) each $\sigma^2_{e_i}$ was expressed as a deviation from the average for the year, 4) procedure 3 was repeated using standard deviations, 5) the variance estimates were not adjusted, and 6) the estimates of standard deviations were not adjusted.

Results and Discussion

Estimates of the sire component of variance and the average within sire variance by the two methods of analysis ($k_i = 1$ for all i and $k_i \neq k_j$) and Bartlett's chi-square statistic for testing heterogeneity of the within sire variances are shown in Tables 1-5. The within sire variances were not homogeneous ($P < .05$) for the overall analyses for all breeds and for all except one year of the Holstein data. The records for the other breeds are not as numerous as the Holstein records, nevertheless about half the yearly tests of heterogeneity of variance are significant for the Ayrshire, Guernsey, and Jersey breeds.

These results which indicate differences in variation among daughters of different sires are in agreement with those found by Johnson (3), Wadell et al. (8) and Van Vleck and Barr (7). Possible biological models have been discussed in the earlier reports.

The concern in this study was, however, to determine the effect of this heterogeneity on estimates of genetic variance ($4\hat{\sigma}^2_s$ or $4\sigma^2_s$). Comparison of the two estimates of the sire variance shows no real difference between them for any of the overall analyses or for most of the analyses of yearly data.

Similarly, estimates of heritability obtained from four times the ratio of the sire variance component to the sire plus the average within sire variance are not generally different (Tables 1-5). These results demonstrate quite conclusively that heterogeneity of variances within sire groups does not explain the difference in heri-

tability estimates from daughter-dam and paternal half-sib analyses.

There is some possibility that the heterogeneity of variance in sire groups is due by chance to the particular herds where the daughters make their records since Lee and Henderson (6) have shown heterogeneity of within herd variances. The number of records in each sire by herd subclass is so small that simultaneous estimation of the effects of sire and herd on heterogeneity is impractical. The similarity of within sire variances from year to year, however, should provide a minimum estimate of how much of the heterogeneity is due to sire effects. Therefore, repeatability of within sire variances was computed for the Holstein data considering the estimates of variances from one year to another as repeated measurements of within sire variance. Only variances estimated from records of 50 or more daughters per year were included in this analysis. The intra class correlations which are estimates of repeatability are shown in Table 6 for the six ways the variances were expressed and for weighting the estimated variances equally and by the number of records in the estimated variances.

Depending on the method of expressing the variances the repeatability values suggest that 40 to 60% of the differences in within sire variances are attributable to effects contributed by the sires. The reason is not clear why the variances not corrected for yearly changes in variance have higher repeatability than the corrected variances. Van Vleck and Barr (7) reported a product-moment correlation of .33 between within sire variances of first and second records.

If within group variances are as different as the results suggest, then what is the appropriate

TABLE 6. Repeatability of within sire variances from year to year for 128,720 records in 707 sire by year groups by 287 sires.

Yearly Observa-tion ^a	Repeatability estimates	
	Observa-tions weighted equally	Observa-tions weighted by n_i
$\sigma^2_{e_i} / \sigma^2_{2e}$.39	.45
$\sigma^2_{1e_i} / \sigma^2_{2e}$.39	.45
$\sigma^2_{e_i} - \sigma^2_{2e}$.44	.49
$\sigma^2_{1e_i} - \sigma^2_{2e}$.41	.46
$\sigma^2_{e_i}$.58	.63
$\sigma^2_{1e_i}$.56	.63

^a $\sigma^2_{1e_i}$ are the estimates of within sire variances for a particular year. σ^2_{2e} is the unweighted average of $\sigma^2_{e_i}$ for a particular year.

procedure to follow in estimating the genetic value or daughter superiority of these sires? The application of the general theory of the selection index (5) would lead to the use of the appropriate within group variance. For example in the simple case when each of p daughters, all in different herds, has one record each, the selection index procedure leads to a regression coefficient of $p/(p + \sigma_{e_i}^2/\sigma_s^2)$ for estimating daughter superiority. $\sigma_{e_i}^2$ is the true within sire variance for the i^{th} sire group. This, however, can only be estimated. With small numbers of records the sampling variance of such estimates is high, the well known expression for the variance of an estimated variance being $2\sigma_{e_i}^4/(n_i - 1)$. Moreover, for sires with large numbers of daughters the regression coefficient is not greatly affected by the ratio, $\sigma_{e_i}^2/\sigma_s^2$. Examination of estimates of daughter superiority for 54 sires, each with more than 500 daughters, shows a maximum difference of only 2 kg of milk between estimates using $\sigma_{e_i}^2$ and those using $\hat{\sigma}_{e_i}^2$. The differences in the methods were greater for 43 sires with between 50 and 60 daughters, the usual number for evaluation of Holstein sires. The extreme differences were +22 and -12 kg. Even these differences have little practical importance in sire selection. The sampling variance of $\sigma_{e_i}^2$ is, of course, much larger for only 50-60 daughters than for more than 500 daughters.

The ratio, $\sigma_{e_i}^2/\sigma_s^2$, also is important in determining the variance of true daughter superiority when the estimated daughter superiority is known. For the simplest case with only one record per daughter this variance is $[1 - p/(p + \sigma_{e_i}^2/\sigma_s^2)]\sigma_s^2$. This expression is, of course, slightly more complicated for unequal numbers of records per daughter and for environmental correlations between daughters in the same herd. The value of this variance depends on knowing the true σ_s^2 and $\sigma_{e_i}^2$. Although the sampling variances of $\sigma_{e_i}^2$ are quite large, some idea of possible differences in computing the variance from $R_i = p/(p + \sigma_{e_i}^2/\sigma_s^2)$ as opposed to $R = p/(p + \hat{\sigma}_{e_i}^2/\hat{\sigma}_s^2)$ can be examined. The ratio, $[(1 - R_i)/(1 - R)]^{1/2}$, gives the relative change in the range for probability statements about a true daughter superiority value given the estimate of daughter superiority.

For the sires with more than 500 daughters the extreme values of this ratio were .82 and

1.16. For the sires with 50-60 daughters the extremes were .59 to 1.24.

Conclusions

These results confirm earlier studies that some sires have daughters with records which are more variable than records of daughters of other sires. This heterogeneity of variance has little effect on the estimate of the among sire component of variance and thus does not explain differences between estimates of heritability from daughter-dam regression and from paternal half-sister analyses for variance components. The repeatability of the within sire variance from a group of daughters in one year to groups in other years is about 50% which may indicate that not all the differences in variances are due to confounding with specific herd or year effects but also some confounding of environmental effects with the effect of the sire on uniformity occurs. The differences in within sire variances are not important in estimating genetic value but are slightly more useful for making probability statements about true genetic value.

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