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Environmental Correlations in Sire Evaluation

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Abstract

Correlations were computed among averages of first lactation deviations from herd-mate averages of groups of artificially sired daughters of the same Holstein bulls. The groups were constructed by specifying the time interval between animals in the different groups. Comparison of the actual correlations with the expected correlations suggests that environmental correlations are small or nil among artificially sired half-sibs in New York. The correlations between initial and later groups of 20 or 40 daughter records at different time intervals are so close to the expected correlations that there is no support for the view that accuracy of prediction in sire evaluation is being over-estimated due to failure to properly account for environmental correlations among contiguous half-sibs in artificial insemination.

Lush (3, 4) and Lush and McGilliard (5) have demonstrated the effect of environmental correlations among daughters of the same sire on sire evaluation. Bereskin and Lush (1) have discussed this problem and have presented evidence from Iowa DHIA data which indicates a significant effect of environmental correla-

tions on predicting the production of future daughters. Heidhues et al. (2) and McDaniel and Corley (6), however, reported no significant departure from the expected correlations among the first ten, second ten, etc., daughters of a sire. Results presented in this paper suggest that under conditions of artificial insemination in New York, environmental correlations are not important in evaluation of sires used artificially.

Data, Methods, and Results

First-lactation milk production records (305-day, 2×, M.E.) of artificially sired Holstein cows were expressed as deviations from their herd-mate averages and used in the analyses, providing certain conditions were met. The records were sorted into order according to the birth date of the cow. Sire groups for analysis were determined in several ways. These methods are described in Table 1. For example, analysis (20:12, 12, 12) included 44 sire groups, all having at least 80 daughters distributed according to birth date into four equal groups, with a minimum time difference of 12 months for birth dates between individuals in first and second groups, between individuals in the second and third groups, and between individuals in the third and fourth groups. No restriction was placed on animals in a group except that if records of the first 20 daughters born were included in the first group, then records of all

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TABLE 1
Description of selection procedure for records included in the analyses

Analysis	No. of daughters per group	No. of groups	No. of sires	Minimum birthdate difference between cows in adjacent groups (months)
20:12,12,12	20	4	44	12
20:8,8,8	20	4	62	8
20:12	20	2	133	12
20:24	20	2	90	24
20:36	20	2	62	36
20:48	20	2	32	48
40:12	40	2	101	12
40:24	40	2	71	24
40:36	40	2	43	36
40:48	40	2	23	48

daughters born less than 12 months after the last animal in the first group were discarded. The records of the first 20 daughters born at least 12 months after the last animal in the first group were included in the second group.

Components of variance and covariance for an among and within sire group model were estimated for pairs of groups. For example, the first group of daughters for analysis (20:12, 12, 12) contained 20 records for each sire. The pair of groups could have been the first ten and the second ten records of the first group of 20, with Record 1 corresponding to Record 11 for the covariance analysis. Other combinations were first ten of the first group with the second ten of the second group, etc. Pairs were also made of the first group of 20 with the second group of 20, etc., for estimates of covariances.

Heritability estimates were obtained for each group by multiplying the intrasire correlations by four. These estimates are shown in Table 2. Genetic correlations among the groups considering genotype expression at the different time periods as different characteristics were computed from the sire components of variance and covariance. Estimates were pooled for analyses where the time interval between groups was approximately equal, by simply averaging the estimates. For example, in analysis (20:12, 12, 12) there were four estimates of the correlation between the first ten and the second ten records of a group, and three estimates of the correlation between records of cows born in adjacent groups.

Product moment correlations between daughter averages of the various pairs of groups were computed and averaged, similarly. These estimates were compared with the expected correlations which were computed as $\{[n_1/(n_1 + e_1/s_1)][n_2/(n_2 + e_2/s_2)]\}^{1/2}$ where n was the number of records in the group, e was the estimated within sire component of variance, and s was the estimated sire component of variance. The subscripts refer to the first or second group of the pair. The expected and actual correlations are given in Table 3.

Discussion

The heritability estimates given in Table 2 illustrate the variability of such estimates from relatively small numbers of sire groups and numbers of daughters per sire group. Examination of the estimates when the same sires had daughters in four groups with 8- or 12-month birth intervals between groups does not suggest any pattern of increase or decrease in the estimates with time. The first and third groups had low estimates and the second and fourth groups

TABLE 2
Estimates of heritability from multiplying the paternal half-sib correlation by four for records of several groups of daughters separated by specific time intervals

Analysis	No. sires	No. daughters per group	Group											
			One			Two			Three			Four		
			All	F ^a	L ^b	All	F ^a	L ^b	All	F ^a	L ^b	All	F ^a	L ^b
20:12,12,12	44	20	.10	.02	.14	.20	.13	.27	.10	.11	.06	.19	.19	.26
20:8,8,8	62	20	.11	.07	.11	.31	.45	.27	.37	.27	.10	.26	.26	.45
20:12	133	20	.25	.32	.20	.27	.23	.30
20:24	90	20	.14	.16	.13	.15	.09	.29
20:36	62	20	.11	.08	.15	.11	.02	.28
20:48	32	20	.04	.04	.11	.16	-.01	.21
40:12	101	40	.24	.19	.34	.21	.18	.28
40:24	71	40	.18	.12	.24	.22	.20	.23
40:36	43	40	.11	.06	.15	.15	.15	.15
40:48	23	40	.04	-.02	.07	.06	.06	.08

^a First half of the whole group.

^b Second half of the whole group.

TABLE 3
Mean expected (E) and actual (A) correlations between groups of progeny specified months apart in age

Time interval between group	Correlations between two halves of a group or between groups									
	Zero			One			Two			Genetic correlations
	E	A	E	E	A	E	E	A	E	
Analysis										
	Ten daughters per group									
20:12,12,12	.25 ^a	.28 ^a	.21 ^b	.10 ^b	.32 ^c	.14 ^d	.10 ^d	.37 ^d	1.31 ^a	.71 ^b
20:8,8,8	.38 ^a	.38 ^a	.40 ^b	.34 ^b	.28 ^c	.25 ^d	.37 ^d	.99 ^c	1.04 ^a	.77 ^b
20:12	.41 ^c	.41 ^c	.42 ^d	.49 ^d	1.03 ^d	1.14 ^d
20:24	.29 ^c	.24 ^c	.23 ^d	.35 ^d81 ^c	1.42 ^d
20:36	.18 ^c	.17 ^c	.09 ^d	.23 ^d68 ^c	2.74 ^d
20:48	.10 ^c	.21 ^c	.03 ^d	.28 ^d	3.03 ^c	8.37 ^d
	Twenty daughters per group									
20:12,12,1241 ^b	.40 ^b	.49 ^c	.41 ^d	.55 ^d	.56 ^d97 ^b
20:8,8,853 ^b	.42 ^b	.50 ^c	.50 ^d77 ^b
20:1259 ^d	.60 ^d	1.03 ^d
20:2443 ^d	.54 ^d	1.20 ^d
20:3636 ^d	.45 ^d	1.30 ^d
20:4826 ^d	.35 ^d	1.09 ^d
40:12	.61 ^c	.48 ^c	.50 ^d	.56 ^d84 ^c	1.12 ^d
40:24	.49 ^c	.54 ^c	.44 ^d	.47 ^d	1.07 ^c	1.10 ^d
40:36	.38 ^c	.40 ^c	.33 ^d	.49 ^d97 ^c	1.30 ^d
40:48	.21 ^c	.19 ^c	.14 ^d	.15 ^d88 ^c	1.80 ^d
	Forty daughters per group									
40:1271 ^d	.68 ^d98 ^d
40:2468 ^d	.59 ^d87 ^d
40:3657 ^d	.41 ^d73 ^d
40:4832 ^d	.34 ^d	1.12 ^d

^a Average of four estimates, e.g., first half of first group with second half of first group, first half of second group with second half of second group, etc. ^b Average of three estimates, e.g., first half of first group with first half of second group, first half of second group with first half of third group, and first half of third group with first half of fourth group, or first group with second group, second group with third group, and third group with fourth group. ^c Average of two estimates, similarly as above. ^d A single estimate, similarly as above.

had estimates above average. Comparison of groups of the same size but with different numbers of sires suggests, however, that the estimates decrease with increasing time interval. The number of sires included in the analyses also decreases. Although not given in the table, the mean deviation for the first group of daughters increases as the time interval between the pair of groups increases. The fewer sires had daughters with higher deviations in the first group than the more sires for the analyses of groups with shorter intervals between them. In other words, more highly selected sires had daughters over a longer time span than did less highly selected sires. This selection could reduce the estimate of heritability. The reduced number of sires and records also increases the sampling errors of the estimates.

The more important aspect of the study is the comparison of the expected and actual correlations between groups of daughters born in different time periods. The actual correlation is $(s_{12} + c_{12})/[(s_1 + c_1 + e_1/n_1)(s_2 + c_2 + e_2/n_2)]^{1/2}$, an expression similar to one given by Bereskin and Lush (1); s_{12} is the genetic covariance between paternal half-sibs in the two groups, due to their having the same sire, c_{12} is the environmental covariance between the two groups, c_1 is the environmental covariance among half-sibs in Group 1, and c_2 is the environmental covariance among half-sibs in Group 2.

Some assumptions likely to be true are that $c_{12} = 0$, $s_{12} = s_1 = s_2 = s$, $c_1 = c_2 = c$, and $e_1 = e_2 = e$. In this study $n_1 = n_2 = n$. Therefore, the expression can be rewritten as $s/(s + c + e/n)$. If, however, the estimates of s contain c , the expected correlation based on those estimates will be $(s + c)/(s + c + e/n)$. Thus, the correlations actually computed should be $c/(s + c + e/n)$ smaller than expected from the biased estimate of s , which really estimates $s + c$.

Examination of Table 3 leads to the conclusion that c is small or nil for this population of artificially sired Holstein cows in the New York DHIA program. All the differences between expected and actual correlations, however, are not independent. Nevertheless, in 15 comparisons the expected was larger than the actual correlations; in 22 comparisons the actual was larger than the expected correlation; and in one comparison the actual was equal to the expected correlation. Analyses (20:12, 12, 12) and (20:8, 8, 8) should be more meaningful than the other analyses in comparing correlations for pairs of groups at larger time intervals since, logically, c_{12} should become smaller as the interval increases. Thus, the assumption

that $c_{12} = 0$ would become more valid as the time interval increases. There was an almost even distribution of plus and minus differences between actual and expected correlations for these analyses. No trend with time interval is apparent. These results do not agree with those of Bereskin and Lush (1), who reported an actual correlation of .30 as opposed to an expected correlation of .62 for a pair of proofs with about 19 daughter deviations in each group, which were said to be similar to proofs made in artificial insemination.

Genetic correlations considering each time interval as a different environment were estimated from the sire components of variance and covariance. If environmental correlations are important, this correlation is really $(s_{12} + c_{12})/[(s_1 + c_1)(s_2 + c_2)]^{1/2}$. If $c_{12} = 0$, $s_{12} = s_1 = s_2 = s$, and $c_1 = c_2 = c$, this expression is $s/(s + c)$. Thus, if the genetic correlation does not equal unity, the reason is the environmental correlation. The sampling errors of the estimates of genetic correlations shown in Table 3 must be relatively large, since some estimates are outside the upper limit of unity. Nevertheless, there is no evidence that environmental correlations are important, since most of the estimates are near unity. No trends are apparent with increasing time interval between groups. Actually, the correlations between groups were often larger for more extreme time intervals between groups than correlations between the first and last half of the same group.

Conclusions

The evidence presented here suggests that environmental correlations are small or nil among artificially sired half-sibs when those half-sibs are grouped according to time intervals corresponding to an initial sire evaluation. This evidence does not preclude a small environmental correlation masked by sampling errors, but does rule out a large environmental correlation. This possible source of error in sire evaluation in artificial insemination for New York Holsteins, however, appears unimportant, since first decisions are rarely made on more than 20-50 daughter records. The correlations between initial and later groups of 20 or 40 daughter records at different time intervals are so close to the expected correlations that there is no support to the view that accuracy of prediction is being over-estimated due to failure to account for environmental correlations among contiguous half-sibs in artificial insemination.

Natural service sire evaluation creates a different situation. The low correlations between natural service and artificial service evaluations

reported by Meek and Van Vleck (7) suggest that environmental correlations in natural service proofs are important and should be considered in the regression of the sire's true genetic value on daughter average, as suggested recently by Bereskin and Lush (1).

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