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Sire Effects in Different Housing Systems

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Abstract

Over 1,000 Holstein herds in New York's Dairy Herd Improvement Cooperative were classified as to housing system. The two housing systems considered were stanchions and free stalls. First-lactation records (21,285) produced in these herds by daughters sired through artificial insemination were analyzed to determine if housing system would affect sire ranking. The study covered records started in 1964 through 1967.

The sire component of variance was estimated for each housing system for deviations of these records from their adjusted herd-mate averages. The covariance between the means of daughters in each housing system was computed. The genetic correlation between sire effects in the two systems was determined by dividing this covariance by the geometric mean of the sire components of variance for the two housing systems. The estimated correlation was near unity for each year of the study, indicating essentially complete agreement between sire rankings in the two housing systems.

Introduction

There has been interest in the effect of the increasing numbers of free-stall-housed cows in New York on the present sire selection system. If housing system introduces a bias into the present method, this bias should be evaluated and corrected.

The question of whether housing system actually defines statistically different groups of records was considered recently (7). That analysis concluded that groups of records classified by housing system did not really differ in their mean or variance to any important degree. The question of homogeneity of sire effects in different housing systems remains. This question may be studied from the point of view of considering milk production to be a different trait in each housing system. This general method was proposed by Falconer (2). These different traits may then have different

genetic variances and, therefore, different heritabilities. If these variances and heritabilities do differ substantially, it would indicate that the genotypes influencing production were different for the two housing systems.

One test to determine the similarity of two traits is to compute the genetic correlation between them. If housing system really defines different effects on the animal, then a different genotype would be required for high production in one housing system than in the other. It would be possible for sires to transmit genes for differential adaptability to different housing systems. These differences would result in changed rankings of sires for milk yield between two housing systems, just as there is a difference in sire rankings for the traits of milk production and per cent fat.

If the sire rankings were affected, the correlation between sire effects in the two housing systems would be less than one. If this correlation were low, selection may be biased against the high sires in the less common environment and would point out a sire-by-housing-system interaction.

A study of Ontario records (4) to investigate the interaction between sire and type of housing system was unable to determine whether housing system affected sire ranking due to an insufficient number of sires with adequate numbers of daughters in both systems.

Experimental Procedure

First-lactation, artificial insemination (AI) daughter Dairy Herd Improvement Cooperative (DHIC) records from New York herds, each with over 44 Holstein cows, were accumulated. Only records produced by cows in stanchions (Housing System 1) or free stalls (Housing System 2) were included. Each record was the deviation of the cow's 2 \times , 305-day mature equivalent milk record from its adjusted herd-mate average (3).

The means for each sire's daughter records in each housing system were computed for all sires with three or more daughters in each housing system in a particular year. These means were used to estimate the covariance between daughter averages in the two housing types, according to the following formula:

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$$\hat{\sigma}_{s_1s_2} = \left[\sum \bar{P}_{1i}\bar{P}_{2i} - \frac{(\sum \bar{P}_{1i})(\sum \bar{P}_{2i})}{S} \right] / (S - 1)$$

where \bar{P}_{1i} = progeny mean of the i^{th} sire in Housing System 1,

\bar{P}_{2i} = progeny mean of the i^{th} sire in Housing System 2, and

S = number of sires.

The sire component of variance was estimated with the one-way classification, random effects model for records in each housing system.

$P_{ij} = \mu + s_i + w_{ij}$, where

μ = population mean

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

w_{ij} = the random effect common to the j^{th} daughter of the i^{th} sire with mean zero and variance σ_w^2 .

If the sire and residual effects are each independent and mutually uncorrelated, the formulas for estimating the variance components are as usual:

$$\hat{\sigma}_w^2 = \left[\frac{\sum \sum P_{ij}^2}{n_i} - \frac{(\sum P_i)^2}{n_i} \right] / (n_i - S), \text{ and}$$

$$\hat{\sigma}_s^2 = \left[\frac{\sum \frac{P_i^2}{n_i} - \frac{P_i^2}{n_i} - (S - 1)\hat{\sigma}_w^2 \right] / \left(n_i - \frac{1}{n_i} \sum n_i^2 \right) \text{ where}$$

n_i = number of daughters of the i^{th} sire, and

n = total number of daughters of all sires in that housing type.

The genetic correlation was then estimated by the formula

$$r_g = \frac{\hat{\sigma}_{s_1s_2}}{\sqrt{\hat{\sigma}_{s_1}^2 \hat{\sigma}_{s_2}^2}} \text{ where}$$

$\hat{\sigma}_{s_1s_2}$ = the covariance between progeny record groups in different housing systems,

$\hat{\sigma}_{s_1}^2$ = the sire component of variance of records from Housing System 1, and

$\hat{\sigma}_{s_2}^2$ = the sire component from Housing System 2.

This general method has been used by Mason and Robertson (5) and Van Vleck (6). The expectations of these components are $\frac{1}{4} \sigma_{s_1s_2}$, $\frac{1}{4} \sigma_{s_1}^2$, $\frac{1}{4} \sigma_{s_2}^2$, respectively, and show that the component by component expectation of this procedure is the genetic correlation. Heritabilities were computed for each housing system in each year by the usual formula:

$$h = \frac{4 \hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_w^2}$$

Results and Discussion

The estimated correlations between daughter records for daughters freshening in 1965 through 1968 are listed in Table 1 along with the other relevant information for each daughter group. As the Table indicates, the estimated genetic correlation was near unity for each year of the study and yielded a simple average of 1.04 for the four years. The Table also shows there was little difference between the mature equivalent means of records in the two housing types and that the residual vari-

TABLE 1. Genetic correlation between housing systems, and heritabilities and means within housing system by years for 1964 to 1967.

Year	Number sires	HS ^a	Number cows	Mean (kg)	Var (w)kg ²	Var (s)kg ²	h	r _g
1964	42	1	4,058	6,986	1,147,449	65,808	0.22	0.76
		2	537	7,129	1,280,565	174,386	0.48	
1965	53	1	4,191	7,129	1,243,771	69,477	0.21	1.31
		2	871	7,122	1,190,920	33,045	0.11	
1966	66	1	4,723	7,102	1,198,029	84,748	0.26	1.04
		2	1,158	7,170	1,120,626	107,310	0.35	
1967	69	1	4,480	6,995	1,218,944	71,801	0.22	1.08
		2	1,267	7,000	1,198,404	27,806	0.09	
Mean		1		7,053	1,202,048	72,959	0.23	1.04
		2		7,105	1,198,404	85,636	0.26	

^a Housing System 1, stanchions. Housing System 2, free stalls.

ances are also similar. These results agree with those of Burdick and McGilliard (1), who found no interaction between sire group and housing types defined as stanchion, loose housing, and a combination of stanchions and loose housing.

The heritabilities listed show some dissimilarity due to differences in the sire components of variance. The average of these estimates over year and housing system is .24, as expected from other analyses (6).

The relative numbers of daughter records from free-stall systems has been steadily increasing during the past 4 years, adding confidence to the estimates from the most recent years.

Conclusions

On the basis of these New York data the two housing systems appear not to affect sire proofs. The groups of daughter records in each system were highly correlated, which suggests that housing system did not separate progeny into heterogeneous groups. Rather, sire effects were nearly the same in both sys-

tems, with superior sires having high daughters in both housing systems.

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