

May 1965

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# LINEARITY OF HERITABILITY OF HOLSTEIN FIRST-LACTATION MILK PRODUCTION

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## ABSTRACT

The regression of daughter on dam first-lactation milk deviations from herd-mate averages was found to be linear from an analysis of 47,400 Holstein pairs. The linear equation was  $y = -25.6 + .210(x - 27.6)$  and the quadratic equation was  $y = -25.6 + .208(x - 27.6) + .0000222(x^2 - 44131.4)$  with correlation coefficients, .18258 and .18268, respectively. These results suggest that selection response can be predicted adequately even with very large selection differentials.

Linearity of heritability implies that selection response will be linearly related to the selection differential over all possible phenotypic values. Recently, artificial insemination organizations have begun mating highly selected sires and dams to produce sons for sampling in artificial insemination. The agreement between the expected and actual genetic value of these sons will depend on whether response to selection is linearly related to the selection differential. This study provides further evidence that selection response can be predicted adequately, even with very large selection differentials. The evidence is based on daughter-dam regression over a large range of phenotypic values of the dams. The evidence supports the findings of a similar study by Bradford and Van Vleck (2), with about 10% as much data. Their results were discussed primarily in terms of the theory of canalization of phenotypic development (5).

## METHODS AND RESULTS

Records of 47,400 pairs of Holstein cows in which both daughter and dam had a first-lactation record in the same herd between 1950 and 1963 were taken from the files of the New York Dairy Records Processing Center. The paired records were sorted on the deviation of the dam's first milk record ( $2 \times$ , M.E., 305-day) from the average of her herd-mates (3). The regression of daughter on dam deviations was then done for each 5% of the data. These regressions and the standard errors and the deviation and mature equivalent means of the daughters and dams are given in Table 1. The equation for curvilinear regression of daughter on dam deviation was  $y = -25.6 + .208(x - 27.6) + .0000222(x^2 - 44131.4)$  where  $y$  is the predicted daughter deviation, and  $x$  is the dam deviation. The multiple correlation coefficient for the quadratic regression was 0.18268. The

means of the daughter deviations by 5% groups are plotted against dam deviations in Figure 1. The linear regression line is drawn through the points. The linear regression equation was  $y = -25.6 + .210(x - 27.6)$ . The correlation coefficient was .18258. Carrying the correlation to an unreasonable number of decimal places merely emphasizes the fit of the linear regression to the data.

## DISCUSSION AND CONCLUSIONS

The results indicate, in agreement with Bradford and Van Vleck (2) and in disagreement with Beardsley, Bratton, and Salisbury (1), that heritability is essentially constant over the entire range of phenotypes of the dams. There is no indication of curvilinearity of daughter-dam regression. Beardsley et al. (1) found evidence for lower heritability as deviations from the mean for milk fat production increased. Their results were based on fewer data and a different trait and also may have been influenced by a differential increase with time in herd mean production between lower and higher level herds, since they did not analyze records as deviations. In the present study the actual regression for the upper 5% of the data was 0.17, which indicates a level of response very close to the average regression over all pairs.

The standard errors of the estimates are very high for the estimates, especially for the middle groups, where the range of the dam deviations is severely restricted. To obtain another view of the situation, the regressions were estimated for each quartile of the data. The estimates and standard errors were .21 (.020), .17 (.055), .30 (.055), and .14 (.020) from high to low dam deviations, respectively. The estimates for the high and low halves of the data were: .21 (.012), and .19 (.012). These groupings also showed no differences in heritability at different phenotypic values of the dams.

Received for publication May 24, 1965.

TABLE 1  
Regression of daughter on dam records with pairs grouped by dam deviations

Group <sup>a</sup>	Daughter on dam regression		Averages ( <i>ten's of pounds</i> )			
	<i>b</i>	<i>s<sub>b</sub></i>	Deviations		Mature equivalent	
			Daughter	Dam	Daughter	Dam
1	.17	.055	68	471	1,430	1,738
2	.55	.220	41	328	1,393	1,592
3	-.23	.351	27	265	1,369	1,521
4	.37	.386	10	218	1,342	1,474
5	.10	.480	9	178	1,335	1,433
6	-.20	.557	-2	146	1,331	1,401
7	.55	.587	-10	117	1,320	1,372
8	-.41	.617	-4	89	1,317	1,338
9	.45	.664	-19	64	1,302	1,318
10	.52	.631	-20	38	1,311	1,301
11	.77	.635	-21	13	1,304	1,272
12	-.99	.652	-32	-12	1,299	1,253
13	-.59	.605	-47	-38	1,279	1,224
14	.96	.603	-50	-65	1,268	1,193
15	.12	.533	-52	-94	1,271	1,177
16	.22	.499	-71	-126	1,246	1,138
17	.34	.417	-65	-162	1,258	1,114
18	.31	.320	-72	-206	1,248	1,073
19	.06	.232	-95	-267	1,224	1,025
20	.11	.054	-105	-406	1,232	908
All	.21	.005	-26	27	1,304	1,293
Variances			57,150	43,372		

<sup>a</sup> Arranged in descending order of dam deviations. Each group contains 2,370 pairs.

Some practical conclusions can be inferred from the results. The fraction of superiority transmitted from a cow to her daughter is probably the same whether the cow is the best or poorest cow in a herd. Superior cows, by extrapolation to male offspring, should also produce sons likely to sire superior daughters, as predicted by the usual methods from linear heritability and normal selection differentials. Whether an analysis involving sires would produce the same linear regression is unknown, since the trait of milk production is obviously sex-limited. There is, however, no reason to believe that the results should be different. The mating of superior cows and superior sires, therefore, should produce sons and daughters

which have average genetic merit for milk production close to what is predicted from linear heritability. The prediction should hold for relatively intense selection (top 5% of cows and top 10% of sires with evaluation in A.I.), which is nearly within the range of concern to the artificial insemination industry. The predictions, of course, have the usual sampling variances, so that the true values of some offspring will be closer to the expected values than others. These sampling variances can be determined by methods presented by Henderson (4), as well as others.

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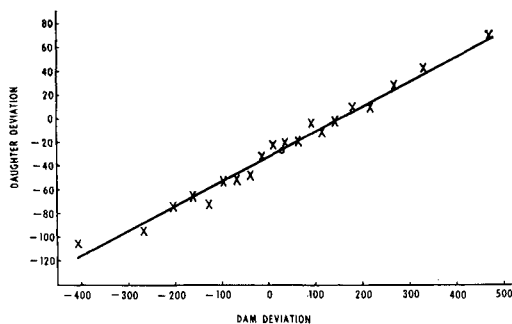


FIG. 1. Regression of daughter milk deviation from herd-mate average on dam deviation in pounds  $\times$  ten. Each point represents the means for 2,370 pairs, or 5% of the total.