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Genetic Change in Milk Yield Estimated from Simultaneous Genetic Evaluation of Bulls and Cows

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ABSTRACT

Genetic trend for milk yield in the artificially sired Holstein population in the northeastern United States was estimated from solutions for simultaneous genetic evaluations of bulls and cows for an animal model using mixed model equations and including all known relationships among the population by years of birth of 1960 to 1980 (1978 for bulls). First lactation milk records of 1,074,971 artificially sired cows sired by 6000 bulls in 20,065 herds were used. Averages of estimated genetic value by year of birth were similar from solutions after 10, 20, and 30 rounds of iteration of the mixed model equations. The trend in genetic value of bulls that entered artificial insemination was marked by slight negative change for three periods totaling 9 yr and substantial positive change averaging 105 kg/yr for the other 9 yr, which suggests that the dairy industry sacrificed milk yield in genetic value of bulls put into artificial insemination during those periods to selection criteria other than milk yield. There was little change in average genetic value of registered cows from 1960 to 1970. Gain in nonregistered cows totaled 177 kg for the same period. Gain from 1970 to 1980 was similar for both registered and nonregistered cows, 39.5 and 38.1 kg/yr, respectively. Average genetic value of nonregistered cows exceeded that of registered cows each year except 1960.

INTRODUCTION

An ideal way to estimate genetic change is to average known genetic values for animals born in each of many time periods. Genetic values, however, are unknown, so an alternative is to substitute "best" estimates of genetic values for known genetic values in the averages. This procedure has been used using United States Department of Agriculture (USDA) sire proofs and cow indexes and Northeast sire proofs and cow estimated transmitting abilities (3, 5). All information has not been used in sire evaluation or in cow evaluation, and the relationship between estimates of genetic change for sires and for cows is not clear. Method of grouping animals also may influence estimates of genetic change. Grouping in most genetic evaluations has been done only for bulls. Whether or not incorporation of bull proofs into cow evaluation procedures establishes the same genetic base for cows and bulls is not known. Simultaneous evaluation of bulls and cows, which incorporates all known relationships among them and utilizes a common grouping system accounting for selection on ancestors, would seem to provide estimates of genetic change more accurate than separate evaluations that ignore certain relationships and that may not establish the same base for bulls and cows.

Westell (9, 10, 11) developed a method of incorporating all known relationships for an animal model based on principles outlined by Henderson (1). She also developed (9, 11) a method of grouping to account for fraction of genes contributed by ancestors that do not have records in the data file and whose ancestors also are not known. The kind of selection practiced on the ancestors, whether a male or female path, was also considered.

This paper reports on genetic change in Holstein bulls used artificially and in cows sired artificially using estimates of genetic values obtained from Westell's (9, 10, 11) analysis of a population of artificially-sired Holsteins in the northeastern United States.

MATERIALS AND METHODS

The mixed model evaluation procedure is described by Westell (9). Only first lactation milk records (2 ×, 305-d, mature equivalent) of artificially sired Holsteins (1,074,971 in 20,065 herds) were used and were obtained from the Northeast Dairy Records Processing Laboratory. After inclusion of all relatives that could be found by tracing pedigrees developed from the all lactation file, there were 1,741,356 equations including 1,505,938 cow, 229,394 herd-year-season, 6000 sire, and 24 genetic group equations. Prediction of additive genetic value was the solution for the genetic value of the cow expressed as a deviation from group effects plus the sum of solutions for the appropriate group effects weighted by their fractional contributions to the genetic value of the animal. A form of block iteration was used to obtain solutions with iteration within a herd block and rounds of iteration across herds, sires and groups.

Estimates of genetic value by year for both cows and bulls were calculated by averaging the predictions of genetic value for all cows or bulls born in each year. The averages were similar for solutions after 10, 20, or 30 rounds of iteration. In fact, the plots for genetic trend in bulls were almost identical at 10, 20, and 30 rounds.

RESULTS AND DISCUSSION

Figure 1 shows the genetic trend for AI bulls and for registered and grade cows. The numbers of animals are in Table 1. Average annual increase for bulls used by artificial insemination (AI) bull studs was 47 kg, which is similar to the average of two periods (1960 to 1968 and 1968 to 1977) reported by Lee et al. (4) based on twice the Modified Contemporary Comparisons calculated by the USDA. This is also greater than the 26 kg/yr reported by Powell (6) for 1960 to 1977 based on Modified Contemporary Comparisons of sires of first lactation cows (7) but less than reported by Powell et al. (8) of 55 kg for 1970 to 1977 and 98 kg for 1977 to 1983 weighted by number of daughters freshening in each year. Regressions of the weighted average of genetic value of Holstein sires on year reported for a somewhat earlier time period as summarized by Hintz et al. (3) were smaller (36 kg/yr) using Henderson's (2) intraherd mixed model procedure.

The trend shown in Figure 1 for bulls measures the genetic value of bulls entering service and is not a measure of genetic value transmitted to their progeny, which would require weighting estimated bull genetic value by number of progeny. What is distinctive about the trend is that for three periods 1960 to 1962, 1964 to 1967, and 1971 to 1975 change was negative although on a practical basis, zero. Change was positive and relatively large for three other time periods of an equal number of years, 1962 to 1964, 1967 to 1971, and 1975 to 1978. Gain in genetic value for the nine "positive" years averaged 105 kg/yr. The gain in the positive years approaches the theoretically optimum gain when allowance is made for selection for other production and nonproduction traits and time lag to equilibrium. For half the period, however, no gain was made. The question of why no gain was made for three periods cannot be answered from the data but, nevertheless, is a question that the industry—AI studs, breed associations, and dairy herd managers—should address. The periods of no gain during the 18-yr period

TABLE 1. Number of animals in averages of genetic values by year of birth.

| Year | Bulls | Cows | |
		Registered	Nonregistered
1960	103	5842	4719
1	89	7232	5679
2	136	8644	6189
3	140	9554	7024
4	186	10,911	8218
5	186	12,082	8551
6	193	13,339	10,734
7	189	15,514	14,529
8	186	16,025	17,121
9	245	16,784	18,690
1970	311	17,286	20,202
1	447	17,964	22,545
2	347	18,340	24,430
3	313	18,518	25,970
4	291	21,494	25,705
5	264	24,632	24,562
6	307	27,121	27,117
7	275	31,298	30,835
8	65	33,687	35,472
9		37,134	42,376
1980		24,037	27,836
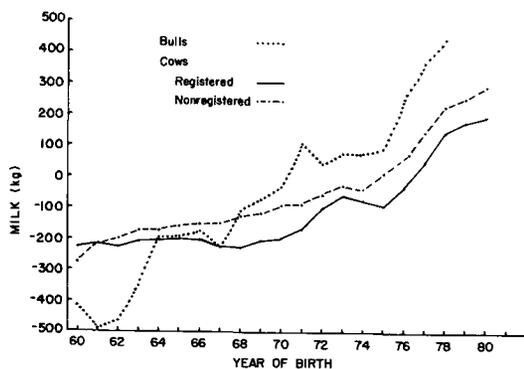
Figure 1. Averages of predicted genetic values by year of birth in the northeast United States for Holstein bulls used in artificial insemination and for registered and nonregistered cows sired artificially.

indicate that genetic value for milk of bulls sampled by bull studs has been sacrificed for other selection criteria. The number of bulls listed in Table 1 represents many bull studs since the regional bull stud was introducing only a small fraction of those numbers each year. Bulls from the regional bull stud, however, would have sired more than half of the cows.

Trends in genetic value of cows represent selection of available sires by dairy managers and selection of dams of replacement heifers. Sire contribution to the cow trend would be the result of average usage of sires from nearly one generation earlier. From 1960 to about 1970 the total change in genetic value of the registered cow population was less than 30 kg. In the same period the average genetic value of nonregistered cows exceeded the registered cows except in 1960. Total change in the nonregistered cows was 177 kg for the 10 yr. From 1970 on, total gains in the registered and nonregistered populations were similar, 395 kg and 381 kg, respectively. The trend lines for the registered and nonregistered populations are remarkably parallel after 1968 except that the difference became smaller from 1972 to 1974. These estimates and patterns of change are similar to those obtained from twice cow indexes by Lee et al. (4).

A majority of the cows were sired by bulls from one bull stud, which may partially account for the more uniform pattern of trend in cows as compared with bulls since the bull trend was not weighted by number of daughters. Breeders of cows may also have been more consistent in their breeding goals than bull studs.

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