Estimates of Genetic Trend in an Artificial Insemination Progeny Test Program and Their Association with Herd Characteristics

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ABSTRACT

Individual lactation records from Holstein cows in 3449 herds participating in an AI stud's young sire sampling program from 1971 to 1987 were used to characterize the sampling program and to estimate genetic merit and trend. Average genetic merit of cows in sampling program herds was consistently superior to the average genetic merit of cows in the US population. Genetic trend of sires of first-crop cows was 58 kg of milk and 1.5 kg of fat/yr from 1971 to 1978 and 176 kg of milk and 5.5 kg of fat/yr from 1979 to 1987. The average genetic merit of sires of first-crop cows born after 1983 was equivalent to or exceeded the genetic level of sires of other cows in the herd. Within-herd-year means and standard deviations of yield, genetic evaluation, and management traits (herd-year characteristics) were computed for a subset of 341 herds contributing first-crop daughters for at least 10 yr. The average of each herd-year characteristic during 10 or more years was used to predict within-herd genetic trend. Herd characteristics explained up to 51% of differences in within-herd genetic trends. Average sire genetic merit of daughters other than first-crop daughters accounted for up to 80% of the explained differences. Other herd characteristics suggested that herds with larger within-herd standard deviation milk yields, a larger number of young sires represented, younger cows, and greater percentage of cows sired by AI sires made greater genetic improvement. Results indicated that the average genetic merit of cows and the rate of within-herd genetic improvement are higher in herds that participate in a young sire sampling program.

(**Key words**: progeny test, genetic trend, herd characteristics)

Abbreviation key: **ME** = mature equivalent, **NFC** = not first crop, **PGA** = Program for Genetic Advancement.

INTRODUCTION

A key to genetic improvement in US dairy cattle has been the progeny testing programs initiated by AI studs during the 1960s. These programs identify bulls with superior genes for milk, fat, protein, and type so that they can be intensively utilized by dairy farmers and AI studs as sires of future dams and sires. These two pathways account for over 60% of all genetic progress made in dairy cattle (16). Thus, the importance of an AI stud's young sire sampling program in its long-term survival cannot be overemphasized. The decline in the number of non-AI-sampled bulls brought into the stud and the apparent increased bias of first-crop evaluations of these bulls over time (7, 11) have further emphasized the importance of AI sampling programs.

The design and importance of these AI sampling programs has been described by

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many researchers (3, 18, 19). The implementation of progeny testing programs was credited with increasing the rate of genetic improvement from 1964 to 1974, although the rate of progress was less than maximum (19). To increase the rate of genetic gain, researchers stressed the need to sample more young bulls, increase the number of herds on test, and, therefore, increase the number of cows available to breed to young sires, improve the percentage and accuracy of sire identified cows, and exercise greater selectivity in choosing the parents of future AI bulls (2, 18, 19).

The number of Holstein bulls sampled per year by AI studs in the US increased from 545 in 1975 to 1273 in 1986 (12). Milk pedigree indexes of AI young sires increased at a rate of 28 kg/yr for bulls progeny tested from 1970 to 1975 and further increased to a rate of 51 kg/yr for bulls sampled from 1980 to 1985 (12). The increased number of bulls sampled and the greater selectivity of milk pedigree indexes of sample sires should have increased the rate of genetic improvement in the general US Holstein population and in the AI studs' cooperating progeny test herds.

White (19) thought that many dairy farmers who have herds on test do not participate in young sire sampling programs because of the unknown genetic risk of young bulls compared with the near certainty of older proven bulls. Powell and Freeman (13) examined genetic trend within progeny test herds of an AI stud and found significant genetic progress. However, it would have been useful to compare the genetic trend and merit of progeny test herds with other herds not on a sampling program to determine what effect the sampling program had on genetic trend and merit within these herds. The objectives of our research were to examine characteristics of a major AI stud's cooperating progeny test herds, to estimate genetic trend and merit within these progeny test herds, to compare genetic trend and merit resulting from the use of young sires to that from use of proven sires, and to determine which herd characteristics were important in predicting genetic progress within a herd.

MATERIALS AND METHODS

Herds that had participated in Select Sires progeny test program, Program for Genetic Advancement (**PGA**), and Holstein sires sampled through PGA were identified by Select Sires Inc., Plain City, Ohio. Herd information included DHIA herd code, Select Sires regional code, and year entering or leaving PGA. Sample sire information included registration number and year entered PGA.

Lactation records and January 1990 animal model evaluations for all cows born after 1970 in herds that participated in Select Sires PGA, January 1990 animal model sire evaluations, and the Modified Contemporary Comparison sire history tape were supplied by Animal Improvement Programs Laboratory, USDA. The Modified Contemporary Comparison history tape was used as described by Meinert and Pearson (7) to determine sire's initial first-crop genetic evaluation. Only daughters of PGA bulls conceived prior to initial first-crop proof were considered first crop. All other cows were classified as not first crop (**NFC**).

The number of first-crop daughters and the number of herds contributing first-crop daughters were examined by state and birth year. Percentage of cows in each birth year classified as first-crop daughters were calculated for each PGA herd-birth year. Yearly and overall averages of percentage of first-crop daughters and number of first-crop daughters were computed for the PGA population.

The January 1990 cow and sire animal model genetic evaluations were used to calculate genetic trend within the herd and within the Select Sires PGA population. Cows were removed when PTA was missing or when the cow did not contribute to her sire's PTA because of no first lactation record or no management mates. Approximately 5% of the data were deleted because of this edit. Sires' milk and fat PTA were added to the record that included the cow's own PTA information. All herd-birth years that occurred before the herd started on PGA or that did not contain first-crop daughters were removed. For each sire sampled through PGA, the number of first-crop daughters in our data was compared with the number of daughters included in the bull's second to last first-crop Modified Contemporary Comparison proof as in work by Meinert and Pearson (7). For each sire, the time between his first PGA first-crop daughters' birth dates and his first published first-crop evaluation and the time between his first and last PGA first-crop daughters' birth dates were computed. Yearly averages of these two variables were examined to indicate efficiency of the sampling program over time.

Means by birth year for cow's PTA (subset 1) milk and fat yields, sire's PTA milk and fat yields for first-crop daughters (subset 2), and sire's PTA for cows classified as NFC (subset 3) were computed. Segmented regression was utilized [similar to methods described by Lee et al. (5)] for these three PTA averages to calculate overall genetic trend for the Select Sires PGA population using SAS NLIN segmented regression technique (17). The model's join points (year in which change in trend of average PTA occurred) were determined iteratively rather than by inspection. Convergence criterion used was the change in sum of squared errors from the $i - 1$ to iteration i less than 10^{-8}. The model simplified to simple linear regression when the sum of squared errors was smaller, fitting one (no joint point found) rather than two segments. Error terms used in the analysis of this study were not independently and identically distributed; however, the effect of this should have been minimal because dependent variables analyzed were herd means of PTA rather than individual PTA.

The following model was used to calculate genetic trends in the PGA population:

$$\overline{Y}_i = I_1\, a_1 + I_2\, a_2 + I_1\, b_1\, BY_i + I_2\, b_2\, BY_i + e_i$$

where

I_1 = 1 if $BY \le JP$; otherwise 0;
I_2 = 1 if $BY > JP$; otherwise 0;
$\overline{Y}_i$ = average cow's (cow's sire's) PTA milk or fat yield in birth year i;
a_1, a_2 = intercepts for first and second trend periods, respectively;
b_1, b_2 = regression of average cow's (cow's sire's) PTA on birth year of cow for the first and second trend periods (BY), respectively;
JP = join point; and
e_i = error.

Genetic trends were computed as twice the regression coefficients and were compared with the overall US population trends computed from yearly PTA of all cows provided by USDA (VanRaden, 1990, personal communication).

Herd-birth year means of cow's PTA milk and fat (subset 1) for all cows, herd-birth year means of sire's PTA milk and fat for first-crop cows (subset 2), and sire's PTA milk and fat for NFC cows (subset 3) were computed separately. Herds having less than 4 birth years were eliminated. Unweighted regression analysis using the following model was used for each subset to estimate genetic trend after fitting herds.

$$\overline{PTA}_{ij} = a + H_i + bBY_j + e_{ij}$$

where

$\overline{PTA}_{ij}$ = average cow's (cow's sire's) PTA milk or fat yield in birth year j and herd i;
a = intercept;
H_i = fixed effect of herd i;
b = regression of average cow's (cow's sire's) PTA milk or fat yield on birth year of cow; and
e_{ij} = error.

If two trend periods were found in the genetic trend estimates ignoring herd, then each subset was split into the two trend periods, and each subset period was fitted using this model that considered the effect of herd. This was preferred to the SAS NLIN segmented regression technique (17) because the NLIN procedure was not computationally feasible with the effect of herd in the model. Within-herd genetic trend was computed as twice the within-herd regression of average PTA on birth year of cow. Within-herd genetic trends from the three subsets were compared.

To examine yearly differences in average genetic merit of sires' of first-crop cows versus sires' of NFC cows, the following model was used:

$$\overline{PTA}_{ijk} = a + H_i + BY \times FC_j + e_{ijk}$$

where

$\overline{PTA}_{ijk}$ = average cow's sire's PTA milk or fat yield in herd i and first-crop status × birth year subclass j;

a = intercept;
H_i = fixed effect of herd i;
$BY \times FC_j$ = fixed effect of birth year by first-crop status subclass j; and
e_{ijk} = error.

For each birth year, orthogonal contrasts to examine effect of birth year by first-crop status subclass were constructed.

For herds that had at least 10 birth years with first-crop daughters in Select Sires PGA, the within-herd birth year means of cow's PTA milk and fat yields were used to compute estimates of genetic trend for each individual herd using the model:

$$\overline{PTA}_{ij} = a_i + b_i\, BY_j + e_{ij}$$

where

$\overline{PTA}_{ij}$ = average cow's PTA milk or fat yield in birth year j within herd i;
a_i = intercept for herd i;
b_i = regression of average cow's PTA milk or fat yield on birth year of cow for herd i;
BY_j = birth year j; and
e_{ij} = error.

Individual herd genetic trends were computed as twice the within-herd regressions.

Herd-year means and within-herd-year standard deviations for each of the variables included in the individual lactation records were calculated. These means and standard deviations were designated as herd-year characteristics. Variables included mature equivalent (**ME**) milk, fat, and fat percentage; age (years); lactation number; sum of sire by herd interaction plus permanent environment effects for milk and fat yields [computed as cow's predicted producing ability minus twice cow's PTA (20)]; cow's PTA milk, fat, and fat percentage; PTA milk and fat for sires of first-crop cows; PTA milk and fat for sires of NFC cows; and reliability of PTA for the cow and her sire.

Herd-year means or values only were computed for the following variables: percentage of cow's having AI sires, percentage of cows registered, percentage of cows that were first-crop daughters of PGA sires, percentage of cows having changes of birth date, number of sires represented, number of young sires represented, herd size, and state and Select Sires sampling region. Percentage of cows having changes of birth date was used as an indication of herd record-keeping management level. Herd-years not containing at least one first lactation, first-crop daughter were removed. Average herd-year characteristics during the 10 yr or more were used to predict the within-herd genetic trend calculated from all cow's PTA.

Stepwise regression (17), with a significance level of .20 for entry or exit, was used to screen variables useful in predicting within-herd genetic trend from all cows' PTA. Then, diagnostic tools were utilized to remove variables that were redundant because of collinearity. Next, all possible regression models were examined that included the variables that were significant in the stepwise regression and passed the collinearity test. Prediction sum of squares, Mallow's CP statistic, adjusted R^2, and mean squares error statistics were examined and used to select the best model for predicting genetic trend (10).

In order to gain additional insight on effects of herd characteristics (those significant in predicting within-herd genetic trend for milk and fat yields) on within-herd genetic trend, herds were divided into low, medium, and high genetic trend groups. The low group included herds less than 1 SD below the average within-herd genetic trend, the high group included herds greater than 1 standard deviations above, and the medium group included herds within 1 SD. The average herd characteristic was computed for each group and compared. This was done separately for milk and fat yields.

RESULTS AND DISCUSSION

Characteristics of Progeny Testing Program

A total of 47,839 first-crop Holstein daughters from 15,891 herd birth years from 3449 herds in 42 states contributed information to PGA bulls. The Select Sire's PGA program has grown greatly since 1971. The number of bulls receiving initial first-crop evaluations through the PGA program increased linearly from 33 bulls in 1974 to 176 bulls in 1989. Six states (Ohio, Indiana, Illinois, Michigan, Vir-

TABLE 1. Statistics of Program for Genetic Advancement herds' percentage of young sire usage, number of first-crop daughters, and number of herds contributing first-crop daughters by year of birth.

Birth year	Total first-crop daughters	Number of herds	Percentage of young sire use		Number of first-crop daughters			
			$\overline{X}$	SD	$\overline{X}$	SD	Min[1]	Max
1971	139	89	16	17	1.6	.8	1	4
1972	704	234	20	15	3.0	2.5	1	17
1973	912	302	21	14	3.0	3.0	1	38
1974	1221	392	20	16	3.1	2.9	1	35
1975	1872	497	21	15	3.8	4.7	1	77
1976	2350	566	20	14	4.2	5.9	1	93
1977	2400	602	19	15	4.0	5.4	1	64
1978	3433	867	19	14	4.0	5.7	1	90
1979	3895	997	18	14	3.9	5.2	1	79
1980	4551	1148	18	14	4.0	5.3	1	100
1981	4709	1217	16	13	3.9	4.7	1	76
1982	5553	1465	16	12	3.8	4.9	1	86
1983	5718	1538	15	12	3.7	5.2	1	104
1984	5490	1518	15	13	3.6	4.5	1	101
1985	5766	1586	14	10	3.6	4.2	1	64
1986	6747	1726	14	11	3.9	5.0	1	86
1987	2734	1147	20	17	2.3	2.5	1	28
Total	58,194	3449	17	13	3.6	4.7	1	104

[1] Min = Minimum, Max = maximum.

ginia, and Kentucky) contributed first-crop daughter information in 1971. In 1986, 12 additional states contributed over 100 first-crop daughters. Two states with small herd sizes (Minnesota and Wisconsin) and two states with large herd sizes (Washington and California) contributed an increasing percentage of the total. Table 1 contains yearly averages of percentage of young sire use (percentage of cows contributing information to genetic evaluations that are daughters of young Select Sires) and average number of first-crop daughters contributed per herd. Percentage of young sire use decreased from 21% in 1973 to 14% in 1986. However, the average number of first-crop daughters contributed per PGA herd increased slightly from 3.0 to 3.9 daughters during this same period. The decrease in percentage of young sire use reflected the increasing herd size from 1971 to 1987, and the number of young sires sampled per herd remained the same or increased more slowly.

The average number of first-crop daughters per bull in our data (45 daughters) was less than the average number of daughters included in the bull's second to last first-crop evaluation (52 daughters). To examine this discrepancy, the numbers of first-crop daughters and herds per bull included in our data were compared with those in the list of first-crop daughters contributing to the bull's first-crop evaluation (given to owners of bulls by USDA) for 10 bulls sampled by Select Sires PGA. Results indicated that for these 10 bulls the average bull had 9.7 first-crop daughters producing in 5.8 herds that were not enrolled in the Select Sires PGA program. This discrepancy could be

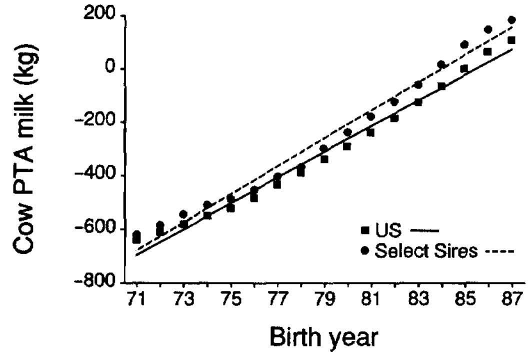

Figure 1. Yearly PTA milk for cows in Select Sires Program for Genetic Advancement herds [(- -O- -); genetic trend ($\hat{g}$) = 105 kg/yr] versus US population [(–■–), $\hat{g}$ = 96 kg].

explained several ways: 1) sale of first-crop daughters to non-PGA herds before first lactation or 2) semen awarded to the original owner of the bull who may use this semen in his herd or may distribute this semen to non-PGA herds. For whatever reason, this discrepancy indicates that AI studs have less than total control over which herds are included in first-crop evaluations of AI-sampled bulls.

The average time between a bull's first PGA first-crop daughters' birth date and his first published first-crop evaluation was 30.7 mo, and the highest average time of 33 mo occurred in 1974 (1st yr of modified contemporary comparison evaluations). The average time between first PGA daughters' birth date and first published evaluation did not significantly change from the 30.7 mo average for the remaining years of 1975 to 1989. This would be as expected due to the average practice of freshening first lactation cows at the age of 27 mo and the average 3- to 4-mo wait until lactation data are used in computing the biannual USDA genetic evaluations. This could be improved upon only if USDA genetic evaluations were computed more frequently and if at least 10 first-crop daughters that were born during the same month of the initial PGA daughter's birth date all freshened near 24 mo of age.

Average time between a bull's first and last PGA first-crop daughters' birth date was 20.7 mo. Average time between first and last PGA daughters' birth date decreased linearly from 23.5 mo in 1975 to 18.8 mo in 1986. Results indicated that PGA herds had improved their time span in using young sire semen and thus increasing the number of first-crop daughters included in initial first-crop proofs evaluations.

Estimates of Genetic Trend

Birth year means of PTA milk and fat yields for the cow and her sire were calculated from 58,194 first-crop daughters and 414,750 NFC daughters born from 1971 to 1987. Yearly averages of PTA milk and the overall estimated genetic trend for cows in the Select Sires PGA population are plotted against those of the US population (VanRaden, 1990, personal communication) in Figure 1. Only one linear time trend was evident. The quadratic form of birth year was added to the model and was significant ($P < .05$). This form of genetic trend is difficult to interpret. Thus, the linear approximation of genetic trend was used for comparison with the other estimates. Genetic trend ($\hat{g}$) for the Select Sires PGA population was slightly larger ($\hat{g}$ = 105 vs. 96 kg of milk, $\hat{g}$ = 3.1 vs. 2.9 kg of fat) than the US population. Least squares means and standard errors (SE = 2.5 to 10 kg of milk, .09 to .33 kg of fat) of birth year average PTA of cows in Select Sires PGA herds indicated that average genetic merit of cows in Select Sires PGA herds was consistently higher than that of the entire US population; differences were greater in the later birth years. Our estimates of genetic trends were considerably larger than those found in previous studies (4, 5, 13, 15), but in agreement with the population trend. Our study utilized animal model estimates of breeding values, but the other studies utilized other methods to calculate estimated breeding values. Larger genetic trend could also be attributed to the increased rates of genetic improvement during the 1980s (5).

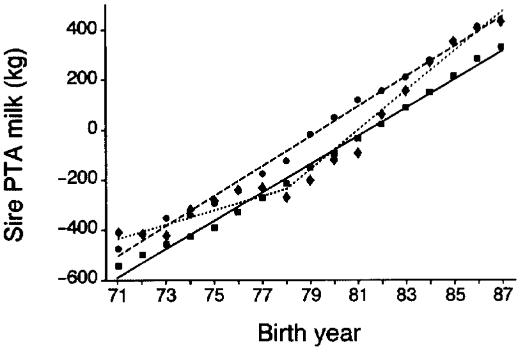

Figure 2. Yearly PTA milk for sires of first-crop cows [(- -◆- -), 1971 to 1978: genetic trend ($\hat{g}$) = 58 kg, 1979 to 1987: $\hat{g}$ = 176 kg] in Select Sires PGA herds, sires of other than first-crop cows [(- -●- -), $\hat{g}$ = 119 kg] in Select Sires Program for Genetic Advancement herds, and sires of cows [(–■–), $\hat{g}$ = 113 kg] in the US population.

Figure 2 contains yearly averages of sire's PTA milk yield for first-crop and NFC cows in the Select Sires PGA population as well as the sire's PTA milk yield for all cows in the US population, respectively. A single linear trend was found both for sire's PTA milk and fat yields of cows born from 1971 to 1987 in the US population ($\hat{g}_{milk}$ = 113 kg, $\hat{g}_{fat}$ = 3.6 kg)

TABLE 2. Genetic trend estimates in Select Sires Program for Genetic Advancement herds fitting and ignoring herd and average PTA for milk and fat yields calculated from all cow's PTA, first-crop cows' sire's PTA, and NFC[1] cows' sire's PTA.

	Milk					Fat				
	$\hat{g}_w$[2]	SE	$\hat{g}_a$[3]	SE	PTA	$\hat{g}_w$	SE	$\hat{g}_a$	SE	PTA
All cows' PTA, kg	119	.4	105	.4	−148	3.6	.02	3.1	.02	−5.6
First-crop cows' sire's PTA, kg										
1971 to 1978	54	4.4	58	3.8	−326	1.2	.16	1.5	.14	−11.4
1979 to 1987	183	2.0	176	1.8	144	5.8	.08	5.5	.07	4
NFC Cows' sire's PTA, kg										
1971 to 1978	126	.6	119	.6	−302	4	.02	3.6	.02	−10.9
1979 to 1987	126	.6	119	.6	223	4	.02	3.6	.02	5.1

[1] Not first crop.

[2] Genetic trend fitting herd.

[3] Genetic trend ignoring herd.

and of NFC cows in Select Sires PGA herds ($\hat{g}_{milk}$ = 119 kg, $\hat{g}_{fat}$ = 3.6 kg). However, two linear trends of sire's PTA milk and fat yields were found in sires of Select Sires first-crop cows. The first trend occurred from 1971 to 1978 ($\hat{g}_{milk}$ = 58 kg, $\hat{g}_{fat}$ = 1.5 kg), and the second trend occurred from 1979 to 1987 ($\hat{g}_{milk}$ = 176 kg, $\hat{g}_{fat}$ = 5.5 kg). Genetic trend in the second period represents some compensatory gain because of the low starting point. During the mid to late 1970s, the genetic merit of young sires having first-crop daughters born during this period increased less rapidly. This may have occurred due to using one or more sires of sons that were not as superior genetically for milk and fat yield as had been thought. However, after this period, the sire's PTA for milk and fat yields of first-crop daughters increased rapidly. For herds in Select Sires PGA, the average genetic merit of young sires used has equaled or exceeded the average genetic merit of other sires used since 1984. McDaniel and Bell (6) found that equivalent genetic progress was made from using the highest pedigreed AI young sires available and top AI proven sires. In both groups, sires were highly selected. This would not be true for all progeny test herds. In some herds, young sires would be compared with elite AI sires, and, in others, they would be compared with a mixture of current AI bulls, inactive AI bulls, and even non-AI bulls (probably used to breed heifers). Powell and Norman (14) found that these non-AI bulls were genetically inferior by 211 kg to the highly selected AI bulls. The type of other sire used has an impact on how good the daughters of young sires appeared to be. In contrast to the study of McDaniel and Bell (6), PGA herds do not select the highest PGA young sires available but are given a random sample of PGA young sires to be used.

Table 2 contains the within-herd and across-herd genetic trend estimates and their standard errors for milk and fat yields calculated from all cows' PTA, PTA for sires of first-crop cows, and PTA for sires of NFC cows born from 1971 to 1987. Also included are the average PTA for cows or cows' sires. Within-herd estimates of genetic trend were significantly larger (although the difference was not great) than the overall genetic trend for the Select Sires PGA population for all subsets except for the 1971 to 1978 milk and fat estimates computed from PTA of sires of first-crop cows. Powell and Freeman (13) also found within-herd estimates of genetic trend were larger than those obtained by ignoring herds, but Powell et al. (15) attributed the difference to using data from one area of the US. However, our study included 3449 herds from 42 US states. Differences between within-herd trends and trends ignoring herd were most likely due to herds entering and leaving PGA during the period of the data generation because only 341 herds of 3449 contributing PGA herds were enrolled for 10 yr or more. Examination of orthogonal contrasts comparing average PTA milk of sires of first-crop and NFC cows by birth year indicated that average genetic merit of sires of NFC cows was not significantly different from genetic merit of sires of first-crop cows for the birth years 1972, 1974 to 1976, and 1984 to 1987. Average genetic merit of milk yield of sires of NFC cows was significantly larger ($P < .05$) than average genetic merit of sires of first-crop cows for the birth years 1973 and 1977 to 1983. Average genetic merit of milk yield of sires of first-crop cows was significantly larger ($P < .05$) than average genetic merit of sires of NFC cows for the birth year 1971. Contrasts of birth year average PTA fat of sires of first-crop and NFC cows indicated that average genetic merit fat yield of sires of first-crop cows was not significantly different

TABLE 3. Herd characteristics of 341 Select Sires Program for Genetic Advancement herds contributing first-crop daughters for at least 10 yr.

Trait	Mean	SD	Minimum	Maximum
$\hat{g}$[1] Milk, kg	118	17	74	178
$\hat{g}$ Fat, kg	3.5	.6	1.8	5.4
Percentage of young sire use	16	6	3	43
Percentage of AI sired	87	12	31	100
Percentage of registered	42	38	0	100
Percentage of birth date change	.003	.05	0	1
Herd size	113	150	5	1672
Number of sires	43	28	4	300
Number of young sires	13	14	1	167
Young sire PTA milk $\bar{X}$,[2] kg	−49	92	−339	252
Young sire PTA fat $\bar{X}$, kg	−2.3	3.1	−12.6	6.9
Other than young sire PTA milk $\bar{X}$, kg	47	90	−214	316
Other than young sire PTA fat $\bar{X}$, kg	−1	2.9	−10.5	7.2
Mature equivalent milk $\bar{X}$, kg	8234	722	6139	10,672
Mature equivalent fat $\bar{X}$, kg	296	28	222	385
Mature equivalent fat percentage	3.62	.14	3.17	4.13
SH + PE[3] milk $\bar{X}$, kg	34	52	−257	184
SH + PE fat $\bar{X}$, kg	1.1	1.7	−7	9
Cow PTA milk $\bar{X}$, kg	−278	79	−495	−56
Cow PTA fat $\bar{X}$, kg	−9.7	2.5	−18	−3
Cow PTA fat $\bar{X}$, %	.01	.01	−.03	.06
Cow reliability $\bar{X}$	.51	.03	.42	.56
Sire reliability $\bar{X}$	.95	.02	.90	.99
Age in years $\bar{X}$	4.1	.5	2	5
Lactation number $\bar{X}$	2.5	.5	1	3
Mature equivalent milk σ,[4] kg	1408	187	929	2758
Mature equivalent fat σ, kg	50	6	36	76
SH + PE milk σ, kg	379	49	246	530
SH + PE fat σ, kg	13.4	1.8	9	19
Cow PTA milk σ, kg	231	26	165	312
Cow PTA fat σ, kg	8.2	1	6	11
Cow PTA fat percentage, σ	.07	.01	.04	.1
Sire PTA milk σ, kg	121	16	63	177
Sire PTA fat σ, kg	4.3	.6	2	6
Sire PTA fat σ, %	.09	.01	.05	.12
Cow reliability σ	.06	.01	.04	.09
Sire reliability σ	.06	.01	.02	.12
Age in years σ	1.9	.3	0	3
Lactation number σ	1.6	.5	0	2

[1] Within-herd genetic trend.

[2] Within-herd mean.

[3] Sire by herd plus permanent environment effect.

[4] Within-herd standard deviation.

from that of sires of NFC cows for the birth years of 1971, 1974, and 1975. Average genetic merit of fat yield of sires of NFC cows was significantly larger ($P < .05$) than average genetic merit of sires of first-crop cows for the birth years 1972, 1973, 1977 to 1983, and 1985. Average genetic merit of fat yield of sires of first-crop cows was significantly larger ($P < .05$) than average genetic merit of sires of NFC cows for the birth years 1976, 1984, 1986, and 1987. The equivalent or greater than average genetic merit of sires of first-crop cows compared with sires of NFC cows for the birth years after 1983 indicates that the use of young sires has not hindered the average genetic merit of the typical PGA herd.

Prediction of Within-Herd Genetic Trend

Means, standard deviations, and ranges of herd-year characteristics for the 341 herds that were enrolled in Select Sire's PGA program for at least 10 yr are in Table 3. Generally, means of the herd characteristics were within ranges found in other studies (1, 8). Ranges of herd characteristics were large, reflecting the diversity of sampling environments for these AI bulls. The average individual herd genetic trends for milk and fat agreed closely to the within-herd genetic trends discussed earlier. The average sire's PTA NFC daughters was larger than that of first-crop daughters. This reflects the intensity of selection of sires utilized to breed the cows in the herd (cows not bred to young sires). Average ME milk and fat yields and fat percentage were higher than national averages during the same period. Within-herd standard deviations for ME milk and fat yields and fat percentage were as variable but had a higher mean, compared with that of other studies (1, 8). This was most likely due to scaling, because ME yield traits were also larger. Percentage of young sire use and percentage of cows sired by AI sires were high, as expected for herds enrolled in a progeny testing program.

The final model for predicting within-herd genetic trend from herd characteristics is in Table 4. Regression coefficients are difficult to interpret because of the covariances involved. Thus, herd group averages of significant herd characteristics used in predicting within-herd genetic trend for milk yield are provided to help with interpretation (Table 4). Also included are the adjusted R^2 and mean square error statistics. The final models selected had the lowest values for prediction sums of squares, small values for Mallow's CP statis-

TABLE 4. Prediction model and mean herd characteristics for genetic trend group means in Select Sires Program for Genetic Advancement herds.

			Herd genetic trend group means[1]		
Herd characteristic	B[2]	SE	Low[3]	Medium	High
NFC[4] Cow's sire's PTA milk $\overline{X}$[5]	.13	.011	–49	49	129
Mature equivalent fat $\overline{X}$	.045	.03	289	295	307
Mature equivalent milk SD	.02	.004	1353	1397	1510
Number of young sires	.15	.051	10	12	19
Cow PTA fat $\overline{X}$	–1.32	.436	–11.1	–9.7	–8.3
Cow reliability $\overline{X}$	.52	.34	.506	.506	.504
Age in years $\overline{X}$	–3.52	1.543	4.2	4.1	3.9
Percentage of AI sired	.13	.063	85	87	90
Percentage of birth date change	–40.9	12.86	.02	0	0
Adjusted R^2 = .45					
Mean square error = 163					

[1] Herds split into <–1 ($\hat{g}$ = 91 kg), –1 to 1 ($\hat{g}$ = 117 kg), and >1 ($\hat{g}$ = 145 kg) standard deviation from the average within-herd genetic trend.

[2] Regression coefficient estimate.

[3] Number of herds was 50 for low, 238 for medium, and 53 for high genetic trend.

[4] Not first crop.

[5] Within-herd mean.

tic, and few problems with multicollinearity. The adjusted R^2 values were .45 and .51 for the models predicting within-herd genetic trend for milk and fat yields, respectively.

The average sire PTA of NFC daughters alone accounted for 80 and 67% of the explained differences in estimates for within-herd milk and fat genetic trends, respectively. Herds that made more genetic improvement had more sires of first-crop daughters represented. A possible explanation was that trend for genetic progress in young sires improved faster than the trend of the other sires. For both milk and fat, herds with higher within-herd ME milk standard deviations made genetic improvement at a faster rate. This agrees with results of Meinert et al. (9), in that herds with larger within-herd variances receive more response from estimated breeding values than expected. Herds having younger cows and cows with lower reliabilities would reflect more recent genetic advances, which resulted in faster genetic improvement for milk yield. Because genetic progress was occurring rapidly, younger cows should have been genetically superior to older selected cows in these herds. Herds having a larger percentage of cows sired by AI sires made faster rates of genetic gain for milk yield.

CONCLUSIONS

The Select Sires PGA program has grown to encompass a large network of herds spread across the nation. Characteristics of these herds were diverse, and means of genetic and phenotypic yield measures were slightly above national averages. Control of which herds contribute to a bull's initial progeny test evaluations was less than expected and was probably due to the sale of first-crop daughters before first calving or to the distribution of semen to the original bull owners. Rate of genetic progress within the Select Sires PGA herd population was large and matched the progress made by the US population. Cows in Select Sires PGA herds were in each year genetically superior to the US population. The rate of genetic progress obtained from using young sires increased from 58 to 176 kg of milk and from 1.5 to 5.5 kg of fat from 1971 to 1978 and from 1979 to 1987. During the mid to late 1980s, the genetic merit of daughters of young sires was equivalent to or exceeded the genetic merit of daughters of other sires in Select Sires PGA herds.

Herd characteristics explained 45 and 51% of the differences in the within-herd genetic trends for milk and fat yields, respectively. The average sire's PTA of daughters of other sires accounted for 80 and 67% of the explainable differences in within-herd genetic trends for milk and fat yields, respectively. This exemplifies the importance of sire selection within a herd. Other herd characteristics also were important in predicting within-herd genetic trend. Herds with larger within-herd standard deviation milk yields, higher average fat yields, a larger number of young sires represented, younger cows, and a greater percentage of cows sired by an AI sire had faster genetic improvement. These herd characteristics could be useful in educating dairy farmers in how to achieve greater rates of genetic improvement.

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