Factors Affecting the Accuracy and Stability of Sire Proofs from Progeny Test Herds

by

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Dissertation submitted to the Faculty of the
Virginia Polytechnic Institute and State University
in partial fulfillment of the requirements for the degree of
Doctor of Philosophy
in
Animal Science (Dairy)

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ABSTRACT

Change in Modified Contemporary Comparison proofs during first and second crop period was computed from up to eight proofs during both periods for AI and non-AI sampled Holstein bulls with repeatability of last evaluation $\geq .90$. Effect of proof number within testing period on the bull's milk or fat evaluation was estimated with bull absorbed. AI and non-AI sampled bulls' proofs increased from initial first crop proof and then remained fairly constant during the remainder of first crop period. With inclusion of second crop daughters, proofs dropped significantly more for non-AI than AI sampled bulls. This drop increased for non-AI sampled bulls born after 1976, but was unchanged for AI sampled bulls. A measure of change was calculated using last second crop proof minus the second to last first crop proof. Expected standard deviation of change was calculated and used to stratify bulls into eight change classes. A larger proportion of non-AI sampled bulls have proofs that dropped than could be explained by chance alone. Results indicated that non-AI sampled bulls were less stable than AI sampled bulls' proofs and that stability of non-AI sampled bulls has diminished over time.

For one of the studs that had stability of their bulls' proofs examined, their young sire sampling program was investigated. Individual phenotypic and genetic records of first crop and non-first crop cows in 3449 herds participating in the AI stud's young sire sampling program from 1971 to 1987 were used to characterize the sampling program, to estimate genetic trend across and within the progeny test herds, and to compute within herd means and standard deviations of various traits (herd characteristics). Herd characteristics of progeny test herds were utilized in predicting within herd genetic trend and in predicting changes in proofs of bulls sampled by the stud.

For bulls sampled by this stud, average herd characteristics and variability of herd characteristics across the contributing herds was calculated and used to predict the measure of proof change in the first study. Average herd-year characteristics and variability of herd-year characteristics explained 39% to 46% of the variation in milk and fat proof changes. In general, variability of herd-year characteristics and average within herd-year standard deviation herd-year characteristic variables explained most of the changes in proofs.

Genetic trend across the progeny test herds was large for milk (105 kg) and fat (3.1 kg) yield. Genetic trend computed from PTAs of sires of first crop cows increased 58 kg milk and 1.5 kg fat per year from 1971 to 1978 and 176 kg milk and 5.5 kg fat per year from 1979-87. The genetic level of daughters of young sires born after 1983 was equivalent or exceeded the genetic level of cows from other sires in the herd. Results indicated that within herd genetic improvement will not be hurt and may actually be enhanced from participating in a young sire sampling program depending upon sire selection of cows not bred to young sires. Herd characteristics explained forty-five and fifty-one percent of the differences in within herd genetic trends for milk and fat yield, respectively. Average sire PTA of non-first crop daughters accounted for 80% and 67% of the explainable differences. Other herd characteristics indicated that herds with larger within herd standard deviation milk yields, larger number of young sires represented, younger cows, less average days open, and greater percentage of cows sired by AI sires made faster rates of genetic improvement.

Acknowledgements

The author wishes to express his appreciation to Dr. Ron E. Pearson on his guidance, knowledge, and encouragement during his work toward both Masters and Doctorate degrees. Special thanks are due to Dr. William E. Vinson, Dr. Bennet G. Cassell, Dr. Ina Hoeschele, Dr. William D. Hohenboken, and Dr. David R. Notter for serving on his graduate committee and for their help in the preparation of this dissertation. The author also appreciates the help and knowledge received from the other faculty of the Dairy Science and Statistics Departments.

The author is indebted to his fellow graduate and Dutch visiting students for their friendship. This has been a very enjoyable atmosphere in which to grow educationally as well as personally.

I would especially like to thank all of my friends that I have made during my stay in Blacksburg, VA. Your friendship during graduate school has helped broaden my horizons.

Most of all the author wishes to thank his family for their encouragement, love, and support during the past four years as well as in the past.

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Introduction

Stability of sire proofs has been of concern to AI companies and dairy farmers ever since genetic evaluations have been computed. Sometimes estimated transmitting abilities (ETA) calculated after second crop daughters are included differ significantly from evaluations based on initial progeny test daughters. A large change in a bull's ETA erodes confidence in genetic evaluations and in the AI company who merchandizes the semen from that particular bull. This is particularly true for bulls whose ETA's drop.

AI companies are affected several ways by change in bull proofs several ways: 1) Mistakes can be made in keeping or culling a young sire graduate from their progeny testing program, or purchasing or not purchasing a breeder proven bull based on first crop proofs. Incorrect decisions lead to either larger costs of maintaining bulls or lost opportunity costs. 2) Large drops in proofs can cause poor public relations with dairy farmers which may lead to lower sales volume. 3) Less than optimal use of outstanding young sires with low repeatabilities (due to risk of drop in ETA) as sire of sons. This increases the generation interval and decreases the genetic progress the stud and population makes.

Some changes in ETA are well within expected bounds, but some are larger than would be expected based on chance alone. Examination of the characteristics of progeny test herds and of the progeny testing program may help explain why certain bulls' proofs change dramatically while others remain constant. If such characteristics were found an AI stud could correct for the discrepancy through careful design of the progeny test program. Careful analysis of an AI stud's progeny test program may help identify progeny test herds that give more accurate first crop daughter information compared to other progeny test herds. Close scrutiny of the AI stud's progeny test program may also yield information on the value of young sire usage in making genetic improvement within a herd.

This study examines the characteristics of a major Artificial Insemination stud's progeny testing program and attempts to determine the extent to which certain herds, herd characteristics, or regions of the country are involved in the cause of greater than expected change in proofs of bulls sampled through their progeny test program.

The specific objectives in the folowing manuscripts were:

Objective 1: To document and compare the proofs of AI and non-AI sampled bulls throughout their evaluation time period.

Objective 2: To examine whether within herd variances used along with herd means of characteristics of progeny test herds contributing daughter information to a bull's first crop proofs would be useful in predicting changes in Modified Contemporary Comparison proofs of AI progeny tested bulls.

Objective 3: To examine characteristics of a major AI studs progeny test program and its herds.

Objective 4: To estimate the genetic trend within these progeny test herds and to determine what herd characteristics were important in predicting this genetic trend.

Objective 5: To compare the genetic trend resulting from the use of young sires versus the use of proven sires.

Review of Literature

Sire Sampling Programs

A key to genetic improvement in U.S. dairy cattle has been the progeny testing programs conducted by AI studs. Around 70% of the progeny testing of bulls is conducted using grade dairy cows (30). The basic ideas of selecting a group of bulls based on their pedigree information, distributing semen of these bulls across many herds in order to obtain daughter production information in different environments, and then extensively using only the bulls with the most favorable genes to produce the next generation had been discussed in scientific literature prior to the 1960s (43,44). In 1955 young sire sampling was experimentally initiated by New York Artificial Breeding Cooperative (28). However, not until the early 1960s were organized young sire sampling programs initiated by most AI organizations (1).

The goal of sampling programs is to identify bulls with superior genes for milk, fat, protein, and/or type so they can enhance the rate of genetic improvement made by dairy farmers and the AI stud through their use as sires of future dams and sires of future sires, respectively. These two pathways represent over 60% of all theoretical genetic progress made in dairy cattle (40). Thus, the importance of an AI stud's young sire sampling program in its long term survival cannot be overemphasized. This is especially true since the accuracy of non-AI sampled bulls' progeny test proofs, another means of replacing bulls in a studs "proven" lineup, appears to be decreasing over time (24,32).

A major deficiency in early AI sampling programs was the insufficient number of bulls sampled which caused an ineffective selection intensity after testing was completed (1). Low numbers number of bulls progeny tested has been attributed to the large investments associated with sampling young sires (1,53,58). The largest of these expenses are the purchase and maintenance costs of bulls. Several years of maintenance costs accumulate before a bull's daughters' yield information allows for the determination of whether his genetic merit is superior enough to enter the proven lineup and start providing income to the stud. Other progeny test costs are in the form of incentives provided to herds enrolled in the sampling program. Incentives include semen of young bulls at a reduced price, better access to superior graduates from the sampling program, reduced prices on proven bulls, and credits for daughters contributing to a bull's first crop proofs.

Kucker (16) described three types of AI sampling programs: 1)Dairyman's Choice, 2)Supervised, and 3)Organized. These three programs differ by the degree of control that the AI organization has on how the bull is sampled. Under the "Dairyman's Choice" the AI stud makes the semen of any young sire available to any dairyman who wants to buy it and thus has no control of what herds and how many herds contribute first crop daughter information to proofs. The second type of sampling program, "Supervised", is operated by AI organizations with large numbers of employed AI technicians. These programs allow the stud to control the uniformity and speed in which bulls are sampled, but not which cows are bred to young sires (e.g. young sires bred to genetically inferior cows). Genetic merit of a young sire's mate is no longer a problem under the USDA Animal Model genetic evaluation system since it corrects for genetic merit of mates (55,56). The third type of sampling program, "Organized", involves a contract between the dairyman and the AI stud which specifically tells what is expected of both parties under the sampling program. This sampling program allows the AI stud to have nearly complete control of which herds will provide daughter information to a bull's first crop proof. This sampling system is the most ideal, but is also the most costly due to incentives provided in the contracts and personell costs in administrating the program.

Bayley (1) pointed out that progeny testing alone would not result in accelerated genetic progress, but that a young sire sampling program must be properly designed and fully supported by stud management in order to reap genetic benefits. The design and importance of AI sampling programs has been described by many researchers (1,11,16,18,46,50,53,54). The implementation of progeny testing programs was credited with increasing the rate of genetic improvement from 1964-74, although the rate of progress was less than the theoretical maximum (53). To improve the rate of genetic improvement, 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 percent and accuracy of sire identified cows, and exercise greater selectivity in choosing the parents of future AI bulls (1,8,16,46,50,53,54).

Number of bulls sampled per year by AI studs has increased from 545 in 1975 to 1273 in 1986 (33). Milk pedigree indexes of AI young sires rose at a rate of 28 kg/yr for bulls progeny tested from 1970-75 and further increased to a rate of 51 kg/yr for bulls sampled from 1980-85 (33). The increased number of bulls sampled as well as the greater selectivity of milk pedigree indexes of sample sires should have resulted in an increased rate of genetic improvement in the general U.S. Holstein population as well as in the AI studs' cooperating progeny test herds.

Stability of Sire Proofs

Sires of dairy females can be partitioned into three categories: 1) young sires with no daughter production information when used to inseminate cows, 2) sires with daughter production information on only those daughters conceived prior to sire's first proof (first crop daughters), 3) sires with daughter production information from second crop daughters. Approximately 10-15% of bulls progeny tested continue in service in category 2 and very few are in service in category 3. Inaccurate first crop daughter information leads to genetic estimates which are not a true reflection of the bull's genetic merit. If a bull's first crop daughter information underestimates his true genetic merit, he could be mistakenly culled from the AI stud with his true breeding value unknown or kept in the AI stud's active lineup but not used as heavily as his true genetic merit would justify. If a bull's first crop daughter information overestimates genetic merit, he may be used more heavily than he actually should. Inclusion of second crop daughters in this case leads to a drop in his proof and causes dissatisfication among dairymen using the bull. Both of these situations are of great concern to AI companies and dairy farmers.

Researchers have recognized this proof stability problem and have tried to utilize characteristics associated with daughters included in the first crop proofs to predict changes in bulls' proofs. Cassell and Norman (5) examined other variables available on sire summary tapes besides a bull's base PD for their usefulness in predicting future daughters performance. Data included 702 bulls with Modified Contemporary Comparison (MCC) sire summaries computed from October, 1974 to May, 1976. A bull's base proof was the October, 1974 proof that included at least 10 daughters. The bull's subsequent proof, which was required to have an increase of at least 10 daughter equivalents and a ratio of subsequent number of daughter equivalents to base daughter equivalents of 1.05 or greater, was utilized with the base proof in calculating the additional Modifed Contemporay Deviation (MCD) from future daughters. A similar data set using only first lactations in computing PD also was investigated. Stepwise regression was used to determine which variables were most useful in predicting additional daughters' MCD. Results indicated that the most important independent variable in predicting additional MCD was the base PD milk which explained 32.4% of the variation. Bulls with low initial PD underestimated future performance of daughters and bulls with high initial PD overestimated future daughter performance. The fraction of progeny test daughters culled was significant. Bulls with few daughters culled overestimated performance of future daughters while bulls with many daughters culled underestimated future daughters performance. The authors felt this observation was implicative of random chance associated with small number of first crop daughters. The genetic merit of contemporaries of the progeny test daughters was slightly useful in predicting future performance of daughters with contemporaries having low genetic merit overestimating and those having high genetic merit, underestimating future performance of daughters.

Clay et al. (7) investigated change from initial proof to last available proof for 455 bulls having repeatability of latest proof greater than or equal to .90. Proofs were computed using only first lactation records. The bulls' initial proofs ranged from .22 to .99 repeatability. Sires with low initial repeatability were more likely to have their evaluations change with a slightly greater tendency to decrease. Otherwise, little relationship was observed between repeatability and changes in evaluations. Little difference was observed in how AI and non-AI bulls changed from initial to final evaluation. Results from regressing last available PD on initial PD and repeatability indicated that initial repeatability explained only 1% of the variation in final PD and that final evaluations would increase an average of 1.53 kg per percent of initial repeatability.

Honette et al. (13) examined the stability of proofs of 236 bulls with at least one proof exceeding 453 kg of milk. Change in proofs was measured as the first evaluation exceeding 453 kg minus the bull's most recent evaluation. Bulls on the average declined 21 kg while increasing .23 in repeatability. A subset of 76 bulls whose last available evaluation was greater than or equal to 95% repeatability declined on the average of 28 kg while increasing 14% repeatability. The overall average negative change in proofs was determined to be caused by having the measure of change being calculated from the evaluation initially exceeding 453 kg of milk. Within-bull regression of PD milk on repeatability in the linear, quadratic, and cubic forms were computed in order to depict changes of PD milk with increasing repeatability. The prediction equation using all available evaluations was

$$\text{PD milk} = 379 - .3577\ \text{rpt} + .1071\ \text{rpt}^2 - .0009\ \text{rpt}^3$$

The cubic term was the only significant predictor, accounting for 76% of the within-bull variation. Evaluations increased to about 70% repeatability and then declined. The decline in proofs after 70% repeatability was suggested to be caused by a difference in the average genetic or management characteristics between herds in which AI bulls are progeny tested and herds that contain second crop daughters. Recently, Van Raden et al. (45) attributed some of this decline to less genetic variability of projected incomplete lactations of new additional second crop daughters.

Bolgiano et al. (2) examined changes in characteristics of herds in which first and second crop daughters of 20 AI bulls were located. Three of the bulls were denoted as "problem" bulls due to their drop in evaluations. Some of the other bulls had as large of a change as the "problem" bulls, but were not considered "problem" bulls due to either lower initial evaluations or increases in evaluations. Herd characteristics examined were herd size, genetic merit, management, genetic trend, and environmental trend. Results indicated that first crop daughters of "problem" bulls were in significantly better managed (higher producing) herds than the other bulls. Though not significant, "problem" bulls were bred to first crop mates with ETAs that were 53 kg superior to the first crop mates of the other bulls. Other herd characteristics were not different between "problem" bulls and other bulls. It was concluded that preferential treatment could be causing the changes in bull proofs, but the most probable explanation was Mendelian sampling.

Vinson et al. (52) used 160 Holstein sires which had an initial evaluation with repeatability less than .70 and a last evaluation greater than .90 repeatability to measure stability of bull proofs. Stability was measured as the last evaluation minus the initial evaluation. Stepwise regression was used to determine which characteristics of initial progeny test programs were associated with changes in evaluations. Results of the study indicated that the most stable proofs had initial evaluations with larger repeatability and their daughters' contemporaries'sires had larger repeatabilities. These bulls were proven in small, high producing herd-years with low genetic merit of contemporaries. There was less variation across the progeny test herds in the number of contemporary sires and in the producing ability of mates. Bulls whose last evaluation increased were proven in large herds with low genetic merit of contemporaries. There was less than average variation across progeny test herds in the number of contemporary sires and in the producing ability of mates, but larger variation across the progeny test herds in the repeatability of contemporaries' sires. Bulls whose last evaluation decreased from initial evaluation had daughters compared to contemporaries with genetically superior sires and daughters with extremely high milk yield. There was large variation across progeny test herds in the size of herds, in producing ability of mates, and in production of contemporaries. It was concluded that most of the change in evaluations over time was due to Mendelian sampling though careful design of progeny testing programs could help stability.

Lofgren and Vinson (19) examined change in proofs of 1095 AI and 1277 non-AI sampled bulls who had between 10 and 75 daughters in their initial summary and added at least 25 daughters between their initial and last available summary. Stability was measured as the actual difference as well as the absolute difference between the initial and last evaluation. Results showed that AI bulls increased slightly in PD compared to natural service bulls though not significantly. It was suggested that natural service bulls were more stable due to their use under less variable environmental conditions. This was supported by the observation that natural service bulls which entered AI were less stable than the AI bulls and the natural service bulls remaining in natural service. Characteristics of progeny test herds the bulls were sampled in were related to the change using multiple regression. Multiple squared correlations were quite low compared to Vinson et al. (52). It was concluded that random Mendelian sampling was the major cause of stability problems. However, the authors felt a larger proportion of the variation could have been accounted for if variances of the progeny test herd characteristics would have been utilized as independent variables in addition to the genetic merit of mates. Production of daughters in the initial evaluation was associated with large differences in PD changes for both AI and natural service bulls. Bulls with daughters with extremely high production decreased in PD while bulls with extremely low producing daughters increased in PD. Type information helped explain changes in PD, but the differences among bulls were not large except for AI bulls whose sires had high PD type declined 175 kg compared to bulls with low PD type sires.

Additional insight into the expected change in sire proofs may be gained from studies looking at the response to selection in herds with different characteristics. The response to sire selection has been shown to increase with increasing herd mean (21,35). This result has been shown to depend on the relationship between herd mean and within herd variance (26). When herds were characterized by both mean and variance, response was shown to differ only with changing variance. This could help to explain why previous investigations including variability parameters were more successful in explaining change than those which only used mean parameters. Response to selection has also been shown to be dependent upon registry status of the herd (25). While the general relationship between within herd variance and response exists in all herds, it is partially modified by registry status. These studies suggest that bulls sampled primarily in registered herds with high within herd variance would have their genetic merit amplified while bulls sampled primarily in grade herds with small within herd variance would have their ranges of genetic merit reduced. This could be partially responsible for changes from first to second crop proofs. Vinson (51) stated that heterogenous within herd variances should not bias sire genetic evaluations due to the large number of herds generally represented. However, he noted that this may not be the case during the initial progeny test period.

Meyer (27) found that registered herds in Great Britain had larger sire by herd interactions (c^2) than grade herds. Bulls initially sampled in primarily grade or registered herds could have their second crop proofs differ from first crop proofs due to the differences in c^2.

Studies comparing stability of AI and Non-AI sampled Bulls

One area of question examined by researchers has been the stability of breeder proven bulls' evaluations versus the evaluations of graduates of AI progeny testing programs. Meek and Van Vleck (23) examined stability of AI and non-AI sampled bulls that were selected for further use under the daughter-dam and herd-mate comparison evaluation systems. Non-AI proven bulls' second crop proofs declined more than AI proven bulls' proofs under both evaluation methods. Cassell et al. (4) investigated the stability of proofs for Holstein bulls sampled under limited and multiherd conditions that later were used extensively in AI. Non-AI sampled bulls' progeny test proofs were overevaluated 119 kg under the herdmate comparison method, but this decreased to 69 kg when pedigree information was utilized as in the MCC system. Clay et al. (7) using modified contemporary procedures found no differences between AI and non-AI sampled bulls in the change from initial proof to last available proof with repeatability greater than .90 for 455 bulls having daughters calving between 1964-1973.

Norman et al. (31) measured the difference between a bull's initial evaluation and his last available evaluation with an increased repeatability of 30% or more for non-AI sampled bulls that later entered AI sire lineups. For the non-AI sampled Holstein bulls the average evaluation for milk and fat dropped 14 and 0 kg, respectively. They concluded that AI organizations can acquire non-AI sampled bulls and be confident their evaluations are not overestimated. Lofgren and Vinson (19) examined AI and non-AI sampled bulls summarized between 1974 and 1979 and found that natural service bulls which entered AI were less stable than AI bulls. Powell and Shainline (37) found that bulls sampled by AI studs from 1974-78 had better Pedigree Index (PI) than both multiherd sampled and single herd sampled non-AI bulls. Non-AI bulls' proofs changed little from initial to last available proof while AI bulls′ proofs increased. Powell and Norman (36) also found AI sampled bulls to be genetically superior to all non-AI sampled bulls.

Estimates of Genetic Trends

Many studies have examined genetic trend in the female North American Holsteins (3,9,10,12,15,17,34,38,39,49). Several of these earlier studies (3,9,10,49) used the three methods, or slight modifications of those proposed by Smith (43) in calculating genetic trend within herd. Smith′s methods were based on the regression of daughter performance on time. Later studies (12,34,39) have estimated genetic trend (ignoring herd) as twice the regression of sires′ average estimated transmitting ability on time. Lee et. al. (17) estimated genetic trend within sex of offspring in two ways. One method was

$$\hat{g} = \hat{\beta}_S + \hat{\beta}_D$$

where

$\hat{\beta}_S$ = regression of average sire transmitting ability on birth year of son

$\hat{\beta}_D$ = regression of average dam transmitting ability on birth year of daughter

The other method utilized was

$$\hat{g} = 2 \times \hat{\beta}_{ETA}$$

where

$\hat{\beta}_{ETA}$ = regression of average parent transmitting ability on birth year of offspring

In most studies, time was measured as year of daughter's first calving though birth year of daughter was utilized by Lee et al. (17).

Estimates of genetic trend are difficult to compare due to the inclusion of different time periods and different populations in different studies. However, a chronological order can give us an understanding of the progress made throughout time. Early studies (3,9,10,34) using data from the 1950s to 1960s found estimates of genetic trends ranging from 41 kg to 133 kg and -.5 kg to 5.07 kg for milk and fat yield, respectively. Later studies (12,34,39) utilizing data from the 1960s to early 1970s estimated genetic trends ranging from 3 kg to 38 kg milk and 0 kg to 1 kg fat. Lee et al. (17) estimated genetic trends of 54.8 kg milk and 1.5 kg fat during the 1970s. The larger genetic trend estimates during the 1950s appear to be caused by either the use of measures less able to distinguish genetic from environmental changes, or to these estimates being within herd estimates as compared to across herd estimates of genetic trend in later studies. Powell and Freeman found (34) within herd estimates of genetic trend to be larger than across herd estimates.

White (53) felt that many dairymen who have herds on official milk recording programs do not participate in young sire sampling programs due to the unknown genetic risk of young bulls compared to the near certainty of older proven bulls. Powell and Freeman (34) 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 progeny test herds' genetic progress to other herds not on a sampling program in order to see what value or hindrance the sampling program had on genetic progress within these herds. McDaniel and Bell (20) found that equivalent genetic progress was made from use of the highest pedigreed AI young sires available and the top AI proven sires. In both groups, sires were highly selected. This could not be true for all progeny test herds as some sampling programs assign semen to different herds. Schneeberger et al. (42) used simulation to look at the expected income and risk for dairymen using different percentage of young sires and different number of total bulls in the herd. Expected income increased with increase percent young sire use when proven and young sires had equal genetic merit due to less expensive semen of young sires. This still held if genetic merit of proven bulls were slightly better than genetic merit of young sires. Risk of herd genetic improvement increased with percent young sire use, low repeatability of proven bulls, and decreased number of bulls used. McMahon et al. (22) compared the potential income generated from daughters of 292 young bulls sampled in 1983 with daughters of proven bulls available in the July 1983 USDA active sire summary. The authors concluded that the cost of young sire semen must be low and have other incentives associated with its use in order to economically justify replacing the use of the top 30% active proven bulls. The economic value of young sire use within a herd depended upon what active proven bulls would have been utilized.

Identification of Problem Herds

Henderson (11) suggested that identifying herds that provided accurate genetic information would be useful in selecting dams of young sires. Only cows from these herds would be used as dams of young sires entering AI. Henderson listed several characteristics of these herds: mostly registered cows, continuous official test for several years, and extensive use of AI. Similar herd characteristics would probably be useful in identification of herds to use in an AI progeny testing program. The requirement of registered cows appears to be an assumption of more accurate identification of registered animals. Misidentification of cows has been shown to reduce estimates of genetic variance (6,47) and has been blamed for decreases in bull's proofs with the inclusion of large amounts of information from second crop daughters (14). Van Vleck (48) found that biases in evaluation of sires increased as the fraction of misidentifications increased. Identifying current and potential progeny test herds with accurate pedigree information would be useful to AI companies.

Wilhelm and Mao (57) examined herd characteristics of Michigan herds that provided dams of bulls entering an AI stud's sampling program. They found that herds with high within herd variance provided bulls whose proofs were worse than their PI would have indicated and that herds with low within herd variance had bulls whose proofs were slightly better than PI would have indicated. They concluded that bias is introduced through inaccurate genetic evaluations and that within herd variance could be used as an indicator of progeny test herds in which information should be used with caution.

Norman and Dickinson (29) attempted to determine if first crop daughter lactation records that were particularly high or low could be useful in predicting a bull's final genetic evaluation. Daughter's Modified Contemporary Deviation (MCD) was deviated from her sire's average MCD and tested with a Z statistic. Results indicated that the removal of daughters more than -3 standard deviations from the mean increased the predictability of first crop proofs by three percent. A similar approach on a herd basis could be useful in identifying herds that provide more accurate genetic information.

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Analysis of Evaluation Stability of AI and Non-AI Sampled Bulls.

ABSTRACT

Changes in proofs during first crop and second crop period were computed from up to eight Modified Contemporary Comparison (MCC) proofs during both periods for AI and non-AI sampled Holstein bulls with repeatability of last MCC evaluation $\geq .90$. Effect of proof number within testing period on the bull's milk or fat evaluation was estimated with a model including fixed effect of bull besides proof number. For subsets of AI and non-AI sampled bulls born from 1970-75 and from 1976-81, proofs of both types of bulls increased from the initial first crop proof and then remained fairly constant during the remainder of the first crop period. With the inclusion of second crop daughters, proofs dropped significantly more for non-AI than AI sampled bulls born from 1970-75 (milk:108 kg vs 28 kg, fat:3.5 kg vs 1 kg). This reduction was larger for non-AI sampled bulls born after 1976 (milk:184 kg, fat:7 kg), but was unchanged for

AI sampled bulls. Two measures of change were calculated: last second crop proof minus the second to last first crop proof (Difference1), and last second crop proof minus the initial first crop proof (Difference2). Expected standard deviation of change for each proof was calculated and used to stratify bulls into eight change classes. Percentages of bulls in each class were compared. Measures of change between proofs of first crop and second crop period gave different impressions of the stability of AI versus non-AI sampled bulls. Difference1 indicated that non-AI sampled bulls dropped considerably while AI sampled bulls remained nearly constant. However, Difference2 indicated that non-AI bulls changed relatively little while AI sampled bulls increased greatly. A larger proportion of non-AI sampled bulls had first crop proofs that dropped more than could be explained by chance alone. Results indicated that non-AI sampled bulls' proofs were less stable than AI sampled bulls' proofs and that stability of proofs of non-AI sampled bulls has diminished over time. It appears that daughters of many non-AI sampled bulls included during the first crop period have received some kind of preferential treatment.

INTRODUCTION

Stability of sire proofs has been of concern to AI companies and dairy farmers ever since genetic evaluations have been computed. Sometimes estimated transmitting abilities (ETA) calculated after second crop daughters are included differ significantly from evaluations based on first crop daughters. A large swing in a bull's ETA causes dairy farmers to lose confidence in genetic evaluations and in the AI company who merchandizes the semen from that particular bull. This is particularly true for bulls whose ETA's drop.

AI companies are affected by change in bull proofs several ways: 1) Mistakes can be made in keeping or culling a young sire graduate from their progeny testing program, or purchasing or not purchasing a breeder proven bull based on first crop proofs. Incorrect decisions lead to either larger costs of maintaining bulls or lost opportunity costs. 2) Large drops in proofs can cause poor public relations with dairy farmers which may lead to lower sales volume. 3) Less than optimal use of outstanding young sires with low repeatabilities (due to risk of drop in ETA) as sire of sons. This increases the generation interval and decreases the genetic progress the stud and population makes.

One question examined by researchers has concerned the stability of breeder proven bulls' evaluations versus the evaluations of graduates of AI progeny testing programs. Meek and Van Vleck (5) examined stability of AI and non-AI sampled bulls that were selected for further use under the daughter-dam and herd-mate comparison evaluation systems. Non-AI proven bulls' second crop proofs declined more than AI proven bulls' proofs under both evaluation methods. Cassell et al. (2) investigated the stability of proofs for Holstein bulls sampled under limited and multiherd conditions that later were used extensively in AI. Non-AI sampled bulls' progeny test proofs were overevaluated 119 kg under the herdmate comparison method, but this decreased to 69 kg when pedigree information was utilized as in the MCC system (2).

Norman et al. (6) measured the difference between a bull's initial evaluation and his last available evaluation for non-AI sampled bulls that entered AI lineups and which increased repeatability ≥ 30%. Average evaluation for milk and fat dropped 14 and 0 kg, respectively, for non-AI sampled Holstein bulls. They concluded that AI organizations can acquire non-AI sampled bulls and be confident their evaluations are not upwardly biased.

In all of these studies stability was measured as the difference between two particular evaluations during a bull's evaluation time period. However, no literature was found that documented stability continually throughout the time period a bull is evaluated. The purpose of this study was to document and compare the proofs of AI and non-AI sampled bulls throughout their evaluation time period.

MATERIAL and METHODS

All Modified Contemporary Comparison (MCC) proofs for each Holstein bull entering a U.S. AI stud were obtained from the Animal Improvement Programs Laboratory (AIPL), USDA. Proofs were required to have NAAB code, year of birth of first AI daughter, and at least ten daughters with records used in computation. Bulls born before 1970 were deleted so that bulls would have at least three first crop proofs after the MCC was implemented in 1974. If a bull's first proof included records from more than seventy five daughters, the bull was eliminated.

First crop proofs were all evaluations that occurred before a bull added more than fifty daughters to his initial first crop proof. Evaluations occurring at least thirty-six months after the initial first crop proof and that added at least fifty new daughters were considered "second crop" proofs. For each bull, proofs were numbered from 1,2,3.. and 51,52,53.. for the first crop and second crop periods, respectively. During the first crop period each proof number after the initial first crop proof, 1, represented a six month period. Similarly, each second crop proof number with 51 subtracted from it represented a six month period after the initial second crop proof. Bulls were classified as non-AI sampled if the date of their initial first crop proof occurred less than two years after the first AI daughters were born. Otherwise bulls were considered AI sampled.

A data set was formed that included the first eight first crop proofs and the first eight second crop proofs of all bulls with a last MCC evaluation with repeatability greater than or equal to .90. The effect of proof number with bull absorbed was estimated using the GLM procedure in SAS for milk and fat evaluations for AI-birth year subsets of the data. Subsets included AI sampled bulls born from 1970 to 1975, non-AI sampled bulls born from 1970 to 1975, AI sampled bulls born from 1976 to 1981, and non-AI sampled bulls born from 1976 to 1981.

Two measures of change were calculated for each bull. One measure was the last available second crop proof minus the second to last first crop proof. Second to last first crop proof was utilized rather than last first crop proof in order to limit the possible inclusion of second crop daughters. The other measure of change was the last available second crop proof minus the initial first crop proof. Expected standard deviation of change was calculated for each difference of each bull as described by Powell and Norman (7):

$$E(\sigma_\Delta) = \sqrt{\mathrm{Rpt}_i - \mathrm{Rpt}_j} \times \sigma_S$$

where

Rpt_i, Rpt_j are the repeatabilities of the bull's second crop and first crop proofs and

σ_S is the sires' genetic standard deviation for milk or fat. $E(\sigma_\Delta)$ were used to stratify bulls into eight SD subclasses based on each measure of change. Percentages of bulls in each subclass were compared for AI and non-AI sampled bulls over time and to expectations from a normal distribution.

RESULTS and DISCUSSION

The number of AI and non-AI bulls included in the study are in Table 1. Fewer bulls in the 1976-81 subset would be expected since some bulls have not had sufficient time for second crop daughters to be incorporated into their proof. AI sampled bulls' average age when they reached .90 repeatability was 9.7 years while non-AI sampled bulls' average age was 10.8 years. The older age of non-AI sampled bulls can be attributed to the time-lag between first crop proofs, purchase or leasing of the bull by an AI organization, and the distribution of semen to produce second crop daughters. Thus many of the bulls born in 1979, 1980, and 1981 that were not available to the general public would not have reached .90 repeatability (or had second crop daughters) when the final MCC evaluation was run in January 1989.

Lifetime Trends in Bulls born 1970-75

Milk: Estimates of effects of proof number expressed as a deviation from initial first crop proof for AI and non-AI bulls born 1970-75 are plotted in Figure 1. Both AI and non-AI sampled bulls' proofs increased after their initial proof. This can be explained by characteristics of the group of bulls examined. All of these bulls were returned to active service. The fact that these bulls returned to service implies that they received better than average genes from their parents. Thus, their daughter deviations were greater than suggested from their ancestors genetic merit. As more daughter information was added, more of the weight was moved from pedigree to daughter performance, which led to an increase in the proof. Another possible factor contributing to the increase could be that lactation extension factors were conservative and underestimate completed lactation performance. This would agree with VanRaden et al. (8) who found that projected records had less phenotypic and genetic variance than completed records. After the initial increase, proofs were relatively stable during the first crop period. Average non-AI and AI sampled bulls reached a high of 88 and 82 kg (compared to initial first crop proof), respectively, during their 4th and 5th first crop proofs.

Of great interest is what happens to bulls' proofs when second crop daughter information is incorporated. AI sampled bulls' second crop proofs generally agreed with the proofs of the first crop period. Proofs dropped slightly (28 kg) but gradually increased toward the highest first crop proof. This slight drop could be caused by the inclusion of incomplete records of second crop daughters. However, non-AI bulls' proofs dropped sharply (108 kg) to the level of the initial first crop proof with the addition of second crop daughters. The initial first crop proof was influenced greatly by the genetic merit of the parents due to small number of daughters and a prevalence of incomplete records. This decrease to the initial first crop proof level indicated that the average non-AI bull received only average genes from its parents. The inflated proofs during the first crop period suggested that an average non-AI sampled bull's initial progeny test daughters received preferential treatment.

Fat: Patterns of fat proofs of bulls born 1970-75 (Figure 2) were similar to those found for milk. Both AI and non-AI sampled bulls' proofs increased from the initial first crop proof. Second crop proofs of AI sampled bulls reflected the peak of the first crop proofs. Non-AI sampled bulls' second crop proofs dropped consistently over 3 proofs to the level of their initial first crop proof. First crop proofs were excellent indicators of the genetic merit of AI sampled bulls, but not for non-AI sampled bulls. It appears that non-AI sampled bulls' initial daughters were preferentially treated causing an over-estimation of the genetic merit of non-AI bulls during the period when decisions on purchasing or leasing such bulls were being made by AI studs.

Lifetime Trends in Bulls born 1976-81

Milk: Estimates of milk proofs for AI and non-AI sampled bulls born from 1976 to 1981 are in Figure 3. As was the case for bulls born from 1970-75, both AI and non-AI sampled bulls′ proofs increased from the initial first crop proof. AI sampled bulls increased to a high of 69 kg (compared to the intial first crop proof) at the 4th proof. Non-AI sampled bulls reached a high of 123 kg at the second first crop proof. This was a considerably higher peak than for non-AI bulls born in 1970-75. AI sampled bulls′ proofs during the first crop period were fairly constant after the increase occurred following the initial first crop proof. Non-AI sampled bulls fluctuated during the remaining first crop period after the increase occurred following the initital first crop proof.

A large difference between AI and non-AI sampled bulls can be seen with the inclusion of second crop daughters. AI sampled bulls dropped (27 kg), about the same as bulls born 1970-75 (28 kg), and then rebounded to near the level of the highest first crop proof. Non-AI sampled bulls dropped even more than the 1970-75 non-AI sampled bulls, 184 kg from the highest first crop proof to the lowest second crop proof. Second crop proofs were considerably lower than the level of the initial first crop proof which suggested that the initial first crop proof may have been overevaluated.

Comparing the group of bulls born in 1976-81 to the bulls born in 1970-75, several conclusions can be made. First, average AI sampled bulls′ proofs were very constant from the first crop period through the second crop period for both data sets with the 1976-81 bulls′ proofs being slightly less variable. Second, non-AI sampled bulls′ proofs dropped considerably when second crop daughters were included. The decline was greater for bulls born in 1976-81. Results suggest greater bias in proofs of non-AI sampled bulls in more recent years of birth.

Fat: Fat proofs for AI and non-AI sampled bulls born from 1976-81 (Figure 4) exhibited the same general pattern observed for milk yield. The increase of 4.8 kg after the initial first crop proof was larger than the 3 kg increase for 1970-75 non-AI sampled bulls. Non-AI sampled bulls born 1976-81 dropped twice as far (7 kg) as 1970-75 non-AI sampled bulls (3.5 kg) when second crop daughters were included. AI sampled bulls increased 2 kg from the first initial progeny test proof and then gradually declined to .5 kg in the later second crop proofs. No explanation for this slight linear decline was evident. In general, AI sampled bulls had more stable proofs than their non-AI counterparts.

Measures of Change in Proofs: Means and standard deviations for the two measures of change in proofs for milk and fat for bulls born 1970-75 and 1976-81 are in Table 2. Difference1 was intended to compare "best" genetic evaluation of first crop daughters to most recently available second crop proof. Difference2 compared first available first crop evaluation, even one based on as few as 10 first crop daughters, to the last available second crop proof. Researchers (1,3,4,9) have generally used Difference2 variables to measure stability of bull proofs.

Difference1 Measure of Stability: Generally for Difference1 the mean change for AI sampled bulls born in 1970-75 and 1976-81 approached the expected value of zero for milk and fat. An exception was that the average fat change (-1.6 kg) which was negative for AI sampled bulls born 1976-81. The mean change for non-AI sampled bulls born in

1970-75 and 1976-81 was highly negative for milk and fat yield. The drop in proofs was more drastic for non-AI sampled bulls born 1976-81 than for bulls born 1970-75.

Observed standard deviations of changes in milk and fat yield proofs for AI and non-AI sampled bulls in both birth year subsets were slightly larger than expected. The exception was the standard deviation of milk change for non-AI bulls born 1976-81. This standard deviation was considerably larger (254 kg vs 182 kg) than expected.

Difference2 Measure of Stability: For the last proof minus the initial first crop proof, the mean change for AI sampled bulls was greater than the expected value for milk and fat yield. Mean milk and fat yield change for non-AI sampled bulls was close to zero for 1970-75 born bulls, but negative for 1976-81 born bulls. The close agreement of the final proof with the initial first crop proof for non-AI sampled bulls coincided with results of Clay et al. (3). However, this does not mean that the average non-AI sampled bull's proof was stable or as stable as the proof of an average AI sampled bull. From examining proofs throughout non-AI sampled bulls' first crop and second crop periods it was evident that Difference1 more accurately depicted changes in proofs compared to Difference2. Difference2 ignored the large increase of first crop proofs after the initial first crop proof which gives a misleading indication of proof stability of non-AI sampled bulls.

Frequency Distribution of Proof Changes: According to Figures 1-4, Difference1 appeared to better explain what was occurring in AI and non-AI sampled bulls' proofs throughout the first crop and second crop periods. Therefore only the Difference1 measure of stability was utilized in examining what proportion of AI and non-AI sampled bulls' proofs changed.

Some change between proofs can be expected due to Mendelian sampling and other random effects. Random chance would cause the expected change to have a mean of zero and a normal distribution. Hence, we would expect that 68% of the bulls would lie within ±1 SD, 95% would lie within ± 2 SD, and 99% would lie within ± 3 SD from the expected mean change of zero. Expected standard deviations of change used to stratify non-AI sampled bulls into SD classes were larger due to lower repeatabilities of progeny test proofs.

Tables 3 and 4 contain the frequency distribution of Difference1 milk and fat proof change measures for bulls born 1970-75 and 1976-81, respectively. For AI sampled bulls born 1970-75 and 1976-81, the frequency of bulls in each SD class followed the normal distribution expected due to chance. Slightly more AI sampled bulls had fat proofs that decreased more than expected. However a larger proportion of non-AI sampled bulls' proofs dropped in the 1970-75 and 1976-81 birth groups, respectively. The excess frequency of non-AI bulls with negative change was in the classes representing drops of greater than 1 SD. There were both AI and non-AI sampled bulls whose proofs dropped excessively (> 1 SD). However, a larger proportion of non-AI sampled bulls dropped excessively, especially for the bulls born 1976-81.

CONCLUSIONS

The average proof of AI sampled bulls stayed relatively constant after initial increases during the first several first crop proofs and a slight reduction with the inclusion of the first second crop daughters. However, the first crop proofs after initial first crop proof of non-AI sampled bulls tended to overestimate their apparent genetic merit. Information from the two different birth groups showed that stability of proofs of non-AI sampled bulls has decreased over time.

The two measures of change demonstrated that looking at two proofs at different time periods of a bull's life can give dissimilar conclusions on stability of non-AI sampled bulls. Difference1, the last second crop proof minus the second to last first crop proof, more accurately depicted the change in proofs throughout the first crop and second crop periods as compared to Difference2. Difference2, the last proof minus the initial first crop proof, ignored the large increases of first crop proofs after the initial first crop proof. Future studies should use Difference1 rather than Difference2 to measure changes in proofs throughout the first crop and second crop periods.

Some AI and non-AI sampled bulls had large increases and some had large decreases in proofs from first crop to second crop period. However, a larger proportion of non-AI bulls had sizeable declines in proofs than can be explained by chance alone. The proportion of non-AI sampled bulls with sizeable decreases has increased in more recent birth years. It appears that for many non-AI sampled bulls, first crop daughters have received some kind of preferential treatment. AI studs should proceed with caution in purchasing or leasing non-AI sampled bulls. Dairymen should be cautious of and limit the use of non-AI sampled bulls in their breeding programs.

ACKNOWLEDGEMENT

Supply of data by USDA Animal Improvement Programs Laboratory at Beltsville, Maryland is gratefully acknowledged. Select Sires, Inc. and VA/NC Select Sires provided partial financial support.

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Table 1. Number of AI and non-AI sampled bulls included in each year subset.

Year Subset	AI	Non-AI
1970-75	762	175
1976-81	469	42

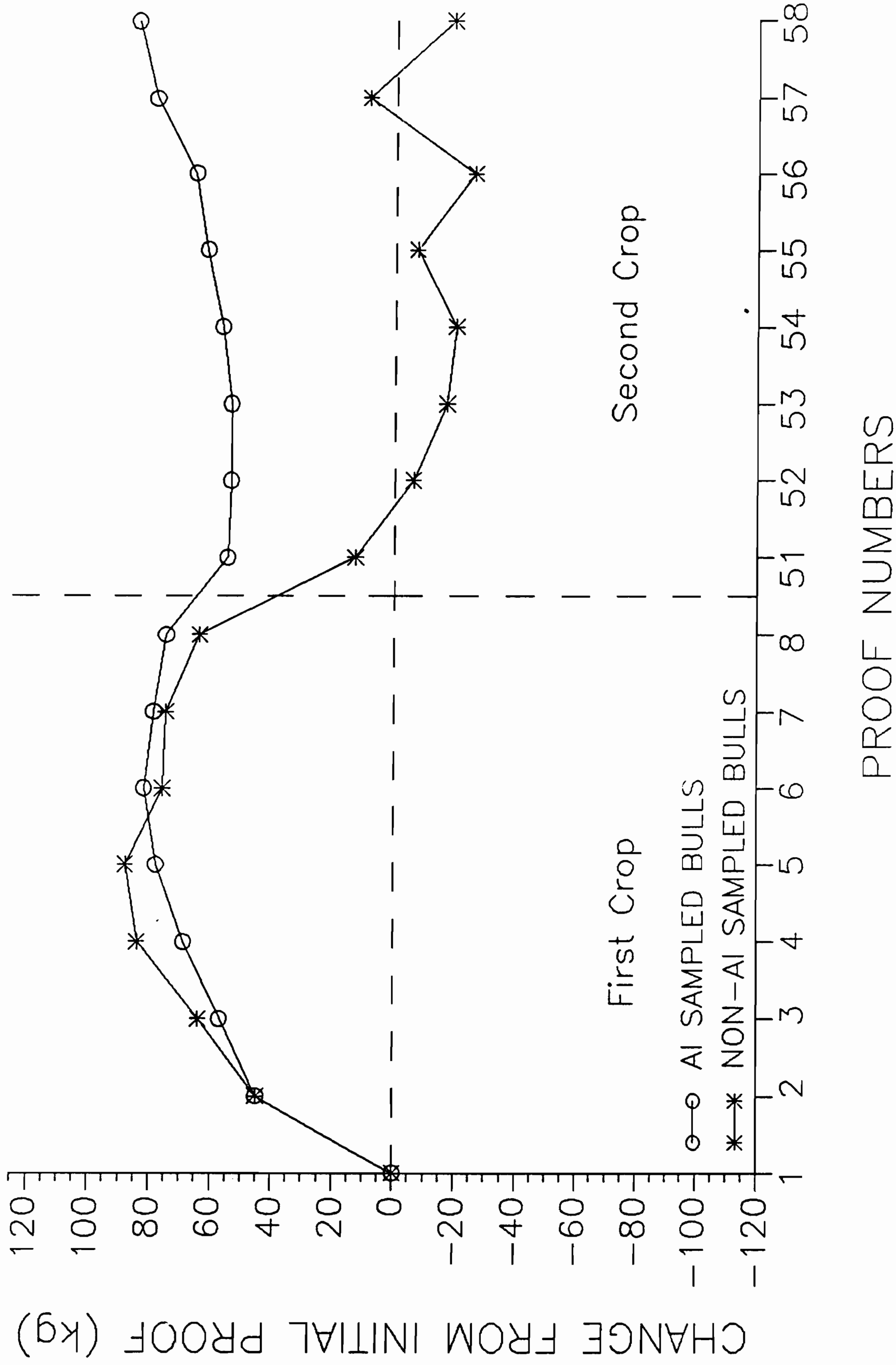

Figure1. Changes of milk proofs for AI and non-AI bulls born 1970-75.

Figure 2. Changes of fat proofs for AI and non-AI bulls born from 1970-75.

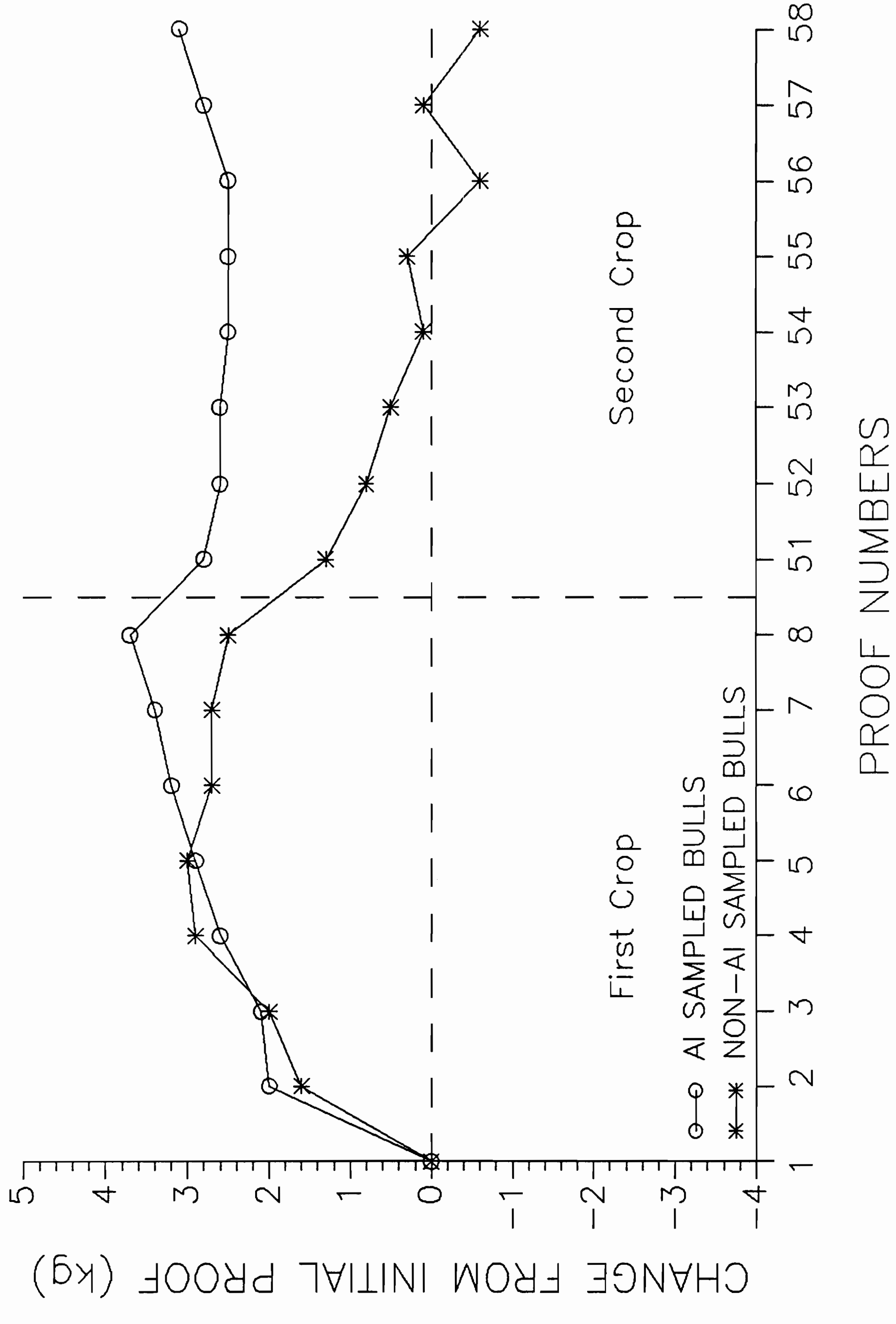

Figure 3. Changes of milk proofs for AI and non-AI bulls born 1976-81.

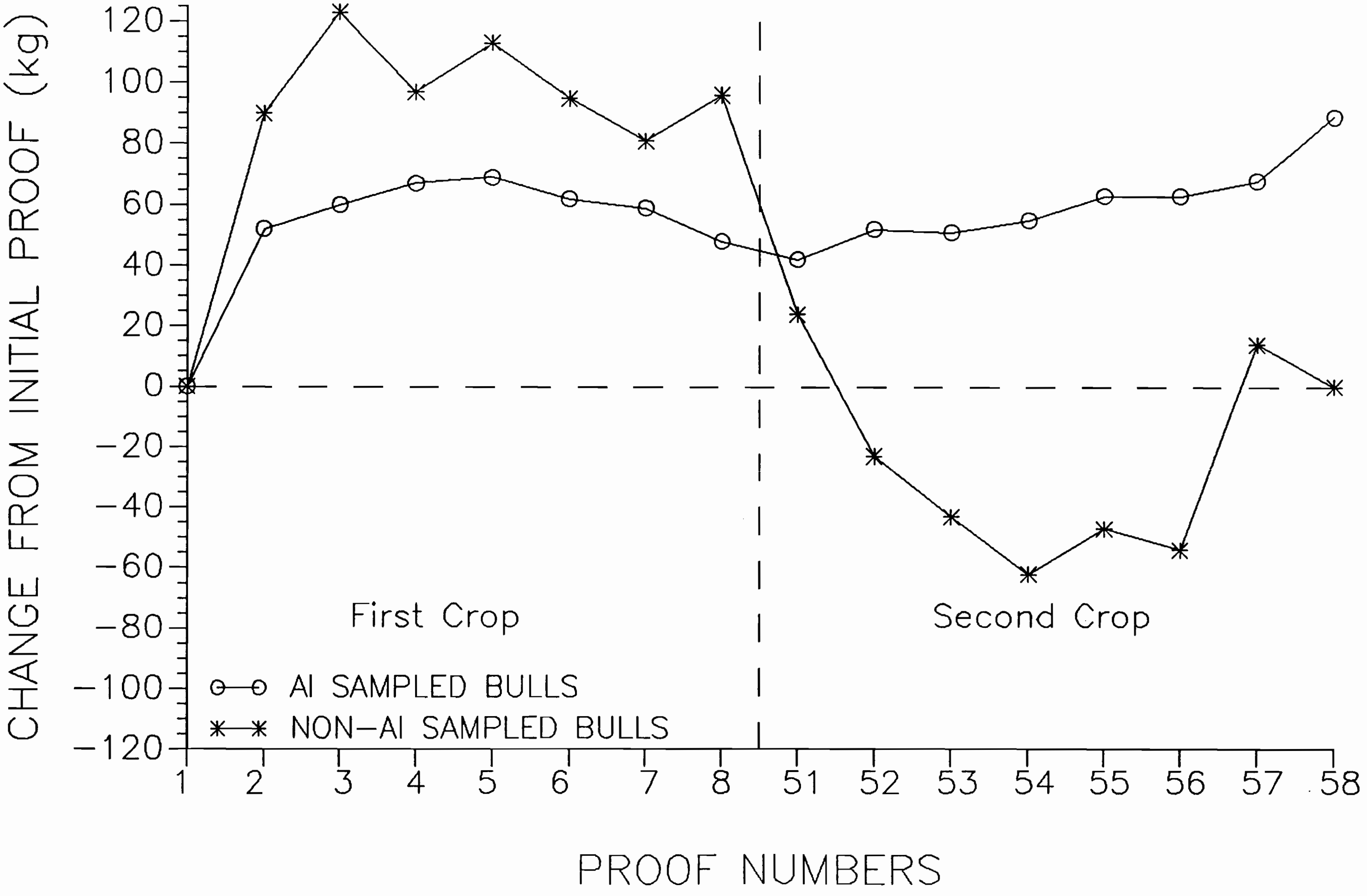

Figure 4. Changes of fat proofs for AI and non-AI bulls born 1976–81.

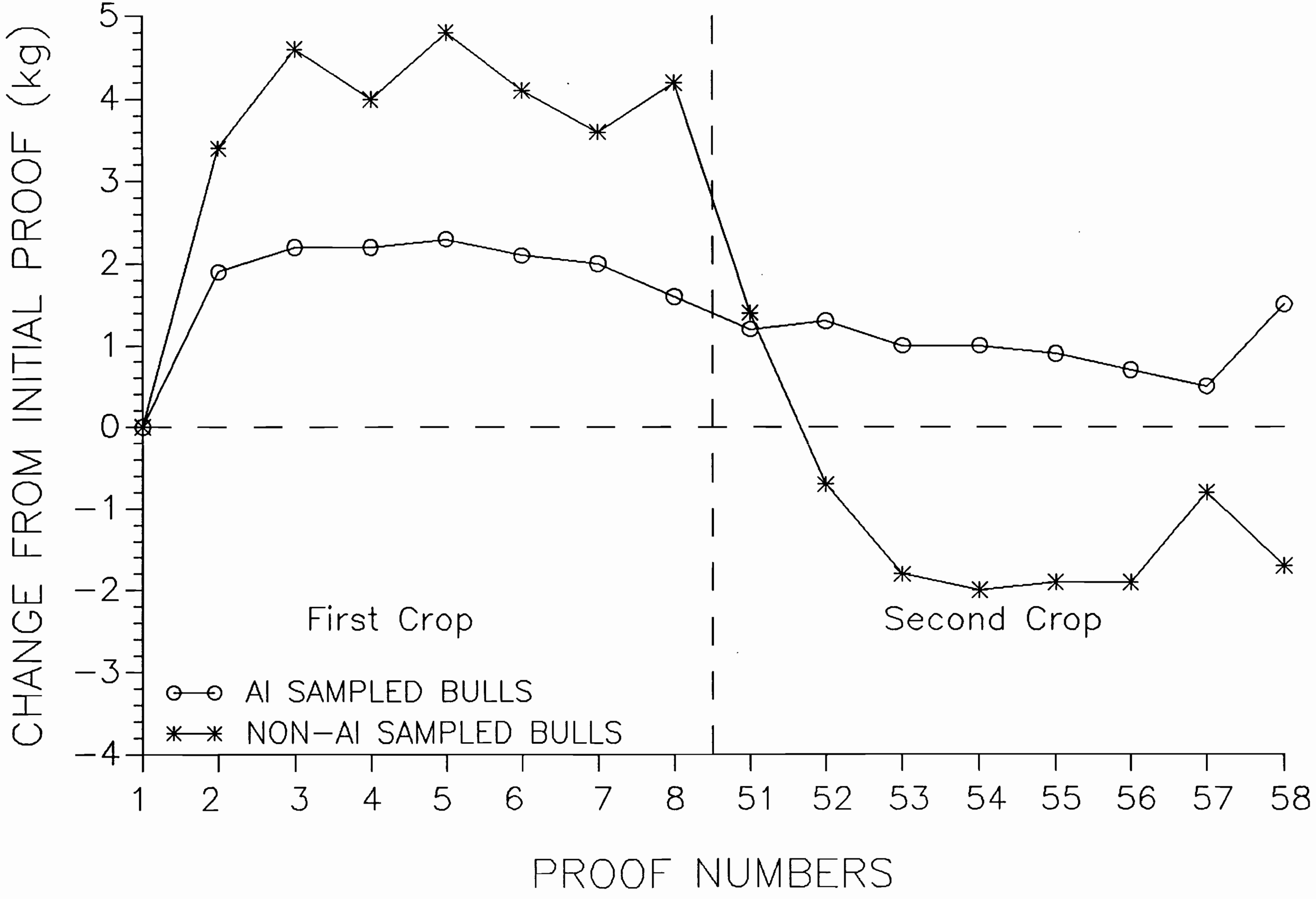

Table 2. Means and standard deviations for measures of change in proofs for bulls born 1970–75 and 1976–81.

	1970–75				1976–81			
	AI		Non–AI		AI		Non–AI	
	$\bar{X}$	SD	$\bar{X}$	SD	$\bar{X}$	SD	$\bar{X}$	SD
Difference1[a]								
Milk (kg)	−17	145	−98	218	−20	152	−147	254
Fat (kg)	−.6	5.4	−3.2	7.6	−1.6	5.3	−6.0	7.1
Repeatability	.21	.10	.44	.12	.20	.08	.38	.10
Difference2[b]								
Milk (kg)	88	211	1	266	85	242	−47	280
Fat (kg)	3.0	7.8	.2	8.5	1.9	8.0	−1.8	8.0
Repeatability	.53	.10	.68	.07	.51	.11	.64	.08

[a] Difference between Last available 2nd crop proof and second to last progeny test proof.

[b] Difference between Last available 2nd crop proof and first progeny test proof.

Table 3. Percentage of bulls born 1970–75 falling into each of the eight single standard deviation subclasses.

	Decrease				Increase			
	>3 SD	2–3 SD	1–2 SD	0–1 SD	0–1 SD	1–2 SD	2–3 SD	>3 SD
AI								
Milk	.9	3.5	15.8	32.5	32.3	12.2	2.1	.7
Fat	.3	3.8	15.2	35.2	29.6	12.7	2.5	.7
Non–AI								
Milk	3.4	2.3	24.6	37.7	22.9	8.6	.6	.0
Fat	2.3	5.1	18.3	42.3	23.4	7.4	1.1	.0

Table 4. Percentage of bulls born 1976–81 falling into each of the eight single standard deviation subclasses.

	Decrease				Increase			
	>3 SD	2–3 SD	1–2 SD	0–1 SD	0–1 SD	1–2 SD	2–3 SD	>3 SD
AI								
Milk	.6	5.0	14.5	35.2	30.8	10.7	3.0	.3
Fat	.6	4.1	19.8	37.9	27.5	8.0	1.8	.3
Non–AI								
Milk	7.1	11.9	23.8	31.0	19.0	7.1	.0	.0
Fat	2.4	9.5	28.6	47.6	11.9	.0	.0	.0

Prediction of Proof Changes from Average and Variability of Herd Characteristics Across Progeny Test Herds

ABSTRACT

Changes in milk and fat proofs for 112 bulls sampled under Select Sires, Inc., Program for Genetic Advancement were measured. Measurement of Modified Contemporary Comparison changes were last available 2nd crop proof minus second to last first crop proof. For each bull the average and standard deviation of herd-year characteristics across contributing herds was calculated and used to predict proof changes. Herd-year characteristics were within herd-year means and standard deviations of phenotypic production, genetic evaluation, and cow characteristic variables. Means and standard deviations of herd-year characteristics explained 39% to 46% of the variation in milk and fat proof changes. In general, standard deviations of herd-year characteristics and average within herd-year standard deviations of herd-year variables were most useful in predicting change in Modified Contemporary Comparison proofs. Impact of significant herd-year characteristics was determined by examining the means for bulls that increased more than 1 SD, decreased more than 1 SD, and those which changed less than 1 SD. In general, the larger the average within herd standard deviation of contributing progeny test herds' genetic merit and phenotypic production variables, the more likely the bull's proof would change. Bulls sampled across herds that were more uniform in their average genetic merit of sires were more likely to have their second crop proofs decrease wheras bulls sampled across herds that were more diverse in their average genetic merit of sires were more likely to have their second crop proofs increase. Bulls sampled across herds with a smaller percentage of young sire usage were more likely to have their second crop proofs change. bulls sampled across herds that were more diverse in their within herd standard deviations of environmental effects (phenotypic yields and sire by herd plus permanent environment effects) were more likely to have their second crop proofs increase. Results indicated that standard deviation and averages of progeny test herd characteristics can help explain changes in proofs.

INTRODUCTION

Sires of dairy females can be partitioned into three categories: 1) young sires with no daughter production information when used to inseminate cows, 2) sires with daughter production information on only those daughters conceived prior to sire's first proof (first crop daughters), 3) sires with daughter production information from second crop daughters. Approximately 10-15% of bulls that are progeny tested continue in service in category 2 and very few are in service in category 3. Inaccurate first crop daughter information leads to genetic estimates which are not a true reflection of the bull's genetic merit. If a bull's first crop daughter information underestimates his true genetic merit, he could be mistakenly culled from the AI stud with his true breeding value unknown or kept in the AI stud's active lineup but not used as heavily as his true genetic merit would justify. If a bull's first crop daughter information overestimates his genetic merit, he may be overused. Inclusion of second crop daughters in this case leads to a drop in his proof and causes dissatisfication with the dairymen that used him. Both of these situations are of great concern to AI companies and dairy farmers.

Researchers (1,2,4,12) have recognized the problem of proof stability and have tried to utilize characteristics associated with the daughters included in the original first crop proof to predict changes in bulls' proofs. Cassell and Norman (2) examined variables available on sire summary tapes besides a bull's first crop proof for their usefulness in predicting future second crop daughters' performance. Bulls whose first crop proofs underestimated their genetic merit had lower initial first crop proofs, a greater percentage of first crop daughters culled, and first crop daughters compared to contemporaries with high genetic merit. Bulls whose first crop proofs overestimated their genetic merit had higher initial first crop proofs, fewer first crop daughters culled, and first crop daughters compared to contemporaries with low genetic merit.

Clay et al. (3) found that bulls with low initial repeatability were more likely to have their evaluations change with slightly greater tendency for evaluations to decrease. Bolgiano et al. (1) examined changes in characteristics of herds in which first and second crop daughters of 20 AI bulls were located. Three bulls whose second crop proofs changed dramatically were denoted as problem bulls. Problem bulls had first crop daughters in better managed (higher producing) herds and were mated to first crop mates with higher ETAs for milk yield. They concluded that preferential treatment could be leading to changes in bull proofs, but the most probable explanation was Mendelian sampling.

Vinson et al. (12) used 160 Holstein sires with an initial first crop evaluation with repeatability less than .70 and a last evaluation with greater than .90 repeatability to measure stability of bull proofs. Both the average progeny test herd-year characteristics and the variability of the herd-year characteristics across the progeny test herds were used in predicting proof changes. Results indicated that bulls with most stable proofs had initial evaluations with larger repeatability and their daughters′ contemporaries′ sires also had larger repeatabilities. These bulls were proven in small, high producing herd-years with low genetic merit of contemporaries. There was less variation across progeny test herds in the number of contemporary sires and in the producing ability of mates. Bulls whose second crop proofs increased were proven in large herds with low genetic merit of contemporaries. There was less than average variation across the progeny test herds in the number of contemporary sires and in the producing ability of mates, but larger variation across the progeny test herds in the repeatability of proofs of contemporaries′ sires. Bulls whose last evaluation decreased from initial evaluation had daughters compared to contemporaries with genetically superior sires and daughters with extremely high milk yield. There was large variation across the progeny test herds in the size of herds, in the producing ability of mates, and in the production of contemporaries. Conclusions were that careful design of progeny testing programs could increase stability, though authors felt most change in evaluations was due to Mendelian sampling since only thirty percent of the variation was explained from herd-year characteristics.

Lofgren and Vinson (4) examined 1095 AI and 1277 non-AI sampled bulls with 10 to 75 daughters in their initial summary and added at least 25 daughters between their initial and last available summary. Average characteristics of a bull's first crop evaluations explained relatively little of the variation in change from first crop to second crop proofs. They concluded that random Mendelian sampling was the major cause of changes in proofs. However, they felt a larger proportion of the variation could have been accounted for if variances of herd characteristics across the progeny test herds had been utilized as independent variables as well as if genetic merit of mates had been considered.

Studies (6,7) suggest that bulls sampled primarily in registered herds with high within herd variance would have their genetic merit magnified while bulls sampled primarily in grade herds with small within herd variance would have their genetic merit diminished. This could be partially responsible for changes from first crop proofs to second crop proofs.

The purpose of our study was to examine whether within herd variances used along with herd means of characteristics of progeny test herds contributing daughter information to a bull's first crop proofs would be useful in predicting changes in Modified Contemporary Comparison (MCC) proofs of AI progeny tested bulls.

DATA

The identity of all herds that participated in Select Sires' progeny test program, Program for Genetic Adavancement (PGA), and all sires sampled through PGA were provided by Select Sires. Herd information included DHIA herd code, USDA regional code, and year of entering or leaving PGA. Sample sire information included registration number, super sampler status (was bull available to general public), and year entered PGA.

Lactation yield records and January 1990 AM evaluations for all cows in herds that have participated in Select Sires' PGA were obtained from Animal Improvement Programs Laboratory (AIPL), USDA. Individual cow records were removed prior to calculations if birthdate or year of calving was missing, record was unuseable for genetic evaluations, or mature equivalent (ME) milk or fat yield was missing. The January 1990 AM genetic sire evaluations and the MCC sire history tape were also obtained. The MCC history tape was utilized as in (5) to determine which genetic evaluation was the sire's initial "first crop" proof. Daughters of PGA bulls conceived prior to their initial first crop proof were considered first crop. Daughters conceived after the first proof of PGA sires and daughters of all other sires were classified as "non-first crop".

METHODS

Bulls sampled through Select Sires PGA program which received second crop MCC proofs with repeatability greater than or equal to .90 were identified. Bulls designated as super samplers (available to the general public immediately after being used in the progeny test herds) were deleted. For each bull the last available second crop MCC proof minus the second to last first crop MCC proof as described in (5) was calculated to measure proof stability.

An attempt to measure proof change under the animal model retrospectively was unsuccessfully. First crop animal model proofs were approximated for each bull based on just first crop daughters from Select Sires PGA herds and the technique explained by Wiggans and Van Raden (13). First crop proof was subtracted from January 1990 second crop animal model proof to yield the measure of change. This method appeared to be unsuccessful due to the feedback (dependency) between the information (i.e. daughter yield deviations and parent averages) used to compute first crop proofs and the second crop proofs.

The expected standard deviation of change in MCC and fat proofs was calculated as described by Powell and Norman (10):

$$E(\sigma_{\Delta}) = \sqrt{R_i - R_j} \times \sigma_S$$

R_i, R_j were the repeatabilities the respective second and first crop proofs. σ_S was one-half the additive genetic standard deviation for milk (295 kg) or fat (11 kg). $E(\sigma_{\Delta})$ were used to stratify bulls into eight SD subclasses based on each measure of MCC change. Percentage of bulls in each subclass was compared to expectations from a normal distribution.

Means and standard deviations of herd-year characteristics represented in each sire's first crop proof (bull's sample herd characteristics) were computed to determine the degree that they could predict the subsequent change in proof. This was accomplished by first computing means and standard deviations, or percentages or counts of cow characteristics for each herd-year. These were designated as herd-year characteristics. Means and within herd-year standard deviations of the following cow characteristics were calculated: mature equivalent milk, fat, and fat percent; lactation number; sum of sire by herd interaction plus permanent environment for milk and fat yield (computed as cow's Predicted Producing Ability (PPA) minus two time cow's PTA (14)); cow's PTA milk, fat, and fat percent; cow's sire's PTA milk, fat, and fat percent; and reliability of cow's and cow's sire's PTA. Means only were computed for the variables: percentage of cows registered and percentage of cows that are first crop daughters of PGA sires. Values only were computed for the variables: number of sires represented, number of young sires represented, percentage of sires represented that were young sires, herd size, state, and USDA region. Herd-years contributing first crop daughters to each PGA bull were identified and the mean and standard deviation of all herd characteristics were calculated. Number of PGA herds contributing daughters to a bull's first crop proof, number of states and USDA regions represented, and difference between number of PGA herds and number of herds in the second to last first crop proof was also calculated for all bulls. These variables were designated as bull's sample herd characteristics and were used to predict change in bulls' MCC proofs. Due to the large number of independent variables examined, interactions were not included in the developement of prediction equations. Stepwise regression, with a significance level of .20 for entry or exit, was used to screen variables useful in predicting bulls' proof changes. Then condition numbers were utilized to remove variables that were found to be redundant due to collinearity (8). Variables passing the multicollinearity test were used to run all possible regression models. PRESS, CP, Adjusted R^2, and Mean Square Error statistics were examined and used to select the best model for predicting proof changes (8). This procedure is more fully detailed in Appendix A. Mean of all bulls that dropped or increased more than one standard deviation and those which changed less than one standard deviation was calculated for each significant bull sample herd characteristic for use in interpretation of these significant dependent variables.

RESULTS and DISCUSSION

Changes in MCC Evaluations

Table 1 contains the means, standard deviations, and ranges of milk and fat proof changes under the MCC evaluation system for the 112 PGA graduates with repeatability of second crop MCC proofs greater than or equal to .90. The average proof declined 9.1 kg milk and 1.9 kg fat.

Percentage of 112 Select Sires PGA graduate bulls that fell into each of the eight single expected standard deviation (SD) subclasses for MCC measure of change for milk and fat are in Table 2. The frequency of bulls in each MCC milk and fat change SD subclass approximated the normal distribution expected due to chance. A slightly larger proportion of bulls had MCC fat proofs that decreased 1-2 SD and 2-3 SD than expected. This resulted in 64.3% of the bulls having MCC fat proofs that decreased compared to 48.3% of the bulls having MCC milk proofs that decreased. However, this had little impact on the change.

Bulls' Sample-herd Characteristics

The mean, SD, mininum and maximum value, and correlations of all bull's sample-herd characteristics with change in his milk and fat proofs for the 112 bulls are in Appendix B. Bull's sample-herd characteristics are means and standard deviations of herd-year characteristics for PGA herd-years included in his first crop proof. To simplify

Appendix B and Tables 4-5, notation was developed for certain variables and the description of this notation is in Table 3. The average bull was sampled in 31 PGA herds located in 12 different states in 6 different USDA regions. The average difference of 6 non-PGA herds contributing information to the bull's first crop proofs was probably due to the distribution of semen to the former owner (breeder) of the bull and/or the sale of first crop daughters (or cows pregnant with first crop daughters) to non-PGA herds prior to initiation of first lactation. The average bull was sampled in herds that were predominantly grade which agreed with Norman and Powell (9). Herds contributing daughter information to a bull's first crop proof had average herd size of 167 cows. This seemed high, however the inclusion of just one herd (out of the 30 generally represented) with herd size of 1000 would greatly inflate average herd size. Average percent young sire use was 18.6%. There were 48 different sires represented in the average herd. Approximately one-third of the sires were PGA young sires. The large number of sires represented was most likely due to a large number of young sires required to be utilized by herds enrolled in a sampling program and/or one herd with large herd size having more sires represented and thus inflating the average value. Results from Appendix B indicated that randomly assigning bulls to herds was not equivalent to each bulls being used in a uniformly homogeneous group of herds.

Predicting Changes in Proofs from Bulls' Sample-herd Characteristics

Tables 4-5 contain the variables, average herd-year characteristics or variability of herd-year characteristics across the PGA herds contributing daughter information to a bull's first crop proof, that were significant in explaining changes in a bull's milk or fat, MCC proofs. The final model's statistics and each significant variable's estimated regression coefficient are also included in the tables. Means of bull's sample-herd characteristics for three bull change groups are presented in Tables 4 and 5 as well. Means of bull's sample-herd characteristics for each group were used to interpret the significant herd characteristics due to the difficulty in interpretting partial regression coefficients.

Final models selected had R^2 values of .39 and .46 for predicting changes in bulls' MCC milk and fat proofs, respectively. The amount of variation explained by variables included in the models was larger than previous studies (2,4,12). Originally, herd characteristics of fat yield were not allowed to enter the model used to predict changes in milk proofs. However, R^2 value was considerably smaller (.18) than when herd characteristics of fat yields were allowed to enter the models. Generally, herd characteristics of fat yield were more important in explaining both milk and fat proof changes than herd characteristics of milk yield. No explanation for this was evident. The inclusion of variables measuring the variability of herd-year characteristics across the PGA herds contributing first crop daughters to the bull's first crop proofs appeared to improve the prediction as suggested by Lofgren and Vinson (4). Vinson et al. (12) explained a larger proportion of changes in milk proofs when using variability of herd characteristics across herds a bull was progeny tested in. The inclusion of within herd standard deviation variables probably improved our ability to predict changes in proofs. Heterogeneous within herd variances have been shown to affect the response to selection within a herd (6,7) and have been blamed for biases of individual cow genetic evaluations (11). Vinson (11) stated that the impact of heterogeneous within herd variances should be minimized in bull proofs due to the large number of herds generally represented. However, heterogeneous within herd variances could have an affect on bull proofs during the first crop proof period when fewer herds are represented. The variables significant in our models were difficult to compare with other studies that examined proof stability due to many of these significant variables (i.e. within herd standard deviation herd-year characteristics and variability of herd-year characteristics across contributing herds) had not been examined extensively or at all previously. These variables probably accounted for some of the variation explained by other variables in other studies.

Interpretation of Significant Herd Characteristics

Interpretation of partial regression coefficients in the final model was nearly impossible. Thus we examined the mean of significant variables for bulls which increased (> +1 SD), were stable (-1 SD to +1 SD) or decreased (< -1 SD) as a way of interpretting the impact of variables. These bull group means of these significant variables are presented in Tables 4 and 5.

MCC Milk Change

Decrease: Bulls whose proofs decreased had less of a difference between the number of PGA herds and all herds contributing first crop daughters and were sampled in herds with smaller percentage of young sire usage which caused the average reliabilities of PTAs of sires to be higher. Averages of bull sample-herd characteristics indicated that decrease bulls were progeny tested in herds that had larger within herd standard deviations of sire by herd plus permanent environent effects, larger within herd standard deviations of genetic merit of cows and their sires, smaller within herd standard deviations of lactation number, and smaller within herd standard deviation of reliability of cows' PTAs.

Standard deviations of bull sample-herd characteristics indicated that bulls whose proofs decreased were sampled across herds that were more uniform in their average genetic merit of sires, but more diverse in their within herd standard deviations of sire by herd plus permanent environment effects.

Increase: Bulls whose proofs increased substantially were progeny tested in herds with a smaller percentage of young sire usage which caused the reliabilities of PTAs of sires to be larger. Averages of bull sample-herd characteristics indicated that increase bulls were sampled in herds with larger within herd standard deviations of sire by herd plus permanent environment effects, larger within herd standard deviations of genetic merit of cows and their sires, but smaller within herd standard deviations of lactation number.

Standard deviations of bull sample-herd characteristics indicated increase bulls were sampled across herds that were more diverse in their within herd standard deviations of sire by herd plus permanent environment effects, within herd standard deviations of genetic merit of cows, and average genetic merit of sires. However, increase bulls were progeny tested across herds more uniform in their average reliabilities of PTAs of sires.

Stable: Bulls whose proofs were stable were progeny tested in herds with a larger percentage of young sire usage which caused the reliabilities of PTAs of sires to be smaller. Averages of bull sample-herd characteristics indicated that stable bulls were sampled in herds with smaller within herd standard deviations of genetic merit and smaller within herd standard deviations of sire by herd plus permanent environment effects. Standard deviations of bull sample-herd characteristics indicated stable bulls were sampled across herds that were intermediate in their diversity of average genetic merit of sires, more uniform in their within herd standard deviations of sire by herd plus permanent environment effects, and more uniform in their within herd standard deviations of genetic merit of cows.

REGION: USDA region contributing the most first crop daughter information to a bull's first crop proofs was important in explaining changes in bulls' milk proofs. However, there were only 19 of the 112 bulls that weren't predominantly sampled in region 1 (Indiana, Michigan, and Ohio). Regions causing the significance had only contributed the most first crop daughter information to one bull each. The bull sampled predominantly in region 3 (North Carolina, South Carolina, Georgia, Florida, Tennessee, Alabama, Mississippi, Arkansas, Louisianna, and Texas) had his proof increase (312 kg) while the bull sampled predominantly in region 4 (Illinois, Iowa, Missouri, Nebraska, Kansas, Oklahoma, and Colorado) had his proof decrease (-156 kg). Whether these region effects are real and repeatable was questionable.

MCC Fat Change

Decrease: Bulls whose fat proofs decreased were sampled in fewer number of PGA herds and had slightly more states represented in their first crop proofs. Averages of bull sample-herd characteristics indicated that decrease bulls were sampled in herds with a smaller percentage of young sire usage and larger average mature equivalent fat yields. Decrease bulls were progeny tested in herds with slightly larger within herd standard deviations of mature equivalent fat yields and larger within herd standard deviations of PTA fat percent of sires.

Standard deviations of bull sample-herd characteristics indicated that decrease bulls were sampled across herds that were more uniform in their average genetic merit fat yield of sires, more uniform in their within herd standard deviations of mature equivalent fat yields, more homogenous in their within herd standard deviations of sire by herd plus permanent environment effects, but more diverse in their within herd standard deviations of PTA fat percent of cows.

Increase: Bulls whose fat proofs increased were sampled in a greater number of PGA herds and had more states and USDA regions represented in their first crop proofs. Averages of bull sample-herd characteristics indicated that decrease bulls were sampled in herds with a smaller percentage of young sire usage, larger average mature equivalent fat yield, higher average genetic merit fat yield of sires, larger within herd standard deviations of mature equivalent fat yield, greater within herd standard deviations of genetic merit fat yield of cows, and smaller within herd standard deviations of gentic mmerit fat percent of sires.

Standard deviations of bull sample-herd characteristics indicated that increase bulls were sampled across herds that were more diverse in their average genetic merit fat yield of sires, more variable in their within herd standard deviations of mature equivalent fat yield, and more heterogeneous in their within herd standard deviations of sire by herd plus permanent environment effects.

Stable: Bulls whose proofs were stable were progeny tested in intermediate number of PGA herds, fewer number of states represented, intermediate number of USDA regions represented, and larger percentage of young sire usage. Averages of bull sample-herd characteristics indicated that stable bulls were sampled in herds with smaller average phenotypic fat yields, lower average genetic merit of sires, smaller within herd standard deviations of phenotypic fat yield, and intermediate within herd standard deviations of genetic merit fat percent of sires. Standard deviations of bull sample-herd characteristics indicated stable bulls were sampled across herds that were intermediate in their diversity of average genetic merit of sires, more uniform in their within herd standard deviations of sire by herd plus permanent environment effects, and intermediate in their diversity of within herd standard deviations of phenotypic fat yield.

SUMMARY

Average changes in MCC milk and fat proofs of the 112 bulls sampled through the PGA program were nearly normally distributed around a mean of zero with extreme changes of -479.5 to 508.9 kg milk and -20.4 to 11.3 kg fat. Ranges of the bull sample-herd characteristics were examined and indicated that not all bulls were sampled across herds with the same average herd characteristics. Similarly, the ranges of the standard deviation of bull sample-herd characteristics indicated that some bulls were sampled across herds with more uniform herd characteristics while other bulls were sampled across herds with widely diverse herd characteristics.

Bull's sample-herd characteristics of first crop proofs explained more variation (39% and 46%) than in previous studies. Standard deviations of herd-year characteristics and average within herd-year standard deviations of herd-year variables were most useful in predicting change in Modified Contemporary Comparison proofs. In general, the larger the average within herd standard deviation of contributing progeny test herds' genetic merit and phenotypic production variables, the more likely the bull's proof would change. Bulls sampled across herds that were more uniform in their average genetic merit of sires were more likely to have their second crop proofs decrease wheras bulls sampled across herds that were more diverse in their average genetic merit of sires were more likely to have their second crop proofs increase. Bulls sampled across herds with a smaller percentage of young sire usage were more likely to have their second crop proofs change. Bulls sampled across herds that were more diverse in their within herd standard deviations of environmental effects (phenotypic yields and sire by herd plus permanent environment effects) were more likely to have their second crop proofs increase.

It appears that the careful design of a sire sampling program in order to avoid bulls that vary greatly in their average herd characteristics and diversity of herd characteristics progeny tested under could help diminish changes in proofs. However, this would not eliminate all changes in proofs from first crop to second crop since over 50% of the variation was not explained by these herd characteristics. Mendelian sampling and other random factors would still cause some fluctuations in proofs.

ACKNOWLEDGEMENT

Supply of data by USDA Animal Improvement Programs Laboratory at Beltsville, Maryland is gratefully acknowledged. Select Sires, Inc. and Virginia-North Carolina Select Sires provided partial financial support.

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Table 1. Means, SD, and Ranges of MCC[a] measures of milk and fat proof changes for 112 Select Sires PGA graduates with last MCC proof repeatability >.90.

MCC Change	Mean	SD	Min	Max
Milk (kg)	−9.1	159.1	−479.5	508.9
Fat (kg)	−1.9	5.7	−20.4	11.3
Repeatability	.245	.053	.120	.430

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[a] MCC Difference between last available 2nd crop MCC proof and second to last first crop MCC proof.

Table 2. Percentage of Select Sires PGA graduate bulls (Last MCC proof repeatability > .90) falling into each of the eight single SD[a] subclasses for MCC[b] measure of milk and fat proof changes.

	Decrease				Increase			
	>3 SD	2–3 SD	1–2 SD	0–1 SD	0–1 SD	1–2 SD	2–3 SD	>3 SD
Expected=	.2	2.1	13.6	34.1	34.1	13.6	2.1	.2
MCC								
Milk	.0	4.5	14.3	29.5	38.4	10.7	1.8	.9
Fat	.9	5.4	22.3	35.7	25.9	8.0	1.8	.0

[a] Expected SD change=$(R_i - R_j)^{-.5} \times \sigma_s$

where R_i=repeatability of last available 2nd crop proof,

R_j=repeatability of second to last first crop proof,

and σ_s is one–fourth genetic standard deviation milk (295 kg) or fat (11 kg) yield.

[b] MCC Difference between last available 2nd crop MCC proof and second to last first crop MCC proof.

Table 3. Description of notation used in Appendix B and Tables 4–5.

Notation	Description
ME	Mature equivalent
ID	Identification
SH+PE	Sire by herd plus permanent environment effect
PTA	Predicted transmitting ability
REL	Reliability of PTA
$\bar{X}$	Within herd mean
σ	Within herd standard deviation
R^2	Coefficient of determination

Table 4. Bull's sample–herd characteristics that entered the final model used to predict changes in a bull's milk MCC proofs and bull change group means of significant variables.

			Bull Change Group Means[a]		
			Decrease	Stable	Increase
MCC Change (kg) =			−254	3.6	237
Herd Characteristic	$\hat{B}$[b]	SE[c]			
Number of MCC herds − PGA herds[d]	5.9	3.8	4.9	6.3	6.2
Avg[e](Percent young sire use)	33.1	7.6	17.4	19.1	17.5
Avg(Percent of sires that are young)	−20.6	6.4	32.2	33.2	30.9
Avg(Sire REL $\bar{X}$)	−7228	1996	.956	.948	.957
Avg(Lactation number σ)	−461.8	152.8	1.56	1.58	1.54
Avg(SH+PE fat σ) (kg)	−122.1	32.8	13.7	13.4	13.6
Avg(Sire PTA fat σ) (kg)	77.4	53.0	4.3	4.1	4.6
Avg(Cow PTA fat σ) (kg)	183.9	64.3	8.1	7.9	8.3
Avg(Cow REL σ)	15603	4224	.0605	.0607	.0608
Std[f](Sire PTA milk $\bar{X}$) (kg)	4.1	2.0	44.2	48.5	50.9
Std(Sire PTA fat $\bar{X}$) (kg)	100.8	55.5	1.46	1.63	1.72
Std(Sire REL $\bar{X}$)	−6095	2693	2.46	2.56	2.28
Std(SH+PE milk σ) (kg)	3.2	1.3	70.6	69.1	78.3
Std(Cow PTA milk σ) (kg)	−3.3	1.9	39.8	37.9	42.0
Std(Cow PTA fat percent σ)	−6460	5732	.0128	.0125	.0135
Region	****[g]				

R^2=.46 Intercept = 6210.6

[a] Bulls split into <−1 SD (Decrease), −1 to 1 SD (Stable), and >1 SD (Increase) change groups.

[b] Regression coefficient estimate. [c] Standard error of regression coefficient estimate

[d] Difference between number of all herds and PGA herds contributing daughters to the bull's first crop proofs.

[e] Average herd characteristic across herds contributing daughters to the bull's first crop proofs

[f] Standard deviation of herd characteristic across herds contributing daughters to the bull's first crop proofs.

[g] Categorical data (No $\hat{B}$)

Table 5. Bull's sample–herd characteristics that entered the final model used to predict changes in a bull's fat MCC proofs and bull change group means of significant variables.

			Bull Change Group Means[a]		
			Decrease	Stable	Increase
MCC Change (kg) =			−9.1	−.4	8.1
Herd Characteristic	$\hat{B}$[b]	SE[c]			
Number of PGA herds	.31	.09	29.1	31.0	35.4
Number of states represented	−1.02	.25	12.9	12.1	13.3
Number of regions represented	.89	.69	6.1	6.2	6.7
Avg[d](Percent young sire use)	.41	.15	18.4	18.8	17.5
Avg(ME fat $\bar{X}$)	−.22	.08	287	284	288
Avg(Sire PTA fat $\bar{X}$)	.89	.60	−4.0	−4.1	−3.3
Avg(ME fat σ)	−.70	.33	49.4	48.9	50.4
Avg(Sire PTA fat percent σ)	−175.56	88.2	.086	.085	.084
Avg(Cow PTA fat σ)	5.12	1.95	8.0	8.0	8.4
Std[e](Sire PTA fat $\bar{X}$)	2.89	1.55	1.56	1.61	1.81
Std(ME fat σ)	.80	.24	8.59	8.95	11.59
Std(SH+PE milk σ)	.07	.04	69.0	70.9	74.3
Std(Cow PTA fat percent σ)	−521.66	194.45	.0132	.0125	.0125

R^2=.39 Intercept = 52.21

[a] Bulls split into <−1 SD (Decrease), −1 to 1 SD (Stable), and >1 SD (Increase) change groups.

[b] Regression coefficient estimate. [c] Standard error of regression coefficient estimate

[d] Average herd characteristic across herds contributing daughters to the bull's first crop proofs

[e] Standard deviation of herd characteristic across herds contributing daughters to the bull's first crop proofs.

APPENDIX A

Variables that passed the initial screening significance level of .20 for entry or exit from stepwisse regression were examined for collinearity problems. Collinearity problems were measured using condition numbers. Condition numbers are ratios of the largest to smallest eigen valuees (8). Condition numbers greater than 30 were used as an indication of serious multicollinearity (8). If condition numbers indicated a serious problem with multicollinearity, one of the variables was removed from further consideration.

Next all possible regression models were examined using the remaining significant variables that had no serious problem with multicollinearity. PRESS, CP, Adjusted R-square, and Mean Square Error (MSE) statistics were examined for these models. Prediction Sum of Squares (PRESS) indicates how the model would predict using independent data (8). Models under selection with the lowest PRESS values would be favored. CP statistic measures the bias from underfitting the model and the increased prediction variance from overfitting the model (8). CP values close to the number of variables in the model are favored. Adjusted R-square measures the proportion of variation explained by this model adjusted for the number of variables included (8).

Ideally, we would want to choose the model that had the lowest values for PRESS, CP, and MSE, and the highest Adjusted R-square value. Often one model does not have the best values for all of these statistics and a selection index must be utilized. For our models, the model with the lowest PRESS statistic also had the lowest CP, highest Adjusted R-Square, and lowest MSE. This simplified the final model selection criteria.

Appendix B. Means, SD, and ranges of bull's sample-herd characteristics of herds contributing first crop daughter information to the 112 bulls.

Trait	Mean	SD	Min	Max	r_{milk}[a]	r_{fat}[a]
Number of PGA herds	30.9	7.9	13	49	.06	.20
Number of MCC herds – PGA herds[b]	6	3.9	−4	21	.09	.08
Number of states represented	12.4	3.4	6	23	−.11	−.05
Number of regions represented	6.2	1.0	4	9	.03	.07
Avg[c](Percent young sire use)	18.6	3.9	6.8	26.5	.04	−.03
Avg(Percent registered)	33.9	8.1	16.1	60.7	−.03	−.13
Avg(Percent of sires that are young)	32.7	4.4	19.8	41.3	−.05	−.08
Avg(Number of sires represented)	48.4	13.1	22.5	81.7	−.14	−.08
Avg(Herd size)	167	59	63	380	−.15	−.12
Avg(ME milk $\bar{X}$)	7932	317	6854	8788	−.08	−.06
Avg(ME fat $\bar{X}$)	285	10.9	251	312	−.09	−.09
Avg(ME fat percent $\bar{X}$)	3.62	.04	3.52	3.77	−.04	−.08
Avg(SH+PE milk $\bar{X}$)	23.9	19.6	−49	92	−.01	.01
Avg(SH+PE fat $\bar{X}$)	.95	.71	−1.6	3.8	.02	.01
Avg(Cow PTA milk $\bar{X}$)	−420	99	−582	−171	−.04	.01
Avg(Cow PTA fat $\bar{X}$)	−13.9	2.8	−18.4	−6.1	−.04	.02
Avg(Cow PTA fat percent $\bar{X}$)	.02	.012	−.005	.039	.06	−.01
Avg(Cow REL $\bar{X}$)	.49	.009	.47	.52	−.10	−.03
Avg(Sire PTA milk $\bar{X}$)	−86	54	−187	51	.01	.04
Avg(Sire PTA fat $\bar{X}$)	−4.0	1.7	−7.1	1.0	.02	.07
Avg(Sire PTA fat percent $\bar{X}$)	−.018	.011	−.042	.016	.03	.11
Avg(Sire REL $\bar{X}$)	.95	.016	.89	.98	−.09	−.04
Avg(Lactation number $\bar{X}$)	2.5	.12	2.23	2.82	−.06	−.08
Avg(ME milk σ)	1388	100	1086	1610	−.13	−.03
Avg(ME fat σ)	49.2	3.4	40.1	56.0	−.12	−.02
Avg(ME fat percent σ)	.38	.019	.33	.43	.01	−.04

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[a] Correlation of herd trait with change in bulls MCC milk or fat proof.

[b] Difference between number of all herds and PGA herds contributing daughters to the bull's first crop proofs

[c] Average herd characteristic across herds contributing daughters to the bull's first crop proofs.

Appendix B contd. Means, SD, and ranges of bull's sample−herd characteristics of herds contributing first crop daughter information to the 112 bulls.

Trait	Mean	SD	Min	Max	r_{milk}^{a}	r_{fat}^{a}
Avg[b](SH+PE milk σ)	379	22	314	429	−.14	−.06
Avg(SH+PE fat σ)	13.5	.8	11.4	15.0	−.15	−.02
Avg(Cow PTA milk σ)	221	17.4	181	266	−.07	−.02
Avg(Cow PTA fat σ)	8.0	.6	6.8	9.2	−.04	.05
Avg(Cow PTA fat percent σ)	.070	.003	.064	.078	−.03	−.10
Avg(Cow REL σ)	.061	.004	.052	.071	.11	−.06
Avg(Sire PTA milk σ)	116	13	85	146	.08	−.02
Avg(Sire PTA fat σ)	4.2	.6	3.1	5.2	.03	.10
Avg(Sire PTA fat percent σ)	.085	.006	.063	.100	−.02	−.15
Avg(Sire REL σ)	.069	.009	.043	.086	.02	−.04
Avg(Lactation number σ)	1.57	.108	1.35	1.82	−.09	−.13
Std[c](Percent young sire use)	9.8	2.9	4.2	19.2	.12	.09
Std(Percent registered)	37.8	3.5	26.9	45.4	−.03	−.11
Std(Percent of sires that are young)	12.0	2.6	7.1	20.6	−.04	−.01
Std(Number of sires represented)	47	21	9	95	−.06	−.03
Std(Herd size)	266	117	38	562	−.07	−.06
Std(ME milk $\bar{X}$)	882	146	557	1259	.05	.11
Std(ME fat $\bar{X}$)	33.6	5.4	22.9	49.3	−.01	.11
Std(ME fat percent $\bar{X}$)	.197	.039	.112	.302	.01	.08
Std(SH+PE milk $\bar{X}$)	85.6	23.0	45.8	173.9	.10	.01
Std(SH+PE fat $\bar{X}$)	3.2	1.0	1.5	7.1	.11	.02
Std(Cow PTA milk $\bar{X}$)	85.6	19.3	46.4	149.7	−.03	−.05
Std(Cow PTA fat $\bar{X}$)	2.68	.70	1.43	6.03	.04	.01
Std(Cow PTA fat percent $\bar{X}$)	.019	.005	.011	.036	−.04	−.09
Std(Cow REL $\bar{X}$)	.040	.006	.026	.063	−.04	−.10
Std(Sire PTA milk $\bar{X}$)	48.1	9.5	31.5	83.3	.27	.11

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[a] Correlation of herd trait with change in bulls MCC milk or fat proof.

[b] Average herd characteristic across PGA herds contributing daughters to the bull's first crop proofs.

[c] Standard deviation of herd characteristic across PGA herds contributing daughters to the bull's first crop proofs.

Appendix B contd. Means, SD, and ranges of bull's sample–herd characteristics of herds contributing first crop daughter information to the 112 bulls.

Trait	Mean	SD	Min	Max	r_{milk}[a]	r_{fat}[a]
Std[c](Sire PTA fat $\bar{X}$)	1.61	.37	.97	3.12	.26	.21
Std(Sire PTA fat percent $\bar{X}$)	.030	.007	.016	.050	.03	−.02
Std(Sire REL $\bar{X}$)	.025	.009	.010	.050	.07	−.01
Std(Lactation number $\bar{X}$)	.63	.08	.44	.85	.11	.09
Std(ME milk σ)	277	130	120	728	.04	.14
Std(ME fat σ)	9.1	2.8	4.5	19.4	.04	.18
Std(ME fat percent σ)	.072	.024	.036	.172	.01	−.03
Std(SH+PE milk σ)	71	12	41	107	.12	.14
Std(SH+PE fat σ)	2.6	.5	1.6	3.8	−.02	.05
Std(Cow PTA milk σ)	38.9	10.2	23.2	77.3	.02	.05
Std(Cow PTA fat σ)	1.37	.30	.85	2.54	.01	.05
Std(Cow PTA fat percent σ)	.013	.003	.008	.026	−.02	−.07
Std(Cow REL σ)	.015	.002	.009	.024	.10	−.01
Std(Sire PTA milk σ)	25.4	6.7	13.2	57.4	.13	.07
Std(Sire PTA fat σ)	.90	.18	.59	1.63	.18	.18
Std(Sire PTA fat percent σ)	.019	.005	.009	.040	.06	−.01
Std(Sire REL σ)	.025	.006	.014	.044	.04	−.03
Std(Lactation number σ)	.58	.08	.44	.79	.04	.09

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[a] Correlation of herd trait with change in bulls MCC milk or fat proof.

[b] Average herd characteristic across PGA herds contributing daughters to the bull's first crop proofs.

[c] Standard deviation of herd characteristic across PGA herds contributing daughters to the bull's first crop proofs.

Estimates of Genetic Trend Within and Across Herds Enrolled in an AI Progeny Test Program and Herd Characteristics Important in Predicting Genetic Trend

ABSTRACT

Individual lactation records from 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 trend. Predicted Transmitting Abilities (PTA) of cows, sires of first crop cows, and sires of other cows were used to estimate overall and within herd genetic trends for milk and fat yield. Milk and fat genetic trend estimates from cows' PTA increased 105 kg and 3.1 kg per year, respectively. PTA's of cows in sampling program herds were consistently superior to those of cows in the average U.S. population. Genetic trend of sires of first crop cows increased 58 kg milk and 1.5 kg fat per year from 1971 to 1978 and 176 kg milk and 5.5 kg fat per year from 1979-87. The genetic level of daughters of young sires born after 1983 was equivalent to or exceeded the genetic level of cows from other sires in the herd. Within herd estimates of genetic trend for milk and fat yield were larger than estimates ignoring herd. Within herd-year means and standard deviations of production, genetic evaluation, and management traits (herd-year characteristics) were computed for a subset of 341 herds contributing first crop daughters for at least ten years. The average of each herd-year characteristic during the ten plus years was used to predict within herd genetic trend for milk and fat yield. Herd characteristics explained forty-five and fifty-one percent of differences in within herd genetic trends for milk and fat yield, respectively. Average sire PTA of non-first crop daughters accounted for 80% and 67% 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, less average days open, and greater percentage of cows sired by AI sires made larger rates of genetic improvement. Results indicated that rate of within herd genetic improvement may be enhanced from participating in a young sire sampling program.

INTRODUCTION

A key to genetic improvement in U.S. dairy cattle has been the progeny testing programs enacted by AI studs during the 1960s. These programs identify bulls with superior genes for milk, fat, protein, and type so they can be intensively utilized by dairy farmers and AI studs as sires of future dams and sires of future sires, respectively. These two pathways represent over 60% of all genetic progress made in dairy cattle (24). Thus, the importance of an AI stud's young sire sampling program in its long term survival cannot be overemphasized. This is especially true since the accuracy of non-AI sampled bulls' progeny test proofs, another source of replacing bulls in a stud's "proven" lineup, appears to be decreasing over time (14,19).

The design and importance of these AI sampling programs has been described by many researchers (1,8,11,28,30,31,32). The implementation of progeny testing programs was credited with increasing the rate of genetic improvement from 1964-74, although the rate of progress was not ideal (31). 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 percent and accuracy of sire identified cows, and exercise greater selectivity in choosing the parents of future AI bulls (1,4,11,28,30,31,32).

Number of bulls sampled per year by AI studs has increased from 545 in 1975 to 1273 in 1986 (20). Milk pedigree indexes of AI young sires increased at a rate of 28 kg/yr for bulls progeny tested from 1970-75 and further increased to a rate of 51 kg/yr for bulls sampled from 1980-85 (20). The increased number of bulls sampled as well as the greater selectivity of milk pedigree indexes of sample sires should have resulted in an increased rate of genetic improvement in the general U.S. Holstein population as well as in the AI studs' cooperating progeny test herds.

Many studies have estimated genetic trend in North American Holsteins females (2,6,7,9,10,12,21,23,29). Several earlier studies (2,6,7,29) used the three methods, or slight modifications, proposed by Smith (26) in calculating genetic trend within herd. Smith's methods were based on the regression of daughter performance on time. Later studies (9,21,23) estimated genetic trend (ignoring herd) as twice the regression of sires' average estimated transmitting ability on time. Lee et. al. (12) estimated genetic trend within sex of offspring two ways. One method was

$$\hat{g} = \hat{\beta}_S + \hat{\beta}_D$$

where

$\hat{\beta}_{\mathrm{S}}$ = regression of average sire transmitting ability on birth year of son

$\hat{\beta}_{\mathrm{D}}$ = regression of average dam transmitting ability on birth year of daughter

The other method utilized was

$$\hat{g} = 2 \times \hat{\beta}_{\mathrm{ETA}}$$

where

$\hat{\beta}_{\mathrm{ETA}}$ = regression of average parent transmitting ability on birth year of offspring

In most studies, time was measured as year of daughter's first calving though birth year of daughter was utilized by Lee et al. (12).

Estimates of genetic trend are difficult to compare since studies include different time periods as well as different subsamples of the U.S. Holstein population. Studies (2,6,7,21) using data from the 1950s to 1960s reported estimates of annual genetic trend ranging from 41 kg to 133 kg and -.5 kg to 5.07 kg for milk and fat yield, respectively. Studies (9,18,23) utilizing data from 1960s to early 1970s estimated genetic trends ranging from 3 kg to 38 kg milk and 0 kg to 1 kg fat. Lee and Freeman (12) estimated genetic trends of 54.8 kg milk and 1.5 kg fat during the 1970s. The larger genetic trend estimates during the 1950s appear to be caused by either less sophisticated measures of distinguishing genetic changes from environmental changes or to these estimates being within herd estimates rather than across herd estimates of genetic trend. Powell and Freeman found (21) within herd estimates of genetic trend to be larger than across herd estimates.

White (31) felt that many dairymen who have herds on test do not participate in young sire sampling programs due to the unknown genetic risk of young bulls compared to the near certainty of older proven bulls. Powell and Freeman (21) 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 progeny test herds' genetic progress to other herds not on a sampling program in order to see what value or hindrance the sampling program had on genetic progress within these herds. The objectives of our research were to examine characteristics of a major AI stud's cooperating progeny test herds, estimate genetic trend within these progeny test herds, compare genetic trend 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.

DATA

Herds that had participated in Select Sires progeny test program, Program for Genetic Advancement (PGA), and sires sampled through PGA were identified by Select Sires Inc., Plain City, OH. Herd information included DHIA herd code, Select Sires regional code, and year of entering or leaving PGA. Sample sire information included registration number, super sampler status (was bull available to general public), and year entered PGA.

Lactation records and January 1990 animal model evaluations for all cows in herds that participated in Select Sires' PGA were obtained from Animal Improvement Programs Laboratory (AIPL), USDA. The January 1990 animal model sire evaluations and the Modified Contemporary Comparison (MCC) sire history tape also was obtained. MCC history tape was utilized as in (14) to determine sire's initial "first crop" genetic evaluation. Daughters of PGA bulls conceived prior to first initial proof were considered first crop. Daughters of PGA sires conceived after the first proof and daughters of all other sires (purchased proven bulls, other studs' AI bulls, and non-AI bulls) were classified as "non-first crop".

METHODS

The number of first crop daughters and number of herds contributing first crop daughters were examined by state and birth year. Percentage of births that were first crop daughters and number of first crop daughters born and eventually received PTAs were calculated for each PGA herd-birth year. Yearly and overall averages of percentage of births that were first crop daughters and number of first crop daughters were computed and examined for the PGA population.

The January 1990 cow and sire animal model genetic evaluations were utilized in calculating genetic trend within herd and within the Select Sires PGA population. Cows were removed if PTA was missing or the cow did not contribute to her sire's PTA. Sires' milk and fat PTAs were merged with the daughter's own PTA information. Cows were designated as "first crop" or "non-first crop" progeny as previously described. 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 set was compared to the number of daughters included in the bull's second to last first crop MCC proof as in (14).

Means by birth year for cow's PTA milk and fat yield were computed. Means by birth year of sire's PTA milk and fat yield were computed separately for first crop daughters and non-first crop cows. Segmented regression was utilized similar to Lee et al. (12) due to the possibility of different linear time trends in the data. These PTA averages were used to determine overall genetic trend for Select Sires PGA population using SAS NLIN segmented regression technique (25). The model's join points (year where change in trend of average PTA occurred) were determined iteratively by the NLIN procedure rather than by inspection.

The model for the within PGA population trends was:

$$\overline{PTA_i} = a_1 + b_1\ BY_i \text{ if } BY \leq JP$$

else

$$\overline{PTA_i} = a_2 + b_2\ BY_i \text{ if } BY > JP$$

where

$\overline{PTA_i} =$ average cow's (cow's sire's) PTA milk or fat yield in the ith birth year.

a_1 and $a_2 =$ intercepts for first and second trend periods, respectively.

$b_1 =$ regression of average cow's (cow's sire's) PTA on birth year of cow for the first trend period (BY).

$b_2 =$ regression of average cow's (cow's sire's) PTA on birth year of cow for the second trend period (BY).

JP = join point.

If no JP was found, simple linear regression was used to estimate trends.

Seperate segmented regression analyses estimated trends in cows, sires of first crop daughters, and sires of non-first crop cows. Genetic trends for both milk and fat for each trend period were computed as twice the regression coefficients. Genetic trends in the Select Sires PGA herds were compared to overall U.S. population trends. Overall U.S. population genetic trends were computed from yearly PTA of all cows provided by USDA (27).

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

$$\overline{PTA}_{ij} = H_i + b\ BY_j$$

where

$\overline{PTA}_{ij}$ = average cow's (cow's sire's) PTA milk or fat yield in the jth birth year within the ith herd.

H_i) = fixed effect of ith herd.

b = regression of average cow's (cow's sire's) PTA milk or fat yield on birth year of cow.

For both milk and fat, within herd genetic trend was computed as twice the within herd regression of average PTA on birth year of cow. Within herd genetic trends calculated from all cow's PTA, first crop cow's sire's PTA, and non-first crop cow's sire's PTA were compared.

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

$$\overline{PTA}_{ij} = a_i + b_i\ BY_{ij}$$

where

$\overline{PTA}_{ij}$ = average cow's PTA milk or fat yield in the jth birth year within the ith herd.

a_i = intercept for the ith herd.

b_i = regression of average cow's PTA milk or fat yield on birth year of cow for the ith herd.

For both milk and fat, herd genetic trend was computed as twice the within herd regression of average PTA on birth year of cow.

Herd-year means and within herd-year standard deviations for each of the variables included in the individual lactation records were calculated. These were designated as herd-year characteristics. Variables included mature equivalent (M.E.) milk, fat, and fat percent; age in years; lactation number; sum of sire by herd interaction plus permanent environment for milk and fat yield (computed as cow's Predicted Producing Ability (PPA) minus twice cow's PTA (33)); cow's PTA milk, fat, and fat percent; PTA milk, fat, and fat percent for sires of first crop cows; PTA milk, fat, and fat percent for sires of non-first crop cows; reliability of PTA for the cow and her sire; and number of days open in previous lactation (first lactation cow's days open = 0).

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 birthdate, number of sires represented, number of young sires represented, and state and Select Sires sampling region. Herd-years not containing at least one first lactation, first crop daughter were removed. Average herd-year characteristics during the ten or more years were used to predict the within herd genetic trend calculated from all cow's PTAs.

Stepwise regression (25), 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 due to collinearity. Next, all possible regression models were examined that included the variables significant in the stepwise regression and passed the collinearity test. PRESS, CP, Adjusted R^2, and Mean Square Error statistics were examined and used to select the best model for predicting genetic trend. The final model used to predict genetic trend within a herd was selected based on the lowest values for CP and PRESS statistics (17). Further details are explained in Appendix A.

In order to gain additional insight on effects of herd characteristics (those significant in predicting within herd genetic trend for milk and fat) 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 from the average within herd genetic trend, the high group included herds greater than +1 SD, and the medium group included herds between -1 SD and +1 SD. The average herd characteristic was computed for each group and compared. This was done separately for milk and fat yield.

RESULTS and DISCUSSION

Characteristics of Progeny Testing Program

Numbers of Select Sire's PGA herds and first crop daughters by state and birth year are presented in Appendix B. A total of 58,194 first crop 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 immensely since 1971. Six states (Ohio, Indiana, Illinois, oichigan, Virginia, and Kentucky) contributed first crop daughter information in 1971. States that contributed over 100 first crop daughters in 1986 (1987 has incomplete information) and were not contributing information in 1971 included Pennsylvania, Wisconsin, Iowa, Minnesota, North Carolina, Florida, Tennessee, Idaho, Arizona, Utah, Washington, and California. Four of these states divergent in herd sizes (Minnesota, Wisconsin, Washington, and California) contributed an increasing percent of the total. Table 1 contains yearly averages of percent young sire use (percent of cows born that are daughters of Select young sires) and average number of first crop daughters contributed per herd. Percent young sire use decreased from 18% in 1973 to 13% in 1986. However, the average number of first crop daughters contributed per PGA herd increased slightly from 2.6 to 3.3 daughters during this same time period. The decrease in percent young sire use was a reflection of the increasing herd size from 1971 to 1987 while the number of young sires sampled per herd remained the same or increased at a slower rate.

The average number of first crop daughters per bull in our data set (45 daughters) was less than the average number of daughters included in the bull's second to last first crop proof (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 USDA "1202" list of daughters contributing to a bull's proof for 10 bulls sampled by Select Sires PGA. Results indicated that the average bull had 9.7 first crop daughters producing in 5.8 herds that were not enrolled in Select Sires PGA program. This discrepancy could be 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 proofs of AI sampled bulls.

Estimates of Genetic Trend

Birthyear means of PTA milk and fat yield for the cow and her sire were calculated from 58,194 first crop and 414,750 non-first crop daughters born from 1971-87. Yearly averages of PTA milk and fat yield and the overall estimated genetic trend for cows in the Select Sires PGA population are plotted against those of the U.S. population (27) in Figures 1 and 2, respectively. Only one linear time trend was evident. Genetic trend ($\hat{g}$) for the Select Sires PGA population was nearly identical ($\hat{g}$ = 105 kg vs 106 kg milk, $\hat{g}$ = 3.1 kg vs 3.2 kg fat) to the U.S. population. However, average PTAs of cows in Select Sires PGA herds were consistently higher (100 kg milk, 1.1 kg fat) than those of the entire U.S. population for both milk and fat during the entire time period. Our estimates of genetic trends were considerably larger than those found in previous studies (9,12,21,23). Our study utilized animal model estimates of breeding values (EBV) whereas other studies have utilized less accurate methods to calculate EBV. Larger genetic trend could also attributed to the increased genetic improvement during the 1980's.

Figures 3 and 4 contain yearly averages of sire's PTA milk and fat yield for first crop and non-first crop cows in the Select Sires PGA population as well as the sire's PTA milk and fat yield for all cows in the U.S. population, respectively. Genetic trend for each population (U.S. population, Select PGA first crop cows, Select PGA non-first crop cows) was also included in Figures 3 and 4. A single linear trend was found for both sire's PTA milk and fat yield in the U.S. population ($\hat{g}_{milk}$ = 125 kg, $\hat{g}_{fat}$ = 4.0 kg) and Select Sires non-first crop cows ($\hat{g}_{milk}$ = 119 kg, $\hat{g}_{fat}$ = 3.6 kg) born from 1971-87. However, two linear trends of sire's PTA milk and fat were found in sires of Select Sires first crop cows. The first trend occurred from 1971-78 ($\hat{g}_{milk}$ = 58 kg, $\hat{g}_{fat}$ = 1.5 kg) while the second trend occurred from 1979-87 ($\hat{g}_{milk}$ = 176 kg, $\hat{g}_{fat}$ = 5.5 kg). Genetic trend in the second period represents some compensotory gain due to the low starting point. During the mid to late 1970's the genetic level of young sires having first crop daughters born during this time 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 expected. However after this time period, the sire's PTA for milk and fat yield of first crop daughters increased rapidly. For herds in Select Sires PGA, the genetic progress made through using just young sires has exceeded the genetic progress made from using other sires since 1984. McDaniel and Bell (13) 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 to elite AI sires and in others they would be compared to a mixture of current AI bulls, non-active AI bulls, and even non-AI bulls (probably used to breed heifers). Powell and Norman (22) found that these non-AI bulls were genetically inferior by 211 kg to the highly selected AI bulls. The type of other sire is important in determining how good the young sire really is within a herd.

Table 2 contains the within and across herd genetic trend estimates for milk and fat yield calculated from all cows' PTA, PTA for sires of first crop cows, PTA for sires of non-first crop cows born 1971-87. Also included are the average PTAs for cows or cow's sires. Within herd estimates of genetic trend were slightly larger than the overall genetic trend for the Select Sires PGA population. Powell and Freeman (21) have also found within herd estimates of genetic trend to be larger than those obtained by ignoring herds, but Powell et al. (23) attributed the difference to using data from one area of the U.S.. However, our study included 3449 herds from 42 U.S. states. Differences between within herd trends and trends ignoring herd were most likely due to herds entering and leaving during the time period of the data since only 341 herds of 3449 contributing PGA herds were enrolled for 10 years or more. Both within and across herd genetic trends for milk and fat yield calculated from PTAs of sires of first crop cows were somewhat larger than the trends calculated from PTAs of sires of non-first crop cows, but the average PTAs of sires of non-first crop cows were greater indicating that they were better genetically.

Prediction of Within Herd Genetic Trend

Appendix C contains 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 ten years. Generally, means of the herd characteristics were within ranges found by other studies (3,5,15,18). Ranges of herd characteristics were large reflecting the diversity of sampling environments for these AI bulls. Within herd genetic trends for milk and fat agreed closely to the within herd genetic trends discussed earlier. The average sire's PTA of non-first crop 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). The average PTA's of cows and cow's sires were larger than U.S. averages (27) during this same time period which was a reflection of the value of young sire usage as well as the incentives of young sire programs which allow for the purchase of active AI sire's semen at a reduced cost. Average M.E. milk, fat and fat percent production was higher than national averages during the same time period (18). Within herd standard deviations for M.E. milk, fat, and fat percent were as variable, but had a higher mean compared to other studies (3,15). This was most likely due to scaling since M.E. production traits were also larger. Percentage of young sire use and percentage of cows sired by AI sires were large and were as expected for herds enrolled in a progeny testing program. The number of young sires and sires represented in a herd-year appeared to be high. However, the average herd size was 113 and if sixteen percent (mean percent young sire usage) of the herd was a daughter of a young sire, we can easily explain the average of 12.7 young sires represented.

Significant herd characteristics and their regression coefficients from the "best" model for predicting genetic trend in cows for milk and fat yield in the 341 Select Sires PGA herds are in Tables 3 and 4, respectively. Also included in the tables are the Adjusted R^2, PRESS, CP, and MSE statistics. Low, medium, and high genetic trend herd group averages of significant herd characteristics used in predicting within herd genetic trend for milk and fat yield are in Tables 5 and 6, respectively.

The final models selected had the lowest values for PRESS, small values for the CP statistic, and little problems with multicollinearity. The adjusted R^2 values were .46 and .51 for the models predicting within herd genetic trend for milk and fat yield, respectively. The average sire PTAs of non-first crop daughters alone accounted for 80% and 67% of the explained differences in within herd milk and fat genetic trend estimates, respectively. This was not unexpected due to the part-whole relationship and shows the importance of choosing bulls with the highest PTAs for milk and fat yield as sires to be used within the herd in order to make optimum genetic improvement.

Because of the problems in interpretting partial regression coefficients, results in Tables 5 and 6 were used to interpret impact of significant herd characteristics. Herds that made more genetic improvement had more sires of first crop daughters represented. This could be interpreted as the more young sires used the greater the chance of sampling genetically superior bulls that can have a large impact on the genetic improvement within the herd. Another possibility was that young sires were better than the other sires used at the same time. For both milk and fat, herds with higher within herd M.E. milk standard deviations made genetic improvement at a faster rate. This would agree with

(16) in that herds with larger within herd variances receive more response from estimated breeding values than expected. Herds with less average days open made genetic improvement for milk and fat yield at a faster rate. This could be a reflection of younger herd age since the days open value was from the previous lactation so two year olds were given the value of zero. Herds having younger cows and cows with lower reliabilities would have a reduced generation interval which resulted in a faster rate of genetic improvement for milk yield. Since genetic progress was occurring at a rapid rate, younger cows should be 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. This would agree with (22) who found AI sires superior to naturally serviced sires.

SUMMARY

Select Sires PGA program has grown to encompass a large network of herds spread across the nation. Characteristics of these herds were diverse, but means of genetic and phenotypic yield measures were above national averages. Control of what herds contribute information to a bull's initial progeny test proofs was less than expected and probably due to the sale of first crop daughters before first calving and/or the distribution of semen to original bull owners. Rate of genetic progress within the Select Sires PGA herd population was large and matched the progress made by the U.S. population. Cows in Select Sires PGA herds were in each year genetically superior to the U.S. population. The rate of genetic progress obtained from using young sires increased from 58 kg to 176 kg milk and from 1.5 kg to 5.5 kg fat from 1971-78 to 1979-87. During the mid to late 1980's, the genetic level of daughters of young sires was equivalent or exceeded the genetic level 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, respectively. The average sire's PTA of daughters of "other sires" accounted for eighty and sixty-seven percent 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, a larger number of young sires represented, younger cows, less average days open, and a greater percentage of cows sired by an AI sire made faster rates of genetic improvement. These herd characteristics could be useful in educating dairy farmers in how to achieve greater rates of genetic improvement.

ACKNOWLEDGEMENT

Supply of data by USDA Animal Improvement Programs Laboratory at Beltsville, Maryland is gratefully acknowledged. Select Sires, Inc. and Virginia-North Carolina Select Sires provided partial financial support.

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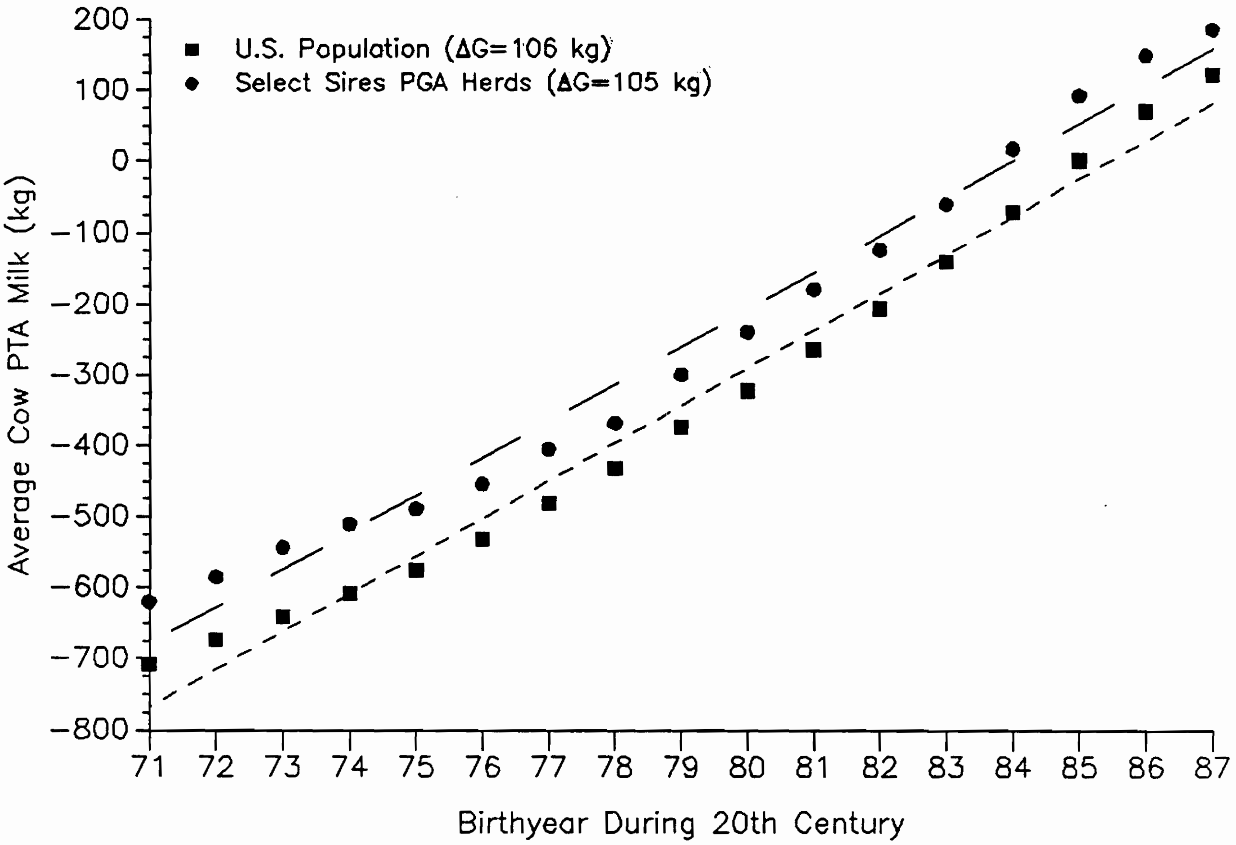

Figure 1. Yearly PTA Milk for Cows in Select Sires PGA Herds vs U.S Population.

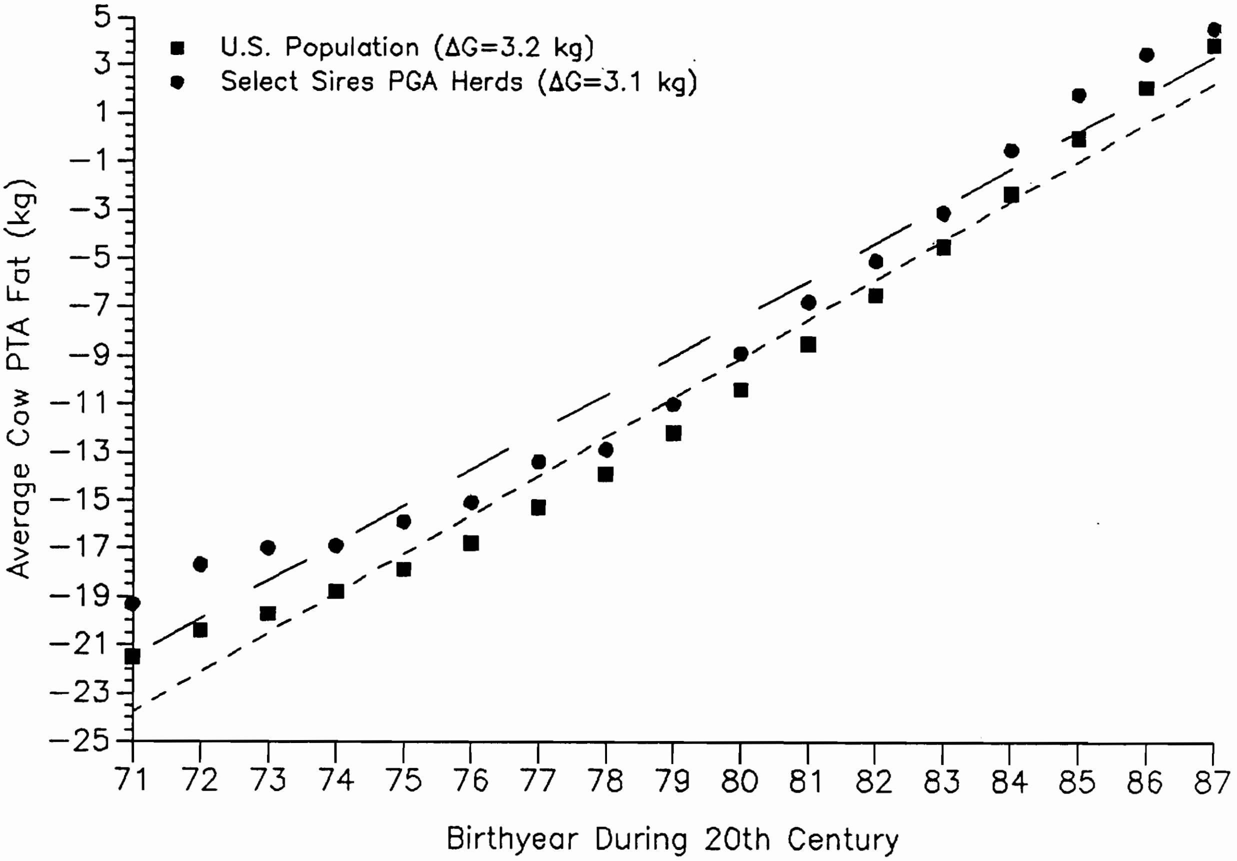

Figure 2. Yearly PTA Fat for Cows in Select Sires PGA Herds vs U.S Population.

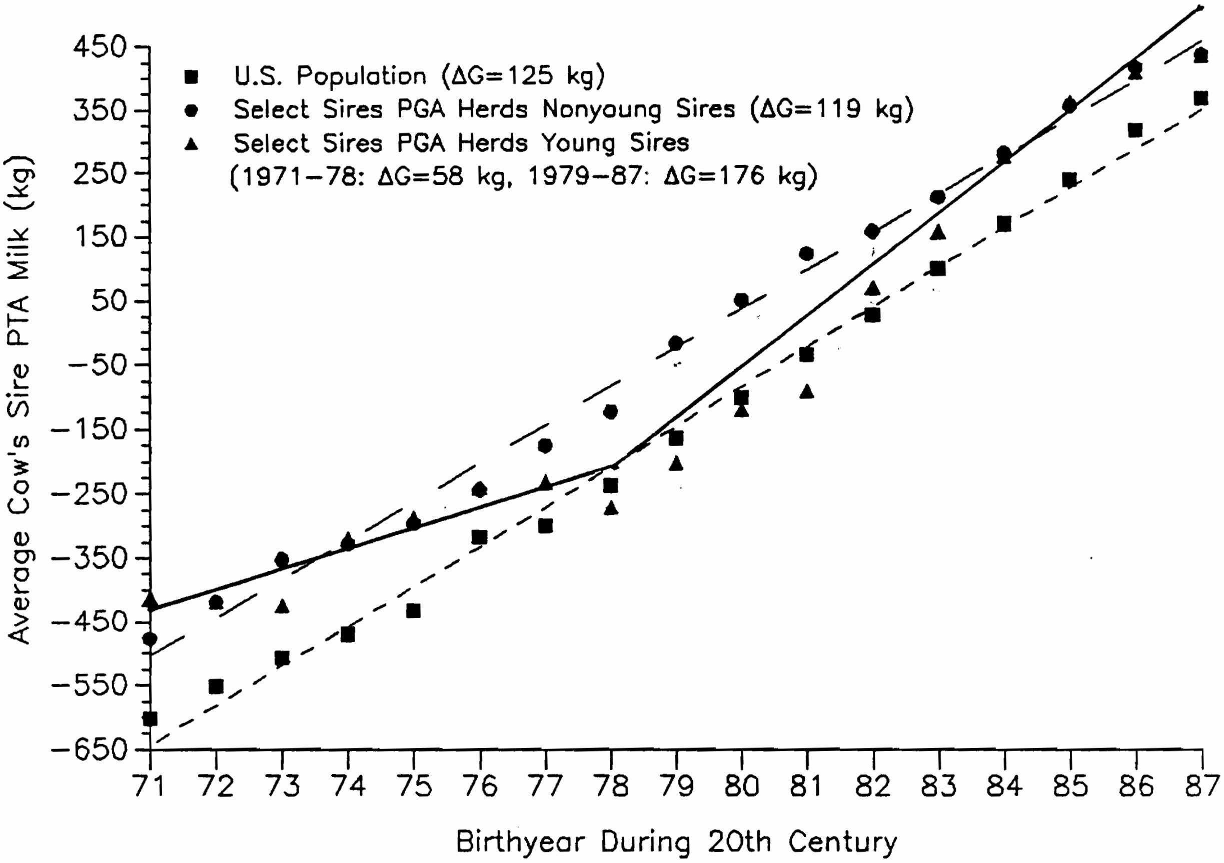

Fig. 3. Yearly Sire PTA Milk for Cows in Select Sires PGA Herds vs US Population

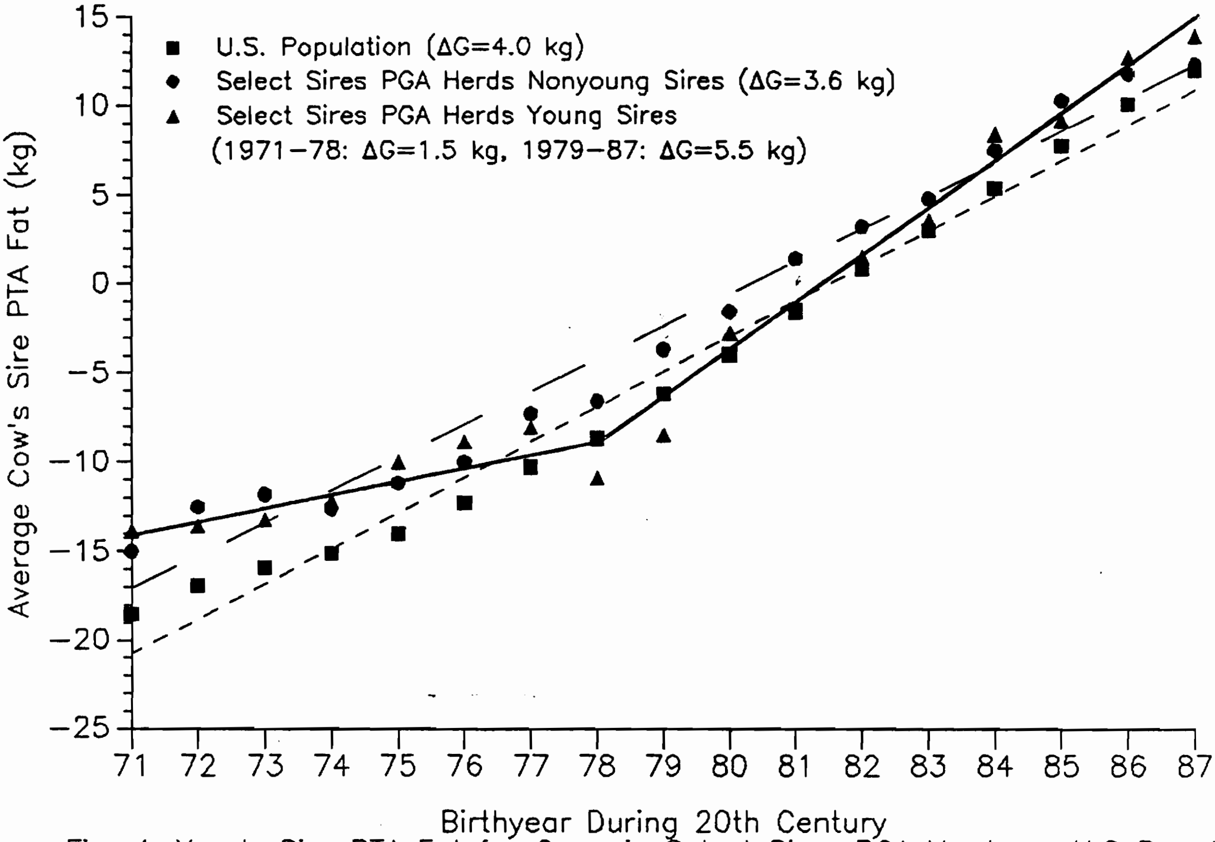

Fig. 4. Yearly Sire PTA Fat for Cows in Select Sires PGA Herds vs U.S Population

Table 1. Means, standard deviations, and ranges of PGA herds' percent young sire usage and number of first crop daughters contributed by year of birth.

	Percent Young Sire Usage				Number First Crop Daughters			
Year	Mean	SD	Min	Max	Mean	SD	Min	Max
1971	14	15	1	100	1.4	.8	1	4
1972	17	10	2	50	2.5	2.0	1	17
1973	18	13	2	100	2.6	2.5	1	32
1974	17	15	1	100	2.5	2.5	1	29
1975	17	12	2	100	3.0	4.0	1	69
1976	16	11	1	75	3.2	4.4	1	57
1977	16	14	1	100	3.1	4.0	1	50
1978	15	13	<1	100	3.1	4.2	1	54
1979	15	12	<1	100	3.1	4.0	1	48
1980	15	13	<1	100	3.2	4.3	1	70
1981	14	13	1	100	3.2	3.7	1	51
1982	13	11	<1	100	3.2	4.1	1	59
1983	13	11	<1	100	3.1	4.4	1	80
1984	13	12	<1	100	3.1	4.0	1	101
1985	12	9	<1	100	3.1	3.4	1	50
1986	13	10	<1	100	3.3	3.9	1	81
1987	19	17	1	100	2.1	1.9	1	20
ALL	14	12	<1	100	3.0	3.8	1	101

Table 2. Genetic trend estimates after and without fitting herd and average PTA for milk and fat yield calculated from all cow's PTA, first crop cow's sire's PTA, and non–first crop cow's sire's PTA.

Data	Milk			Fat		
	G_w^1	G_a^2	$\overline{PTA}$	G_w	G_a	$\overline{PTA}$
All cow's PTA (kg)	119	105	−148	3.6	3.1	−5.6
First crop cow's sire's PTA (kg)						
1971–78	136	58	−326	4.4	1.5	−11.4
1979–87	136	176	144	4.4	5.5	4.0
Non–first crop cow's sire's PTA (kg)						
1971–78	126	119	−302	4.0	3.6	−10.9
1979–87	126	119	223	4.0	3.6	5.1

[1] Genetic trend fitting herd

[2] Genetic trend without fitting herd

Table 3. Herd characterisitcs entering and statistics of the final model used to predict within herd genetic trend for milk yield.

Herd Characteristic	$\hat{B}^5$	SE^6
Non-first crop cow's sire's PTA milk $\bar{X}^1$	.13	.013
First crop cow's sire's PTA milk $\bar{X}$	.015	.010
ME^2 milk σ^3	.02	.004
ME fat percent σ	−29.6	18.97
Number young sires	.14	.051
Cow PTA fat $\bar{X}$	−1.43	.435
Cow PTA fat percent $\bar{X}$	95.6	59.60
Cow REL^4 $\bar{X}$	.95	.340
Age in years $\bar{X}$	−3.04	1.632
Days open $\bar{X}$	−.10	.043
Percent AI sired	.12	.064
Percent birthdate change	−40.2	12.82

Statistics

Adjusted[7] R^2	CP[8]	PRESS[9]	MSE[10]
.46	14.7	57086	160

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[1] Within herd mean, [2] Mature equivalent, [3] Within herd standard deviation

[4] Reliability of PTA, [5] Regression coefficient estimate

[6] Standard error of regression coefficient estimate

[7] Coefficient of determination adjusted for number of variables in model

[8] Mallows CP statistic, [9] Prediction Sum of Squares, [10] Mean square error

Table 4. Herd characterisitcs entering and statistics of the final model used to predict within herd genetic trend for fat yield.

Herd Characteristic	$\hat{B}$[5]	SE[6]
Non-first crop cow's sire's PTA fat $\bar{X}$[1]	.11	.012
First crop cow's sire's PTA fat $\bar{X}$[1]	.03	.009
ME[2] milk σ[3]	.0007	.0001
ME fat percent σ	−2.63	.684
Number young sires	.007	.002
Cow PTA fat $\bar{X}$	−.05	.014
Cow PTA fat percent $\bar{X}$	−3.78	1.80
Sire REL[4] $\bar{X}$	.03	.017
Cow PTA fat percent σ	11.0	2.83
Sire PTA fat percent σ	−6.66	2.40
Sire PTA milk σ	.003	.002
Days open $\bar{X}$	−.004	.001
Percent birthdate change	−1.66	.413

Statistics			
Adjusted[7] R^2	CP[8]	PRESS[9]	MSE[10]
.51	14	60	.167

[1] Within herd mean, [2] Mature equivalent, [3] Within herd standard deviation

[4] Reliability of PTA, [5] Regression coefficient estimate

[6] Standard error of regression coefficient estimate

[7] Coefficient of determination adjusted for number of variables in model

[8] Mallows CP statistic, [9] Prediction Sum of Squares, [10] Mean square error

Table 5. Low, medium, and high genetic trend herd group[1] means of significant herd characteristics predicting within herd genetic trend for milk yield.

	Low (50)[7]	Medium (238)	High (53)
$\hat{G}^2$ milk (kg) =	91	117	145
Herd Characteristic			
Non–first crop cow's sire's PTA milk $\bar{X}^3$ (kg)	–49	49	129
First crop cow's sire's PTA milk $\bar{X}$ (kg)	–121	–46	2
ME[4] milk σ^5 (kg)	1353	1397	1510
ME fat percent σ	.382	.383	.389
Number young sires	10	12	19
Cow PTA fat $\bar{X}$ (kg)	–11.1	–9.7	–8.3
Cow PTA fat percent $\bar{X}$	.011	.004	.003
Cow REL[6] $\bar{X}$	.506	.506	.504
Age in years $\bar{X}$	4.2	4.1	3.9
Days open $\bar{X}$	116	111	107
Percent AI sired	85	87	90
Percent birthdate change	.02	0	0

[1] Herds divided into <–1, –1 to +1, and >+1 standard deviations from the genetic trend mean
[2] Within herd genetic trend, [3] Within herd mean, [4] Mature equivalent
[5] Within herd standard deviation, [6] Reliability of PTA, [7] Number herds

Table 6. Low, medium, and high genetic trend herd group[1] means of significant herd characteristics predicting within herd genetic trend for fat yield.

	Low (56)[7]	Medium (214)	High (71)
$\hat{G}^2$ fat (kg)=	2.6	3.4	4.3
Herd Characteristic			
Non–first crop cow's sire's PTA fat $\bar{X}^3$ (kg)	−3.6	−1.0	1.2
First crop cow's sire's PTA fat $\bar{X}$ (kg)	−4.5	−2.3	−.5
ME^4 milk σ^5 (kg)	1348	1395	1493
ME fat percent σ	.385	.383	.387
Number young sires	10	12	17
Cow PTA fat $\bar{X}$ (kg)	−10.9	−9.8	−8.4
Cow PTA fat percent $\bar{X}$	.011	.004	.004
Sire REL^6 $\bar{X}$	.946	.952	.959
Cow PTA fat percent σ	.073	.074	.076
Sire PTA fat percent σ	.088	.088	.089
Sire PTA milk σ (kg)	118	120	126
Days open $\bar{X}$	116	111	107
Percent birthdate change	.02	0	0

[1] Herds divided into <−1, −1 to +1, and >+1 standard deviations from the genetic trend mean
[2] Within herd genetic trend, [3] Within herd mean, [4] Mature equivalent
[5] Within herd standard deviation, [6] Reliability of PTA, [7] Number herds

APPENDIX A

Variables that passed the initial screening significance level of .20 for entry or exit from stepwisse regression were examined for collinearity problems. Collinearity problems were measured using condition numbers. Condition numbers are ratios of the largest to smallest eigen valuees (18). Condition numbers greater than 30 were used as an indication of serious multicollinearity (18). If condition numbers indicated a serious problem with multicollinearity, one of the variables was removed from further consideration.

Next all possible regression models were examined using the remaining significant variables that had no serious problem with multicollinearity. PRESS, CP, Adjusted R-square, and Mean Square Error (MSE) statistics were examined for these models. Prediction Sum of Squares (PRESS) indicates how the model would predict using independent data (18). Models under selection with the lowest PRESS values would be favored. CP statistic measures the bias from underfitting the model and the increased prediction variance from overfitting the model (18). CP values close to the number of variables in the model are favored. Adjusted R-square measures the proportion of variation explained by this model adjusted for the number of variables included (18).

Ideally, we would want to choose the model that had the lowest values for PRESS, CP, and MSE, and the highest Adjusted R-square value. Often one model does not have the best values for all of these statistics and a selection index must be utilized. For our models, the model with the lowest PRESS statistic also had the lowest CP, highest Adjusted R-Square, and lowest MSE. This simplified the final model selection criteria.

Appendix B. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

	STATE					
Year	CT	NY	NJ	PA	OH	IN
1971	–	–	–	–	43 (26)	3 (2)
1972	–	–	–	–	153 (57)	13 (4)
1973	–	–	–	–	151 (62)	10 (5)
1974	–	1 (1)	–	–	171 (67)	27 (9)
1975	–	–	–	–	264 (76)	19 (8)
1976	–	–	–	–	294 (79)	34 (14)
1977	–	–	–	–	284 (84)	42 (15)
1978	–	–	–	5 (2)	406 (103)	61 (27)
1979	–	–	–	5 (2)	446 (117)	74 (30)
1980	–	2 (2)	–	17 (10)	432 (114)	99 (32)
1981	–	2 (1)	–	38 (21)	409 (113)	102 (33)
1982	–	–	–	59 (25)	430 (119)	120 (42)
1983	–	–	13 (5)	122 (43)	445 (119)	92 (37)
1984	–	4 (3)	7 (4)	126 (45)	411 (119)	97 (33)
1985	–	4 (2)	6 (4)	139 (52)	406 (112)	95 (37)
1986	–	5 (3)	18 (6)	160 (61)	450 (118)	84 (29)
1987[2]	2 (1)	26 (10)	4 (3)	82 (43)	189 (91)	46 (22)
Total	2 (1)	44 (22)	48 (22)	753 (304)	5384 (1576)	1018 (379)
Herds[3]	1	16	8	101	248	77

[1] Number of PGA herd–birthyears in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix B contd. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

Year	STATE					
	IL	MI	WI	MN	IA	MO
1971	11 (7)	47 (32)	–	–	–	–
1972	65 (25)	179 (61)	–	–	–	–
1973	109 (45)	248 (73)	9 (2)	1 (1)	–	–
1974	63 (33)	280 (89)	21 (8)	–	–	2 (2)
1975	69 (28)	407 (121)	18 (6)	–	4 (2)	9 (3)
1976	85 (42)	537 (131)	20 (9)	–	7 (2)	15 (2)
1977	79 (33)	522 (137)	15 (11)	–	2 (1)	11 (5)
1978	130 (47)	663 (175)	128 (72)	22 (6)	4 (3)	23 (7)
1979	171 (63)	762 (194)	206 (89)	34 (14)	6 (4)	41 (14)
1980	216 (76)	829 (211)	303 (129)	58 (21)	14 (7)	30 (13)
1981	325 (109)	739 (199)	382 (156)	65 (34)	34 (14)	33 (10)
1982	338 (111)	837 (208)	557 (230)	179 (86)	69 (33)	40 (12)
1983	397 (133)	779 (209)	621 (241)	222 (88)	80 (37)	42 (15)
1984	334 (116)	848 (210)	633 (262)	246 (95)	80 (35)	46 (13)
1985	334 (110)	758 (192)	703 (273)	272 (110)	125 (46)	44 (15)
1986	401 (123)	831 (206)	758 (272)	436 (161)	171 (55)	57 (15)
1987[2]	120 (61)	311 (140)	346 (181)	204 (112)	74 (39)	19 (13)
Total	3247(1162)	9577(2588)	4720(1941)	1739(728)	670(278)	412(139)
Herds[3]	224	445	558	256	89	28

[1] Number of PGA herds in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix B contd. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

	STATE					
Year	ND	SD	NE	KS	MD	VA
1971	–	–	–	–	–	26 (17)
1972	–	–	–	–	–	151 (44)
1973	–	–	–	–	–	203 (65)
1974	–	–	–	–	–	343 (94)
1975	–	1 (1)	–	2 (2)	–	492 (114)
1976	–	–	–	–	–	454 (117)
1977	–	–	–	–	–	447 (115)
1978	–	–	3 (2)	2 (1)	–	547 (131)
1979	1 (1)	1 (1)	12 (3)	2 (2)	–	553 (139)
1980	–	5 (2)	16 (4)	1 (1)	–	643 (140)
1981	–	3 (2)	22 (6)	–	–	614 (144)
1982	1 (1)	35 (9)	31 (9)	–	–	658 (144)
1983	–	27 (9)	27 (8)	16 (11)	15 (6)	590 (138)
1984	1 (1)	32 (11)	27 (6)	52 (20)	28 (6)	508 (117)
1985	5 (2)	38 (15)	38 (7)	63 (24)	36 (11)	559 (130)
1986	5 (3)	53 (18)	32 (9)	83 (31)	39 (8)	615 (134)
1987[2]	4 (2)	40 (15)	22 (5)	32 (19)	16 (7)	205 (80)
Total	17 (10)	235 (83)	230 (59)	253 (111)	134 (38)	7608 (1863)
Herds[3]	5	29	14	41	14	263

[1] Number of PGA herds in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix B contd. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

	STATE					
Year	WV	NC	SC	GA	FL	KY
1971	–	–	–	–	–	9 (5)
1972	–	5 (2)	–	–	–	48 (16)
1973	–	5 (1)	–	–	–	62 (16)
1974	–	18 (9)	1 (1)	–	4 (1)	87 (23)
1975	–	43 (18)	–	–	5 (1)	88 (23)
1976	–	56 (12)	7 (3)	–	–	85 (24)
1977	–	70 (18)	–	3 (3)	8 (2)	89 (24)
1978	–	96 (30)	5 (3)	7 (1)	23 (3)	90 (33)
1979	–	95 (30)	9 (3)	18 (3)	29 (3)	107 (30)
1980	–	118 (37)	5 (2)	22 (6)	32 (4)	140 (39)
1981	–	163 (39)	3 (2)	20 (3)	59 (5)	107 (28)
1982	–	131 (40)	27 (11)	24 (4)	104 (7)	108 (34)
1983	4 (1)	163 (46)	33 (9)	43 (8)	90 (6)	101 (35)
1984	3 (1)	172 (43)	38 (13)	49 (9)	79 (6)	76 (28)
1985	8 (1)	161 (43)	41 (10)	27 (12)	121 (7)	94 (31)
1986	9 (2)	183 (45)	40 (10)	53 (13)	131 (8)	118 (32)
1987[2]	5 (2)	61 (26)	22 (10)	22 (7)	26 (8)	44 (19)
Total	29 (7)	1540 (439)	231 (77)	288 (69)	710 (61)	1453 (440)
Herds[3]	3	79	18	19	12	76

[1] Number of PGA herds in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix B contd. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

	STATE					
Year	TN	AL	MS	AR	LA	OK
1971	–	–	–	–	–	–
1972	33 (11)	10 (3)	19 (5)	1 (1)	–	–
1973	39 (10)	16 (5)	13 (4)	3 (1)	–	–
1974	54 (14)	19 (6)	21 (8)	–	–	–
1975	49 (19)	18 (4)	24 (11)	2 (1)	–	–
1976	62 (19)	30 (8)	22 (8)	3 (1)	–	–
1977	59 (16)	28 (8)	25 (15)	3 (2)	2 (2)	–
1978	104 (32)	41 (9)	38 (12)	5 (2)	10 (5)	–
1979	136 (36)	30 (13)	83 (26)	13 (3)	12 (5)	–
1980	195 (44)	44 (11)	96 (25)	23 (6)	22 (6)	1 (1)
1981	126 (36)	29 (8)	83 (29)	20 (7)	48 (14)	–
1982	149 (39)	39 (12)	133 (33)	16 (6)	52 (17)	4 (2)
1983	154 (42)	29 (8)	104 (35)	13 (6)	56 (15)	8 (3)
1984	150 (43)	45 (14)	80 (29)	13 (7)	39 (13)	7 (3)
1985	148 (44)	27 (13)	78 (24)	15 (5)	45 (14)	17 (3)
1986	174 (52)	43 (12)	83 (28)	25 (6)	48 (15)	8 (2)
1987[2]	37 (20)	8 (4)	15 (12)	10 (2)	9 (6)	4 (3)
Total	1169 (477)	456 (138)	917 (304)	165 (56)	343 (112)	49 (17)
Herds[3]	96	28	75	15	29	6

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[1] Number of PGA herds in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix B contd. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

	STATE					
Year	TX	MT	ID	WY	CO	NM
1971	–	–	–	–	–	–
1972	–	–	2 (1)	–	–	22 (2)
1973	10 (3)	–	3 (2)	–	1 (1)	27 (4)
1974	27 (4)	–	4 (4)	1 (1)	3 (1)	46 (6)
1975	32 (7)	1 (1)	39 (12)	24 (3)	22 (3)	140 (7)
1976	60 (11)	–	30 (7)	37 (5)	22 (2)	241 (10)
1977	40 (10)	3 (3)	44 (16)	20 (2)	36 (5)	233 (9)
1978	53 (14)	4 (2)	103 (27)	16 (5)	40 (4)	196 (8)
1979	69 (16)	3 (3)	90 (20)	16 (5)	47 (5)	202 (9)
1980	94 (20)	3 (2)	97 (27)	26 (4)	38 (5)	170 (10)
1981	83 (21)	13 (4)	106 (27)	11 (1)	39 (6)	146 (10)
1982	84 (24)	31 (8)	121 (26)	1 (1)	19 (1)	133 (10)
1983	78 (25)	18 (6)	108 (27)	–	30 (4)	181 (8)
1984	57 (17)	20 (5)	89 (22)	–	36 (4)	119 (8)
1985	56 (21)	12 (4)	131 (28)	–	18 (2)	45 (5)
1986	58 (16)	12 (4)	147 (26)	–	28 (2)	36 (3)
1987[2]	25 (12)	–	43 (14)	–	10 (2)	17 (2)
Total	826 (221)	120 (42)	1157 (286)	152 (27)	389 (47)	1954 (112)
Herds[3]	53	13	75	5	12	14

[1] Number of PGA herds in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix B contd. Number of first crop daughters and Select PGA herds contributing initial period information to PGA bulls by state and year of birth[1].

	STATE					
Year	AZ	UT	NV	WA	OR	CA
1971	–	–	–	–	–	–
1972	–	3 (1)	–	–	–	–
1973	–	1 (1)	–	1 (1)	–	–
1974	–	16 (6)	4 (1)	1 (1)	6 (2)	1 (1)
1975	–	22 (8)	10 (1)	1 (1)	9 (3)	58 (13)
1976	18 (2)	80 (15)	11 (1)	13 (9)	12 (6)	115 (27)
1977	36 (4)	66 (12)	11 (1)	108 (16)	37 (16)	77 (17)
1978	26 (5)	102 (16)	7 (2)	269 (30)	56 (17)	148 (31)
1979	66 (6)	96 (22)	–	211 (27)	49 (16)	201 (43)
1980	105 (7)	93 (27)	7 (1)	265 (34)	59 (22)	231 (46)
1981	87 (7)	117 (26)	2 (1)	291 (40)	67 (17)	321 (44)
1982	135 (6)	140 (27)	1 (1)	267 (41)	67 (20)	413 (66)
1983	142 (7)	102 (24)	–	287 (39)	43 (16)	443 (69)
1984	149 (7)	118 (25)	6 (1)	246 (48)	48 (17)	371 (59)
1985	152 (5)	137 (34)	–	297 (46)	52 (19)	459 (73)
1986	147 (6)	134 (32)	–	385 (63)	82 (19)	605 (78)
1987[2]	80 (8)	57 (25)	–	203 (53)	19 (7)	275 (61)
Total	1143 (70)	1284 (301)	59 (10)	2845 (449)	606 (197)	3718 (628)
Herds[3]	18	66	3	104	46	167

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[1] Number of PGA herds in parentheses and number of first crop daughters outside of parentheses.

[2] Incomplete information for this year.

[3] Number of PGA herds represented.

Appendix C. Herd characteristics of 341 Select Sires PGA herds contributing first crop daughters for at least ten years.

Trait	Mean	SD	Min	Max
$\hat{G}^1$ milk (kg)	118	17	74	178
$\hat{G}$ fat (kg)	3.5	.6	1.8	5.4
Percent young sire use	16	6	3	43
Percent AI sired	87	12	31	100
Percent Registered	42	38	0	100
Percent birthdate change	.003	.05	0	1
Herd size	113	150	5	1672
Number sires	43	28	4	300
Number 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
Proven sire PTA milk $\bar{X}$ (kg)	47	90	−214	316
Proven sire PTA fat $\bar{X}$ (kg)	−1.0	2.9	−10.5	7.2
ME^3 milk $\bar{X}$ (kg)	8234	722	6139	10672
ME fat $\bar{X}$ (kg)	296	28	222	385
ME fat percent $\bar{X}$	3.62	.14	3.17	4.13
$SH+PE^4$ milk $\bar{X}$ (kg)	34	52	−257	184
SH+PE fat $\bar{X}$ (kg)	1.1	1.7	−7.0	9.0
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 percent $\bar{X}$	.01	.01	−.03	.06

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[1] Within herd genetic trend

[2] Within herd mean

[3] Mature equivalent

[4] Sire by herd plus permanent environment effect

Appendix C. contd. Herd characteristics of 341 Select Sires PGA herds contributing first crop daughters for at least ten years.

Trait	Mean	SD	Min	Max
Cow REL[1] $\bar{X}$[2]	.51	.03	.42	.56
Sire REL $\bar{X}$	.95	.02	.90	.99
Age in years $\bar{X}$	4.1	.5	2.0	5.0
Lactation number $\bar{X}$	2.5	.5	1.0	3.0
Days Open $\bar{X}$	111	18	22	163
ME[3] milk σ[4] (kg)	1408	187	929	2758
ME fat σ (kg)	50	6	36	76
ME fat percent σ	.38	.04	.23	.61
SH+PE[5] 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	1.0	6	11
Cow PTA fat percent σ	.07	.01	.04	.10
Sire PTA milk σ (kg)	121	16	63	177
Sire PTA fat σ (kg)	4.3	.6	2	6
Sire PTA fat percent σ	.09	.01	.05	.12
Cow REL σ	.06	.01	.04	.09
Sire REL σ	.06	.01	.02	.12
Age in years σ	1.9	.3	.0	3.0
Lactation number σ	1.6	.5	.0	2.0
Days open σ	88	40	31	384

[1] Reliability of PTA

[2] Within herd mean

[3] Mature equivalent

[4] Within herd standard deviation

[5] Sire by herd plus permanent environment effect

VITA

Todd Richard Meinert was born December 15, 1961 in Freeport, Illinois. He graduated from Orangeville High School in Orangeville, Illinois in June 1980. From 1961 to 1980 he was living and working with his family on a registered Brown Swiss farm in Davis, Illinois. The author was involved with 4-H, FFA, and basketball during this time period.

In August 1980 the author entered Iowa State University and received the Bachelor of Science degree in Dairy Science in May 1984. He then enrolled at Virginia Polytechnic Institute and State University and received a Masters of Science degree in Dairy Science Genetics in May 1987. From May to August 1987, the author worked at Wageningen Agriculure University in The Netherlands on research estimating genetic parameters of fat/protein ratio and other milk components. In August 1987 the author returned to Virginia Polytechnic Institute and State University to continue his pursuit of a Doctor of Philosophy degree in Animal Science in the area of Dairy Cattle Genetics. Awards and Honors received by the author include the 1987 Virginia Tech Dairy Science Teaching Assistant Award and 3rd Place 1990 ADSA Graduate Student Paper Contest. The author has the following publications:

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