

# **Characteristics of progeny test herds and their effects on the genetic evaluation of young sires**

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## **Abstract**

Our purpose was to examine characteristics of progeny test herds and their effects on the genetic evaluation of young sires. Data for a study of response to pedigree selection by stud were evaluated from 6238 Holstein sires in four USDA animal model evaluations from January 1995 to February 1997. When data were restricted to the nine major semen producing organizations, a common intercept and slope for prediction of daughter yield deviation from pedigree merit were appropriate for milk but  $R^2$  was low at 0.14. We detected no important differences in response to pedigree selection among progeny testing methods used by major semen producing organizations.

Data for a study of specific progeny test herds were 4154 Holstein progeny test herds from two AI studs and 6361 remaining herds from two states. We grouped herds into four categories, 21st Century Genetics and Genex progeny test herds, other Minnesota herds and other New York herds. Herds were described by DHI profile and average cow evaluation data. Cows with extreme yield deviations ( $\pm 3$  herd standard deviations) were identified, as were daughters of progeny test bulls with extreme daughter performance relative to pedigree merit of the bull. 21st Century Genetics and Genex appear to have chosen the larger, genetically superior and better managed herds from within their regions in which to conduct their progeny testing. We were not able to predict if a bull was going to exceed or fail to meet pedigree prediction by characteristics of the progeny test herds in which he was sampled.

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# Introduction

A quality progeny test for a young bull requires the efforts of many people, substantial capital, and top quality management. Permanently impacting the dairy industry by the purchase of a young sire is every sire analyst's objective. The sire analyst, although highly regarded, is a very small part of the entire picture of progeny testing. The initial purchase price of a young bull is substantial but represents a small portion of the amount spent to maintain and progeny test a young bull.

Studs utilize the progeny test of a young bull to establish a market value for his semen. Market value is maintained if there is stability in the bull's evaluation. The accuracy of the progeny test is essential to create consumer confidence for an AI organization. Inaccuracy in a young sire's evaluation may also lead to less or more than optimal use of a young bull as a sire of male and female replacements.

In the highly competitive AI industry, many half and even full brother combinations appear in more than one AI organization. A half brother released earlier than other brothers may generate more revenue for an AI organization. Progeny testing is centered on speed and accuracy of producing milking daughters from young sires. Efficient allocation and distribution of young sire semen is essential in reducing days to a bull's progeny test results.

Progeny test semen is distributed to herds at a relatively low price or even free, and in some cases incentives for milking young sire daughters are used to entice farmers to use young sire semen. These incentives and willingness by farmers to participate in progeny test programs may give a choice to AI organizations on which herds they should allow to participate.

The choice of which herds to allow to participate in progeny testing may be a difficult decision, especially for member-owned cooperatives. Member relations may be strained by excluding member herds whose performances in critical areas such as age at first freshening, conception rates, and calf mortality are marginal. Inclusion of all member herds may increase expense of progeny testing substantially and accuracy of progeny test results can be compromised if such issues are ignored.

## **The objectives of this study were:**

1. To evaluate response to pedigree selection through progeny test programs conducted by AI and private organizations for Holsteins in the United States. Evidence of differences between organizations was of primary interest.
2. To compare herds in two current progeny test programs and to other herds in the same region.
3. To predict whether a bull was going to exceed or fail to meet pedigree prediction from characteristics of the progeny test herds in which he was sampled.

# Review of Literature

Progeny testing programs are important for continued genetic improvement in United States dairy cattle. Progeny testing identifies bulls with superior genetic merit for milk, protein, fat, and other traits of economic importance. Bulls identified with superior genetic merit are utilized by dairy producers and AI studs as sires of future dams and sires (30).

A limited number of daughters of an individual bull enables an AI organization to determine if a bull received a better or worse than expected sample of genes from his parents. Increased accuracy of parental evaluation is a bonus of large numbers of progeny. Mendelian segregation makes progeny testing necessary to evaluate the gene sample inherited by a young sire from his parents.

## Genetic evaluations

A persistent increase in the complexity of genetic evaluations has significantly impacted the history of dairy cattle breeding. Information used to evaluate animals has expanded from physical appearance to records of yields, to the further inclusion of correlated traits and information on relatives (18).

The theory required for genetic evaluation utilizing an animal model was initiated by Henderson (17) in 1949. His theory referred to an animal model as a method of cow and sire evaluation in which the performance of an animal is used to estimate the breeding value of that individual (5). Only recently, as a result of computational advances, has the impact of Henderson's theory been realized.

The animal model replaced the Modified Contemporary Comparison (MCC), a procedure for genetic evaluation which was used from 1974 to 1989. The following factors supported the adoption of the animal model for genetic evaluations. First, the model uses all sources of information including performance, parents, and progeny, in an optimal manner. Second, the animal model system has established statistical properties (best linear unbiased prediction) and is endorsed by the scientific community. Third, the adoption of the animal model as the national system of sire and cow evaluation adds credibility to evaluations in the global market (5).

Genetic evaluations for yield traits are calculated at the Animal Improvement Programs Laboratory (AIPL) four times a year since May 1997 from data received from the dairy records processing centers in the United States. AIPL performs numerous checks on incoming data from dairy processing centers to screen for reasonable values and consistency with existing data (28). Prior to analysis, data are adjusted for age-season of calving, length of lactation, and number of milkings per day (58). An adjustment for heterogeneous variance is likewise applied. The adjustment for heterogeneous variance considers both residual and genetic variances, and was implemented to reduce the apparent underestimation of PTA's of progeny-tested bulls in low variance herds (64). The adjustment also increases the number of elite cows in average variance herds, but decreases the number in higher variance herds (64). Adjustment for heterogeneous variance increased differences among bulls. However, the anticipated reduction in evaluation bias for AI non-stud bulls was not observed (43).

The current animal model describes a cow's lactation as the sum of the effect of her management group (m), genetic merit (a), permanent environment (p), interaction of her herd and sire (c), calving age and parity (v), and unexplained residual (e) using the following model (57):

$$Y = m + a + p + c + v + e$$



In the above model, effect of the herd environment is accounted for by management groups. Each lactation record is assigned to a management group (59, 60) defined by several factors. First, groups are delineated by a herd-year-season of freshening classification. Two month calving seasons were chosen to make management groups as uniform as possible, a change from the MCC which used a five month rolling seasons, resulting in 12 overlapping seasons (59). Secondly, groups are defined by registry status (registered or grade), an approach that attempts to account for different management of registered and grade cows in the same herd (39). Third, the definition of management groups includes parity, in order to compare animals with similar survival histories. Lactation number is limited to five lactations, thus limiting the time period in which a cow contributes data to her own evaluation. With advancing parity, later lactation records become less useful in estimating genetic merit (38). Cows with missing first-lactation records are excluded from evaluations affecting relatives, to reduce selection bias (64). In January 1995, age-parity factors for cows of the same age but differing in lactation number and in time periods were implemented (47). Genetic trend was reduced, and comparisons of animals born in different years were improved with the new age-lactation factors (47).

If management groups include less than five cows, grouping requirements are relaxed until a group size of five is reached. Boundaries between groups are relaxed as follows: 1) season is increased to 4 months, 2) registered-grade distinction is removed, 3) season is increased to 6 months, 4) parity distinction is removed, and 5) season is increased to 12 months in increments of 2 months (60). A management group including only one daughter of a sire does not contribute to that sire's evaluation (64).

Breeding value of a cow producing a record is referred to as genetic merit (a). All known relationships with other animals are included in the estimation of genetic merit (5). Pedigree data on all known relationships go back to 1950, and lactation data back to 1960 calvings are included (64). Data from all known relatives were not included in the MCC where only sire and maternal grandsire information (later, dam evaluation) were considered for sire evaluation. For cows, the MCC ignored all progeny and maternal half sibs performance.

Permanent environmental effects (p) affect all lactations of a cow, but are not transmitted to offspring (5). A loss of a quarter due to mastitis would be an example of a permanent environmental effect. Proper consideration of permanent environment effects prevents confusion with genetic effects. The interaction of herd and sire (c) is the environmental correlation among a sire's daughters in the same herd (5, 32). Herd-sire interaction has been credited with causing genetic evaluations based on natural service to be acceptable predictors of the bulls' future AI evaluations (32, 33). Herd-sire interaction has been shown to increase the correlation between early evaluations of bulls with daughters in few herds, and their later evaluations on widespread data (18).

The calving age and parity adjustment (v) was included in the animal model in January 1995. The previous approach considered the effect of age group within parity (60). Calving age, calving year, and region defined effects. The adjustment was implemented from findings of Wiggans and VanRaden (64) who reported, previous to the calving-parity adjustment, that age adjustment factors over-adjusted lactation records of second lactation cows. Estimates of genetic trend were shown to be quite sensitive to age adjustments (58). The incorporation of a parity effect eliminated upward trend in evaluations of bulls as additional daughter information was included. The inclusion of parity effects in the model improved accuracy of comparisons of animals born in different years.

A cow's predicted genetic merit ( $\hat{a}$ ) is computed as a weighted combination of three sources of information: 1) average of its sires' ( $\hat{a}_s$ ) and dam's ( $\hat{a}_d$ ) predicted merits, 2) the cow's yield deviation (YD, missing for bulls) where:

$$YD = \frac{\sum [w_{len} (y - \hat{m} - \hat{a} - \hat{p} - \hat{v})]}{\sum w_{len}}$$

and 3) average of contributions from progeny (63). An estimate of the effect is indicated by  $\hat{a}$ ,  $\sum$  indicates summation, and the lactation length weight is  $w_{len}$  (5, 60). Lactation weight depends on test plan (standard or am-pm), number of tests, lactation number (first or later) and number of supervised test days, or other test days (46). A new source of differences in lactation weight in February 1997 came from the use of owner sampler records. Owner sampler tests receive 50% credit, whereas official tests receive full credit (48). Records from 10,849 cows, calving after July 1, 1996, were included in the February 1997 summary from owner sampler records. Data from owner sampler herds were included if (46):

- 1) valid identification in the herd (cow, sire, and birth date) was greater than 40%,
- 2) there was reasonable agreement between bulk tank measurements and the sum of individual cow milk weights (between 81% and 117% of recorded milk shipped),
- 3) The number of outliers in the herd was below a ceiling based on size. Outliers are based on interquartile ranges for deviated milk yield. If a herd has 6.4% possible outliers or more then all data are deleted for that herd (48).

A progeny contribution is twice the progeny's predicted merit ( $\hat{a}_p$ ) minus the mate's predicted merit ( $\hat{a}_m$ ). Estimates of unknown-parent group effects are substituted for unknown parents or mates. Furthermore,  $\hat{a}$  is represented as follows (63):

$$\hat{a} = w_1 \frac{\hat{a}_s + \hat{a}_d}{2} + w_2 (YD) + w_3 (\overline{2\hat{a}_p - \hat{a}_m})$$

The  $w$ 's are weighting factors that sum to 1. For  $w_1$ , the numerator is 2 if both parents are evaluated, 4/3 if only one parent is evaluated, or 1 if neither parent is evaluated. For  $w_2$  the numerator is  $(\sum w_{len})[h^2/(1-r)]$ . For  $w_3$ , the numerator is half the number of progeny, but progeny of unknown parents only count 2/3. The three  $w$ 's have the same denominator, which is the sum of the  $w_1$ ,  $w_2$ , and  $w_3$ . Bull evaluations are computed in the same way except with  $w_2$  set to 0 (63).

If a parent or mate is unknown, its value is replaced by a group (56) effect for unidentified parent (phantom) and the weight given that term is reduced (17). Animals are placed into genetic groups to account for selection as suggested by Henderson in 1949 (17), when they cannot be accounted for by known genetic relationships. Sires are assigned to groups based on discretionary criteria such as year of birth, stud, year of entry into service, geographical region, or pedigree information (19). Pollak and Quaas (37) reported that the need for grouping decreases as genetic relationship information among animals becomes more complete. Simultaneous sire and cow evaluations developed by Westell and Van Vleck (56) in 1987 minimized the need for genetic groups. Nonetheless, groups are required to represent differences in genetic values of unknown parents which may be from different populations.

Prior to the work of Westell et al. (55), a majority of models for animal evaluations used only a single group effect for an animal without consideration of unknown data. Simple rules for

constructing group equations and group contributions to animal equations were developed (43, 56). Westell and VanVleck (56) developed phantom parents as an alternative to a single group effect for animals not having records. Phantom parents are used only to assist computing solutions for the mixed model equations in the animal model. A sire or dam is assigned to the phantom group if both parents are unknown, or only have one progeny and no yield record of their own (59). Groups are formed so those parents of the same expected genetic merit are in the same group (56, 63). The animal model does not assume that all unknown ancestors are genetically equal (5); therefore, four parallel phantom genetic groups corresponding to the four selection paths were assigned for each path, (44) allowing each genetic group to have different selection intensities. Within these four paths, year of birth of unknown parents is used to define groups. These four path values assigned for each animal made the animal model impractical for large populations due to computer storage problems. Wiggans et al. (59) developed ways to reduce the storage requirement and make the animal model feasible.

The operational steps of evaluations by the animal model are as follows. 1) Processing of lactation data, 2) processing of pedigree data, 3) preparation for computation of solutions, 4) iteration until satisfactory convergence, 5) calculation of reliability, 6) computation of supplemental evaluations, which include cows that lack first lactation records, and 7) adjustment of breeding values to a genetic base and calculation of transmitting ability (59).

Iterations (repeated calculation) allow the contribution of each animal to affect all its relatives (5, 63). Iteration is useful because each effect is estimated from records adjusted for all other effects in previous rounds of iteration. By revising estimates repeatedly for each effect, a final solution is reached where the estimate for each term is adjusted for all other terms calculated by the system (59).

Another improvement in the animal model was the ability to accommodate changes in the genetic mean and variance (18). Genetic means and variances seldom are constant but change as a result of finite population size or selection (18). Inbreeding and genetic drift accumulate each generation in a closed, finite population, thereby affecting both genetic means and variance. Genetic variance can be altered by linkage disequilibrium (3), changes in gene frequency, and establishment of covariances between genotypic values.

Heritability in the animal model was increased to .30 in August 1997. This change in heritability was shown to improve the ability of evaluations based on first-crop daughter records to predict later daughter performance (48, 57). Limiting the impact of evaluations with large deviations to within 4 herd-year standard deviations from management group average (48, 57) had a large impact on individual genetic evaluations (64). Even with the increase in heritability, the correlation between repeated records of the same cow (repeatability) remained at 0.55. Repeatability is the sum of variation due to heritability, herd-sire interaction, and permanent environment (63). With the increase in heritability, the proportion of overall variation was reduced from 0.14 to 0.10 for herd-sire interaction and from 0.16 to 0.15 for permanent environment. Larger differences in evaluations for bulls with small numbers of daughters or proven in few herds are expected to result from changing the relative proportion of variation assigned to heritability.

The genetic base, a reference point for comparing animals (63), was established by setting the genetic value of the average cow born in a base year to 0 (58). The genetic base is updated every five years to encourage dairy producers to continue to make rapid genetic advancement.

The base is subtracted from predicted breeding value of all individual animals processed by the animal model (61). All calculations are made within breed.

Predicted transmitting ability (PTA) includes parent average (PA), individual yield deviation (only in cows), and progeny contributions through daughter yield deviation (DYD). DYD is the weighted average of daughter yield deviated from contemporaries and adjusted for genetic merit of contemporaries' dams for milk, fat, or protein. As a sire accumulates more daughter information and reliability increases, more weight is given to DYD in calculating PTA and less emphasis is placed on pedigree.

## **Within herd variance**

In genetic evaluations, within herd variance has a notable effect on sire and a potentially more serious effect on cow evaluations. Initial studies of within-herd variance focused on the association of herd variances with herd averages. Most studies, with two exceptions (23, 24), reported that environmental variances increased with herd averages (1, 4, 11, 12, 20, 26, 40).

For three independent analyses, Hill et al. (20) obtained records on first lactation daughters of British Friesian sires. Herds were first separated on mean production into high and low levels of average production. The groups of low and high milk yield herds had heritabilities of 0.24 and 0.30 respectively. The data were also split into two groups by within-herd variance, and again by within year-season coefficient of variation using variances and means computed from the previous splits. An increase in milk yield per herd from low to high in mean and variance of yield both within and between sires were reported. Higher heritability was found in herds with larger coefficients of variation. Therefore, progeny test bulls were evaluated more accurately when sampled in herds with higher mean or variance for production. Hill et al. (20) concluded for British herds with higher production levels that there was a corresponding increase in heritability for milk yield, fat, and protein. Powell and Norman (38) obtained similar results with United States data from 1979 herd-average milk yields. They reported that heritability estimated in five herd-average groups ranged from 0.26 in the lowest to 0.35 for the highest group.

Two studies (23, 24) did not report increases in heritability as production levels increased. In 1962, Legates (23) used Guernsey, Jersey, and Holstein daughter-dam pairs to estimate heritability for fat yield and its relationship with herd-average levels. Increases in phenotypic and genetic variance were present as milk yield increased but the coefficient of variation declined. Consequently, no significant relationship was reported between herd production levels and heritability estimates. The author reported no need to use different heritability estimates for herds at different production levels.

Lofgen et al. (24) did not find an increase in heritability as production levels increased, using data from Holstein and Jersey cows born after 1963. Three groups of herd means and variances were formed using modified contemporary average and heritability was estimated in each group. The lowest heritability was the middle group with higher estimates in the extreme groups. Lofgren et al. (24) concluded a possible reason for the contrast was that older data were used in the previous study as well as a different method of analysis.

McDaniel et al. (26) reported that daughters in herds with higher milk production also had increased variation among their evaluations. Relationships among breeding values of 40 first lactation Holstein sires were calculated at different levels of production. Sire's progeny were classified into one of four groups based on milk yield of herdmates. Correlations among sire

progeny averages at the different herdmate levels were high (0.88 to 0.96) and indicated that bulls ranked in about the same order at all production levels.

Progeny in a more variable herd will influence a sire's evaluation to a greater extent than daughters in a less variable herd (52). Therefore, bulls of above average genetic merit with a large percentage of daughters in herds with high variance levels generally will be over-evaluated if heterogeneous variance is not considered (52). Progeny in herds with lower variances will have less effect on a bull's summary. Adequately sampled sires will not be likely to be affected greatly by variability of daughters by virtue of equal distribution of a sire's progeny across many herds (51, 52).

Within-herd variance has potentially serious effects on cow evaluations if variation remains constant in the same herd over years (2). Approximately half of the bias in a dam's index is reflected in the index of her daughter. Furthermore, with most daughter-dam pairs in the same herd, within-herd variation has a cumulative effect over several generations.

Powell et al. (40) used MCC to illustrate that herds with higher milk production per cow tended to use bulls with higher predicted differences and to have higher cow indexes. A larger proportion of cows in these herds will attain elite status for production than in herds with lower production. A cow's elite status should reflect genetic superiority and not environmental opportunity. The work concluded that genetically superior cows with higher yields seem to result from herds with higher heritability. Higher heritability would also be associated with larger within herd variance.

Hill (19) concluded that using the same intensity of selection among members of two groups of equal size with the same mean but different variances will cause three-quarters of the selected animals to come from the more variable group. Everett et al. (14) using 7398 Holstein herds with equal genetic merit reported 10% of the cows qualified for elite status in herds with larger variance and none qualified in the lower variance herds. Large within-herd variation causes more cows to reach elite status and be selected as future AI bull mothers than in herds with small within herd variation.

Incorrect selection of bull mothers may be the result of selection from herds with large within-herd variation. Wilhelm and Mao (66) reported that young bulls selected from Michigan herds with low within herd variance appeared to be genetically superior to those selected from herds with high within herd variance. Mao et al. (65), during the same time period, looked at 209 bulls from herds in northeastern United States and reported no evidence that cows from herds with low within herd milk variation were superior to those from high variation herds.

## **The Artificial Insemination Industry**

### **Early History**

In the earliest years of the AI industry, semen freezing techniques were not perfected. Consequently semen had to be used quickly and in a location relatively close to point of semen collection. As a result, many bull studs were needed. Consequently, most bulls were proven in a single herd, and it was difficult to determine if the high production of bulls' daughter was caused by genetic merit of the bull or by extremely good management (31). Many of the proven service

sires were a disappointment when their daughters came into production. Due in part to the perfection of semen freezing techniques, today's AI industry is in a period of consolidation into larger and presumably more efficient operations.

C.R. Henderson in 1950 experimented with herdmate comparison methods to provide a more accurate prediction of which bulls would produce the best daughters in AI service (31). As a result of Henderson's research (17), young sire sampling was experimentally initiated by New York Artificial Breeding Cooperative in 1955. Herdmate comparison summaries published by Cornell in the mid 1950's were attributable to Henderson's research. The United States Department of Agriculture (USDA) began publishing herdmate sire comparisons in 1962 (32).

## **Progeny testing**

Mendelian segregation makes progeny testing important to identify the gene sample inherited by a young sire from his parents (15). Only by examining daughters in a progeny test can bulls with favorable Mendelian segregation be reliably identified as better than their PA. A progeny test results from the sons of the best pedigreed sires being mated to the best pedigreed dams. The young bull is brought into the AI center at an early age or may even be born at the AI center. The first semen is distributed to many herds to obtain daughters for an accurate evaluation of each bull. After the distribution of the first semen is completed, the young bull is held in a rearing environment until evaluations of the daughters are complete. Once the daughters are evaluated, the top 10 to 15% of bulls are put into widespread service.

Throughout the years, an increasing number of bulls have entered AI. Larger numbers of progeny test bulls increased opportunity for selection intensity, and, thus, the opportunity for obtaining a highly marketable bull. The number of bulls entering AI from the years 1975 through 1983 increased substantially. At the same time, the percentage sampled through private organizations or herds began to decrease (35, 42). Growth of AI sampling programs leaves studs less dependent on AI non-stud bulls (corresponding to AI privately sampled bulls in this study) and natural service sires as the numbers for both declined notably over time (7, 35). Cassell et al. (7) reported numbers of AI sampled bulls rose from less than 500 bulls in the 1970 birth year to over 1100 of those born in 1981, enabling a considerable increase in selection intensity into the 1980's.

## **Preferential treatment of bull dams**

The financial gain and name recognition of having a bull enter AI creates a temptation for giving a potential bull mother preferential treatment. Preferential treatment is any management practice that increases production and is applied to one or several cows, but not to their equally worthy contemporaries (21). A dairy producer may not intentionally give individual cows preferential treatment or may not realize favoritism at all. Preferential treatment may involve providing better or more feed, different housing, or even breeding a cow one more time where another cow would not receive that one last chance. Unfortunately, intentional preferential treatment may also occur so that a cow would be chosen as a bull mother or sold at a higher price.

The overestimation of genetic merit of bull dams contributes to overestimation of parent average. A cow's inflated evaluation can remain until information from her progeny, particularly her sons, causes her evaluation to reflect her actual genetic merit more accurately (41).

Kuhn et al. (21) using simulated data, reported potential for substantial bias from 15 kg to 893 kg in female PTA's from cows that received preferential treatment. Weigel et al. (54) reported similar results with simulated data.

Accurate first-crop daughter information is a necessity for genetic progress when the 10 to 15% of young sires that graduate to the proven lineup will receive very heavy use. Overestimation of a bull's genetic merit will result in heavier use than true genetic merit justifies. Underestimation of a bull may result in a bull being culled from the AI organization with his true genetic merit unknown. Both cases are of great interest to the AI organization in addition to the dairy producers as they reduce potential genetic progress and can erode producers' confidence.

Clay et al. (9) studied 455 bulls having a final proof with MCC repeatability exceeding 90%. They used these sires to examine relationships between initial repeatabilities and final evaluations. Were more variable with lower initial MCC repeatabilities with a slightly greater tendency to decline than evaluations with high initial repeatabilities. When last available PD was regressed on initial PD, initial MCC repeatability explained only 1% of the variation in final PD. Final evaluations increased 1.53 kg per percent increase of initial MCC and have repeatability, which may indicate heavier use of better production pedigrees by farmers doing the sampling.

Stability of bull proofs was researched by Vinson et al. (53) using 160 Holstein sires. These bulls' final evaluations had an initial MCC repeatability less than 70% and a final evaluation exceeding 90% repeatability. Stability was measured by subtracting the last evaluation from the initial evaluation of a sire. Results were similar to Clay et al. (9) in that higher initial MCC repeatabilities resulted in more stable final proofs. Bulls with the most stable proofs were tested in moderate sized, high producing herds, with low genetic merit of contemporaries. The bulls whose evaluations increased from initial to final evaluations were sampled in large herds with low genetic merit of mates. Vinson et al. (53) concluded that much of the change over time in evaluations of sires was from Mendelian sampling variation but proper design of progeny testing programs could help in a bull's stability.

Cassell et al. (6) reported that genetic evaluations for milk yield under the MCC for Holsteins with limited, non AI sampling were inflated 69 kg when later evaluations were compared to first progeny results. Norman et al. (34) reported that non AI bulls entering AI service from 1975 through 1978 were not overestimated. However, later MCC studies (29, 34) comparing non AI and latest evaluations reported that early evaluations were overestimated, particularly for bulls born after 1975.

In the early years of the animal model, Powell et al. (42) compared DYD milk with PA for bulls in different sampling categories using 22,930 bulls from July 1990 evaluations. A higher DYD than expected from PA for a group of bulls would suggest selective treatment of daughters. Furthermore, a negative mean for DYD minus PA would suggest that PA was inflated, perhaps because of inflated dam PTA. AI bulls produced a mean of DYD minus PA of -9 kg of milk compared to -46 kg for non AI bulls. Low coefficients of determination was reported, indicating that variation not accounted for by sampling status, year, or reliability were considerable. Powell et al. (42) concluded that non AI bulls should be considered cautiously for mating but not dismissed. A declining proof on a non AI sampled bull may be disappointing but will not reduce genetic progress in a herd if the bull was genetically superior to the AI sampled bull that might have been used instead (7).

# Characteristics of progeny test herds

## Identification problems

An increase in the number of usable records from current progeny test herds would benefit AI organizations substantially. Benefits could: 1) support the progeny testing of more bulls; 2) result in more progeny test daughters per bull and higher accuracy for first-crop genetic evaluation; 3) result in a reduction of the units of semen needed to obtain a sufficient number of daughters for first-crop evaluation (27).

## Misidentification

VanVleck (49) raised questions about valid identification in a study of differences in heritability estimates from parent offspring compare to paternal half-sibs methods. Lower heritability was found when estimated by paternal half sib methods. The author concluded misidentification of sires of cows could be a substantial problem. Heritability was estimated to be 64% of its true value when only 80% of cows were identified correctly by sire. Therefore, misidentification of sires' daughters leads to substantial underestimation of heritability (50).

In a simulation study, Christensen et al. (8) determined influences of misidentification to be more serious for bulls with a small progeny group sizes than for bulls with larger progeny groups. For bulls with large progeny groups, a certain proportion of misidentification will reduce the differences between bulls but not change the bull's ranking. For bulls with a smaller progeny group, a change in his ranking compared to other bulls could occur. Geldermann et al. (16) reported similar results using 15 German tested bulls from the insemination period 1977 to 1978. The 15 bulls had a misidentification rate of 4 to 23% within their progeny group. Differences between the breeding values changed once misidentified animals were removed. For example, one bull was ranked 11<sup>th</sup> out of 15 on milk fat yield when all the daughters were included. The same bull was ranked 4<sup>th</sup> once evaluation included only correctly identified daughters.

Misidentification is expected to reduce the differences between the estimated breeding value. Cows misrepresented as daughters of an exceptionally high bull would be over evaluated, as their true sire would likely be of lower genetic merit. Therefore, the estimated breeding values would be closer to average than true breeding values. Misidentification reduces apparent genetic variation.

## Missing identification

Missing sire identification is the primary reason why lactation records do not contribute to genetic evaluations. Genetic evaluations during 1984 were computed with 48% of records from approved test plans being eliminated (60). Slightly over 25% of records from usable plans did not include sire identification. During January 1992, 35% of records were eliminated; 31% of records submitted for genetic evaluations were excluded because of missing sire identification (36).

Meinert et al. (27) reported only a small increase in usable official records from 1968 to 1978 but a steeper linear increase from 1979 to 1988. This increase in correct identifications could be a result of better heifer record systems and improved education on the values of identification. From 1988 to 1990, usability of official records changed little, possibly as a result of larger herd sizes and a high proportion of grade cows. Sire identification was less complete in the grade population (13).



Meinert et al. (28) reported that the mean percentages of records that were usable for herds participating in AI progeny test programs were 77% in 1991 and 78% in 1992. The percentages of usable records for non participating herds were 62% in 1991 and 60% in 1992. Progeny test herds had larger mean herd sizes, higher mean standardized milk yield and larger standard deviations of milk yields, younger cows, and a lower percentage of registered cows than non participating herds. The authors observed a lower percentage of registered cows and higher mean yield for herds participating in progeny test programs.

## **Registration status**

Animals recorded by the Holstein Association with both parent lines tracing back to original importation into North America from Europe are considered registered Holsteins. A grade individual has a less complete record of ancestry. The impact of the grade population is nevertheless substantial with 65% of all daughters in an average AI bull proof being grade (33). Grade data are expected to have more impact in the future. The percentage of usable records for genetic evaluations from registered cows declined from 64% in 1969 to 42% in 1990 with the balance of records contributed by grade cows (27). Without the presence of grade animals in the dairy population, only one third of the current AI bulls could have been sampled.

Powell and Norman (39) studied preferential treatment according to registry status using cows with calving dates from 1960 to 1984 that were enrolled in official DHIA test programs and that passed edits for use in MCC genetic evaluations. Consequently, sire identification was present on all individuals but missing dam identification did not exclude individuals. Only about one-third of grade cows on official test were identified by sire. Within the same herd and year, average milk yields of registered cows generally were higher than those of grade cows but as cows aged, production of grade cattle surpassed that of registered cows (10). The grade cows had a higher culling rate than did the registered cows. There were 70% more sire-identified grades than registered 2-year-old cows in the data but by the age of 5 years, only 8% more grades than registered cows were still milking. Dentine et al. (10), using July 1983 summary information on a random sample of cows that calved for the first time between 1965 and 1980, reported registered 2-year-old cows out-produced grades in the same herd by 99 kg milk. However, increased intensity of culling among grade cows resulted in registered cows out-producing grades by only 21 kg over all lactations.

Herds with more grade cows tended to have a higher average sire predicted difference (PD), but within a typical herd, registered cows were sired by bulls with higher PD (39). Powell and Norman (39) reported that registered cows received preferential treatment within herds with a mix of registered and grade cows. Approximately 19.1% of the herds had at least one registered and one grade cow (10). Preferential treatment of registered over grade cattle was about 90 kg milk per lactation, which resulted in about 3 kg in cow index across herds (39). The authors assumed herds with a mixture of registered and grade cows might represent management systems that were attempting to increase the proportion of registered cows.

## **Daughters receiving preferential treatment**

Preferential treatment of bull dams is one way that bias in predicting transmitting ability may occur. Another source of bias in a bull's proof is preferential treatment of his daughters. In a simulation study, Kuhn and Freeman (22) reported no more than 5 to 6% of a bull's daughters, when distributed across herds, can receive preferential treatment without causing the bull's evaluation to be inflated by 5%. If a sire's dam received preferential treatment equivalent to increased milk yield less than 2268 kg, then 20 to 30 daughters without preferential treatment were necessary to obtain an approximately unbiased evaluation of the bull. Bias in a sire's PTA when daughters receive preferential treatment can be substantial.

Major AI organizations are in constant competition in every aspect of the AI industry. Progeny testing is no exception. AI organizations must identify and market superior bulls and the sampling programs must accurately demonstrate the genetic merit of the bull. For a 10% increase in accuracy, an AI organization would need to increase the number of daughters per bull from 50 to 200. If total progeny test daughters remained constant, only 25% as many bulls could be sampled (25). Can accuracy be improved by more careful selection of progeny test herds? Are there efficiencies to be gained within the design of current progeny test programs?

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# Influences of Progeny Test Programs on Genetic Evaluations of Young Sires

## Abstract

Our purpose was to examine differences among AI progeny test programs in effectiveness in identifying elite young sires for milk and protein. Data were from 6238 Holstein sires in five USDA animal model evaluations from January 1995 to February 1997. Bulls were required to be no older than 8 years of age and to have at least 10 daughters in production at the time of the evaluation. Bulls were grouped by sampling method into nine major AI organizations, bulls with daughters averaging less than 150 days in milk, bulls sampled in over 100 herds, bulls sampled in organizations with controller numbers greater than or equal to 30, and bulls with no connection to a sampling organization. From the major AI organizations, bulls with daughters averaging less than 150 days in milk and bulls sampled in over 100 herds were removed from the studs and placed into two separate groups. A model predicting daughter yield deviation included effects of organization or sampling method, parent average (free of progeny information), and the interaction of organization or sampling method and parent average. When all data were used, a common intercept for milk was appropriate for all sampling methods but the slopes were different ( $R^2 = 0.44$ ). Neither a common intercept nor slope was appropriate for protein. When data were restricted to the nine major organizations, a common intercept and slope were appropriate for milk, and  $R^2$  declined to 0.14. For protein, a common intercept and slope were found, and  $R^2$  declined to 0.15. We detected no important differences in response to pedigree selection among progeny-testing methods used by major semen producing organizations but a difference was detected among NAAB sampling status codes.

## Introduction

Progeny testing (PT) programs were developed by AI organizations in many countries at least partially as a result of the ideas of C.R. Henderson (5) in 1964. Substantial genetic progress in milk yield has resulted from conventional progeny testing (18). Currently, AI organizations in the free market system of the United States have the unique challenge of competing among themselves in addition to facing global competition. Availability of across country ranking of sires (16) enables international comparisons and intensified international competition. Competitive AI markets demand that AI organizations select superior bulls on pedigree merit and sample those bulls in an unbiased manner to demonstrate the genetic merit of each bull accurately.

The selection of superior bulls for sampling accounts for 70 to 76% of the total genetic gain possible in the dairy cattle population (12, 17, 19). Selection of superior bulls has been difficult because of possible biases in genetic evaluation of parents, particularly bull dams. Bias in female predicted transmitting ability (PTA) has been shown to increase as preferential treatment increases (6). As additional related animals receive preferential treatment, bias increases (6) as well as difficulty in selecting an unbiased bull dam pedigree.

Ferris and Wiggans (4) and Samuelson and Pearson (13) compared pedigree merit calculated by the animal model to evaluations based on the Modified Contemporary Comparison (MCC) and concluded that parent average from the animal model was more accurate in predicting



evaluations of AI sampled bulls than pedigree index from the MCC. Even with the improvement of parent average in the animal model, Powell et al. (11) and Samuelson and Pearson (13) reported differences between daughter yield deviation (DYD) and PA. Samuelson and Pearson (13) concluded that a combination of overestimated PAs and error (and) or biased evaluations of the daughters could be a possible cause for these differences.

PTA is based upon parent average (PA), individual yield deviation (only in cows), and progeny contributions through DYD. DYD is the weighted average of daughter yield deviated from contemporaries and adjusted for genetic merit of contemporaries' dams. As a sire accumulates more daughter information and reliability increases, more weight is given to DYD in calculating PTA. Mendelian segregation makes progeny testing necessary to identify the gene sample inherited by a young sire from his parents (3). Only by examining daughters in a progeny test can bulls with favorable samples of genes from their parents be reliably identified as better or worse than their PA. Evaluations from second-crop daughter information showed a decline compared to evaluations from first-crop daughter information (1, 8) under the MCC. A similar result was found for the animal model by Van Der Werf et al. (20), who reported an average drop in breeding values of 30 kg in evaluations from first versus second-crop daughter information using Dutch data. As a decline in evaluations was observed under both systems, problems with progeny testing schemes could be the cause.

Progeny testing is an expensive venture; with only about 1 of every 10 progeny tested bulls returned to active service. Genetic gain and net returns from semen sales may not be maximized by the same progeny group size (2). A cost estimate for each active sire is \$350,000 (21). An active bull ranking in the top percentile produces \$282,000 higher returns for an AI organization than a bull in the middle percentile (7). A free market system demands that AI organizations select superior bulls and that sampling programs demonstrate the genetic merit of each bull accurately. The objective of this study was to evaluate response to pedigree selection through progeny test programs conducted by AI and private organizations for Holsteins in the United States. Evidence of differences between organizations was of primary interest.

## **Materials and Methods**

Data were from 6238 Holstein sires from five USDA animal model evaluations (January 1995 to February 1997). We used the USDA animal model evaluations as a source of bull identification, age, number of daughters and herds, DYD, PA, and controlling organization. Genetic evaluations prior to January 1995 were excluded from this project because of major changes in the animal model system in January 1995. For instance, use of new age adjustment factors in January 1995 (9) and succeeding evaluations compromised valid comparisons with earlier animal model genetic evaluations.

Progeny testing programs have proven effective, although not perfect, in identifying bulls receiving favorable gene samples from parents. These programs vary in how they are administrated and regional scope among AI organizations and other industry groups. To evaluate the sampling method, we eliminated effects of second-crop daughters of bulls returned to active service by including only sires less than 8 years of age at the time of evaluation. Bulls without a birth date, or without sire or dam identification were discarded. Sires with less than 100% US daughters or with less than ten daughters in their DYD at the time of latest summary were also discarded.

Sampling controller numbers were used to identify the organization that performed the initial sampling on each young bull. Bulls with controller numbers less than 30 were placed in their respective organizational sampling controller groups and considered to be sampled by a major AI organization. The nine major AI organizations used in the study were identified by letters A to I. These organizations sample sires with a relatively large number of daughters in many dissimilar herds. Because such organizations have little vested interest in which bulls excel within their program, environmental effects and preferential treatment should be minimized in their sampling programs.

In major organizations, bulls with daughters averaging less than 150 days in milk were considered “AI preliminary sampled” and were grouped together. Bulls sampled in more than 100 herds were grouped separately as “AI heavily sampled sires.” Many major organizations make these bulls available for use in non progeny test herds, unlike the use of traditionally sampled young sires. A bull may be placed into the AI heavily sampled category if he has a unique pedigree, extreme pedigree merit in a certain trait, or carries the red coat color factor.

All sires with sampling controller numbers equal to or greater than 30 were placed in one group called “AI privately sampled.” Sires in this group often were sampled with the intention of developing a bull in which major AI organizations would have a marketing interest. Sires with no sampling controller number were considered to be herd sires and were grouped together. These sires were generally not sampled with the intention of developing a bull in which AI organizations would have a marketing interest. A bull was included in only one category.

All sires with DYD milk available in January 1995 or before were discarded except for bulls in the herd sires group. Herd sires would have no pedigree information in USDA files, whereas bulls with any form of sampling controller number would have been reported to USDA as “in sampling.” We wanted to examine influences of PA unaffected by DYD of daughters (11). Therefore, PA milk and protein from the evaluation prior to a bull’s first DYD were used for all sires except those in the herd sire group. For herd sires, first PA would only be available when first DYD was calculated, and that PA was used in this study. Influences of DYD on PA for herd sires would be less than for a bull sampled in AI because of fewer daughters in a very limited number of herds.

Our first analysis compared PA, DYD, number of herds, and daughters per herd among organizations as defined above. Tests of differences among organizations and sampling status codes (15) were made using the following model:

$$y_{ij} = \mu + \text{Org}_j + \varepsilon_{ij} \quad [1]$$

- $y_{ij}$  = DYD and PA for milk or protein, daughters per herd, Initial PA-Current PA of bull i in org j
- $\mu$  = Overall mean
- $\text{Org}_j$  = Effect of jth organization or sampling status code (15)
- $\varepsilon_{ij}$  = Error for the ith bull in the jth organization.

Regression of DYD on PA by organization or sampling status code (15) was examined using the following model:

$$y_{ij} = \mu + \text{Org}_j + b_1(\overline{\text{PA}_{ij}} - \overline{\text{PA}_{..}}) + [b_{1j}(\overline{\text{PA}_{ij}} - \overline{\text{PA}_{.j}})] + \varepsilon_{ij} \quad [2]$$

$y_{ij}$  = DYD for milk or protein of bull  $i$  in Org  $j$   
 $\mu$  = Overall mean  
 $\text{Org}_j$  = Effect of  $j$ th organization or sampling status code (15)  
 $b_1$  = Overall linear regression of  $y_{ij}$  on  $\text{PA}_{ij}$   
 $\overline{\text{PA}_{ii}} - \overline{\text{PA}_{..}}$  = Difference between PA and overall average PA  
 $b_{1i}$  = Linear regression of  $y_{ij}$  on PA within organization  $j$   
 $\overline{\text{PA}_{ii}} - \overline{\text{PA}_{.i}}$  = Difference between PA and organization average PA  
 $\varepsilon_{ij}$  = Error for the  $i$ th bull in the  $j$ th organization.

Analysis was by the general linear models (GLM) procedure of SAS (14). We divided intercept and regression of DYD on PA into overall and organization effects to test differences between organizations in response to pedigree selection.

### Sampling Status Codes

In 1990, the National Association of Animal Breeders (NAAB) added sampling codes to its cross-reference program to identify the method used to sample bulls (15). NAAB considered bulls with semen distributed to at least 40 herds to be stud sampled (code S) or multi-herd sampled (code M). Code “S” bulls were sampled by an organization that owned (or leased) the bull, processed and marketed semen, and distributed semen to 40 or more herds; for our purposes considered “AI sampled.” If the organization in charge of sampling did not market semen, the bull was considered multi-herd sampled. Bulls not reported to NAAB as S or M by 3 years of age were designated as other sampling status (code O). Bulls not reported to NAAB at all had no code assigned. For our purposes, bulls not reported to NAAB were given a “none” status (code N). Bulls with an NAAB code of a major AI organization but a sampling code of M, O, or N were placed into a separate sampling group (code M, N, O, to AI). We used model 1 with “sampling code” replacing “organization” for analysis.

### Results and Discussion

Summary statistics characterizing progeny test programs of the different organizations are in Table 1. Of 6238 sires with information on first-crop daughters for milk and protein, 2846 were herd sires. The smallest group included 51 AI heavily sampled young sires.

Number of daughters per bull differed ( $P < 0.01$ ) among the organizations with a coefficient of determination ( $R^2$ ) of 0.78 in Table 1. Typical herd sires were used in very few herds with several daughters in each herd; AI heavily used young sires were actively marketed by major AI organizations and used in many herds (Table 1). The AI heavily sampled group showed the greatest variation in the number of herds and daughters, probably because these bulls were not so much sampled as marketed. AI preliminary sampled bulls were sampled as usual for young sires but had incomplete progeny data at latest sire summary.

The subset of data including only the nine major AI organizations was analyzed separately. Number of daughters and herds differed ( $P < 0.01$ ) between organizations, but the  $R^2$  was

reduced dramatically from the full data set to 0.24. Among the major organizations, organization F had the least variation in number of herds and daughters per herd. The greatest variation in the number of herds and daughters per herd was organization I.

Standard deviations within organization (Table 1) reveal the characteristics of pedigree selection and progeny testing systems. The herd sire group had the greatest variation for PA milk with a standard deviation of 268 kg. AI heavily and AI privately sampled bulls were more variable in PA milk than young sires in major organizations. Variability in PA milk for AI heavily and AI privately sampled bulls may be an indication of a multi-focused selection goal. The organization that had the least amount of variation among sires in PA milk was A, suggesting careful or conservative pedigree selection by this organization. Variation among sires in DYD for organization A in Table 1, on the other hand, was second highest among the major organizations. The AI preliminary sampled group showed substantial variation among sires in DYD, possibility due to a high number of records in progress.

Table 2 shows least squares means by organization for PA and DYD milk and protein. Model 1 was used to test differences among the organizations. The initial PA's and DYD's for milk and protein differed significantly ( $P < 0.01$ ) among all organizations for milk and protein. Among the major organizations, only PA protein was not different ( $P > 0.01$ ) between organizations.

The highest average PA for milk and protein were among bulls in the AI preliminary and AI heavily sampled groups. Genetic trend could contribute to such a result for the AI preliminary group and selection intensity on PA could affect the AI heavily sampled group. Genetic trend could affect PA if an organization increased or decreased the number of sires sampled through the period of time in our study. Our data cover only a few birth years and results due to genetic trend should not be large. Therefore selection intensity may play a larger roll in low PA's. Low PA for herd sires is likely due to low selection intensity.

The AI heavily sampled bulls had relatively high PA's for milk and protein but lower DYD for both than other organizations. AI heavily sampled bulls may have unique pedigrees. Bulls with red coat color or out of a popular cow family could contribute to the AI heavily sampled group. Biased PA's may occur more often in bulls from popular cow families. Kuhn et al. (6) found that bias was large for cows with multiple progeny per year. As the number of embryo transfer daughters per dam increased from 10 to 20, bias on dams increased by 15% and bias on embryo transfer daughters increased 7%.

Among all organizations, a substantially higher  $R^2$  resulted for initial PA milk and protein than for DYD milk and protein. Removing herd sires and the privately, AI heavily, and AI preliminary sampled bulls dropped  $R^2$  substantially. The reduced  $R^2$  from the analysis may be due to lack of variance among the mean PA of bulls sampled by each of the major organizations. Major organizations sampled 1735 sires. The three most frequently used sires of sons, Rothrock Tradition Leadman, To-Mar Blackstar, and Southwind Bell of Bar-Lee accounted for 45% of the young sires undergoing evaluations in this group. The frequency of the three most used sires, Rothrock Tradition Leadman, To-Mar Blackstar, and Walkway Chief Mark, decreased to 31% of 6238 total sires in the total data. Differences existed for DYD milk among major organizations but only a small amount of the variation was accounted for.

Table 3 shows differences between PA at the last evaluation without daughter information (initial PA) and most current PA (PA affected by the son's DYD). Model 1 was used to test differences between organizations. All organizations experienced significant changes between

initial PA and current PA except the AI preliminary sampled bulls. Sources of change included Mendelian segregation, errors, and biases in estimating sire and dam evaluations. PA's for milk in all groups except the herd sire and AI preliminary sampled group declined. AI heavily sampled sires showed the greatest decline in milk and protein among all groups examined. Such a decline may be due to an upwardly biased evaluation of parents of AI heavily used young sires and is consistent with the differences in PA and DYD in Table 1. Over evaluation of parents may have occurred in all groups where PA dropped.

Samuelson and Pearson (13) reported that sires of bulls receiving first evaluations averaged 99% reliability while dams' reliability averaged approximately 65%. Powell et al. (11) reported similar results among all bulls but found 70% reliability for dams of AI bulls and 61% reliability for dams of non-AI bulls. Because sires of sons are evaluated more accurately than dams of sons, the effect of preferential treatment of bull dams may explain a substantial part of the drop in PA. The small change in PA milk of herd sires may indicate little preferential treatment of dams for bulls in that group. However, limited progeny data on herd sires and AI preliminary sampled sires reduced the impact of DYD on PA for these bulls. Changes in PA were significantly different ( $P < 0.01$ ) among all organizations for milk and protein, but  $R^2$  values were only 0.03 and 0.02 respectively.

Among the nine major organizations, organization C showed the least amount of change between initial and current PA milk, possibly indicating cautious pedigree selection. Organization A had the largest differences among the major organizations, possibly indicating greater pedigree selection risk. Even with the apparent differences between I and C, no differences among the nine major organizations were found for change in PA for milk and protein with  $R^2$  of 0.01 for both traits.

Table 4 shows equations for DYD milk and protein predicted from PA unaffected by progeny data on the son. Model 2 was used for analysis. Intercepts and regression coefficients by organization were obtained by summing the overall intercept or coefficient with effects of each organization.

When all organizations were studied, a common intercept of 5.76 kg for milk ( $P > 0.01$ ) was appropriate, but the slopes were heterogenous ( $P < 0.01$ ;  $R^2 = 0.44$ ). Response to pedigree selection in the herd sire group was the closest to the expected value of 1.0 with a regression coefficient of 0.97. For protein, there was a difference ( $P < 0.01$ ;  $R^2 = 0.48$ ) between both intercepts and slopes among all organizations.

When data were restricted to the nine major organizations, a common intercept of 28.32 kg and slope of 0.70 were appropriate for milk, but  $R^2$  declined to 0.14. Ferris and Wiggans (4) reported an overall intercept for the AI sampled bulls of -9 kg and a slope of 1.08 ( $R^2 = 0.56$ ). Ferris and Wiggans (4) used the first PA's calculated under the animal model and bulls returned to service.

For protein, a common intercept of 1.21 kg and regression coefficient of 0.70 were found, and  $R^2$  declined to 0.15 for the nine major AI organizations (Table 4). The sampling programs operated by the major AI organizations resulted in similar DYD from similar pedigrees. Our research provided no evidence of different progeny test effectiveness for different major AI organizations when similar pedigrees were sampled.

## Sampling Status Codes

Means values for sampling codes are in Table 5. The largest group of sires were the “no sampling status” group followed closely by “AI sampled.” Small numbers of bulls were reported in the “multi-herd sampled”, “other sampling status,” and “M, N, O to AI” groups. The small number of “M, N, O to AI” bulls entering major AI groups was consistent with findings of Cassell et al. (1), who reported fewer non-AI sampled bulls entering major AI organizations in the early 1980s than previous years. This trend may be due to a substantial increase in the number for bulls sampled through progeny test programs of major AI organizations (10). Numbers of daughters and herds per bull in the “bulls entering AI” groups were larger than in the “multi-herd sampled” group, an indication that AI sire analysts are acquiring bulls sampled in larger numbers of herds and daughters per bull than average multi-herd sampled bulls.

The PA was highest for “M, N, O to AI” bulls (537 kg) followed by “AI sampled” and “multi-herd sampled” bulls. Results for protein were similar. “M, N, O to AI” bulls had the highest DYD, reflecting greater selection on daughter performances following progeny testing. No other group of bulls in Table 5 was so selected on progeny performance. Meinert et al. (8) reported that when non AI sampled bulls received second-crop daughter information, a substantial drop in DYD occurred. “Multi-herd sampled” and “other sampling” groups had comparable DYD for milk and protein, despite the superior initial PA for the “multi-herd sampled” group. PA’s for milk and protein dropped for all sampling methods except “no sampling” and “M, N, O to AI” groups.

Table 6 is based on analysis using model 2. Intercepts and regression coefficients by sampling status were obtained by summing the overall intercept or coefficient with effects of each sampling status method. A common intercept of 23.02 kg for milk ( $P > 0.01$ ) was appropriate for all sampling status groups, but the slopes were different ( $P < 0.01$ ;  $R^2 = 0.44$ ). Bulls entering major AI organizations and bulls with no sampling status had coefficients closest to expectation at 1.01 and 0.97, respectively. There was a significant difference ( $P < 0.01$ ;  $R^2 = 0.48$ ) between both intercepts and slopes for protein among sampling status groups.

## Conclusions

Differences among organizations were observed in the average number of daughters per bull sampled. Average pedigree merit of bulls differed among major organizations for PA milk but not for protein. Changes in probable genetic merit following progeny test differed by organization, possibility as a result of inflated initial PA from preferential treatment or risk factors associated with pedigree selection. Apparent genetic merit declined over time except for AI preliminary bulls and herd sire sampled groups.

One overall intercept for milk fit all organizations, but there were differences among organizations in the intercept for protein and the regression of DYD on PA for both milk and protein. There was no significant difference in the intercepts or regression coefficients among the major organizations. However, the average regression was significantly less than 1 (0.70) for this highly selected group of young sires. We conclude that the sampling programs operated by the major AI organizations produced similar DYD when similar pedigrees were sampled. No one organization appears uniquely effective in locating superior gene samples among progeny tested bulls.

For sampling methods, “multi-herd sampled” and “other sampling status” groups were comparable in DYD for milk and protein, but bulls in the “multi-herd sampled” group were considerably higher in initial PA for milk and protein. PA’s for milk and protein declined for all sampling methods except the “no sampling status” and “M, N, O to AI” groups. A common intercept was appropriate for all sampling status groups, but the slopes were different for milk. There was a significant difference between both intercept and slopes for protein among sampling status groups.

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**Table 1. Characteristics of progeny test programs of different organizations using January 1995 to February 1997 USDA animal model genetic evaluations.<sup>1</sup>**

Organization or group	Number of Bulls	Number of Herds		Number of Daughters		Within organization SD			
						Milk (kg)		Protein (kg)	
		$\bar{X}$	SD	$\bar{X}$	SD	PA <sup>2</sup>	DYD <sup>3</sup>	PA <sup>2</sup>	DYD <sup>3</sup>
A	67	33	11	48	18	103	326	4	9
B	272	42	13	53	18	133	338	5	10
C	228	52	11	61	15	140	309	5	9
D	145	52	14	64	18	131	299	4	8
E	150	45	14	65	22	145	300	5	9
F	227	30	9	39	15	164	340	5	10
G	237	42	14	51	18	150	308	5	10
H	54	36	11	59	21	148	308	5	9
I	355	49	17	73	25	152	297	5	9
AI preliminary sampled	600	23	11	28	14	152	389	5	12
AI heavily sampled	51	168	87	249	150	237	308	7	9
AI privately sampled	1006	17	10	35	23	223	353	7	10
Herd sires	2846	2	3	17	9	268	322	8	10
R <sup>2</sup> for all organizations		0.78		0.62					
R <sup>2</sup> for nine major AI organizations		0.24		0.24					

<sup>1</sup> Number of daughters and herds differed significantly ( $P < 0.01$ ) among organization for all data and for a subset of the data including only nine major US AI organizations.

<sup>2</sup> Parent Average (PA) = Latest PA before first-crop daughter information became available

<sup>3</sup> Daughter Yield Deviation (DYD) = Latest DYD for the bull before second-crop daughter information became available.

**Table 2. Least square means of initial parent average and current daughter yield deviation for milk and protein using January 1995 to February 1997 USDA animal model.**

Organization or group	Number of Bulls	Milk <sup>1</sup> (kg)				Protein <sup>1</sup> (kg)			
		Initial PA <sup>2</sup>		DYD <sup>3</sup>		Initial PA <sup>2</sup>		DYD <sup>3</sup>	
		$\bar{X}$	SE	$\bar{X}$	SE	$\bar{X}$	SE	$\bar{X}$	SE
A	67	447	27	301	41	17	0.86	14	1.21
B	272	453	14	326	21	17	0.44	12	0.62
C	228	427	15	396	23	16	0.48	15	0.68
D	145	431	19	383	28	16	0.59	14	0.84
E	150	418	19	274	28	16	0.58	11	0.82
F	227	417	15	359	23	16	0.48	14	0.68
G	237	427	15	383	22	17	0.47	15	0.66
H	54	493	31	343	46	17	0.96	13	1.35
I	355	455	13	349	19	17	0.39	13	0.55
AI preliminary sampled	600	516	10	424	15	20	0.31	17	0.45
AI heavily sampled	51	533	31	380	47	20	0.99	14	1.39
AI privately sampled	1006	362	8	294	12	13	0.26	11	0.37
Herd sires	2846	120	4	118	6	5	0.13	5	0.19
R <sup>2</sup> for all organizations		0.34		0.11		0.42		0.18	
R <sup>2</sup> for nine major US AI organizations		0.01		0.01		0.01		0.02	

<sup>1</sup> PA and DYD for milk and protein differed ( $P < 0.01$ ) among organizations in all cases except for PA protein among the major AI organizations.

<sup>2</sup> Initial Parent Average (PA) = Latest PA before first-crop daughter information became available.

<sup>3</sup> Daughter Yield Deviation (DYD) = Latest DYD for the bull before second-crop daughter information becomes available.

**Table 3. Least square means for differences in initial parent average (PA) and current PA for milk and protein**

Organization or group	Number Of bulls	Change in PA <sup>1</sup>			
		Milk <sup>2</sup> (kg)		Protein <sup>2</sup> (kg)	
		$\bar{X}$	SE	$\bar{X}$	SE
A	67	34	7	0.7	0.2
B	272	18	4	0.6	0.1
C	228	7	4	-0.1	0.1
D	145	18	5	0.5	0.2
E	150	20	5	0.5	0.2
F	227	11	4	0.2	0.1
G	237	14	4	0.2	0.1
H	54	13	8	0.3	0.2
I	355	20	3	0.5	0.1
AI preliminary sampled	600	0	3	0.0	0.1
AI heavily sampled	51	39	8	1.1	0.3
AI privately sampled	1006	2	2	-0.1	0.1
Herd sires	2846	-1	1	0.0	0.0
R <sup>2</sup> for all organizations		0.03		0.02	
R <sup>2</sup> for nine major US AI organizations		0.01		0.01	

<sup>1</sup> Change in PA = Initial PA (Last PA before first-crop daughter information became available) minus Current PA (Latest PA evaluation for a bull before second-crop daughter information became available)

<sup>2</sup> Initial PA minus Current PA for milk and protein differed ( $P < 0.01$ ) among organization in all cases. Initial PA minus current PA milk and protein did not differ significantly ( $P > 0.01$ ) by major organization.

**Table 4. Prediction equation for daughter yield deviation milk and protein using last parent average prior to progeny test results.<sup>1</sup>**

Organization or group	Number of Bulls	Milk <sup>2</sup> (kg)		Protein <sup>2</sup> (kg)	
		Intercept	Coefficient	Intercept	Coefficient
A	67	-12	0.70	6.48	0.44
B	272	-43	0.82	2.18	0.58
C	228	117	0.65	5.27	0.60
D	145	106	0.64	3.61	0.61
E	150	-178	1.08	-2.10	0.80
F	227	28	0.79	3.49	0.66
G	237	-15	0.93	-0.66	0.95
H	54	232	0.23	10.03	0.15
I	355	28	0.70	1.21	0.70
AI preliminary sampled	600	19	0.78	0.51	0.81
AI heavily sampled	51	174	0.39	5.49	0.41
AI privately sampled	1006	16	0.77	1.77	0.70
Herd Sires	2846	6	0.97	0.29	0.93
All organizations		5.76	0.97	0.29	0.93
Nine major AI organizations		28.32	0.70	1.21	0.70
R <sup>2</sup> for all organizations		0.44		0.48	
R <sup>2</sup> for nine major AI organizations		0.14		0.15	

<sup>1</sup> Intercepts and regressions include overall intercept plus individual effects for each organization.

<sup>2</sup> Intercept for protein and slopes for milk and protein differed significantly ( $P < 0.01$ ) among organization for analysis of all data. For milk, the intercept for all organizations did not differ ( $P > 0.01$ ). Intercepts and slopes for milk and protein were not different ( $P > 0.01$ ) for data only from major organizations.

**Table 5. Mean characteristics of progeny test programs of different organizations using January 1995 to February 1997 USDA animal model genetic evaluations.**

Group	Number of Bulls	# of Herds <sup>1</sup>	Number of Daughters <sup>1</sup>	Milk <sup>2</sup> (kg)		Protein <sup>2</sup> (kg)		Change in PA <sup>5</sup>	
				PA <sup>3</sup>	DYD <sup>4</sup>	PA <sup>3</sup>	DYD <sup>4</sup>	Milk <sup>6</sup>	Protein <sup>6</sup>
Multi-herd sampled status	371	20	41	404	298	15	11	15	0.36
No sampling status	2846	2	18	120	119	5	5	-1	-0.04
Other sampling status	387	12	30	336	290	12	11	4	0.07
M,N,O to AI	41	23	45	537	545	20	21	-14	-0.54
AI sampling status	2594	39	53	447	360	17	14	10	0.16
R <sup>2</sup> for sampling status		0.47	0.24	0.33	0.11	0.40	0.16	0.01	0.01

<sup>1</sup> Number of daughters and herds differed significantly ( $P < 0.01$ ) among organization for all bulls.

<sup>2</sup> PA and DYD for milk and protein differed ( $P < 0.01$ ) among sampling status.

<sup>3</sup> Initial Parent Average (PA) = Latest PA before first-crop daughter information became available.

<sup>4</sup> Daughter Yield Deviation (DYD) = Latest DYD for the bull before second-crop daughter information became available.

<sup>5</sup> Change in PA = Initial PA minus current PA (Latest PA evaluation before 2<sup>nd</sup> crop daughters information become available).

<sup>6</sup> Initial PA minus Current PA for milk and protein differed ( $P < 0.01$ ) among sampling status.

**Table 6. Prediction equations for daughter yield deviation milk and protein using last parent average prior to progeny test results.<sup>1</sup>**

Sampling status	Number Of bulls	Milk <sup>2</sup> ( kg)		Protein <sup>2</sup> (kg)	
		Intercept	Coefficient	Intercept	Coefficient
Multi-herd sampled status	371	-29.64	0.81	0.37	0.74
No sampling status	2846	5.82	0.97	0.30	0.93
Other sampling status	387	55.86	0.70	3.10	0.62
M,N,O to AI	41	4.47	1.01	5.42	0.77
Stud sampling status	2594	23.02	0.75	1.74	0.71
R <sup>2</sup> for all sampling status		0.44		0.48	

<sup>1</sup> Intercepts and regressions include overall intercept plus individual effects for each organization.

<sup>2</sup> Intercept for protein and slopes for milk and protein differed significantly ( $P < 0.01$ ) by sampling status. For milk, the intercept for sampling status did not differ ( $P > 0.01$ ).

# **Comparisons of cows and herds in two progeny test programs and two corresponding states.**

## **Abstract**

Data were USDA genetic evaluations on cows and DHI herd profiles from 4154 Holstein progeny test herds from two AI studs, 21st Century Genetics and Genex, and 6361 additional herds from Minnesota and New York. We grouped herds into four locations, 21st Century Genetics, other Minnesota herds, Genex progeny test herds, and other New York herds. Herds contributing fewer than 10 cows with genetic evaluations and records from cows with birth dates from January 1989 to March 1995 were eliminated. Data included 83% and 74%, respectively, of first-crop daughters of 21st Century Genetics and Genex progeny test bulls with genetic evaluations from January 1995 to February 1997. Herds were characterized by DHI profile and cow evaluation data. Daughters of progeny test bulls with extreme daughter performance relative to pedigree merit of the bull were identified but did not appear in disproportionate numbers among progeny of bulls likely to be culled or considered for further uses. The two semen marketing organizations appear to have selected the larger, genetically superior and better managed herds from within their respective regions for progeny testing purposes. We were not able to predict whether a bull was going to exceed or fail to meet pedigree prediction from characteristics of the progeny test herds in which he was sampled. The differences between the parent average and daughter yield deviations for typical young sires appear to result from Mendelian segregation of genes.

## **Introduction**

The dairy cow population in the United States declined to less than 10 million for the first time in modern history during the 1990's (6). Even with a decline in the dairy population, the average amount of milk produced has progressively increased (6), due in part to rapid genetic progress for milk production (12). AI organizations have helped to accelerate genetic progress by increasing the number of bulls sampled from 857 in 1980 to 1526 in 1995 (7), and in the process helped reduce the number of cows necessary to produce the equivalent amount of milk. Reduction in the cow population increased competition among AI organizations for semen sales and top quality herds in which to progeny test young sires.

AI organizations make conscious decisions balancing the rate of genetic gain with net returns from semen sales (1). Rate of genetic gain is maximized by sampling many bulls with 57 to 61 daughters per bull (1). Genetic gain increases as the number of bulls sampled and the size of progeny groups increases, but at a diminishing rate (1, 4). The optimal size of progeny groups from Dekkers et al. (1) was larger than previous studies, (4, 10, 11) which reported optimal size between 30 and 50 daughters per bull. Net returns from semen sales which equals returns from semen sales minus cost of sampling would be maximized with 95 to 110 daughters per bull. The increase in daughters per bull would reduce the number of bulls sampled in a fixed population (1). For many AI organizations, sampling programs are a compromise between maximizing the rate of genetic improvement and net returns from semen sales.

A possible solution to the compromise between maximizing the rate of genetic improvement and net returns from semen sales is to increase the number of herds for progeny



testing. As a result, more bulls could be sampled and progeny group sizes increased. However, herds already participating in AI progeny test programs have an average percentage of usable records of 77% in 1991 for official DHIA test plans (7). The percentage of usable records in all official test plans was 64% in 1990 (7). Therefore, due to lower sire identification more semen would need to be distributed into non participating herds to produce a lactating daughter. Such expansion would add to costs and possibly reduce net returns. Our purpose was to compare herds in two current progeny test programs to other herds in their respective regions and to evaluate the possibility of improving those programs by elimination of existing herds and/or addition of new herds. A further objective was to study the effect of progeny test daughters and their corresponding herds on the genetic evaluation of young sires.

## **Materials and Methods**

We examined progeny test herds from two AI organizations, 21<sup>st</sup> Century Genetics and Genex. 21<sup>st</sup> Century Genetics supplied 2968 Holstein herd codes and Genex provided 1444 Holstein herd codes from herds enrolled in their respective progeny test programs. Individual cow records and DHI herd profile data were obtained from USDA Animal Improvement Programs Laboratory. Genetic evaluations of Holstein young sires were from one of five USDA animal model evaluations (January 1995 to February 1997). Herd codes from 21<sup>st</sup> Century Genetics included 218 herds with no genetic information compared to 44 such herds for Genex. The number of herds that had herd profiles, an indication the herds were still in business, but no cows with genetic evaluations were 161 for 21<sup>st</sup> Century Genetics and 24 for Genex. Lack of genetic evaluations from these herds may indicate lack of identification or possibly a change in type of test to a program unacceptable for genetic evaluations (14). Individual cow and DHI herd profile data were obtained from all remaining Holstein herds in Minnesota and New York. These states were selected because of the predominance of herds from these states in the two progeny test programs.

We grouped herds into four locations, 21<sup>st</sup> Century Genetics, Minnesota non progeny test herds, Genex progeny test herds and New York non progeny test herds. Herds were eliminated from the study if they contributed fewer than 10 cows with genetic evaluations for cows with birth dates from January 1989 to March 1995. Our data did not include all first-crop daughters of bulls progeny tested by the two studs during the time covered by the study. The percentages of daughters of young sires from 21<sup>st</sup> Century Genetics and Genex that were present in our data are shown in Table 1. Percentage of young sire daughters in data used in the study was somewhat higher at 83% for 21<sup>st</sup> Century Genetics than 74% for Genex. Possibly Genex only supplied current progeny test herds, which could be one reason for the difference. Also, Genex may not have as strict a policy on distribution of young sire semen only to progeny test herds. Finally, number of cattle bought and sold between herds may be different among the regions.

Characteristics of progeny test and other herds were determined by three methods. First, herd means from all cows with individual genetic evaluations formed a herd history. A second related method used means of cows freshening within the most recent year of test for each herd with the herd required to be on test for at least a year. A third method used yearly DHI herd summary information provided to USDA by regional records processing centers. These three methods of characterizing the herds were merged onto each cow's individual record.

Differences in characteristics of cows and their herds between locations were measured using the model 1:

$$Y_{ij} = \mu + L_i + e_{ij} \quad [1]$$

where  $Y_{ij}$  is the cows of herd characteristics of the  $j$ th cow or herd in the  $i$ th location and location is determined by the progeny test program or state where the cow or herd is located.

Holstein bulls progeny tested by 21<sup>st</sup> Century Genetics and Genex with DYD from USDA animal model evaluations between January 1995 to February 1997 were used to study the impact of progeny test herds on results of pedigree selection. The parent average (PA) from the genetic evaluation prior to daughters performance data minus his most recent daughter yield deviation (DYD) prior to any second-crop daughter data was calculated for each bull. The 20% of bulls with the largest negative difference were placed in the group of top 20% bulls. A negative difference means that DYD exceeded PA, a desirable result. The middle 60% of the bulls were grouped together and the remaining 20% of bulls with the largest positive difference were put in the bottom 20% group of bulls. Each young sire's group was merged into his daughters' individual record.

Differences in characteristics of cows and their herds between groups of young sires (top 20%, middle 60%, bottom 20%) for DYD compared to PA were measured using model 2:

$$Y_{ijk} = \mu + G_i + S_j(G_i) + e_{ijk} \quad [2]$$

where  $Y_{ijk}$  is the characteristic of  $k$ th cow or herd by (or affecting the proof of) the  $j$ th sire in the  $i$ th group where group is defined by performance of each sire's progeny relative to his pedigree merit. Tests of significance for differences between groups were performed.

## Results and Discussion

Table 2 shows the average number of cows per herd with genetic evaluations within the last year of test compared with DHI herd profile information by state. Progeny test programs at 21<sup>st</sup> Century Genetics and Genex included herds from many states but with no duplication in states. Minnesota and Wisconsin accounted for 85% of the herds contributing to genetic evaluations for 21<sup>st</sup> Century Genetics, New York and Pennsylvania 76% of the herds contributing to genetic evaluations of Genex's sampling programs.

For both 21<sup>st</sup> Century Genetics and Genex, not all cows in the progeny test herds had genetic evaluations. Even though a cow was considered completely identified in the DHI herd profile, she had a 35% probability of being rejected from genetic evaluations for reasons other than sire, dam, and (or) birth date not reported (9). Other possible reasons for rejection may include animals birth date conflicting with information for maternal sister, sire or dam conflicts with existing information, and animal birth dates conflicting with existing information. Cows that did not freshen within the last year of test were excluded from our data. Herds considered as mixed herds were included as long as they produced ten Holstein cows with genetic evaluations during the time of the study. The data were from the time period when genetic evaluations were calculated twice a year. Therefore, many first lactation cows currently in the herds had no genetic evaluation. The addition of quarterly genetic evaluation will reduce the numbers without predicted transmitting abilities (PTA) for this reason. Lack of identification of daughters is still a primary reason for differences between the two estimates of herd size.

Non progeny test herds are indicated in Table 2 for each progeny test program. Non progeny test herds are indicated below the progeny test programs herds. Number of cows per herd with genetic evaluations within the last year compared with DHI herd profile for the herds by state are indicated by Table 2. Genex and 21<sup>st</sup> Century Genetics progeny test herds are larger

than non participating herds, a possible indication of the two progeny test programs selecting larger herds to sample progeny test bulls.

Comparisons of cows in progeny test herds to cows in other herds using genetic evaluations from USDA animal model and DHI data are in Table 3. Data included 486,691 Holstein cows from herds enrolled in 21<sup>st</sup> Century Genetics and Genex AI progeny test programs. An additional 495,591 cows from Minnesota and New York herds not included in progeny test herds were also included in the data. All  $R^2$  from model 1 were low, indicating that the herd groups used explained little of the variations present in the data for any of the observations. A significant difference ( $P < 0.01$ ) among groups in the percentage of animals registered was observed ( $R^2 = 0.055$ ). 21<sup>st</sup> Century Genetics and Minnesota herds had the lowest percentage of registered cows at 20% followed by Genex at 31% and remaining cows in New York with the largest percent registered at 45%. The percentage difference in cows registered between Genex and New York may be an indication of registered producers not choosing to participate in the Genex progeny test program or vice versa. Meinert et al. (7) reported 34% registration for herds participating in all United States progeny test programs. Our research indicated a drop from 7 to 9% in registration occurring from dam to daughter for all groups. Majeskie (6) also reported this downward trend in registration.

Inbreeding coefficient was significantly different ( $P < 0.01$ ) among the groups ( $R^2 = 0.004$ ). Minnesota had the highest inbreeding at 2.8% and Genex the lowest at 2.4%. Smith et al. (12) reported 1.2% average inbreeding for cows classified by the Holstein Association from 1983 to 1990. Our result was more similar to the results of Wiggans et al. (15), who reported a mean inbreeding of all Holsteins born in 1990 of 2.6%. Smith et al. (12) reported that registered cows had higher coefficients of inbreeding than grade cows. Our results were different as Minnesota herds had the highest inbreeding among the locations and the lowest registration. Larger herds had lower inbreeding in these data, perhaps due to less complete pedigree data or regional differences in inbreeding.

Parent average milk was significantly ( $P < 0.01$ ) higher for cows in the progeny test herds than the other two locations ( $R^2 = 0.024$ ), with Genex at 144 kg followed by 21<sup>st</sup> Century Genetics at 92 kg. Cows from progeny test herds were genetically superior to the remaining population. Meinert et al. (8) reported similar results with data from the Select Sires PGA program from 1979 to 1987.

Cow birth dates ( $R^2 = 0.004$ ) and sire birth dates ( $R^2 = 0.008$ ) were significantly different ( $P < 0.01$ ) among the four locations. Cows in herds in the two progeny test groups were younger and were sired by younger bulls. Age at first calving was significantly different among the four groups ( $R^2 = 0.008$ ). Genex was the only group with average first calving date less than 27 mo but as indicated by Table 6, these herds had the highest mean production level. This supported previous research by Losinger and Heinrichs (5) documenting herds with a mean age of less than 27 mo had higher milk production than operations with a mean age at first calving greater than 27 mo. Daughters calving at a younger age will result in a genetic evaluation on the sire at a younger age.

Table 4 is based on herd averages using all cows with genetic evaluations regardless of year of freshening, whereas Table 5 is based on genetic evaluations of cows freshening within the last year for each herd. Parent average and yield traits in Table 5 were higher for cows freshening within the most recent 12 month period for all groups than for the historic herd summary in Table 4. The  $R^2$  from both Tables 4 and 5 were low for all herd characteristics. The analyses

summarized in Table 5 explain more variation in four of six traits than analyses summarized in Table 4. The reason for the increase in  $R^2$  may be due to less variation in the herd characteristics for the more recent data.

Herd averages based on cows with genetic evaluations within the last year showed that parent average and yield deviation were superior to averages based on longer periods of herd history, such results in consistent with genetic trend in the Holstein breed (13).

As would be expected, more cows were sired by 21<sup>st</sup> Century Genetics and Genex young sires in progeny test herds than in the other two groups (Table 5). Frequencies of young sires from other programs are in Appendix Table A. A difference ( $P < 0.01$ ) between 21<sup>st</sup> Century and Genex ( $R^2 = 0.237$ ) was found through orthogonal contrasts but no difference in young sire usage between the non progeny test herds in the two states was found. Significant differences among the groups remained when all young sires from all studs were included in the calculation ( $R^2 = 0.055$ ). The number of young sires used per herd increased when young sires' daughters from any stud were included. This is consistent with Meinert et al. (7) who reported fifteen percent of herds participating in progeny testing used young sires from more than one progeny test program.

Herd averages in Table 6 are based on characteristics of the DHI herd profile information from the most recent year of DHI testing. Higher rolling herd averages were reported in New York than in Minnesota. Rolling herd average milk was significantly ( $P < 0.01$ ) different among all groups ( $R^2 = 0.018$ ). Orthogonal contrasts showed no significant difference in rolling herd average between the two progeny test programs. Progeny test herds had higher rolling herd averages compared to remaining herds. Our results agree with Losinger and Heinrichs (5) who reported higher rolling herd averages for the Northeast than the Midwest.

For a cow to be considered identified in the DHIA percent identified calculation (Table 6), she is required to have a valid identification, sire identification and birth date. Cows indicated as completely identified for a herd still has the possibility of being rejected from genetic evaluations if other conflicts occur in the record. A cow has a 35% probability of being rejected from genetic evaluations for other reasons even with sire, dam, and birth date reported (9).

Table 6 shows average herd size to be considerable larger than in Table 5, an indication of lack of animal identification in the DHI herd profiles. Number of cows per herd was significantly different ( $P < 0.01$ ) among the groups ( $R^2 = 0.024$ ). Percentage of cows in individual herds with genetic evaluations was significantly different among the groups ( $R^2 = 0.055$ ) but, non progeny test herds contributed essentially the same proportion of records useful for genetic evaluations as progeny test herds. Meinert et al. (7) reported 77% of records from progeny test herds in all major studs were usable. 21<sup>st</sup> Century Genetics herds had 67% usable records and Genex herds had 68% usable from these data. Difference from Meinert et al. (7) may have resulted from inclusion of owner sampler records in our study. Also, if a cow did not freshen soon enough for the genetic evaluations included in this study she was excluded from our data. Finally, herds including crossbred cows were included in our data as long as they produced 10 Holstein cows with genetic evaluations during the time of the study.

Comparisons of daughters of young sire using differences between parent average and daughter yield deviation for milk to categorize young sires and three standard deviations of DYD for milk above and below herd mean to categorize young sire daughters are in Table 7. Each individual cow's yield deviation was subtracted from the herd mean yield deviation and the difference was divided by the within-herd standard deviation of yield deviation to form groups of

cows, the result being cows ranked three or more standard deviations above the mean, cows in between, and cows more than three standard deviations below the mean.

Percentages of cows three standard deviations above and below would theoretically be 0.5% in each category with 99% of cows in the middle category. Elite cows three standard deviations above the mean appeared less frequently than the anticipated 0.5% in both 21<sup>st</sup> Century Genetics and Genex, but a surplus of cows three standard deviations below the mean was observed. Similar results occurred for protein as shown in Appendix Table B1.

Exceptional DYD's appeared with nearly equal frequency for young bulls in the top 20% and middle 60% which were negative as indicated by Table 7. It is possible that a few very poor daughters put bulls in the lowest 20% group, but unlikely that such daughters kept them out of the top 20% group.

Comparisons of daughters of young sires using differences between parent average and daughter yield deviation for milk to categorize young sires are in Table 8. We examined the predicted transmitting ability (PTA) for sire and dam separately. The sire's PTA milk for 21<sup>st</sup> Century Genetics ( $R^2 = 0.553$ ) and Genex ( $R^2 = 0.529$ ) daughters was significantly higher in the top 20% of bulls than in the lower categories of bulls. The same trend occurred in the PTA's of the dams of the daughters, which were higher in the top 20% of bulls, but  $R^2$  were small and differences were not large for the dam's PTA's.

The daughters of the bulls in the bottom 20% were more highly inbred than the middle and top groups for 21<sup>st</sup> Century Genetics but  $R^2$  was very low at 0.002. No significant differences occurred in the inbreeding amount among the Genex's young sire groups ( $R^2 = 0.000$ ). No significant difference ( $P > 0.01$ ) in registration for cows or their dams were observed among the categories. There was a difference in the age of the bull among the three categories. Bulls in the top 20% were significantly younger than bulls in middle and bottom categories. Results for protein were similar as shown in Appendix Table B2.

Tables 9 and 10 compare herd characteristics based on cows with genetic evaluations within the last year of test and DHI herd profile information by differences between the bull's parent average and daughter yield deviation. Low  $R^2$  may result from herds being repeated in all three categories. Genex had 505 herds with daughters in all three categories and 21<sup>st</sup> Century Genetics had 502 herds with daughters in all three categories.

Herd average yield deviation milk was not significantly different among the categories for 21<sup>st</sup> Century Genetics or Genex. Herd average parent average milk was significantly different for Genex ( $P > 0.01$ ) ( $R^2 = 0.080$ ) but not for 21<sup>st</sup> Century Genetics ( $R^2 = 0.050$ ). The lack of significance for PA and the low  $R^2$  possibly arise from the same herd average appearing in all three categories. Results in Table 8 are different as a cow's pedigree information would only affect the category to which her sire was assigned.

Number of daughters per herd were not significantly different ( $P < 0.01$ ) among the categories for 21<sup>st</sup> Century Genetics ( $R^2 = 0.047$ ) or Genex ( $R^2 = 0.056$ ). The same results occurred using in the herd profile information. Rolling herd average milk from Table 10 was not significantly different ( $P < 0.01$ ) among the categories for 21<sup>st</sup> Century Genetics. Table 9 and 10 clearly show that the herds in which a bull's daughters appear do not control ultimate daughter performance relative to pedigree. Mendelian segregation appears a much more likely explanation for his genetic merit estimated from progeny data.

## **Conclusions**

The theory required for genetic evaluation utilizing an animal model was presented by Henderson (3) in 1949. Only recently, as a result of computational advances, has the impact of Henderson's theory been realized. Our research provides circumstantial evidence of the accuracy of the current genetic evaluation system known as the animal model.

Cows in progeny test herds were younger, sired by younger bulls, had higher PA's and produced more milk than cows in non progeny test herds. 21<sup>st</sup> Century Genetics and Genex appear to have selected the larger, genetically superior and better managed herds from within their respective regions.

We were not able to predict if a bull was going to exceed or fail to meet pedigree prediction by characteristics of the progeny test herds in which he was sampled. The difference between the parent average and the daughter yield deviations for young sires appeared to result from Mendelian segregation of genes (3). Rolling herd average was not significantly different for daughters of successful or disappointing young sires. There appears to be no need for an AI organization to eliminate herds from their progeny test program due to the herds' rolling herd averages. More suitable considerations for eliminating herds from progeny test programs would be percent identification of daughters within the herd or efficient use of young sire semen. Higher producing herds may meet such requirements more often than low producing herds. The animal model appears to be calculating genetic evaluations of bull and cows uniformly using data from highly variable herd management systems.

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**Table 1. Percentage of young sire daughters present in data used in the study.**

Young sires sampled at:	Herds located in				Total
	Progeny test herds		All other herds		
	21 <sup>st</sup> Century	Genex	Minnesota	New York	
21 <sup>st</sup> Century Genetics (%)	76.6	0.2	6.5	0.2	83.5
Genex (%)	0.2	64.3	0.0	9.9	74.4

**Table 2. Number of cows per herd with genetic evaluations within the last year compared with DHI herd profile for the herd by state.**

State	21 <sup>st</sup> Century Genetics						Genex						
	Number of cows per herd with genetic evaluations within the last year			Number of cows per herd from herd profile			Number of cows per herd with genetic evaluations within the last year			Number of cows per herd from herd profile			
	Number of herds	Mean	SD	Number of herds	Mean	SD	Number of herds	Mean	SD	Number of herds	Mean	SD	
Arkansas	12	42	31	11	82	42	Alabama	2	91	91	2	156	120
Illinois	7	34	19	5	81	47	Arizona	3	2087	864	3	4213	2400
Iowa	193	45	51	141	90	90	Connecticut	44	112	82	38	191	162
Kansas	26	41	32	25	83	46	Delaware	5	153	113	5	264	214
Michigan	17	44	92	14	92	37	Louisiana	13	80	46	12	125	60
Minnesota	1341	48	80	1239	80	83	Maine	57	71	54	45	114	91
Non PT Herds	2917	37	28	2033	71	56	Maryland	24	76	34	22	126	70
Missouri	61	47	34	51	98	62	Massachusetts	25	75	40	24	110	51
Nebraska	34	50	41	28	100	72	Mississippi	4	132	67	4	219	79
North Dakota	7	44	34	3	203	218	New Hampshire	25	79	45	23	107	58
Oklahoma	3	54	44	3	106	63	New York	687	78	79	572	135	146
South Dakota	18	50	40	18	112	91	Non PT herds	2767	52	59	1810	103	120
Texas	6	274	182	5	601	196	Ohio	4	118	64	4	190	83
Wisconsin	806	54	38	756	94	95	Pennsylvania	364	63	55	334	92	71
							Vermont	131	68	62	118	114	100
100% ID in herd profile	470	51	26	473	59	31		256	74	58	256	90	73

**Table 3. Comparison of cows with genetic evaluations in progeny test herds to cows in other herds.**

	Progeny test herds		All other herds		R <sup>2</sup>
	21st Century	Genex	Minnesota	New York	
Number of cows	268770	217921	220720	274871	
Cows Registered (%)*	20	31	20	45	0.055
Dams of cows registered (%)*	27	39	27	54	0.056
Inbreeding (%)*	2.7	2.4	2.8	2.6	0.004
Age at first freshening (mo)*	27.9	26.8	28.6	27.9	0.008
Parent average milk (kg)*	92	144	47	62	0.024
Yield deviation milk (kg)*	25	189	-81	7	0.006
Parent average protein (kg)*	3	4	2	2	0.018
Yield deviation protein (kg)*	2	4	-2	0	0.004
Cows birth date*	10/17/91	11/10/91	07/27/91	08/29/91	0.004
Sire birth date*	09/27/84	11/20/84	03/10/84	03/13/84	0.008

\*Significant differences between groups ( $P < 0.01$ )

**Table 4. Characteristics of herds based on all cows with genetic evaluations.**

	Progeny test herds		All other herds		R <sup>2</sup>
	21st Century	Genex	Minnesota	New York	
Number of herds	2532	1390	3021	2849	
Number of cows per herd *	105	157	73	96	0.043
Herd average registration (%)*	18	30	17	41	0.081
Herd average parent average milk (kg)*	81	126	26	29	0.103
Herd average yield deviation milk (kg)*	1	140	-125	-67	0.088
Herd average parent average protein (kg)*	3	3	1	1	0.108
Herd average yield deviation protein (kg)*	1	3	-3	-3	0.078

\*Significant differences between groups ( $P < 0.01$ )

**Table 5. Characteristics of herds based on cows with genetic evaluations freshening within the last year for the herd.**

	Progeny test herds		All other herds		
	21st Century	Genex	Minnesota	New York	R <sup>2</sup>
Number of herds	2532	1390	2917	2767	
Number of cows per herd *	50	79	36	52	0.044
Herd average registration (%)*	18	30	18	41	0.076
Herd average parent average milk (kg)*	134	179	67	67	0.117
Herd average yield deviation milk (kg)*	316	407	137	135	0.099
Herd average parent average protein (kg)*	5	5	2	2	0.132
Herd average yield deviation protein (kg)*	11	11	5	4	0.109
Percent of cows sired by 21 <sup>st</sup> and Genex young sires <sup>1</sup> (%)*	7	10	1	1	0.237
Percent of cows sired by young sires from any stud <sup>2</sup> (%)*	10	13	5	5	0.094

\* Significant differences between groups ( $P < 0.01$ )

<sup>1</sup> Young sire identity was from Vierhout et al. (15). Numerators are based on 21<sup>st</sup> Century and Genex young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

<sup>2</sup> Young sire identity was from Vierhout et al. (15). Numerators are based all young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

**Table 6. Characteristics of herds based on DHI herd profile information.**

	Progeny test herds		All other herds		R <sup>2</sup>
	21st Century	Genex	Minnesota	New York	
Number of herd profiles	2300	1201	2033	1810	
Number of cows per herd*	87	132	71	104	0.024
Percent identified <sup>1</sup> (%)*	81	85	78	84	0.013
Rolling herd average milk (kg)*	8875	8890	8449	8587	0.018
Rolling herd average protein (kg)*	286	283	271	274	0.020
Percent of cows sired by 21 <sup>st</sup> and Genex young sires <sup>2</sup> (%)*	5	7	1	1	0.064
Percent of cows sired by young sires from any stud <sup>3</sup> (%)*	7	9	4	4	0.217
Percent of cows in individual herds with genetic evaluations <sup>4</sup> (%)*	67	68	66	66	0.055

\* Significant differences between groups ( $P < 0.01$ )

<sup>1</sup> Total number of cows with usable identification divided by number of cows.

<sup>2</sup> Young sire identity was from Vierhout et al. (15). Numerators are based on 21<sup>st</sup> Century and Genex young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd profiles.

<sup>3</sup> Young sire identity was from Vierhout et al. (15). Numerators are based all young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd profiles.

<sup>4</sup> Numerators are based on all cows with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd

**Table 7. Frequency of daughters of young sires using differences between parent average and daughter yield deviation for milk to categorize young sires and three standard deviations of yield deviation for milk above and below herd mean to categorize cows.**

	Genex young sire daughters			Total Freq.
	Cows with YD milk 3SD Below	All other cows	Cows with YD milk 3SD Above	
	Freq.	Freq.	Freq.	
Bottom 20 percent of young bulls	25	1971	1	1997
Middle 60 percent of young bulls	65	6623	18	6706
Top 20 % of young bulls	8	1894	10	1912
<b>Total</b>	98	10488	29	10615

  

	21 <sup>st</sup> Century Genetics young sire daughters			Total Freq.
	Cows with YD milk 3SD Below	All other cows	Cows with YD milk 3SD Above	
	Freq.	Freq.	Freq.	
Bottom 20% of young bulls	28	1923	4	1955
Middle 60% of young bulls	48	5543	8	5599
Top 20% of young bulls	11	1837	10	1858
<b>Total</b>	87	9303	22	9412

**Table 8. Comparison of daughters of young sires<sup>1</sup> using difference between parent average and daughter yield deviation for milk to categorize young sires.**

Trait or Variable	Young sires <sup>1</sup> in 21 <sup>st</sup> Century Genetics: Parent average milk compared to daughter yield deviation				Young sires <sup>1</sup> in Genex: Parent average milk compared to daughter yield deviation			
	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>
Number of bulls	47	141	46		55	162	54	
Number of daughters	1951	5571	1857		2007	6712	1915	
Cows registered (%)	11	10	10	0.000	23	21	21	0.001
Dams of cows registered (%)	17	15	14	0.001	33	30	30	0.001
Inbreeding (%) <sup>†</sup>	3.03	2.94	2.81	0.002	2.58	2.55	2.58	0.000
Age at first freshening (mo)	27.1	27.2	27.1	0.000	26.1	26.3	26.0	0.001
Yield deviation milk (kg) <sup>‡g</sup>	-140	228	670	0.039	-96	330	740	0.043
Predicted transmitting ability milk sire (kg) <sup>‡g</sup>	136	399	693	0.553	92	432	695	0.529
Predicted transmitting ability milk dam (kg) <sup>g</sup>	-39	-26	-19	0.001	-13	-23	-3	0.001
Yield deviation protein (kg) <sup>‡g</sup>	1	10	22	0.031	3	12	23	0.030
Predicted transmitting ability protein sire (kg) <sup>‡g</sup>	9	16	24	0.398	8	17	24	0.390
Predicted transmitting ability protein dam (kg) <sup>g</sup>	-1.30	-1.03	-0.70	0.001	-0.97	-1.41	-0.80	0.001
Cows birth date <sup>2,g</sup>	7/14/93	7/27/93	7/21/93	0.001	9/18/93	8/13/93	10/11/93	0.016
Sire birth date <sup>2,t,g</sup>	4/24/91	5/23/91	5/24/91	0.005	6/17/91	4/28/91	07/14/91	0.029

<sup>g</sup> Significant ( $P < 0.01$ ) for Genex.

<sup>†</sup> Significant ( $P < 0.01$ ) for 21<sup>st</sup> Century Genetics.

<sup>1</sup> Young sire identity was from Vierhout et al. (15).

<sup>2</sup> Analyzed as days since January 1, 1960.



**Table 9. Comparison of herd characteristics based on cows with genetic evaluation and fresh date within the last 12 months using difference between parent average and daughter yield deviation for milk to categorize young sires<sup>1</sup>. Herd averages are repeated for each cow.**

Trait or Variable	Young sires <sup>1</sup> in 21 <sup>st</sup> Century Genetics: Parent average milk compared to daughter yield deviation				Young sires <sup>1</sup> in Genex: Parent average milk compared to daughter yield deviation			
	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>
Number of bulls	47	141	46		55	162	54	
Number of daughters	1945	5561	1855		2007	6712	1915	
Number of cows per herd	72	74	71	0.047	145	142	141	0.056
Herd average registration (%)	13	12	12	0.050	25	25	26	0.076
Herd average parent average milk (kg)	152	155	156	0.050	198	200	208	0.080
Herd average yield deviation milk (kg)	371	372	382	0.045	460	465	480	0.065
Herd average parent average protein (kg) <sup>g</sup>	6	6	6	0.054	6	6	6	0.061
Herd average yield deviation protein (kg)	13	13	14	0.048	13	13	13	0.052
Percent of cows sired by 21 <sup>st</sup> and Genex young sires <sup>2</sup> (%)	17	17	17	0.044	16	16	16	0.044
Percent of cows sired by young sires from any stud <sup>3</sup> (%)	19	20	19	0.044	19	19	19	0.046

<sup>g</sup> Significant ( $P < 0.01$ ) for Genex.

<sup>1</sup> Significant ( $P < 0.01$ ) for 21<sup>st</sup> Century Genetics.

<sup>1</sup> Young sire identity was from Vierhout et al. (15).

<sup>2</sup> Young sire identity was from Vierhout et al. (15). Numerators are based on 21<sup>st</sup> Century and Genex young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

<sup>3</sup> Young sire identity was from Vierhout et al. (15). Numerators are based all young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

**Table 10. Comparison of herd characteristics based on DHI herd profile information using difference between parent average and daughter yield deviation for milk to categorize young sires. Herd averages are repeated for each cow.**

Trait or Variable	Young sires <sup>1</sup> in 21 <sup>st</sup> Century Genetics: Parent average milk compared to daughter yield deviation				Young sires <sup>1</sup> in Genex: Parent average milk compared to daughter yield deviation			
	Bulls in Bottom 20%	All other cows	Bulls in Top 20%	R <sup>2</sup>	Bulls in Bottom 20%	All other cows	Bulls in Top 20%	R <sup>2</sup>
	Number of bulls	47	141	46		55	162	54
Number of daughters	1855	5330	1779		1853	6132	1759	
Number of cows per herd	115	117	114	0.048	228	233	236	0.064
Percent identified <sup>2</sup> (%)	84	85	83	0.035	87	87	87	0.039
Rolling herd average milk (kg)	9149	9107	9084	0.046	9052	9052	9146	0.055
Rolling herd average protein (kg)	295	293	293	0.046	287	287	290	0.051
Percent of cows sired by 21 <sup>st</sup> and Genex young sires <sup>3</sup> (%)	12	12	12	0.044	11	11	11	0.052
Percent of cows sired by young sires from any stud <sup>4</sup> (%)	14	14	14	0.042	12	13	13	0.061
Percent of cows in herd with genetic evaluations <sup>5</sup> (%)	72	72	71	0.032	68	69	69	0.045

<sup>g</sup> Significant ( $P < 0.01$ ) for Genex.

<sup>t</sup> Significant ( $P < 0.01$ ) for 21<sup>st</sup> Century Genetics.

<sup>1</sup> Young sire identity was from Vierhout et al. (15).

<sup>2</sup> Total number of cows with usable identification divided by number of cows.

<sup>3</sup> Young sire identity was from Vierhout et al. (15). Numerators are based on 21<sup>st</sup> Century and Genex young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

<sup>4</sup> Young sire identity was from Vierhout et al. (15). Numerators are based all young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

<sup>5</sup> Numerators are based on all cows with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd profiles.

## Appendix A

**Appendix A. Frequency of young sire daughters freshening within the last year of test in progeny test herds compared with other herds using all daughters with genetic evaluations.**

Organization	21st Century Genetics		Genex		Minnesota		New York	
	Frequency	% of YS	Frequency	% of YS	Frequency	% of YS	Frequency	% of YS
Noba	389	2.9	43	0.3	18	0.3	1	0.0
Select Sires	790	5.8	510	3.7	1146	17.7	738	6.6
Genex	43	0.3	9262	66.3	2	0.0	1628	14.6
Sire Power	304	2.2	362	2.6	219	3.4	857	7.7
Landmark	433	3.2	423	3.0	442	6.8	1147	10.3
Accelerated	591	4.4	221	1.6	534	8.2	659	5.9
21st Century	8222	60.7	22	0.2	757	11.7	29	0.3
Excelsior	31	0.2	44	0.3	25	0.4	26	0.2
ABS Global	839	6.2	735	5.3	1447	22.3	1405	12.6
Privately	489	3.6	790	5.7	739	11.4	1293	11.6
Herd Sires	1407	10.4	1553	11.1	1154	17.8	3344	30.1
Young sires	13,538	11.0	13,965	13.0	6,483	6.0	11,127	8.0
None Young Sires	113,708	89.0	95,839	87.0	99,052	94.0	133,406	92.0

## Appendix B

**Appendix B1. Frequency of daughters of young sires using differences between parent average and daughter yield deviation for protein to categorize young sires to young sire daughters in progeny test programs using three standard deviations of yield deviations for protein above and below herd mean to categorize cows.**

	Genex young sire daughters			
	Cows with YD protein 3SD Below	All other cows	Cows with YD protein 3SD Above	Total
	Freq.	Freq.	Freq.	Freq.
Bottom 20% of young bulls	32	2130	3	2165
Middle 60% of young bulls	54	6358	20	6432
Top 20% of young bulls	11	1993	14	2018
<b>Total</b>	97	10481	37	10615

  

	21 <sup>st</sup> Century Genetics young sire daughters			
	Cows with YD protein 3SD Below	All other cows	Cows with YD protein 3SD Above	Total
	Freq.	Freq.	Freq.	Freq.
Bottom 20% of young bulls	30	1941	2	1973
Middle 60% of young bulls	66	5652	5	5723
Top 20% of young bulls	13	1696	7	1716
<b>Total</b>	109	9289	14	9412

**Appendix B2. Comparison of daughters of young sires<sup>1</sup> using difference between parent average and daughter yield deviation for protein to categorize young sires.**

Trait or Variable	Young sires <sup>1</sup> in 21 <sup>st</sup> Century Genetics: Parent average protein compared to daughter yield deviation				Young sires <sup>1</sup> in Genex: Parent average protein compared to daughter yield deviation			
	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>
Number of bulls	47	142	45		55	162	54	
Number of young sire daughters	1969	5690	1720		2169	6445	2020	
Cows registered (%) <sup>§</sup>	10	10	10	0.000	24	22	18	0.002
Dams of cows registered (%) <sup>§</sup>	16	15	14	0.000	33	31	27	0.002
Inbreeding (%) <sup>†</sup>	3.0	2.9	2.9	0.001	2.6	2.6	2.5	0.000
Age at first freshening (mo) <sup>†</sup>	27.0	27.3	27.0	0.001	26.3	26.2	26.1	0.000
Yield deviation milk (kg) <sup>†,§</sup>	-86	226	654	0.031	-45	343	661	0.033
Predicted transmitting ability milk sire (kg) <sup>†,§</sup>	179	399	671	0.416	146	428	663	0.413
Predicted transmitting ability milk dam (kg) <sup>†,§</sup>	-30	-31	-14	0.001	-23	-19	-5	0.001
Yield deviation protein (kg) <sup>†,§</sup>	-1	10	25	0.041	1	13	23	0.039
Predicted transmitting ability protein sire (kg) <sup>†,§</sup>	8	16	25	0.508	8	17	24	0.493
Predicted transmitting ability protein dam (kg) <sup>†</sup>	-1.1	-1.1	-0.5	0.001	-1.4	-1.3	-0.9	0.000
Cows birth date <sup>2,†,§</sup>	7/29/93	7/10/93	8/31/93	0.012	8/24/93	8/25/93	9/22/93	0.003
Sire birth date <sup>2,†,§</sup>	5/13/91	5/7/91	6/28/91	0.013	5/19/91	5/10/91	6/20/91	0.007

<sup>§</sup> Significant ( $P < 0.01$ ) for Genex.

<sup>†</sup> Significant ( $P < 0.01$ ) for 21<sup>st</sup> Century Genetics.

<sup>1</sup> Young sire identity was from Vierhout et al. (15)

<sup>2</sup> Analyzed as days since January 1, 1960.

**Appendix B3. Comparison of herd characteristics based on cows with genetic evaluation and fresh date within the last 12 months using difference between parent average and daughter yield deviation for protein to categorize young sires. Herd averages are repeated for each cow.**

Trait or Variable	Young sires in 21 <sup>st</sup> Century Genetics: Parent average protein compared to daughter yield deviation				Young sires in Genex: Parent average protein compared to daughter yield deviation			
	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>	Bulls in Bottom 20%	All other bulls	Bulls in Top 20%	R <sup>2</sup>
Number of bulls	47	142	45		55	162	54	
Number of young sire daughters	1963	5683	1715		2169	6445	2020	
Number of cows per herd	73	73	73	0.47	142	143	139	0.056
Herd average registration (%)	13	12	13	0.50	27	25	24	0.076
Herd average parent average milk (kg)	155	154	155	0.50	198	200	208	0.080
Herd average yield deviation milk (kg)	378	371	375	0.045	459	466	481	0.065
Herd average parent average protein (kg) <sup>§</sup>	6	6	6	0.054	6	6	6	0.061
Herd average yield deviation protein (kg)	14	13	13	0.048	13	13	13	0.052
Percent of cows sired by 21 <sup>st</sup> and Genex young sires (%) <sup>1</sup>	17	17	17	0.044	16	16	16	0.044
Percent of cows sired by young sires from all studs (%) <sup>1</sup>	20	20	20	0.044	19	19	19	0.046

<sup>§</sup> Significant ( $P < 0.01$ ) for Genex.

<sup>1</sup> Significant ( $P < 0.01$ ) for 21<sup>st</sup> Century Genetics.

<sup>1</sup> Young sire identity was from Vierhout et al. (15). Numerators are based on 21<sup>st</sup> Century and Genex young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year

<sup>2</sup> Young sire identity was from Vierhout et al. (15). Numerators are based all young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd with genetic evaluations within the last year.

**Appendix B4. Comparison of herd characteristics based on DHI herd profile information using difference between parent average and daughter yield deviation for protein to categorize young sires. Herd averages are repeated for each cow.**

Trait or Variable	Young sires <sup>1</sup> in 21 <sup>st</sup> Century Genetics: Parent average protein compared to daughter yield deviation				Young sires <sup>1</sup> in Genex: Parent average protein compared to daughter yield deviation			
	Bulls in Bottom 20%	All other cows	Bulls in Top 20%	R <sup>2</sup>	Bulls in Bottom 20%	All other cows	Bulls in Top 20%	R <sup>2</sup>
Number of bulls	47	142	45		55	162	54	
Number of young sire daughters	1866	5438	1660		1999	5880	1865	
Number of cows per herd	115	118	117	0.000	235	234	237	0.000
Percent identified <sup>2</sup> (%) <sup>†</sup>	84	85	84	0.000	87	87	86	0.000
Rolling herd average milk (kg)	9140	9105	9129	0.000	9117	9099	9140	0.000
Rolling herd average protein (kg)	295	294	294	0.000	289	288	289	0.000
Percent of cows sired by 21 <sup>st</sup> and Genex young sires <sup>3</sup> (%)	12	12	12	0.000	11	11	11	0.000
Percent of cows sired by young sires <sup>4</sup> (%)	14	14	14	0.000	13	13	12	0.000
Percent of cows in herd with genetic evaluations <sup>5</sup> (%)	72	72	72	0.000	69	69	68	0.000

<sup>‡</sup> Significant ( $P < 0.01$ ) for Genex.

<sup>†</sup> Significant ( $P < 0.01$ ) for 21<sup>st</sup> Century Genetics

<sup>1</sup> Young sire identity was from Vierhout et al. (15).

<sup>2</sup> Total number of cows with usable identification divided by number of cows.

<sup>3</sup> Young sire identity was from Vierhout et al. (15). Numerators are based on 21<sup>st</sup> Century and Genex young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd profiles.

<sup>4</sup> Young sire identity was from Vierhout et al. (15). Numerators are based all young sire daughters with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd profiles.

<sup>5</sup> Numerators are based on all cows with genetic evaluations and a fresh date within the last year for the herd. Denominator is all cows in herd profiles.

## **Vita**

Crystal Nadine Vierhout, daughter of William and Charlotte Vierhout, was born on October 7, 1967 in Melvin, Iowa. She graduated from Sibley-Ocheyeden High School in Sibley, Iowa in May 1986. From 1967 to 1986 she was living and working with her family on a commercial Holstein farm in Melvin, Iowa. The author was involved with 4-H, FFA, music, and sports during this time period.

In August 1986 the author entered Iowa State University and received a Bachelor of Science degree in Dairy Science and Agriculture Business in December 1990. From January 1990 through September 1994, the author worked for 21<sup>st</sup> Century Genetics. In August 1995, she enrolled at Virginia Polytechnic Institute and State University and received a Master of Science degree in Dairy Science in May 1998.