Impact of different strategies and levels of preferential treatment on different methods of bull dam selection

by

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(ABSTRACT)

Three milk, fat yield and final score type records were simulated for each cow in 20 herds of 200 cows over 13 years. At completion of the simulation, cows were ranked by different selection methods and the top 2% were chosen to be bull dams. Preferential treatment was simulated by increasing milk and fat yields by 8, 16, 32, and 48% in separate copies of the simulation. Preferential treatment was given to a limited number of cows in copies of the original herds based on 8 strategies. Cows were chosen to receive preferential treatment for 2nd and 3rd records based on phenotypic records and ETA′s alone and in combination with a phenotypic minimum for final score type. Cows were also chosen to be biased in all records based on phenotypic records of dam, parent average ETA, maternal line and final score type. Bull dam selection methods compared used 2:2:1 milk:fat:type indexes of cow Predicted Transmitting Abilities (PTA), first lactation PTA, (PTA-F), PTA after requiring phenotypic minimums, (PTA-P), 3-generation Pedigree Index (PI-3) and PTA after preselection on 3-generation Pedigree Index (PI-3/PTA). Comparison criterion was average merit on a 2:.2:.1 weighting of true transmitting abilities for milk, fat and type for cows selected in each of 3 replicates of the cow population that were started with different random number seeds. Selection methods PTA and PTA-F gave the highest average true breeding values when no bias was present, and both methods were robust to bias levels of 8 and 16% mean response, and continued to give the best results at these levels for all bias patterns studied. In general, selection on PI-3 and PTA-P gave poor results and should not be considered viable selection methods. Selection ability of PTA was greatly decreased at the 32 and 48% bias levels. Selection on PTA-F continued to be effective when bias did not occur in the first lactation or when bias was based on type score, while selection on PI-3PTA was unaffected by bias at any level. Requiring a

high level of 3-generation Pedigree Index before selection on PTA appears useful for selecting bull dams when very high levels of bias are present.

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Introduction

Artificial Insemination (AI), when combined with selection, has become a powerful tool for genetic improvement of dairy cattle. AI programs for dairy cattle consist of three steps: a) selction of parents to produce sons for sampling, b) random use of a limited amount of semen from young sires to produce daughters for a progeny test evaluation and c) selection among progeny tested young sires to determine which sires will be returned to service and receive heavy use as part of the proven sires offered by the stud. The goal of the AI companies is to obtain young sires with the highest parent average possible for the traits of interest. The companies then rely on the random Mendelian sampling effect to provide a percentage of young sires with genetic values significantly higher than their parents, and on the progeny test data to correctly identify those bulls.

As progeny testing programs and genetic evaluations have become more advanced, genetic evaluations for bulls have become very accurate. The accurate ranking of bulls has made the choice of bulls to sire the next group of young bulls much easier. Although the population of dams is much larger than the population of proven sires, and offers a very high selection intensity, the accuracy of genetic evaluations is much lower and often based on parent average and few own records for most cows. Thus, selection of dams of young sires is diffucult under the best of circumstances. Because of these factors, the choice of dams to produce young sires has been implicated as the most limiting factor in genetic improvement.

There is a potential for large profits from the sale of offspring and embryos from cows of high estimated genetic merit. For this reason, breeders are suspected of giving preferential treatment to cows of high estimated genetic merit which biases the genetic evaluations and further lowers the accuracy of selection of bull dams. It is well known that the production of the dairy cow can be greatly enhanced by the husbandry practices which she receives. The development of new management tools, such as bovine somatotropin (bST), will greatly increase the ability of breeders to provide preferential treatment.

Concern over the accuracy of the genetic evaluations of potential bulls dams has lead to the consideration of alternative methods of bull dam selection. While some recommend the use of only first lactation production records in an attempt to alleviate bias, it is argued that these records may also be biased. Performance testing of dams in different nucleus herd settings have also been studied as an alternative to the progeny test system.

Many studies have attempted to measure the amount of bias present in the group of cows ranked highest for ETA. However, due to Mendelian sampling and reduced variance of selected groups, no method using field data has been developed to estimate the true decrease in selection efficiency that is caused by misranking of dams from preferential treatment.

Computer simulation offers a means to model the current dairy population and examine some of the forms of preferential treatment which are suspected and to measure the effect of different patterns and levels of bias. Bull dam selection methods can then be compared for their ability to withstand different biases.

The primary objective of the study was to determine how different patterns of preferential treatment or bias applied within all herds affect the accuracy of different methods of bull dam selection. A secondary objective is to quantify the amount of bias needed to significantly affect selection decisions by simulating different levels of preferential treatment.

Review of Literature

Genetic progress has long been recognized as a means to improve the efficiency of milk production in dairy cattle. Since selection is the basis for genetic progress, much research has been devoted to methods which improve the efficiency of selection of individuals that produce the next generation.

Estimates for Genetic Gain

Rendel and Robertson (25) examined the problems in measuring genetic gain and put forth a method to estimate genetic gain from the selection applied. They saw the genetic improvement, (I), due to selection as occurring through four pathways:

- Selection of bulls to sire the next generation of bulls (I_{BB})
- Selection of bulls to sire the next generation of cows (I_{BC})
- Selection of cows to produce the next generation of bulls (I_{CB})

- Selection of cows to produce the next generation of cows (I_{CC}).

Further, they demonstrated that the total genetic gain per year equalled the sum of the genetic improvement of animals from each of the four pathways divided by the sum of the generation intervals of the paths. Cow and bull survivability and productive life estimates were then assumed as the average values of the time so that a theoretical value for genetic improvement in a closed system could be calculated.

Using young sires in 60% of the herd was considered optimum for closed systems (25). In a closed population of 10,000 cows, the genetic improvement per year would be expected to be 2.05% of the phenotypic average. Of this improvement, the relative contribution of each path is: I_{BB} 43%, I_{BC} 18%, I_{CB} 33% and I_{CC} 6%. The large percent gain from the sire pathways was credited to the increased reproductive potential of bulls through the use of artificial insemination (AI).

Reasons for the less than theoretical genetic progress for milk production have been investigated by several workers. Van Vleck (33) used the method of Robertson and Rendel to conclude that a genetic gain of 2.05% of the phenotypic average per year was possible, although a greater percent of the total progress could be attributed to the bull to sire cow path, due to an increase in the services per sire. Genetic trends for cow and sire groups in the Northeast U.S. from 1961-74 were presented by Van Vleck (33) to show that actual genetic progress in the U.S. population is much lower than that predicted possible. This was contrasted by results from studies of institutional herds by Freeman (9), Richardson and Bearden (26) and Wilk, et al. (42) where response to selection was equal to or greater than that predicted by differences in estimated breeding values.

Selection for nonproduction traits, increased generation interval and decreased selection intensities were thought to have decreased the actual progress made in the U.S. (33). Also proposed was the over-reliance by bull studs on later records of potential bull dams. In addition to increasing generation interval, the later records by these potential bull dams were thought to be biased upward by preferential treatment.

Alternatively, Meuwissen (16) has suggested that the theoretical rates of genetic improvement are over-estimated. The reduction in genetic variance over time, due to selection, has not been accounted for in many estimates. As shown by Bulmer (2), the decrease in genetic variance would be expected to be significant under the traditional progeny test setting because of the high accuracies of the selections.

Selection of Young Sires

Efficient selection of young sires is often cited as the most limiting factor in overall genetic improvement (33,18), and hence is often studied. In a symposium on young sire selecion for commercial AI, Henderson (11) presented several alternative selection policies and the expected gains of each. Since the choice of sires to breed sires is limited and often clear cut, it was held constant in all alternatives. It was shown that after having sires chosen, reasonable genetic gains could be made simply by choosing the dams of sires at random, but more efficient choices seemed logical. The dam was recommended to be out of a sire with a high estimated breeding value, as well as having high deviations in her own records. It was also recommended as many cows as possible be evaluated before selecting only a small percentage to insure the highest selection intensity possible.

Further, the large amount of variation in young sire true breeding values, given the estimates, was thought to necessitate sampling large numbers of sires with high estimated breeding values each year to achieve the desired results. This was due to the low accuracy of the estimated breeding values, since even if the young sires had large amounts of information from ancestors and sibs, the standard deviation of the Mendelian sampling effect would still be over two-thirds that of the additive genetic standard deviation.

To find the proper weighting of information from various relatives in choosing young sires, many researchers have used the regression of proven sires' progeny test predicted difference (PD) value on relatives in his pedigree. Van Vleck and Carter (35) predicted son's estimated daughter superiority from the daughters of his sire, recors of his dam and daughters of his maternal grand sire (MGS). Evaluation of records from American Breeders Service and Eastern AI Cooperative bulls found poor agreement between theoretical and empirical regression coefficients for relatives. There were differences between studs for both sire actual weights (.40 versus .85) and MGS actual weights (.57 versus .10), while both studs differed from the theoretical weights (.66 for sire and .22 for MGS). Dam's records had a much smaller actual coefficient for both studs (.03 and .05) than predicted by theory (.12). Inclusion of dam's records did not significantly add to the R^2 value of the equation predicting progeny test ETA of son. This did not necessarily mean dam's records are not important, as the average for both studs was quite high, but rather differences among highly selected dams were not important.

Van Vleck also studied the relative selection efficiency of the selection methods of Eastern AI Cooperative in choosing young sires to be sampled (32). It was found that the most efficient index of the potential six sources of pedigree information available used records of the young sire's paternal sisters (sire's PD), dam and paternal sisters of the dam (MGS's PD) in predicting the daughter superiority of the young sire.

The addition of records on the young sire's maternal sisters, dam's maternal sisters and maternal grandam lowered the net efficiency of selection, while the records on paternal sisters of the young sire accounted for 45-50% of the total daughter superiority. Results indictated that the selection methods of the stud had an under-emphasis of the sire's proof and over-emphasis of the dam's and grandam's records. It was rationalized that the stud had more opportunity for selection on the maternal side of the pedigrees of prospective young sires.

Vinson and Freeman (37) found that including the dam with sire in a midparent index gave only a slightly higher R^2 (.22 vs. .20) than regression on sire's PD alone. It should be noted that in the study the sire's regression coefficient was significantly less than that predicted by theory (.40 vs. .87), indicating bias in the proofs of the sires. Dams were found to have an excessively long generation interval, with the average age of dam at time of birth of son being 7 to 8 years.

Improvements in the computation of sire proofs has greatly increased the accuracy of prediction of breeding value over the years and aided selection. However, Rothschild (28) found that models for predicting son's modified contemporary deviation and modified contemporary comparison were similar. When predicting son's MCD or MCC milk ($R^2 = .31$) and fat ($R^2 = .24$) proofs, the sire's PD, MGS's PD and dam's cow index (CI), respectfully, were the most important variables, with addition of more records to dam's CI having little effect. However, when predicting son's PD for fat percent, dam was of more value than the PD of MGS with R^2 also increasing with the number of records used from the dam.

Van Raden et al. (31) analyzed the pedigrees of Select Sires, Inc. bulls to determine the best predictor of son's genetic evaluation from progeny. Sire's PD, dam's CI and MGS's PD gave the best R^2 with coeficients of .408, .153 and .161, respectively. Although the addition of MGS's PD after dam's CI was significant, the converse was not. Also, CI overestimated the genetic value of the population of bull dams. One explanation suggested was that these dams had preferential treatment, which biased their records.

More recently, Ferris and Wiggans (8) and Samuelson and co-workers (29) examined predicting son's Daughter Yield Deviation (DYD) from animal model parent evaluations. Ferris and Wiggans (8) found that the coefficients were below that predicted by theory for PTA of sire, dam and MGS. Although the coefficient for PTA of dam was less than that of sire when in the same model (.36 vs. .41), neither the coefficients or prediction ability were changed with the addition of MGS to the model. Further, when used with PTA of sire, models using PTA of dam and yield deviation of dam both had larger R^2 values than the model with the PTA's of sire and MGS (.22 and .19 vs .14).

Samuelson et al. (29) also found that the coefficients for all relatives were decreased below theoretical values and that the parent average was a better predictor of son's DYD than pedigree index. It was also found that prediction ability increased as accuracy of the son's DYD increased for all predictors (PTA of sire, parent average and Pedigree Index) except PTA of dam. Although it is unclear why prediction from dam did not also increase with accuracy of the DYD of the son, it would seem clear that both studies show an increase in the predictive ability of dam's information over that shown by Van Raden et al. (31).

Funk and Hansen (10) studied the use of two, three and four generation pedigree indexes (PI) for use in predicting genetic merit of unproven sires. In the study of Eastern AI Cooperative sires, the standard deviation of three and four generation PI were greater than that of two generation PI. Accounting for the differences in maternal great-grandsire (MGGS) through the use of three generation PI gave a significant increase in prediction of progeny test ETA of son over two generation PI. Because inclusion of maternal great-great-grandsire (MGGGS) was not significant, it was concluded that three generation PI's may have advantages for selection over conventional two generation indexes.

Use of Dam for Prediction

Due to the improvements in sire evaluation accuracy, the usefulness of maternal records for prediction of son's progeny test proof has been questioned. Butcher and Legates (4) examined several combinations of information from relatives for estimating the true breeding value of AI sires. The theoretical expectations of correlations to breeding value of son followed closely those observed for most sources of information except dam's later lactations. The highest correlation (R^2 =.48) to son's progeny test breeding value was for the index using the sire's PD and the dam's CI based on her first lactation and her sire's PD. Dam's later records were found to be of no value in predicting son's PD, with similar results observed in non-AI bulls.

McCraw and co-workers (13) found that including dam's average deviation in the index gave a higher correlation to son's PD than using PI based on only sire and MGS PD's ($R^2 =$ .37 vs. .32 for milk, .33 vs. .30 for fat-corrected milk). The index included an average of 4.6 records per dam and did over-estimate son's PD and resulted in a negative intercept.

Miller (17), in a symposium on genetic improvement, suggested that there is strong positive assortative mating practiced on high index cattle, even as virgin heifers. This has resulted in a shortened generation interval for the selection of young sires because a potential bull dam will often have a bull calf by a suitable sire by the end of her first lactation. But as a consequence of the earlier identification of potential, the dam's first lactation record may be biased due to preferential treatment. Therefore Miller suggests that all lactations on potential bull dams be ignored when making selections.

Mocquot (18) concluded with Miller (17) that dam-son is the path with the most opportunity for improvement and reviewed several options to conventional young sire selection. Nucleus herd schemes are often suggested as an alternative to conventional progeny testing because these settings would allow for unbiased measurement of several traits. However, it was noted by Mocquot (18) that many factors such as variable numbers of offspring per donor and the effect of inbreeding need to be examined more closely to conclude if nucleus herd settings could provide an economically feasible alternative to progeny testing.

A second method proposed is to purchase bull calves from selected heifers with a high PI (18). After one lactation a second selection would be made to keep the top 1/4 of the bulls based on the dam's first lactation performance. Although theoretical genetic gain is 8-25% greater than conventional methods, largely due to decreased generation interval, this scheme is limited by the fact that the dams may receive preferential treatment in the first lactation since they have been identified as bull dams. Also, because of the lower repeatability and greater costs associated with this type of selection, it was considered optimal to also purchase bulls from older dams in the more conventional method.

Computer simulation has long been recognized as a very useful tool for modeling the genetics of a population. Recently, Burnside and Meyer (3) examined the potential effects of bovine Somatotropin (bST) on sire evaluations. An estimated 15-20% increase in milk yield due to treatment with bST was used in examing the effects of different schemes of within herd application. The researchers concluded that the non-random allocation of bST within herds could be used to systematically bias sire proofs and commented that the effect of nonrandom allocation would have a much greater impact on cow evaluations. This is usually the case, because cow evaluations are much less robust against unidentified environmental enhancers.

Prediction of Daughter's Performance

The studies of the prediction ability of dam's information have not been limited to sons. Deaton and McGilliard (5) designed a selection index to combine information on the milk production of a cow and her close relatives for prediction of milk production of a daughter. Following development, the index was empirically tested by application to a new population of cows with similar information available. It was found that paternal half sisters and daughters could substantially improve the accuracy of estimating the genetic value of a cow. The correlation to the deviation of the first record of an unselected daughter was used as a measure of accuracy in comparing predictors. For this measure, the index of paternal half sisters and daughters gave a 19% increase in accuracy ($r = .166$ versus .140) over using the cow's own phenotypic value. The dam's records and records from maternal sisters added little to the accuracy of the cow's estimate.

McGilliard and Freeman (14) evaluated the usefulness of estimated average transmitting ability (EATA) of cows to predict daughter's first lactation deviated milk yield. The study found a correlation of .18 (vs. expected of .20) between dam's index and daughter deviated yield when both animals were required to be in the same herd. The linear regression slope of 1.15 was higher than the predicted 1.00 and was inaccurate for daughters of dams with extremely high or low indexes, causing overestimation and underestimation, respectively. Deviated yield was simultaneously regressed on groups of relatives in the dam's index. The dam was found to have a larger than expected weight, while maternal grandam and dam's other daughters contributed less than expected.

Westell and Van Vleck (40) compared theoretical and observed regression coefficients of various sources of information on relatives used in prediction of a estimated transmitting ability (ETA) of heifer. The most important differences occurred for ETA of dam when it included all records versus first lactation only. Not only did including all lactations have a much lower than expected regression coefficient but the R^2 was decreased also. The possibility of preferential treatment could not be concluded to be the reason for the discrepancy. In a previous study, Westell and Van Vleck (39) had concluded that the effect of regression coefficients being much smaller was not due to inclusion of herdmates without a first record.

Regression of adjusted daughter deviation on dam's CI was also used as a measure of accuracy by Powell and Norman (22). In general the regressions tended to increase with dam repeatability and fluctuated near unity (.84 to 1.08). The correlation between CI and daughter deviation also tended to increase with dam repeatability and number of records on daughter (up to 3), although correlations were not as high as expected.

When Holstein daughter-dam pairs were divided into 20 groups based on dam's CI, it was shown that daughter deviations from herdmates were higher than expected for the groups of dams with extremely high or low CI's. While extreme adverse health and subsequent early culling of dam for non-genetic reasons could explain the low group response, preferential treatment was assumed to be the case for the daughters of the high CI dam group. Evidence of preferential treatment is supported further by the correlation of dams and daughters in the highest group of .10. The the next highest correlation, .06, was found in the extreme low CI group, while the within group correlation was .00 in most other groups.

It was assumed that increased financial considerations of potential bull dams may cause preferential treatment of high CI cows and their daughters and subsequently bias their evaluations (22). The authors suggest that the weighting of data should be done differently for prediction of merit of sons than for prediction of merit of daughters.

Accuracy of Prediction from Different Lactations

The effect of lowered accuracy of prediction of genetic merit with increasing lactation number (4,28,40) has been extensively studied. Powell and Norman (21) found that first lactation has been overemphasized in its predictive ability. When predicting daughter modified contemporary deviation (MCD) for different lactations or average MCD of lifetime, first lactation of dam was most valuable only when predicting the first lactation of the daughter. Corresponding number of lactation was almost always the best predictor of a lactational MCD of the daughter, and the third lactation was the best predictor of lifetime production. Performance in each lactation was suggested to represent a separate trait rather than a repeated record. Prediction of merit of sons did not follow the same trends of lactational specificity, as the first lactation of the dam was the best predictor of all lactations in daughters of the son. Preferential treatment after the first lactation was assumed to be the reason for the lack of prediction for later records of bull dams.

A similar study by Murphy et al. (19) examined the effectiveness of ETA of dam based on first or all lactations in predicting PD of son. Sire regression weights in the model were close to expected

(.45) as were dam weights based on first lactation (.32). However, using all records on the dam for her ETA resulted in a weight of about one-third (.13) of predicted. Possible sources of explanation were examined. As for different genes controlling different lactations, a genetic correlation of only .20 would be required to explain such a large discrepancy. In a later paper, Van Vleck and Murphy (36) proposed an ETA for the dam based on her first lactation and all herdmate lactations, but it was not successful. The assumption of preferential treatment of potential bull mothers was reinforced by the trend of average ETA of dams based on first lactation (+ 157 kg) to increase over 100 kg when based on later lactations for the same cows (+ 259 kg). It was therefore recommended for bull studs to use ETA for the dams based on first lactation herdmates until evidence for alternative schemes are presented.

Materials and Methods

The Simulation Language for Alternative Modeling (SLAM II) simulation package, supplemented with Fortran subroutines, was used to perform a Monte Carlo simulation. Three milk and fat yield records and three type conformation scores per cow were simulated in 20 herds of 200 cows over 13 years, with the simulation of the cow population being replicated 3 times by using different seeds for the random number generator. The initial population of 267 base generation animals in each herd was uniformly divided into calves, yearlings and first and second lactation cows. Although no pedigree information was generated for base population, a genetic trend constant 86 kg of milk per year was added to the breeding values of all but second lactation cows to simulate moderate selection. Thus, calves, yearlings and first lactation animals had average breeding values of 258, 172 and 86 kg, respectively.

Random standard normal N(0,1) deviates and the additive genetic standard deviations listed in Table 1 were used to generate breeding values. The type conformation score was uncorrelated to the two other traits so that the breeding values for type and milk were generated by simply multiplying the random numbers for each trait by the corresponding genetic standard deviation. The genetic correlation of .70 between milk and fat yield was imposed in the initial generation by simulating the fat yield breeding value with the following formula:

$$BV_{fat} = [R_{milk} \times r_{GG} \times \sigma_{AF}] + [R_{fat} \times \sigma_{AF} \times \sqrt{1 - (r_{GG})^2}\,] \qquad [1]$$

where:

R_{milk} = N(0,1) Random deviate for milk yield breeding value

r_{GG} = Genetic correlation between milk and fat yield

σ_{AF} = Additive genetic standard deviation for fat yield

R_{fat} = N (0,1) Random deviate for fat yield breeding value

For later generations, Mendelian sampling effects were incorporated into the creation of breeding values for the milk and final score traits in the following manner:

$$BV_{off} = (BV_{dam} + BV_{sire}) \times .5 + R_{MS} \times \sigma_A \times .707 \qquad [2]$$

where:

BV_{off} = Breeding value of the offspring for milk or final score

BV_{dam} = Breeding value of the dam for milk or final score

BV_{sire} = Breeding value of the sire for milk or final score

R_{MS} = N(0,1) random deviate for the Mendelian sampling effect
of the offspring for milk or final score

σ_A = Additive genetic standard deviation for milk or final score

To continue the genetic correlation between the milk and fat traits in later generations, the Mendelian sampling term for fat yield was correlated to the Mendelian sampling term for milk yield. Thus, the breeding value for fat was generated as:

$$BV_{offfat} = (BV_{damfat} + BV_{sirefat}) \times .5 + [(R_{MSmilk} \times r_{GG}) + (R_{MSfat} \times \sqrt{1 - (r_{GG})^2}\,)] \times \sigma_A \qquad [3]$$

where:

BV_{offfat} = Breeding value of the offspring for fat yield

BV_{damfat} = Breeding value of the dam for fat yield

$BV_{sirefat}$ = Breeding value of the sire for fat yield

R_{MSmilk} = N(0,1) Random deviate for the Mendelian sampling effect

Table 1. Values assumed for genetic and environmental parameters in simulation.[1]

Parameter	Trait Milk	Fat	Type
Additive genetic SD (σ_A)	567[2,3]	27.7[2,3]	1.87[4]
Permanent environment SD (σ_{PE})	567[2,3]	27.7[2,3]	2.15[8]
Temporary environment SD (σ_{TE})	803[2,3]	32.1[2,3]	1.87[8]
Permatent Herd SD (σ_{PH})	622[2,4]	24.9[2,4]	1.18[6]
Temporary Herd SD (σ_{TH})	254[2,4]	10.2[2,4]	0.76[6]
Population Mean	8626[6]	309[6]	80[5]

[1] Units for values given are in kg for milk and fat and points for type score.

[2] From Meinert et al. (14).

[3] From Maijala and Hanna. (11).

[4] From Bereskin and Freeman (1).

[5] From C.D. Smothers (19).

[6] From Vinson et al. (27).

[7] From Wiggans and VanRaden (30).

[8] From R.E. Pearson (personal communication).

of the offspring for the milk yield

$R_{MS_{fat}}$ = N(0,1) random deviate for the Mendelian sampling effect of the offspring for fat yield

An AI bull population was simulated by generating breeding values of each trait for 100,000 bulls in the same manner as for the first generation females. Rather than simulating a progeny test proof, a normally distributed error of prediction component was added to the true breeding value to produce an estimated breeding value (EBV) of 75% reliability, where reliability is defined as the squared correlation between true and estimated breeding values, for each trait as:

$$\text{EBV} = \text{BV} \times .75 + \sqrt{1-.75} \times \sqrt{.75} \times R_{E1} \times \sigma_A \qquad [4]$$

where:

.75 = The squared correlation of true and estimated breeding value

R_{E1} = N(0,1) random deviate for the 75% reliability error term

σ_A = Genetic standard deviation for the trait

The environmental correlation, r_{EE}, of .94 between milk and fat was used in place of r_{GG} in equation [3] to correlate the milk and fat estimated breeding value error terms in the EBV's. Observed and predicted parameters for the simulated population of 100,000 bulls are shown in Table 2.

The resulting simulated EBV were halved to obtain estimated transmitting abilities (ETA) which in turn were divided by the original additive genetic standard deviation for the trait and combined in a index with weights of 2:2:1 for milk, fat yield and type, respectively. The top 250 of the bulls ranked on the index of progeny test ETA's were then selected for the AI population. Selection of the top .25% approximated the selection of one out of every eight progeny tested sires which in turn have been previously selected from the top 2% of the population.

For subsequent years of the simulation, the top 10,000 bulls on this 2:2:1 index rank were also kept. Genetic trend values equal to 1.3% and 1.0% of the phenotypic mean for milk and fat, respectively

Table 2. Predicted and observed parameters of 75% accuracy ETA of the unselected A.I. bull population.

Parameter[1]	Predicted Value[2]	Observed Value
$\sigma_{\hat{I}}$	3.36	3.35
σ_{I}	3.82	3.82
σ_{ETAM}	245.52	244.66
σ_{TTAM}	283.50	282.73
σ_{ETAF}	9.82	9.81
σ_{TTAF}	11.34	11.34
σ_{ETAT}	.81	.81
σ_{TTAT}	.94	.94
$\sigma_{ETAM,TTAM}$	60,279.63	59,951.86
$\sigma_{ETAF,TTAF}$	96.44	96.49
$\sigma_{ETAT,TTAT}$	.66	.66
$\sigma_{ETAM,ETAF}$	1829.84	1820.61
$\sigma_{TTAM,TTAF}$	2250.42	2243.99
$\sigma_{ETAM,TTAF}$	1687.82	1680.32
$\sigma_{ETAM,\hat{I}}$	747.98	742.43
$\sigma_{TTAM,\hat{I}}$	722.93	718.76
$\sigma_{ETAF,\hat{I}}$	29.92	29.76
$\sigma_{TTAF,\hat{I}}$	28.92	28.85
$\sigma_{ETAT,\hat{I}}$	.70	.70
$\sigma_{TTAT,\hat{I}}$	.70	.71
$\rho_{ETAM,TTAM}$	.87	.87
$\rho_{ETAF,TTAF}$	.87	.87
$\rho_{ETAT,TTAT}$	.87	.87
$\rho_{\hat{I},I}$	.85	.85

[1] I refers to the 2:2:1 weighting of milk (M), fat (F) and type (T) True Transmitting Abilities (TTA's) and $\hat{I}$ refers to the 2:2:1 weighting of Estimated Transmitting Abilities (ETA's)

[2] Units for values given are in kg for milk and fat, points for type and standardized units for the index.

and .1 points for type score were added to the true breeding values of all bulls each year. New errors of prediction were generated for the 10,000 bulls that were kept from the first year and the top 250 bulls were selected to create AI bull populations each year for years 2 through 13.

The high selection intensity applied in choosing the AI bulls resulted in a population which had means and (co)variances much different than that of the original population. Table 3 contains the predicted and observed parameters of the 250 AI bulls, with the derivation of the predictions outlined in Appendix 1.

As shown in Table 3, the resulting bull population had average estimated breeding values for milk and fat of 1357 and 54.1 kg, respectively, compared to averages of roughly 86 and 0 kg for the cow population. Constants of 636 kg milk and 22.7 kg fat were subtracted from the breeding values of all bulls to bring the average breeding values of males and females more in line with the current U.S. Holstein population.

To simulate the increase in accuracy of a bull's proof with the addition of more daughters, a second random deviate was also generated. This random deviate and the previous random deviate were then weighted by the approximate percentage of new and original progeny test daughters that would be included in the proof, Powell and Norman (23), assuming each daughter was from a different herd]. To approximate a 95% accuracy ETA for each trait, the resulting EBV was generated as:

$$\text{EBV} = \text{BV} \times .95 + [\text{R}_{\text{E1}} \times (62 \div 395) + \text{R}_{\text{E2}} \times (333 \div 395)] \times \sqrt{1 - .95} \times \sqrt{.95} \times \sigma_{\text{A}} \quad [5]$$

where:

R_{E1} = Random deviate used for simulating error term of 75% accuracy ETA

62 = Approximate number of daughters in original progeny test ETA

395 = Approximate total number of daughters in 95% accuracy ETA

R_{E2} = Random deviate used for simulating error term of 95% accuracy ETA

333 = Approximate number of new daughters in 95% accuracy ETA

Table 3. Predicted and observed parameters of 75% accuracy ETA of selected A.I. bull populations.[1]

Parameter[1]	Predicted Value[2]	Observed Value[3]
$\sigma'_{\hat{I}}$	.93	.94
σ'_{I}	1.78	2.10
σ'_{ETAM}	119.10	117.80
σ'_{TTAM}	187.34	187.02
σ'_{ETAF}	4.76	4.93
σ'_{TTAF}	7.60	7.60
σ'_{ETAT}	.78	.81
σ'_{TTAT}	.91	.93
$\rho'_{\hat{I},I}$	.41	.40
$\overline{X}'_{ETAM}$	691.47	679.07
$\overline{X}'_{TTAM}$	667.90	652.04
$\overline{X}'_{E_{MI}}$	440.04	438.88
$\overline{X}'_{ETAF}$	27.65	27.07
$\overline{X}'_{TTAF}$	26.70	26.06
$\overline{X}'_{E_{FI}}$	17.60	17.38
$\overline{X}'_{ETAT}$	.65	.71
$\overline{X}'_{TTAT}$	.65	.71
$\overline{X}'_{E_{TI}}$	.38	.40

[1] I refers to the 2:2:1 weighting of milk (M), fat (F) and type (T) True Transmitting Abilities (TTA) and $\hat{I}$ refers to the 2:2:1 weighting of Estimated Transmitting Abilities (ETA); E_{XI} is the prediction error term for the 75% accuracy ETA for trait X.

[2] Units for values given are in kg for milk and fat, points for type and standardized units for the index.

[3] Observed values are the mean of the 13 groups of A.I populations, except for the $\overline{X}'$'s which are the means from year 1 only.

.95 = Squared correlation of true and estimated breeding value

σ_A = Genetic standard deviation for the trait

The resulting means and standard deviations of the milk and type transmitting abilities are shown in Figures 1-4 for the AI bulls of each year in the simulation.

Model for Phenotypic Values

The permanent and temporary environmental effects for milk and type were standard normal N(0,1) deviates times the appropriate standard deviations given in Table 1. Permanent and temporary environmental effects for fat yield were generated using equation [1] to impose a .94 residual correlation to milk. Milk and fat records had a heritability of .25 and a repeatability of .50 between all records. The type conformation trait had a heritability of .30 and a .70 repeatability between all records.

The initial population was randomly assigned to 20 different herds at the beginning of the simulation. The herds themselves were assigned random permanent and yearly (temporary) effects similar to cows. Since no age effects were simulated for any of the traits, mature equivalent records for each trait combined all effects in the model as follows;

$$P_{ijkl} = u_i + A_{ijk} + PE_{ijk} + PH_{ik} + TH_{ikl} + TE_{ijkl} \qquad [6]$$

where:

u_i = mean of population for trait i (Table 1)

PH_{ik} = Permanent Herd effect of the kth herd for trait i.

A_{ijk} = Additive genetic value for the jth cow in the kth herd for trait i

PE_{ijk} = Permanent Environmental effect particular to the jth cow in the kth herd

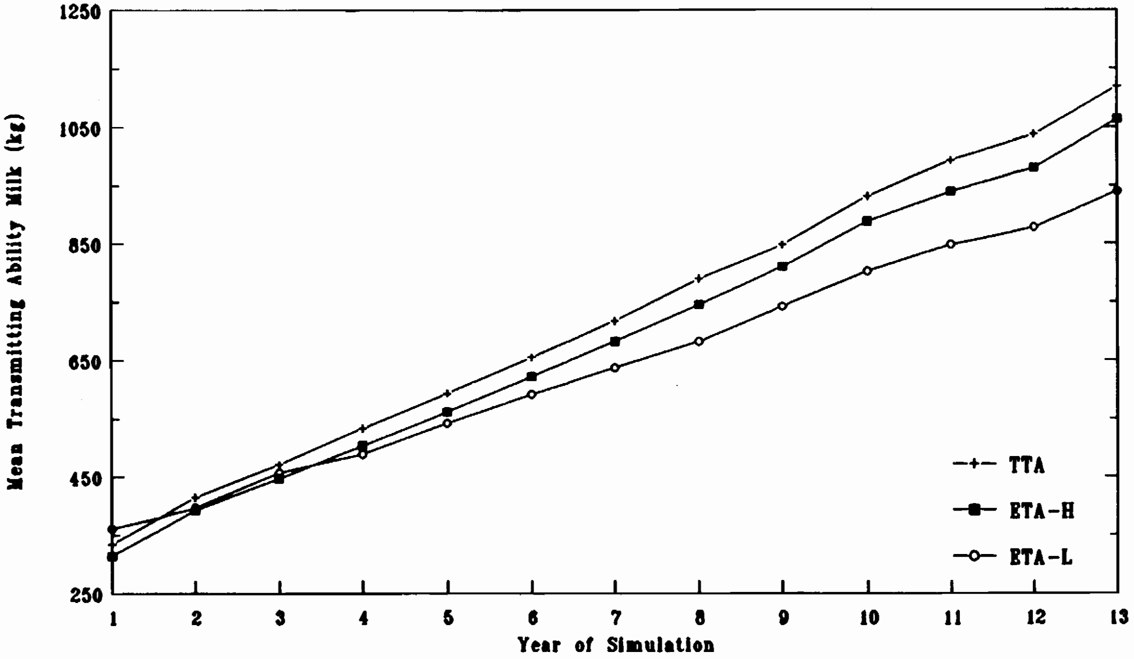

Figure 1. Mean 95% (ETA-H) and 75% accuracy (ETA-L) Estimated Transmitting Abilities and True Transmitting Ability (TTA) milk in the A.I. bulls for each year of the simulation.

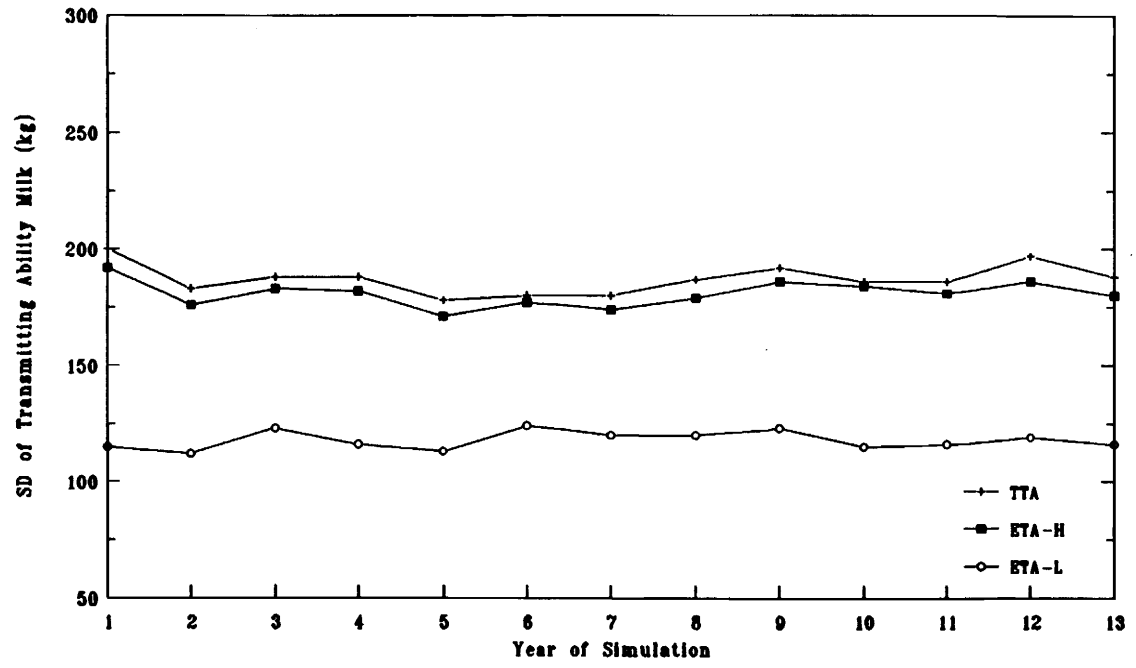

Figure 2. Standard deviation of 95% (ETA-H) and 75% accuracy (ETA-L) Estimated Transmitting Abilities and True Transmitting Ability (TTA) milk in the A.I. bulls for each year of the simulation

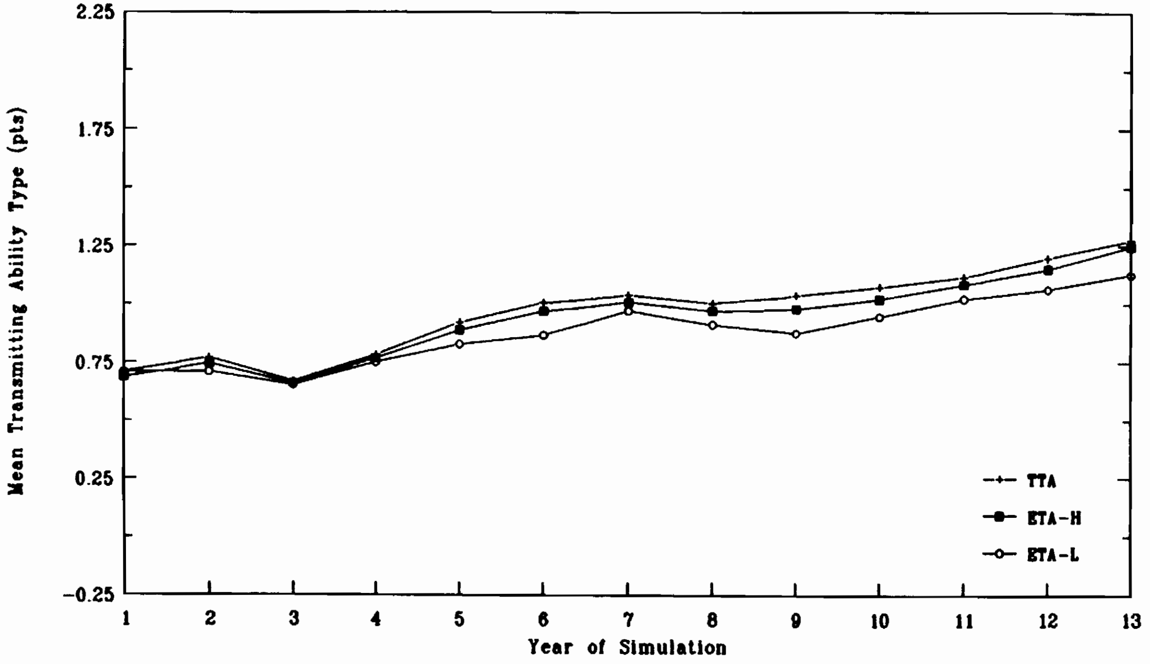

Figure 3. Mean 95% (ETA-H) and 75% accuracy (ETA-L) Estimated Transmitting Abilities and True Transmitting Ability (TTA) type in the A.I. bulls for each year of the simulation.

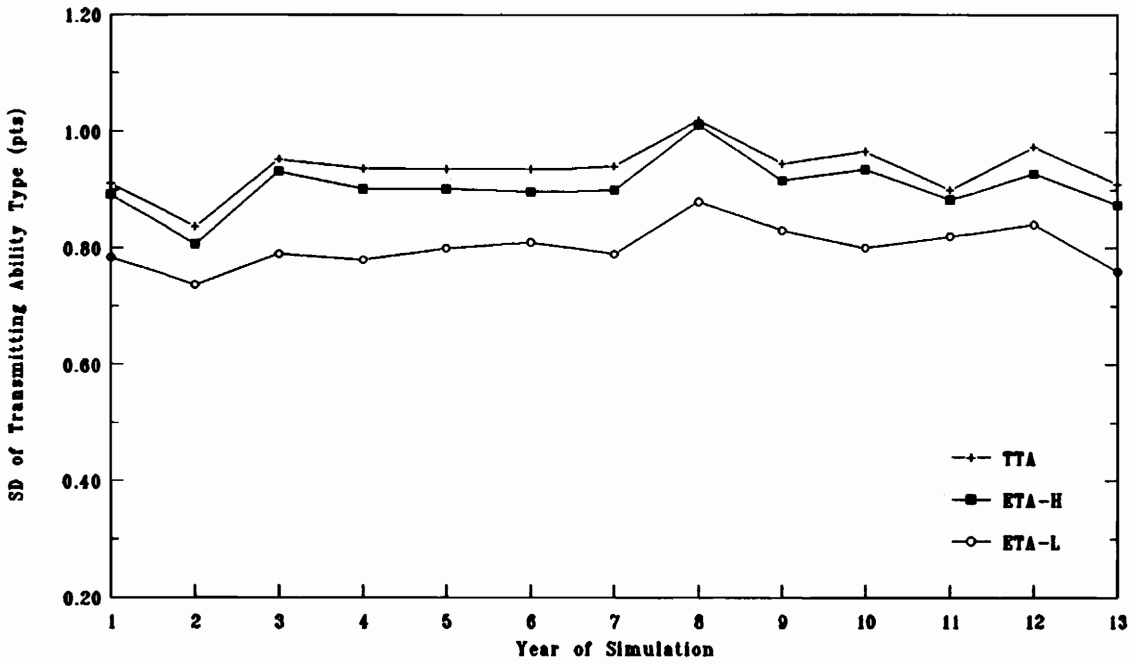

Figure 4. Standard deviation of 95% (ETA-H) and 75% accuracy (ETA-L) Estimated Transmitting Abilities and True Transmitting Ability (TTA) type in the A.I. bulls for each year of the simulation

for trait i

TH_{ikl} = Temporary Herd effect for herd k in year l for trait i.

TE_{ijkl} = Temporary Environmental effect particular to the j^{th} cow in the k^{th} herd in year l for trait i.

An error of prediction term was added to milk and fat yield records to simulate records projected from 90 days using the phenotypic correlations from Dickinson et al. (6) and the same form as that used for correlating traits in equation [1]. The 90 day records were used in genetic evaluations so that cows could be ranked for breeding each year. Since daughters in the simulation were not included in the proofs of the AI bulls, a herdmate comparison evaluation system was used to calculate cow ETA's. All cows, other than paternal half-sibs, were used as herdmates for the calculation of deviations since there were no seasonal effects, age effects or culling in the herds. The steps in calculating the deviations are outlined in Figure 5. A lookup table was used to obtain weighting factors for the average deviation and parent average in calculating the cow index. Because of the large number of herdmates, a fixed number of herdmates was assumed in using the formula of Powell et al. (23) to derive the weighting factors in the tables and the subsequent accuracy of the index.

First generation heifers were mated randomly before their first lactation. In subsequennt generations, cows and heifers were ranked within their respective herd-groups on the 2:2:1 index of milk, fat and type ETA's, calculated from 90 day records for milk and fat, and mated to a bull with rank S in the stud with the following function:

$$\begin{aligned} S &= U\,[1,(2*PR+3)*2.5] \quad \text{for } 1 < PR < 48 \\ &= U\,[1,250] \quad \text{for } 48 < PR < 49 \\ &= U\,[PR*.5-24,250] \quad \text{for } 49 < PR < 100 \end{aligned} \qquad [7]$$

where:

S = Rank of bull in the stud of 250 bulls

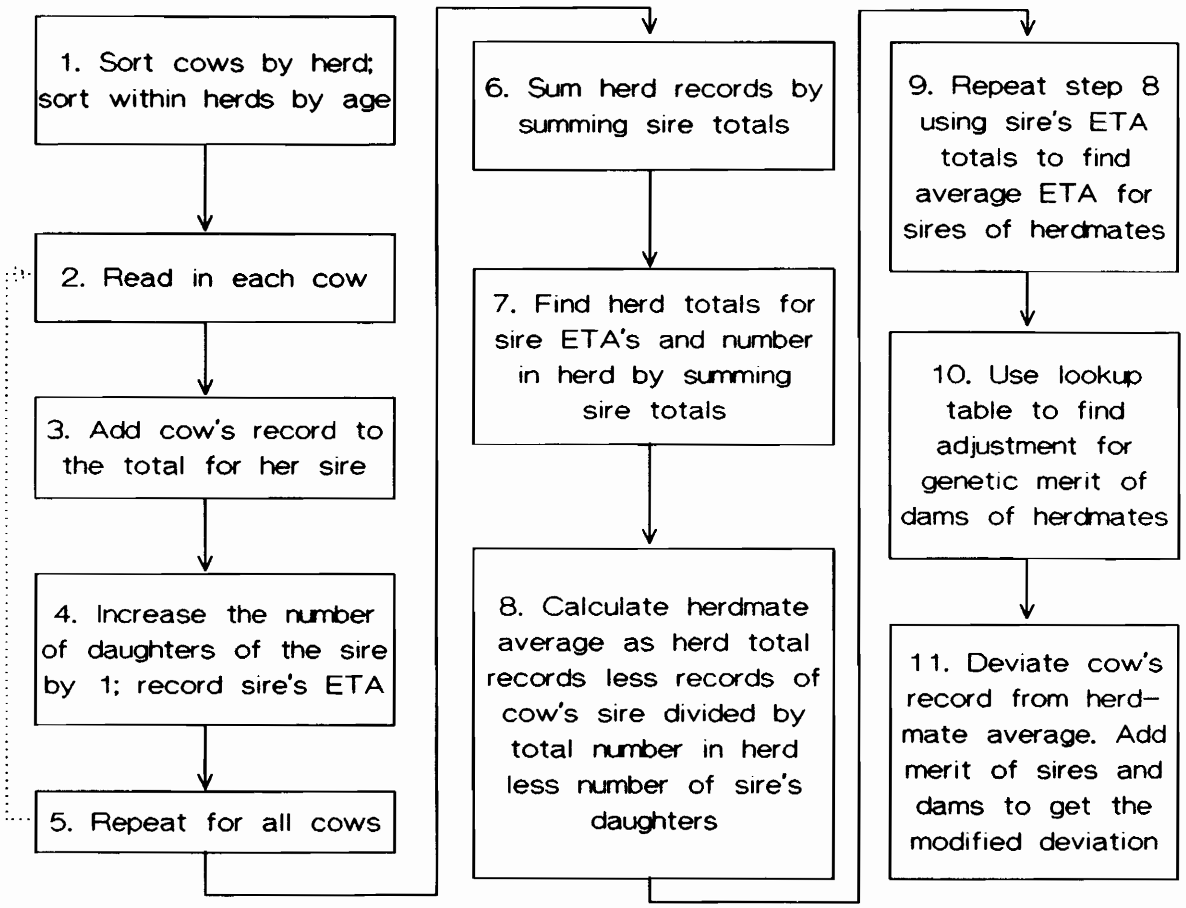

Figure 5. Flowchart showing the steps in calculating the deviations for the herdmate comparison evaluation system used for genetic evaluations.

U = Random sample from a uniform distribution

PR = Percentile rank of the cow or heifer in their herd-group

This function imposes a stronger correlation of mates for cows with higher index rankings and gave cows of decreasing rank a lower probability of being mated to the higher sires. The farther cows were ranked below the 49th percentile, the more the top sires were restricted as possible mates. Table 4 gives the the range of the uniform distribution of bulls, given by rank in stud, which would be available to some example cow herd percentile ranks.

To maintain constant herd size, all matings had a 33% probability of producing a female that would survive to enter the milking herd. All cows were culled 90 days into their third lactation, and the shortened lactations were included in the calculation of estimated transmitting abilities and herd-group rankings.

Preferential Treatment for Bull Dams

After the second lactation of the first generation, 8 different patterns of preferential treatment, which are listed in Figure 6, were applied to separate copies of the herds. The preferential treatment was simulated as a percentage increase in milk and fat records over the control (unbiased) phenotypic records for each year a cow was chosen to be biased. To keep the actual makeup of the herds identical over time, all matings were made based on the ranking of cows in the control copy.

The first 6 bias patterns biased cows if they were above a set percentile rank of the cows in the herd for that year for different measures. The percentile rank was was an attribute of the herd and was constant over all copies of the herd for all years of the simulation. The percent of the cows biased

Table 4. Range of the uniform distribution of mates available to cows of different percentile ranks in the simulation.

Cow percentile rank in herd	Range of mates available [1]
1	1- 12
10	1- 58
20	1-108
30	1-158
40	1-208
50	1-250
60	6-250
70	11-250
80	16-250
90	21-250
100	26-250

[1] Range given is a uniform distribution of rank of bull in stud

Strategy	Records biased	Criteria for bias
IRP-23	2nd and 3rd	Rank on 2:2:1 index of milk, fat and type phenotypic records.
IRP/FS82-23	2nd and 3rd	Same as Phen-LL but requires type score to be greater than 82 points.
IRP-123	all	Same as in Phen-LL, but also biased first lactation if dam was ever chosen to be biased
IRG-23	2nd and 3rd	Rank on 2:2:1 index of milk, fat and type ETA's
IRG/FS82-23	2nd and 3rd	Same as ETA-LL but requires type score to be greater than 82 points.
IRG-123	all	Same as in ETA-LL, but also bias first lactation if dam was ever chosen to be biased
Fam/FS82-123	all	Any descendent of cow biased in year 3 for Phen-P-LL with type score greater than 82 points.
IRP+/FS85-123	all	All first lactation animals scored at least 85 points, and all later lactation animals above herd average on the 2:2:1 phenotypic index and scored at least 85 points were biased. Magnitude of bias was increased as final score increased to 87 points.

Figure 6. Strategies of preferential treatment allocation studied in simulation.

for a herd ranged from 1 to 10% and was set for each herd at the beginning of the simulation and was set by sampling from a uniform distribution of random numbers ranging from 1 to 10.

Different copies of the herds were used to investigate the effect of how the different patterns of preferential treatment of potential AI young sire dams may cause misrankings of these cows. The amount of preferential treatment applied to a cow could range from faster identification of ailments to preferential use of bST. Therefore, four copies of the simulation were conducted with the different preferential treatment levels being simulated as normal with mean increases of 8, 16, 32 and 48% in the milk and fat yield records for the lactation with the standard deviation of the response being 2, 4, 8, and 12%, respectively. The different levels were chosen to determine the ability of different selection methods in tolerating bias.

In the first bias copy, cows were ranked in the herd on a 2:2:1 index of their milk, fat yield and type phenotypic records. If a cow's percentile rank in the herd on the index was equal to or higher than the herd bias percent, the cow then had a preferential treatment component added to the next record. This simulated the situation where a cow which ranks high in the herd for production is managed differently in the subsequent lactation. A second copy was operated similarily but also required that cows selected to be biased have a type score of 82 points or more in the beginning of the next record in order for the bias to occur.

A third copy biased cows as in the first bias pattern, IRP-23, but additionally biased the first lactation records of heifers out of dams which were at one time chosen to be biased. This simulated the scenario of a heifer receiving greater attention because of the high performance of her dam. Copies 4 through 6 were the same as 1 through 3 but used milk, fat and type ETA's rather then phenotypic records for the 2:2:1 index ranking.

The 7th copy used the cows biased in year 3 for copy 2 to establish cow families. For subsequent years of the simulation all of these cows and all of their descendants were biased, regardless of herd-group rank, provided that they had type scores of 82 points or greater in the beginning of the lactation. Therefore, the herd attribute of a set percentile rank of cows to be biased had no affect on this copy after the cow families were establised.

The final copy also was not affected by the set percentage of cows to be biased. This copy biased all first lactation cows with final score greater than 85 points, with all records being expressed on a mature equivialent basis, but required second and third lactation cows to also be above average on herd-group rank for the 2:2:1 index of phenotypic records to be biased. The amount of bias cows received was then correlated to type score. Cows scored 87 or higher received the full amount of bias, while those scored 86 and 85 received one-half and one standard deviation of bias less, respectively. Thus, in the simulation of 8% bias, the mean bias for cows scored 86 and 85 was approximately 7% and 6%, respectively, with bias response not allowed to become negative.

The control copy of the herds had no preferential treatment components added so that the ranking of cows represented the ideal situation and served as a basis for comparison.

At the completion of the simulation, the cows selected to be bull dams in each copy (top 2% of all cows on the 2:2:1 index ranking of milk, fat and type traits) were compared to the cows selected in the control copy. Different bull dam selection policies are listed in Figure 7 and were compared on the effectiveness of each policy at the different levels and types of bias. The first selection policy was the index of cow ETA's calculated from year 13 completed production records, which is labeled PTA to distinguish bull dam selection from the selection of cows to be biased. Other selection policies included selection on cow's first lactation PTA (PTA-F) and requiring minimum values for the cow's year 13 phenotypic type score and complete lactation fat percent before selection on PTA (PTA-P).

The fourth method used was selection on the 2:2:1 index of three generation Pedigree Indexes of the milk, fat and type traits and is labeled PI-3. Selction on PI-3 would be free of any biases due to preferential treatment since the ranking of potential bull dams is not affected by the production on the maternal line of the dams. The final selection method involved selecting the top 4% of the

Policy	Selection criteria
PTA	2:2:1 index of milk, fat and type PTA's
PTA-F	2:2:1 index of milk, fat and type first lactation PTA's
PTA-P	2:2:1 index of milk, fat and type PTA's and phenotypic minimums of 85 points type score and 3.58 percent fat.
PI-3	2:2:1 index of 3-generation Pedigree Indexes for milk, fat and type.
PI-3/PTA	2:2:1 index of milk, fat and type PTA's after having preselected top 4% of cows on PI-3

Figure 7. Bull dam selection policies compared for tolerance to preferential treatment.

cows on PI-3 and then re-ranking them on PTA to select the top half and is labeled PI-3/PTA. Both PI-3/PTA and PTA-F were attempts to limit the impact of preferential treatment while still allowing cow's performance to have input to the selection process.

Selection policies were compared based on the average true breeding value of the 80 cows selected in each of the 3 replicates for each of the bias copies in the simulation at each level of bias. Comparison of selection method means at increasing levels of bias were used to test for tolerance to level of bias.

Results and Discussion

Evaluation of Simulated Populations

Figures 8-11 show the change over time in the means and standard deviations of the transmitting abilities for the milk and type conformational traits for the cows in the control copy. As expected the increase in average transmitting abilities for the cow population followed that of the AI sires (Figures 1 and 3) closely. The change in true transmitting ability for years 6 thru 13 averaged 61 kg and 2.0 kg for milk and fat, and .07 points of type per year. This compared to the trends of 64 kg and 1.7 kg for milk and fat, and .05 points in the AI bull population.

The standard deviation of cow ETA increased in years 4-6 due to the heterogeneity of base and first generation cows, and steadily in all other years due to increasing accuracy of the ETA's. However, true genetic standard deviation for milk in the cow population was gradually reduced by the lower genetic standard deviation of the highly selected AI bull population. This reduction in variance was expected, as predicted by taking the variance of equation [2] (assuming no covariance between sire and dam breeding values) as:

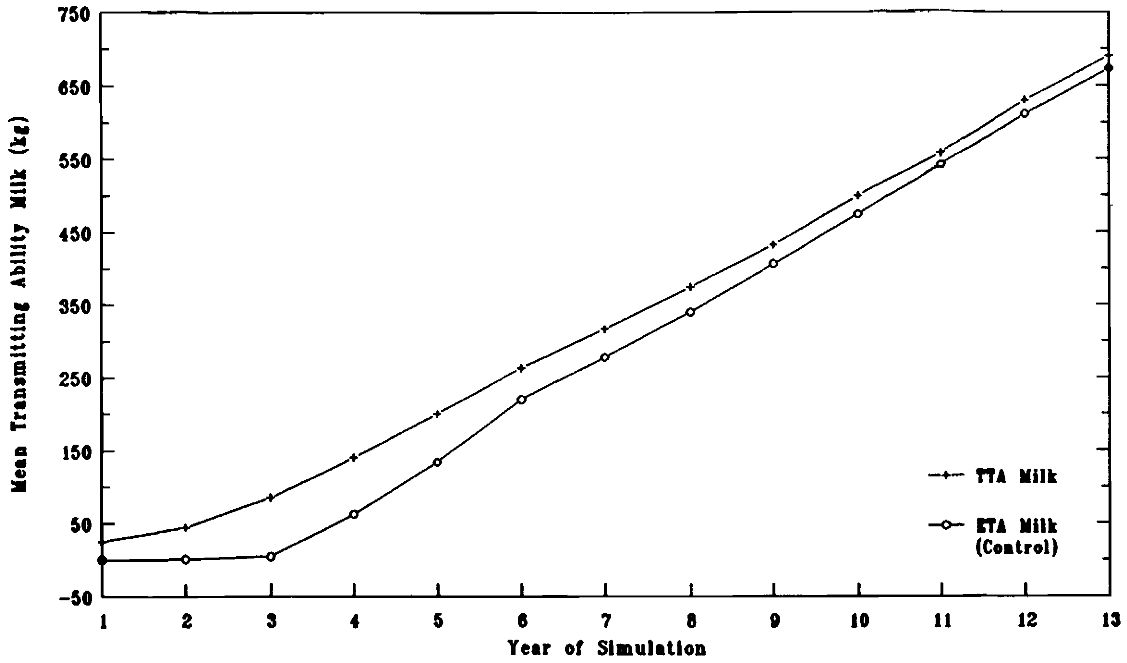

Figure 8. Change in the mean True Transmitting Ability (TTA) and Estimated Transmitting (ETA) milk for the control copy over the simulation.

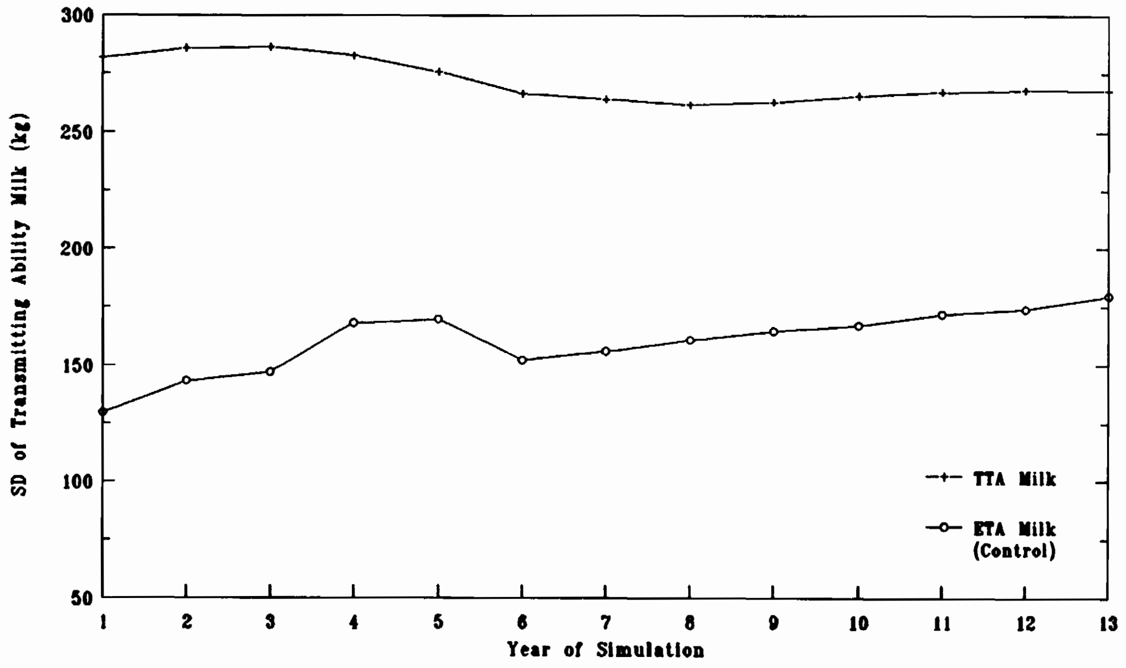

Figure 9. Change in the standard deviation of True Transmitting Ability (TTA) and Estimated Transmitting (ETA) milk for the control copy over the simulation.

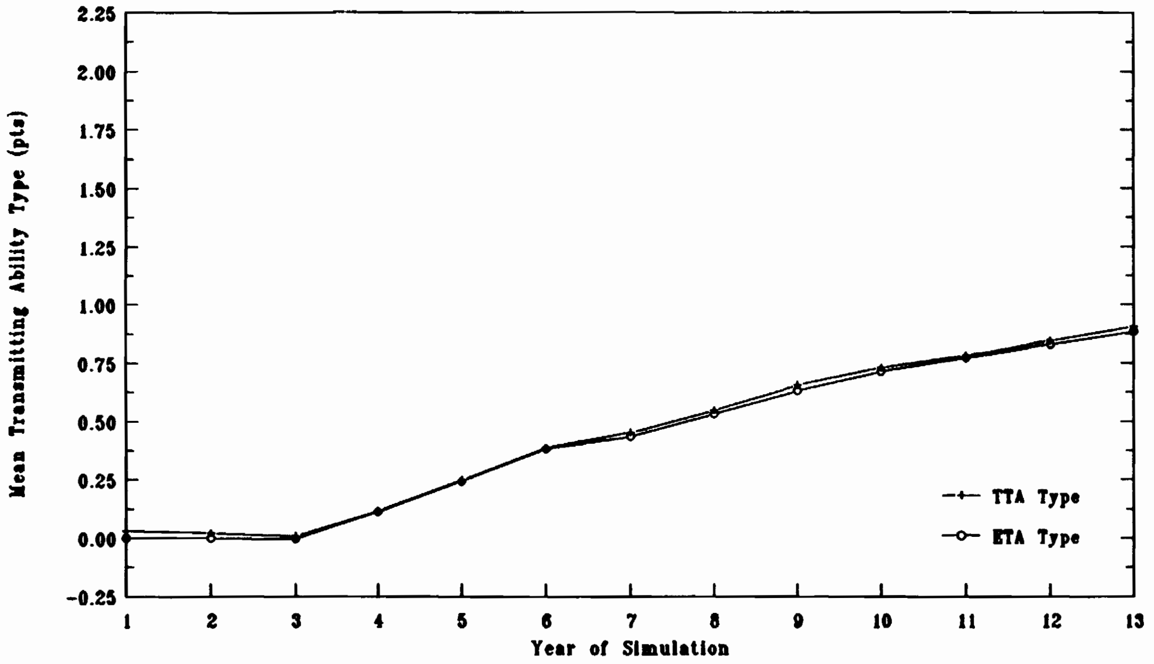

Figure 10. Change in the mean True Transmitting Ability (TTA) and Estimated Transmitting (ETA) type for the control copy over the simulation.

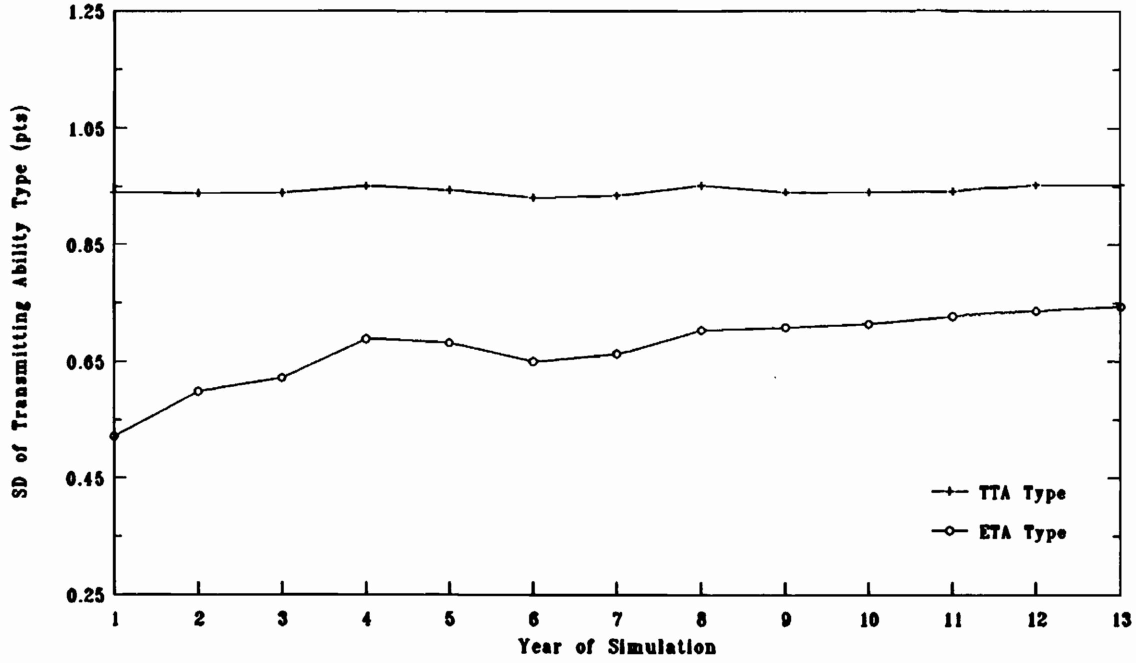

Figure 11. Change in the standard deviations of True Transmitting Ability (TTA) and Estimated Transmitting (ETA) type for the control copy over the simulation.

$$\sigma^2_{BV_{off}} = (\sigma^2_{BV_{dams}} \times .25) + (\sigma^2_{BV_{sires}} \times .25) + (\sigma^2_A \times .5) \qquad [8]$$

where:

$\sigma^2_{BV_{off}}$ = Resulting additive genetic variance for offspring population

$\sigma^2_{BV_{dams}}$ = Additive genetic variance for dam population

$\sigma^2_{BV_{sires}}$ = Additive genetic variance for sire population (= 44% of σ^2_Aformilk)

σ^2_A = Additive genetic variance

If equation [8] is carried out for many generations of random mating, with dams being replaced by the offspring, the static state genetic variance would be equal to the weighted mean of the variances for the sires and the Mendelian sampling term. For milk, where sire additive variance is reduced to 44% of σ^2_A, the genetic variance of the offspring would be reduced over time to 81% of the original variance. While similar results were seen for fat yield, type was not expected to change since the standard deviation in the AI population was not significantly reduced by selection (Table 3).

However, equation [8] assumes there was no covariance between sire and dam breeding values, which was not the case in the simulation. The positive assortative mating imposed by the mating function, equation [7], would be expected to partially counter the reduction in genetic variance. This may be reason for the non-linearity of the change in genetic variance over time and apparent stabilization at 90% of original variance.

Trends in the within herd standard deviation for phenotypic records (Figures 12-16) and cow ETA's (Figures 17-21) over the 13 years of the simulation are presented for 5 of the patterns of bias for all levels of bias. The increase in within-herd standard deviations were examined as potential indicators of bias. Copies where bias was based on ETA were nearly identical to those based on phenotypic records and are not included. The within herd standard deviation in the control copy is also included in each figure as a basis for comparison.

Phenotypic standard deviation was inflated less than 7% for any of the bias copies at the 8 and 16% levels of bias (Figures 12-16). The within-herd standard deviation was increased by the greatest

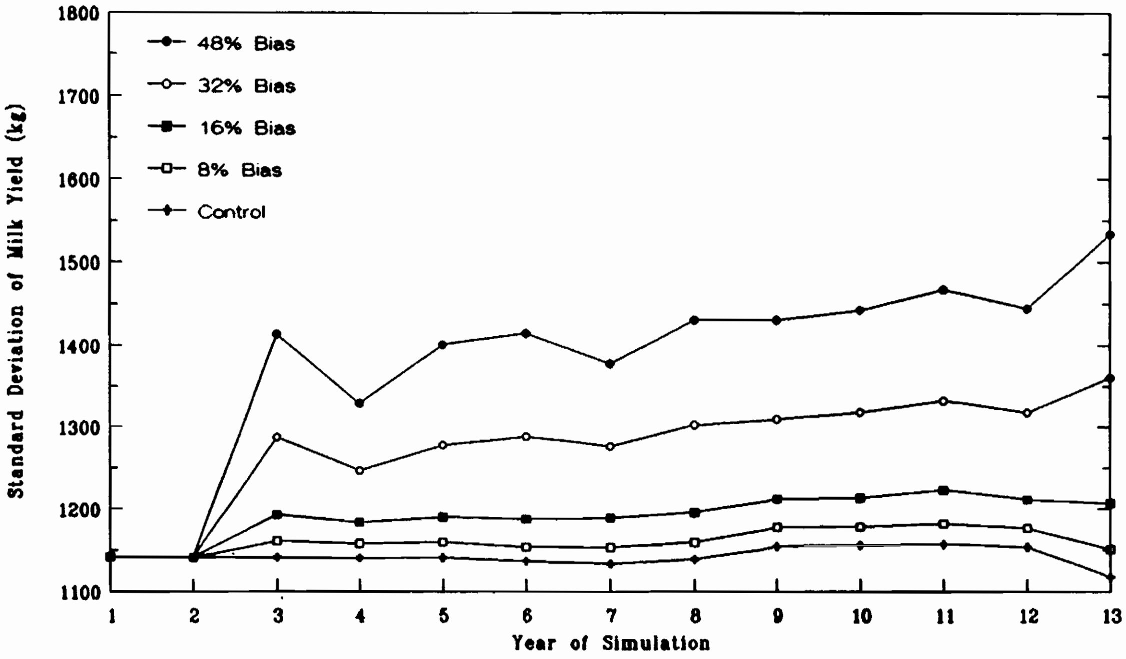

Figure 12. Change in SD of milk records over time when cows are biased in 2nd and 3rd records based on herd rank on 2:2:1 index of milk, fat and type phenotypic records.

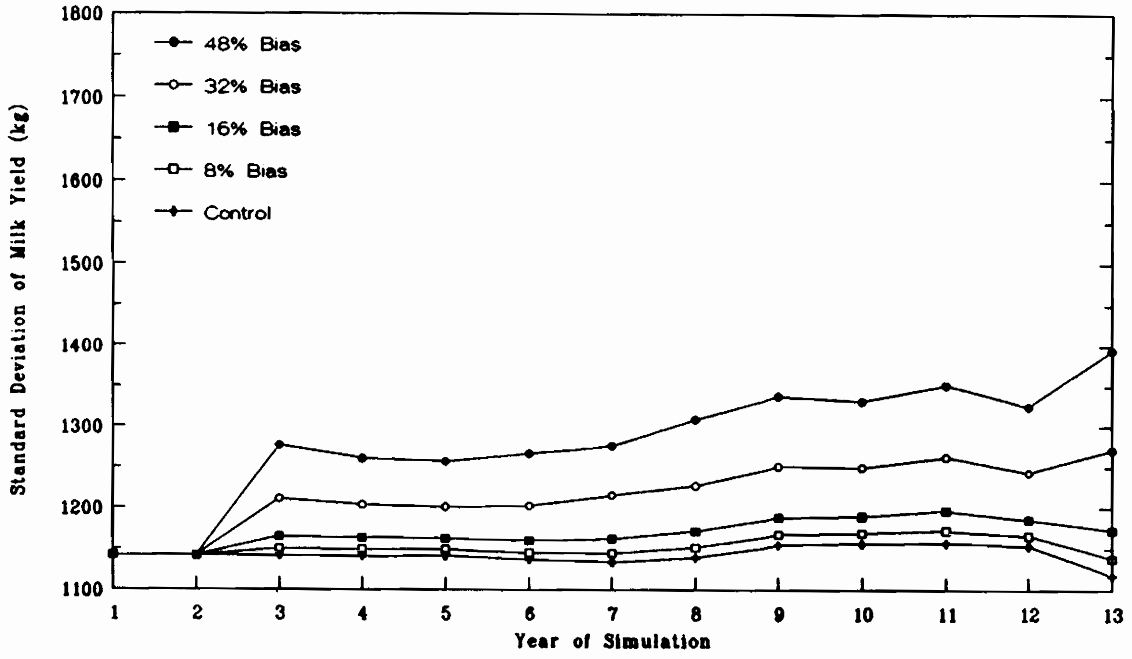

Figure 13. Change in SD of milk records over time when cows are biased in 2nd and 3rd records based on herd rank on 2:2:1 index of milk, fat and type phenotypic records and final score type.

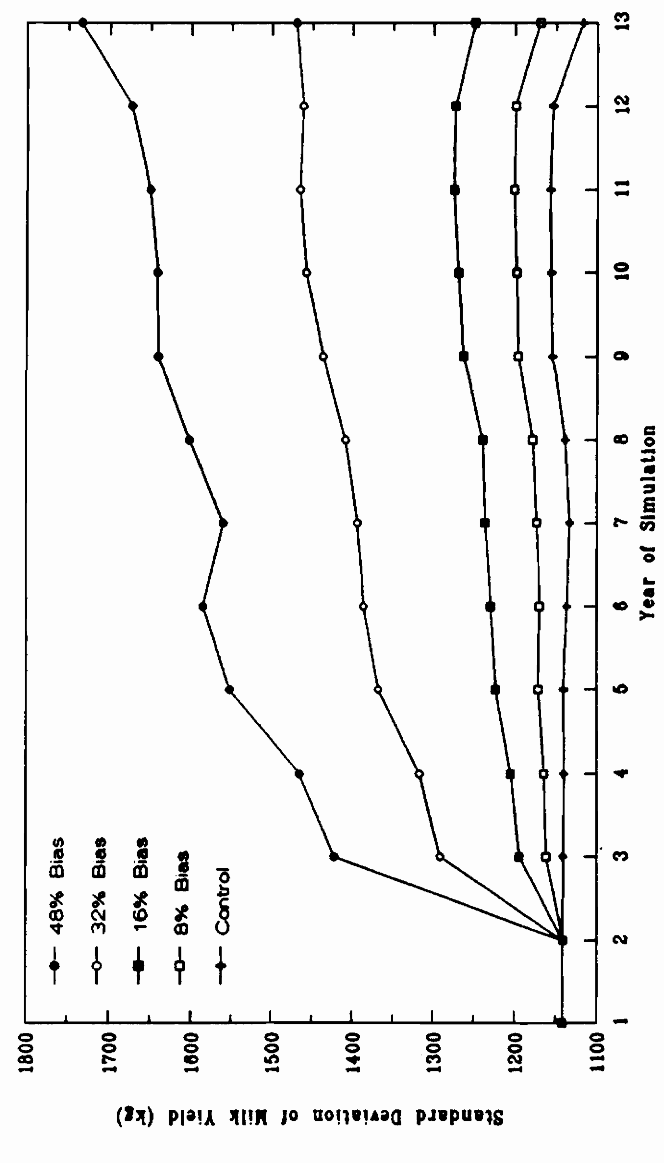

Figure 14. Change in SD of milk records over time when cows are biased in all records based on herd rank on 2:2:1 index of milk, fat and type phenotypic records.

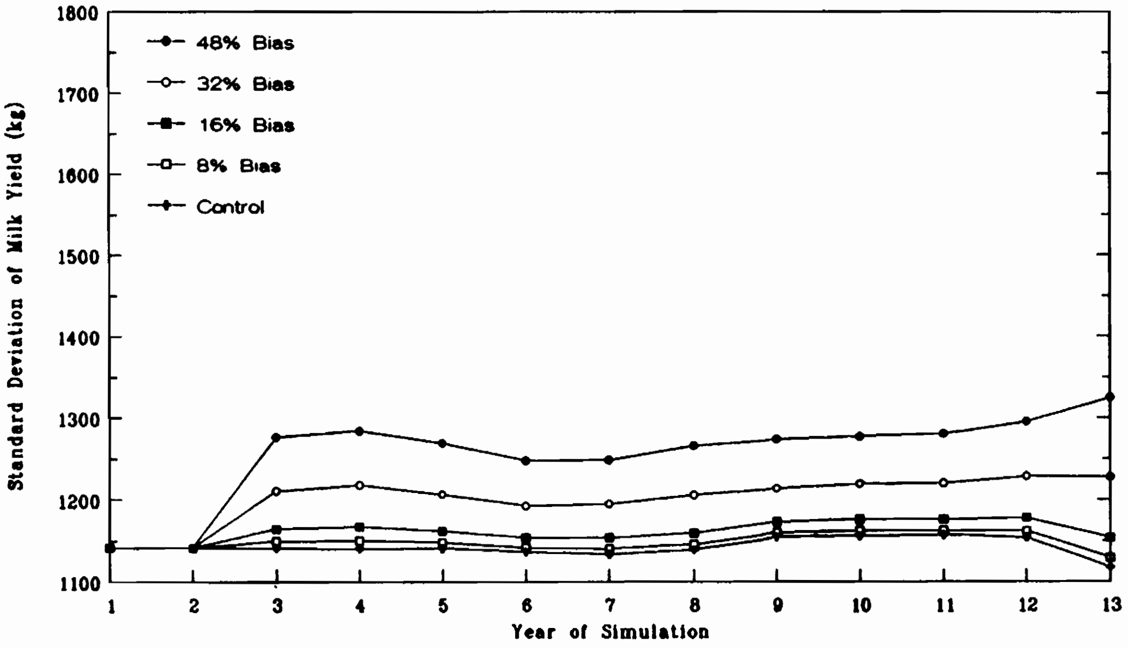

Figure 15. Change in SD of milk records over time when cows are biased in all records based on maternal line and final score type.

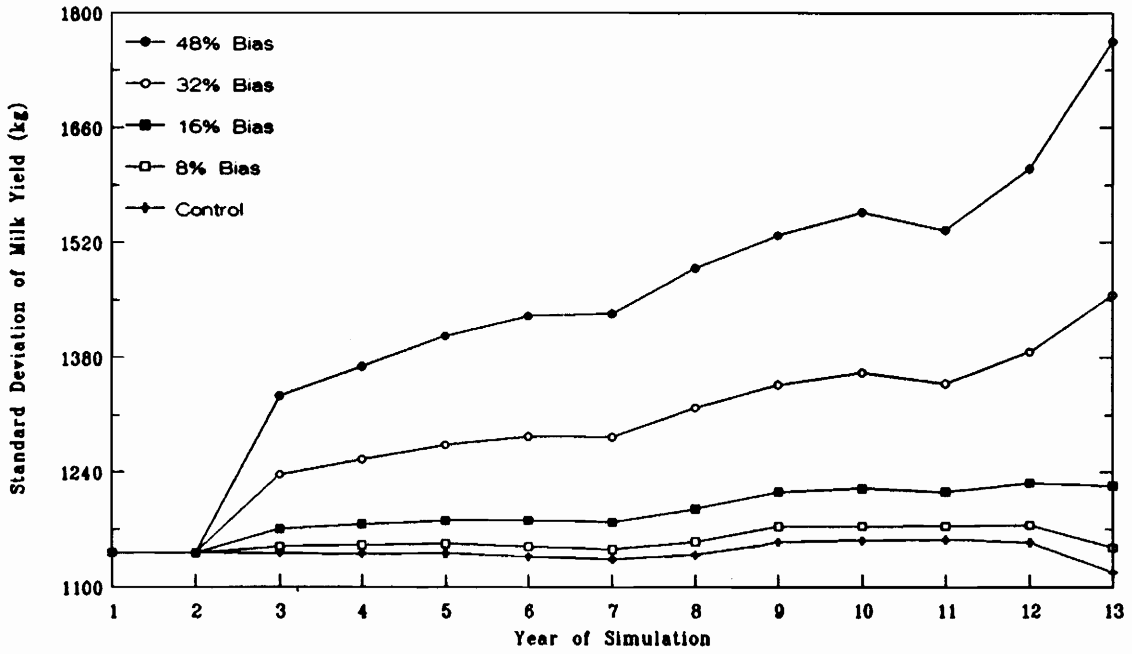

Figure 16. Change in SD of milk records over time when cows are biased based on final score type and above herd average rank on phenotypic records if cow is not first lactation.

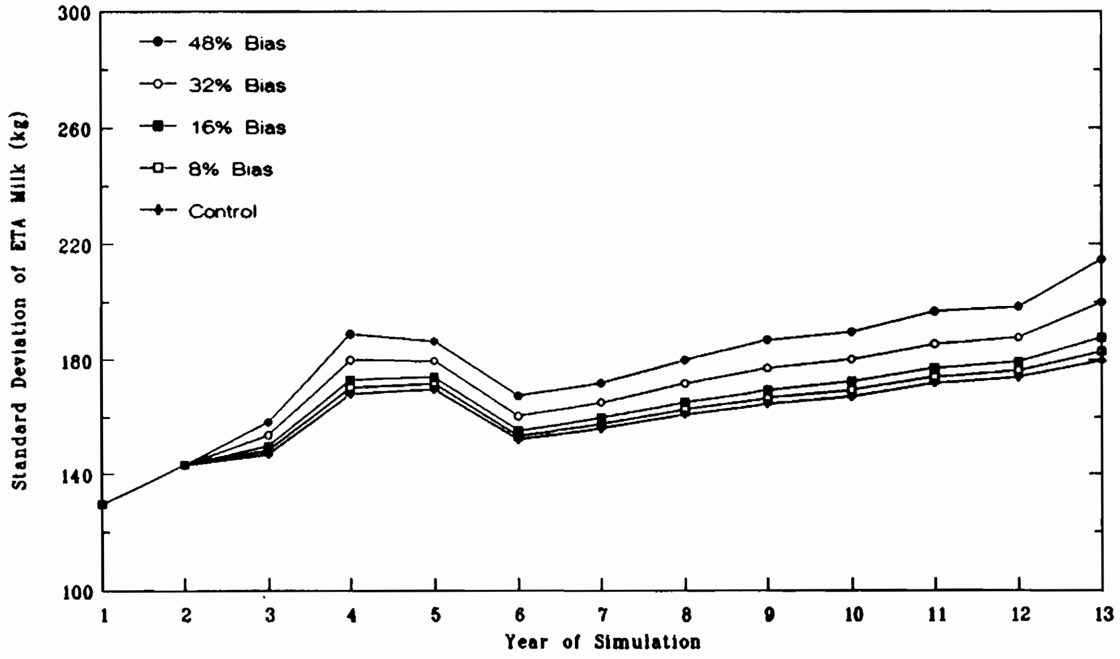

Figure 17. Change in SD of cow ETA milk over time when cows are biased in 2nd and 3rd records based on herd rank on 2:2:1 index of milk, fat and type phenotypic records.

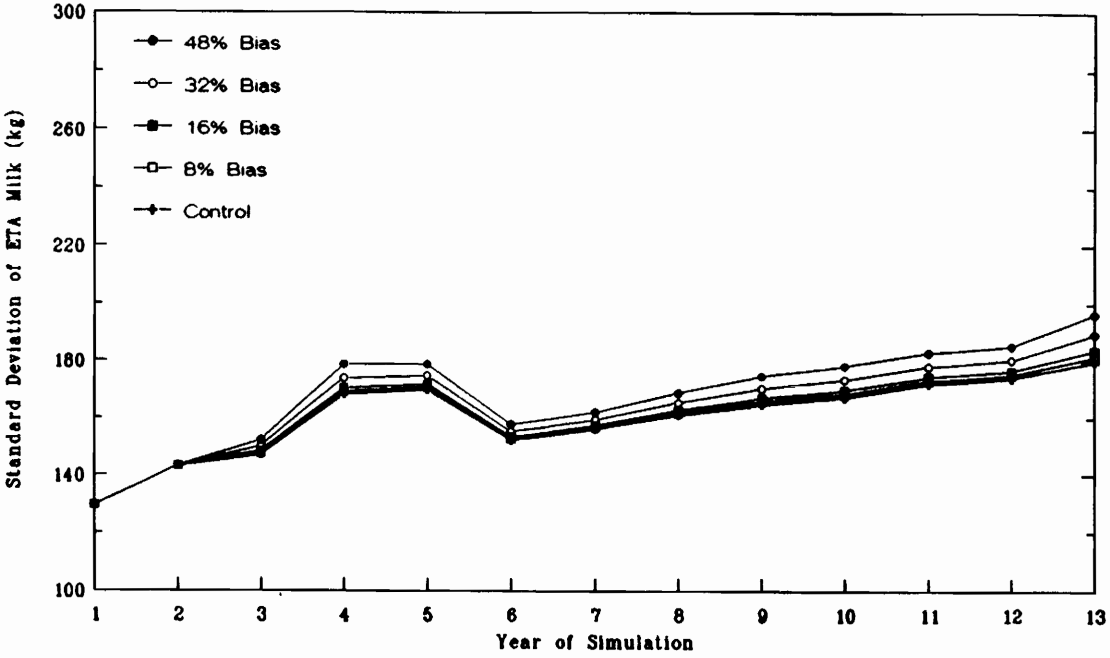

Figure 18. Change in SD of cow ETA milk over time when cows are biased in 2nd and 3rd records based on herd rank on 2:2:1 index of milk, fat and type phenotypic records and final score type.

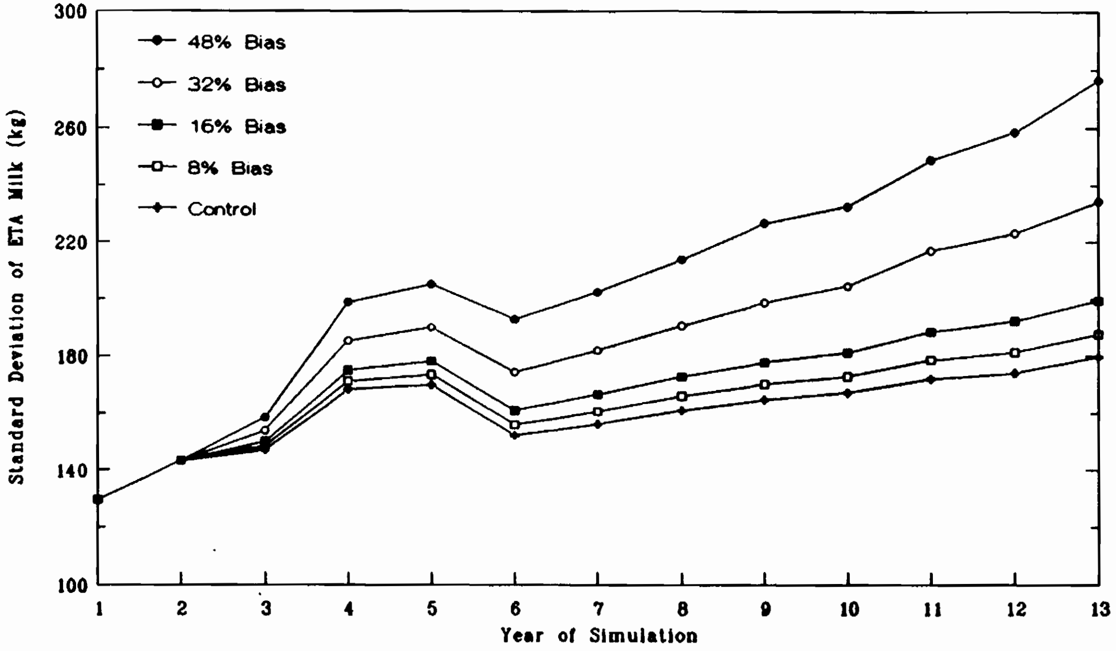

Figure 19. Change in SD of cow ETA milk over time when cows are biased in all records based on herd rank on 2:2:1 index of milk, fat and type phenotypic records.

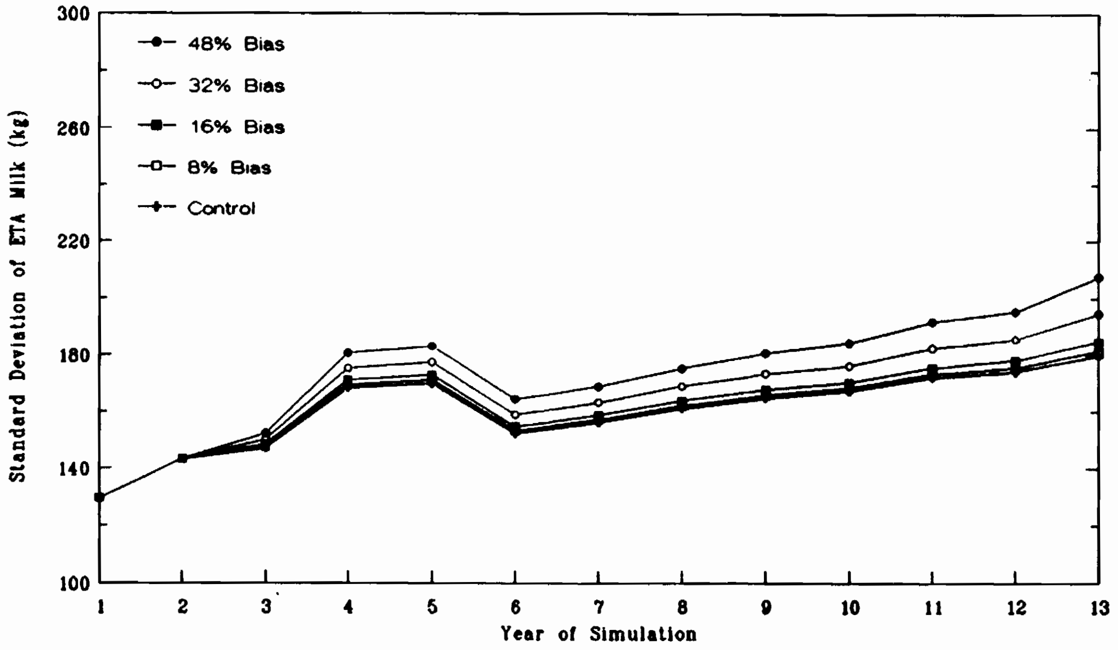

Figure 20. Change in SD of cow ETA milk over time when cows are biased in all records based on maternal line and final score type.

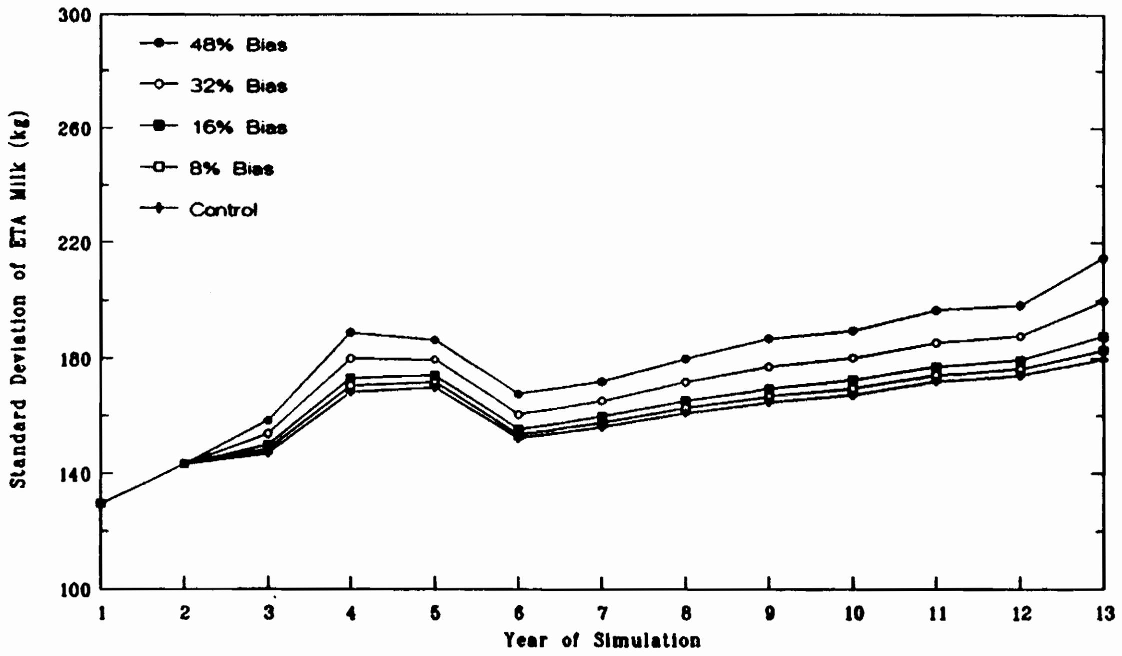

Figure 21. Change in SD of cow ETA milk over time when cows are biased based on final score type and above herd average rank on phenotypic records if cow is not first lactation.

amount for bias levels of 32 and 48% when bias was based on cow ETA or phenotypic records with no phenotypic minmum for type, and the inflation increased slightly over time (Figures 12 and 14). This inflated variance was consistent with the findings of Burnside and Meyer (3). The IRP+/FS85-123 copy also showed increased variance (Figure 16), however the greatest increases were in the last 2 years. This may be due to an increase in the number of cows which received bias because of the genetic trend for final score type over time. Other bias copies requiring a phenotypic minimum for type score had small increases in phenotypic standard deviation (Figures 13 and 15), which may suggest that the increase in phenotypic variance is related to the number of cows which received bias.

The change in standard deviation of ETA over the 13 years of the simulation are in Figures 17-21 for 5 of the bias patterns. Four of the patterns (Figures 17,18,20 and 21) show similar trends with slight increases after year 6. An increase in information in the ETA's due to the use of completed lactations in the genetic evaluations for year 13 may be responsible for the increase in the variance seen in the last year. While the within herd variance of cow ETA's was also increased over the control for all bias copies and levels of bias, only bias copies IRG-123 and IRP-123 (Figure 19) had increases which were very large.

The average percent of cows biased for year 13 in each bias copy and level is listed in Table 5. The differences in the patterns of bias caused differences in the number of cows biased, with those copies with the largest percent biased having the largest inflation in variance.

Correlations between percent of the cows biased in year 13 and the within herd standard deviation for milk phenotypic records (yield) or ETA's for year 13 are presented in Table 6. At the 8% bias level, the correlation for phenotypic standard deviation was positive for the 4 bias copies based on phenotypic records or ETA's with no phenotypic minimums for type score. For the other bias copies the correlation was near zero. This indicates that, for these copies, the differences in the herds for the number of cows biased were not enough to overcome previous differences in the within-herd variances when bias levels were low.

Table 5. Percent of cows that were biased in year 13 for each bias strategy and level.

	Bias Level			
Bias Strategy	8%	16%	32%	48%
IRP-23	3.6	3.7	3.7	3.7
IRP/FS82-23	2.4	2.4	2.2	2.1
IRP-123	7.2	6.8	6.4	5.9
IRG-23	4.0	3.8	3.4	3.4
IRG/FS82-23	3.0	2.8	2.8	2.7
IRG-123	6.5	6.0	5.4	5.2
Fam/FS82-123	2.1	2.0	1.9	1.8
IRP+/FS85-123	9.1	9.5	9.6	9.5

Table 6. Correlation of percent of cows biased to the within-herd SD's of phenotypic milk yield (Yield) and Estimated Transmitting Ability (ETA) for different bias allocation strategies and levels.

Bias Strategy	Bias Level							
	8%		16%		32%		48%	
	Yield	ETA	Yield	ETA	Yield	ETA	Yield	ETA
IRP-23	.13	.44	.55	.60	.82	.83	.91	.92
IRP/FS82-23	-.06	.26	.35	.39	.76	.63	.85	.78
IRP-123	.30	.55	.71	.75	.88	.88	.90	.92
IRG-23	.18	.53	.53	.70	.82	.86	.91	.92
IRG/FS82-23	.02	.43	.40	.62	.75	.83	.88	.91
IRG-123	.29	.66	.66	.82	.85	.92	.91	.94
Fam/FS85-123	-.04	.29	.38	.56	.83	.85	.91	.91
IRP+/FS85-123	.06	.08	.58	.25	.85	.55	.86	.68

The correlation of percent of cows biased to within herd phenotypic variance was greatly increased for all bias strategies as the bias level increased to 16% and above, while differences in the correlations between the copies remained. At the 48% bias level all of the correlations were close to 90%.

The correlation of percent of cows biased to the standard deviation of ETA's (Table 6) was much higher than those for phenotypic variance at the 8% bias level. Bias copy IRP+/FS85-123 was considerably lower than the other copies with a correlation of .10, and continued to have the lowest correlation as bias levels increased. At the 48% level of bias, IRP+/FS85-123 and IRP/FS82-23 were the only bias copies with a correlation of less than 90%, which would indicate that the cows chosen to be biased in these copies for year 13 were not chosen to be biased for multiple lactations and/or were not from maternal families which had been consistently biased. Thus, the large bias in the phenotypic records did not create the extremely high ETA's for milk as in the other bias copies.

With the large changes in within herd variance of ETA, corresponding changes in the covariances and correlations would also be assumed. Table 7 lists the squared correlation of true and estimated transmitting abilities for the entire cow population at the end of year 13. The squared correlation of predicted and true transmitting ability for cows in the control copy of 45% was lower than predicted by the average reliability of 51%. The reduced correlation is probably caused by the reduction in additive genetic variation, as was seen in the bull population.

As bias levels increased above 16%, the correlation was further reduced in all bias copies. At the 48% bias level, the realized accuracy of the ETA's was decreased to nearly half of that in the control copy accuracy in bias copies IRG-123 and IRP-123. Also the decrease in the squared correlation for bias copy Fam/FS82-123 was quite large considering the small number of cows that were biased in this copy.

Table 7. Squared correlation of True and Estimated Transmitting Ability milk for all cows in the presence of different bias allocation strategies and levels.

Bias Strategy	Bias Level 8%	16%	32%	48%
IRP-23	.45	.44	.42	.37
IRP/FS82-23	.45	.45	.44	.41
IRP-123	.44	.42	.34	.26
IRG-23	.45	.44	.41	.37
IRG/FS82-23	.45	.45	.42	.40
IRG-123	.44	.41	.32	.25
Fam/FS85-123	.45	.44	.40	.35
IRP+/FS85-123	.45	.44	.40	.35

Effect of bias on Bull Dam Selection

Eighty bull dams were selected out of a population of approximately 4000 for each bias copy and selection policy in each of the three replicates of the simulation. Mean 2:2:1 index weighting of milk, fat and type true transmitting abilities for the groups of cows selected in year 13 are given in Table 8 and were the primary basis of evaluation of the various systems. The tabulated values are deviations from the mean of cows selected on PTA in the control copy. As expected, selection on PTA gives the highest mean when there is no bias present. The mean index of true transmitting abilities of the three groups of 80 cows selected on PTA in the control copy was 15.76, compared to the 10.14 average for the entire population of possible dams. The standard deviation of the index in the population was 3.54 in year 13.

Selection on PTA-F was only slightly lower (-0.11) than selection on PTA using all lactations in the control copy, while the means of cows selected on PTA-P, PI-3/PTA and PI-3 had values of -1.43, -0.87 and -1.80 which were .4, .25, and .51 standard deviations below that of PTA.

Using PTA and PTA-F as selection methods gave the highest average in all bias strategies when bias levels were 8 or 16%, with PTA-F tending to have a slight advantage in bias stratagies where bias did not occur in the first lactation. However, selection on PTA became less effective as bias level increased to 32%, especially when the bias was applied to all lactations. Although PTA-F remained an effective selection method for many of the bias stratagies, for strategies ETA-AL, Phen-AL and Family it was equally as ineffective as selection on PTA, with both methods being roughly .54 standard deviations below the control copy mean.

While more conservative in the selection of dams, and therefore less effective than PTA or PTA-F at the low bias levels, selection on PI-3/PTA was affected little by the high bias levels. At the 48% bias level, PI-3/PTA was the most effective selection method in all bias strategies where bias oc-

Table 8. Mean 2:2:1 weighting of milk, fat and type true transmitting abilities[1] for cows selected to be bull dams in three replicates by different methods in the presence of different bias allocation st

Bias Strategy	Bull Dam Selection Method				
	PTA	PTA-F	PTA-P	PI-3/PTA	PI-3
Control	0.00	-0.11	-1.43	-0.87	-1.80
			8% Bias Level		
IRP-23	-0.11	-0.17	-1.46	-0.89	-1.80
IRP/FS82-23	-0.17	-0.16	-1.47	-0.89	-1.80
IRP-123	-0.34	-0.40	-1.53	-0.82	-1.80
IRG-23	-0.03	-0.05	-1.55	-0.88	-1.80
IRG/FS82-23	-0.07	-0.16	-1.48	-0.90	-1.80
IRG-123	-0.19	-0.45	-1.53	-0.91	-1.80
Fam/FS82-123	-0.04	-0.25	-1.49	-0.90	-1.80
IRP+/FS85-123	-0.24	-0.14	-1.53	-0.88	-1.80
			16% Bias Level		
IRP-23	-0.39	-0.40	-1.55	-0.92	-1.80
IRP/FS82-23	-0.53	-0.42	-1.52	-0.91	-1.80
IRP-123	-0.60	-0.72	-1.57	-0.84	-1.80
IRG-23	-0.46	-0.28	-1.55	-0.76	-1.80
IRG/FS82-23	-0.42	-0.22	-1.54	-0.84	-1.80
IRG-123	-0.55	-0.60	-1.70	-1.01	-1.80
Fam/FS82-123	-0.44	-0.43	-1.66	-0.90	-1.80
IRP+/FS85-123	-0.58	-0.36	-1.51	-0.83	-1.80
			32% Bias Level		
IRP-23	-0.88	-0.32	-1.61	-0.83	-1.80
IRP/FS82-23	-0.81	-0.33	-1.62	-0.84	-1.80
IRP-123	-1.57	-1.56	-1.92	-0.92	-1.80
IRG-23	-0.96	-0.38	-1.63	-0.93	-1.80
IRG/FS82-23	-0.94	-0.35	-1.56	-0.89	-1.80
IRG-123	-1.36	-1.63	-1.92	-0.97	-1.80
Fam/FS82-123	-2.09	-1.90	-1.83	-0.93	-1.80
IRP+/FS85-123	-1.05	-0.32	-1.83	-0.77	-1.80
			48% Bias Level		
IRP-23	-1.45	-0.55	-1.74	-0.89	-1.80
IRP/FS82-23	-1.36	-0.43	-1.57	-0.86	-1.80
IRP-123	-1.89	-1.95	-2.13	-0.93	-1.80
IRG-23	-1.39	-0.62	-1.65	-0.97	-1.80
IRG/FS82-23	-1.31	-0.63	-1.61	-0.86	-1.80
IRG-123	-1.89	-1.92	-1.93	-1.00	-1.80
Fam/FS82-123	-2.79	-2.60	-1.86	-0.94	-1.80
IRP+/FS85-123	-1.65	-0.37	-2.11	-0.78	-1.80

[1] Tabulated values are the difference from the mean of cows selected in the control copy using cow PTA equal to 15.76, with the standard error of each mean equal to .19.

curred in all lactations, and second to PTA-F in the other bias strategies. However, disregarding all maternal production by using PI-3 alone seems to be too conservative in all bias strategies except Fam/FS82-123.

Selection on PTA after requiring phenotypic minima for fat percent and final score type (PTA-P) was also relatively unaffected by increasing bias. However, roughly 10% of the cows passed the phenotypic minimums, so that selection intensity and the variance of the selected groups, was greatly reduced. As expected, the use of the phenotypic minima greatly changed the ratio of the three traits from the 2:2:1 index of selection. Shown in Table 9 are the mean standardized selection differentials of each of the traits in the index for the group of cows chosen by each selection method in the control copy and all bias copies at the 48% bias level.

The resulting weighting of the true transmitting abilities of cows selected in the control copy on PTA-P was .8:1.15:1 compared to a ratio of 2.8:2.8:1 for the selection methods using PTA and PI-3 had a ratio of 4.4:4.1:1. Clearly the stringent phenotypic minimum for type score in PTA-P selected cows cows which were also high for breeding value type. Similarily, imposing a minimum for fat percent resulted in fat yield having a higher standardized selection differential than milk for the cows selected.

While PI-3 and PI-3/PTA remained constant for these ratios, the other selection methods showed an increase in the standardized selection differential for type in bias strategies that included final score type as a bias criterion.

Accuracy of Bull Dam PTA's

The regression coefficients and R^2 values from the prediction of true transmitting ability milk from cow ETA milk are listed in Table 10 and were very close to the theoretical expectation in the control copy. The R^2 values were higher in the groups of cows selected in the control by methods

Table 9. Mean standardized selection differentials for true transmitting abilities of milk, fat and type for cows selected in three replicates by different methods in the presence of different bias s

Bias Strategy	Bull Dam Selection Method				
	PTA	PTA-F	PTA-P	PI-3/PTA	PI-3
Milk					
Control	1.27	1.26	.68	1.08	.92
48% Bias Level					
IRP-23	.91	1.15	.59	1.10	.92
IRP/FS82-23	.91	1.17	.65	1.09	.92
IRP-123	.80	.80	.50	1.08	.92
IRG-23	.99	1.12	.63	1.08	.92
IRG/FS82-23	.92	1.10	.63	1.10	.92
IRG-123	.84	.85	.56	1.06	.92
Fam/FS85-123	.56	.61	.57	1.08	.92
IRP+/FS85-123	.71	1.16	.46	1.09	.92
Fat					
Control	1.30	1.26	.97	1.08	.87
48% Bias Level					
IRP-23	1.00	1.16	.89	1.07	.87
IRP/FS82-23	.90	1.16	.91	1.08	.87
IRP-123	.86	.84	.76	1.06	.87
IRG-23	.96	1.16	.90	1.06	.87
IRG/FS82-23	.92	1.09	.91	1.08	.87
IRG-123	.87	.84	.84	1.06	.87
Fam/FS85-123	.58	.63	.86	1.06	.87
IRP+/FS85-123	.78	1.14	.78	1.08	.87
Type					
Control	.45	.44	.84	.40	.21
48% Bias Level					
Phen-23	.32	.43	.86	.36	.21
Phen/FS82-23	.60	.49	.89	.40	.21
Phen-123	.38	.37	.90	.38	.21
IRG-23	.31	.42	.85	.36	.21
IRG/FS82-23	.60	.57	.88	.38	.21
IRG-123	.30	.29	.85	.36	.21
Fam/FS85	.53	.50	.84	.38	.21
Phen+/FS85-123	.94	.62	.98	.48	.21

PI-3/PTA and PTA-P, which may suggest that these groups were less variable and/or that there was a scaling effect on prediction, since those groups also had lower means for true breeding value.

In general, the predictive ability of PTA decreased sharply as bias levels increased. This same trend noticed in the population as a whole and resulted in the predictive ability of PTA milk being near zero for many groups selected at the 48% bias level. Interestingly, bias copies IRG-123 and IRP-123, which had the lowest correlations on a population basis for the high bias levels, had the highest R^2 at the 48% bias level for selection methods PTA and PTA-F. This would indicate that most of the cows selected had been biased such that the ranking of cows on ETA, at least within the group of cows selected, was still reasonable.

Table 10. Parameter estimates and R^2 for regression of True Transmitting Ability milk on ETA milk for bull dams selected by different methods in the presence of different bias strategies and levels.

	Bull Dam Selection Method											
Bias Strategy	PTA			PTA-F			PTA-P			PI-3/PTA		
	α	β^1	R^2	α	β	R^2	α	β	R^2	α	β	R^2
Control	-314	1.14	.26	-208	1.10	.26	-113	1.05	.31	-211	1.11	.30
8% Bias Level												
IRP-23	-98	1.02	.23	46	.98	.24	-27	.99	.30	-158	1.08	.30
IRP/FS82-23	-449	1.18	.28	-51	1.03	.25	-70	1.01	.30	-91	1.05	.29
IRP-123	46	.92	.18	262	.84	.16	150	.88	.27	163	.92	.23
IRG-23	67	.93	.21	224	.89	.21	-56	.98	.32	-109	1.04	.29
IRG/FS82-23	-149	1.03	.24	-61	1.01	.25	-10	.96	.29	-220	1.10	.31
IRG-123	181	.84	.18	7	.91	.22	149	.86	.30	337	.81	.21
Fam/FS82-123	-192	1.07	.24	72	.96	.22	68	.93	.25	-37	1.01	.24
IRP+/FS85-123	-522	1.21	.28	-224	1.10	.27	-216	1.07	.30	-245	1.13	.32
16% Bias Level												
IRP-23	150	.87	.21	566	.73	.19	141	.87	.27	104	.95	.27
IRP/FS82-23	-152	1.01	.23	31	.98	.26	26	.94	.27	33	.99	.27
IRP-123	601	.62	.11	588	.62	.13	488	.68	.22	841	.60	.15
IRG-23	33	.87	.22	440	.76	.20	242	.82	.28	330	.84	.23
IRG/FS82-23	159	.84	.19	343	.81	.20	184	.84	.27	81	.95	.27
IRG-123	273	.71	.16	302	.69	.18	626	.58	.19	1051	.47	.10
Fam/FS82-123	548	.69	.11	965	.53	.08	560	.66	.16	719	.66	.14
IRP+/FS85-123	-550	1.17	.29	166	.92	.22	-114	.98	.26	-183	1.10	.32
32% Bias Level												
IRP-23	659	.56	.14	1402	.34	.08	844	.50	.14	897	.58	.15
IRP/FS82-23	720	.58	.11	608	.71	.20	608	.63	.16	396	.82	.24
IRP-123	73	.62	.18	752	.42	.12	1196	.28	.08	1693	.21	.05
IRG-23	358	.64	.16	1200	.40	.10	757	.54	.21	1056	.48	.12
IRG/FS82-23	524	.59	.14	1148	.44	.12	732	.55	.19	701	.65	.19
IRG-123	-65	.64	.18	-250	.70	.24	1521	.14	.02	1906	.11	.02
Fam/FS82-123	1386	.22	.02	1556	.17	.02	1451	.20	.03	1698	.22	.03
IRP+/FS85-123	41	.81	.18	653	.68	.16	-62	.86	.22	185	.92	.27
48% Bias Level												
IRP-23	682	.47	.11	1610	.23	.05	1289	.27	.06	1466	.32	.07
IRP/FS82-23	1249	.31	.05	1207	.43	.10	1140	.36	.08	680	.69	.21
IRP-123	-357	.61	.22	188	.48	.18	1546	.11	.02	1968	.09	.02
IRG-23	232	.59	.18	1389	.29	.08	1172	.33	.12	1544	.26	.06
IRG/FS82-23	710	.46	.11	1353	.32	.09	1148	.33	.11	1333	.37	.10
IRG-123	-757	.70	.27	-356	.61	.25	1881	-.01	.00	2140	.02	.00
Fam/FS82-123	1624	.08	.01	1743	.05	.00	1839	.02	.00	2027	.07	.01
IRP+/FS85-123	164	.66	.14	1167	.44	.10	317	.61	.14	580	.73	.22

[1] Standard error of regression coefficients ranged from .04 to .13.

Summary

A Monte Carlo simulation was conducted to determine the impact of different bull dam selection methods when preferential treatment was applied to selected cows or cow families. The average bias ranged from 8 to 48% and was applied through eight different strategies.

Additive genetic variance for the bulls in the simulated bull stud was reduced to 44% of the original σ^2_A due to selection. Partial assortative mating to the highly selected A.I. population subsequently reduced the additive genetic variance in the cow population for the milk and fat yield traits to 90% of the original variance.

Giving preferential treatment to or biasing a small percentage of cows chosen by various strategies increased the within-herd variances of both the phenotypic records and the ETA's for milk and fat for all bias levels. While the increase in variance of phenotypic records was strongly related to the number of cows which received bias, the increased variance in ETA's was more related to bias strategy. Increase in within-herd variances of ETA's was greatest when bias was based on phenotypic records or ETA's with no phenotypic minima, especially when bias was applied to all lactations.

Bull dams were selected on PTA, PTA based on first lactations, PTA with phenotypic minimums for fat percent and conformational type score, three generation Pedigree Index (PI-3) and PTA after preselection on PI-3. Selection of bull dams on PTA was effective in the presence of bias for bias levels up to 16% for all bias strategies studied. At bias levels of 32% and 48%, efficiency of selection on PTA was greatly reduced especially when bias was based on cow family (Family). Basing selection on first lactation PTA's (PTA-F) was more resistant to bias than PTA in many of the bias copies, but was equally ineffective for bias copies Phen-AL, ETA-AL and Family for all levels of bias.

Disregarding all maternal production through selection of bull dams on three generation Pedigree Index (PI-3) was much less effective than PTA and PTA-F for bias levels of less than 32%. Only in bias copy Family at the highest level of bias did PI-3 show a real advantage over PTA-F.

Use of phenotypic minimums for fat percent and conformational type score before selection of PTA also gave much lower means for cows selected at the lower bias levels. While PTA-P was better than PTA for Family at the highest level of bias, it was worse for several of the other bias strategies at the high level of bias. In addition, requiring phenotypic minimums resulted in decreased selection for milk and increased selection for fat and type.

Preselecting cows on PI-3 before selection on PTA also was examined as a way to minimize the impact of bias on bull dam selection while still allowing cow's production to have some influence on rank. The use of PI-3/PTA as a method of bull dam selection was more conservative than PTA-F, and therefore less efficient at the low levels of bias. However PI-3/PTA was virtually unaffected by any of the bias strategies, even at the highest levels of bias.

Simple regression of ETA milk on True Transmitting Ability milk for cows selected to be bull dams gave coefficients and R^2 near the theoretical expectation for the lower levels of bias. For most of the bias strategy-selection method combinations, prediction was greatly lowered as bias level increased.

Conclusions

Large within-herd phenotypic variances and variances of cow ETA for milk and fat may be an indication of preferential treatment. Unfortunately, the bias strategy which was the most damaging to efficiency of bull dam selection, Family, showed only a small increase in the variance of ETA's. The usefulness of within herd variances as a means of detecting preferential treatment may also be limited by the strong relationship of the increase in variance to the number of cows biased.

Selection on PTA and PTA-F were the most efficient selection methods when no bias was present and also gave the best results at 8 or 16% bias. PTA-F is also resistant to higher levels of bias when bias occurs only in later lactations or when bias is based on conformational type score (IRP+/FS85). However, PTA-F is even less effective than selection on PTA when bias occurs in all lactations for some bias strategies, such as IRP-123 and IRG-123, and equally ineffective for the most damaging bias strategy, Fam/FS82-123.

Requiring phenotypic minima for fat percent and conformational type score greatly reduced the efficiency of selection at low levels of bias and only showed advantages over PTA and PTA-F at high levels of bias in copies where selection had been greatly compromised (Family). Furthermore, there was a change in the weighting of the true transmitting abilities for milk, fat and type in the cows chosen by PTA-P versus those cows chosen using PTA alone. If the change in the weighting of the traits caused by requiring the phenotypic minimums is the desired result, it would seem that modifying the index of selection would be more efficient.

Likewise, it would seem unjustified to disregard all maternal line production information in avoidance of bias by using PI-3 alone as a selection method. However, preselection of cows on PI-3 before selection on PTA proved to be an effective method of largely eliminating the impact of bias while not being prohibitively conservative at low levels of bias.

The recommendation as to which bull dam selection method may be most effective in the current dairy population is difficult, since it is not known what types of bias are most common, or the levels of bias, that currently exist. However, it would seem logical to require potential bull dams to have high values for Pedigree Index if large amounts of bias are suspected.

The predictability of True Transmitting Ability milk from ETA milk for cows selected in the presence of high bias is low for most of the selected groups. Raising selection intensity by sampling multiple sons of the top cows may yield variable results at best, and warrants further study.

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Appendix

Parameters for the simulated bull population are shown in Table 2. Selection of the top 250 from this group of 100,000 bulls gave a selection intensity, i, of 3.1 with the point of truncation, x, that was 2.807 standard deviation units above the mean. The expected mean value of the 2:2:1 weighting of the true transmitting abilities of the selected bulls is then equal to:

$$\mu_I = i \times (r_{I,\hat{I}}) \times \sigma_I \qquad [9]$$

Substituting the values from Table 2 gives an expected value of 10.1 which was slightly over the 10.0 which was observed in the first year. Similarily, equation [9] was used to calculate the expected means for the individual traits in the index with the predictions and the values observed in year 1 listed in Table 2.

The standard deviations and adjusted means of the transmitting abilities of the A.I. populations are shown graphically in Figures b2-b4. Genetic variation in the population was relatively constant over time for each trait but was reduced due to the high selection intensity. As shown by Bulmer (2), the variance of the index of ETA's is expected to be reduced to:

$$\sigma'^2_{\hat{I}} = (1 - k) \times \sigma^2_{\hat{I}} \qquad [10]$$

The factor k is a function of the selection intensity, i, such that

$$k = i \times (i - x) \qquad [11]$$

where x is the distance of the point of truncation from the mean in standard deviation units. Likewise, the reduction in the variance of a variable X, which is correlated to the index of ETA's, can be calculated as

$$\sigma'^2_X = (1 - \rho^2_{X,I} \times k) \times \sigma^2_X \qquad [12]$$

where $\rho^2_{X,I}$ is the square of the correlation between the variable X and the index I. The expected and observed variances for the ETA's of the traits in the index as well as the variances for the true transmitting abilities of the traits and the index are listed in Table 2 for the population of 100,000 unselected A.I. bulls.

Just as variances are reduced by selection, the correlation of the index of ETA's and the index of true transmitting abilities is also lowered. The expected value of the correlation of the index of ETA's and the index of true tranmitting abilities among selected bulls is:

$$\rho'_{I,\hat{I}} = \rho_{I,\hat{I}} \sqrt{\frac{1 - i \times (i - x)}{1 - \rho^2_{I,\hat{I}} \times i \times (i - x)}} \qquad [13]$$

As seen in Table 3, the correlation was reduced to less than half of its valuue prior to selection, or from .85 to .41, with the observed values being close to that expected.

Equation [9] can also be used to predict the average error term (defined as $R_{E1} \times \sigma_A$) for the 75% reliability ETA's for each trait in the index. The predicted values and those observed in year 1 are listed in Table 3. As seen in the graphs of the adjusted means for each year of the simulation in Figures B1-B3, bull ETA's are over-estimated in the first years of the simulation. However, because the error of prediction terms generated for all bulls continued to have a mean of zero, the average error term of the selected bulls remained roughly the same over time while the genetic trend continued to increased. Therefore by year 4, the genetic trend constant became large enough that the average error term of the bulls selected was less than the average true transmitting ability, and ETA's became under-estimated. The reduction of the ETA's by a constant should not have affected the results of the simulation and could have been corrected by simply increasing the mean of the error term for the ETA's by the genetic trend each year.

Vita

The author was born on March 20, 1965 in Manchester, Iowa and was raised on the family dairy farm in eastern Iowa. Following graduation from Beckman High School in Dyersville, Iowa in 1983, the author enrolled at Iowa State University and completed summer internships at Maddox Dairy, Inc. in Burrel, California, Ruann Holsteins, Inc. in East Avon, New York and Select Sires, Inc. of Plain City, Ohio before graduating with a B.S. in Dairy Science in 1987. The author has completed the requirements for the M.S. degree in Dairy Science at Virginia Polytechnic and State University where he is currently pursuing a Ph.D. degree in Animal Science-Dairy Genetics.

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