CHANGES IN GENETIC EVALUATIONS FROM 1ST TO 2ND CROP FOR FINAL SCORE IN HOLSTEINS

by

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(Under the Direction of Ignacy Misztal)

ABSTRACT

The purpose of this study was to investigate the changes of predictive transmitting abilities (PTAs) and PTA trends for final score, from 1st to 2nd crop of daughters for Holstein sires. The PTAs were estimated from 2 datasets: D01 (records classified up to 2001) and D05 (records classified up to 2005). PTA change was the difference between D01 and D05 evaluations. A variety of alternative models were investigated to reduce the PTA changes and to reduce the differences between 1st and 2nd crop trends of both PTA and MS. Allowing separate unknown parent groups for sires and dams together with additional pedigrees reduced the mean PTA change from -0.33, with single trait model, to -0.12. And, reduced the percent of sires showing drops from 74.5% to 56.4%, minimized the differences between 1st and 2nd crop trends.

INDEX WORDS: Final score, Holstein, PTA, trends

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M.V.Sc., Acharya N.G. Ranga Agricultural University, India, 2004.

A Thesis Submitted to the Graduate Faculty of the University of Georgia in Partial Fulfillment of the Requirements for the Degree

MASTER OF SCIENCE

ATHENS, GEORGIA

2006

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December 2006

DEDICATION

To my beloved parents and my dearest brother Balakrishna Reddy

ACKNOWLEGEMENTS

My heartfelt sincere thanks to Dr. Ignacy Misztal for accepting me into his group. His meticulous guidance, constant encouragement and endless support are commendable. I place my deep sense of gratitude and thanks to Dr. Romdhane Rekaya for all his guidance and thought provoking discussions. Also, I would like to thank Dr. Bertrand and Dr. Samuel Aggrey for their kind support.

My special thanks to Shogo Tsuruta for his guidance, suggestions and help during these two years stay at UGA. I admire his talent, hard work and all the kindness, friendship he showed to me.

I would like to thank all the graduate students in animal breeding group at UGA. Special thanks to Marcelo and Georgina for making me interested in SAS. Sincere thanks to Andra and Mike Kelly for their assistance. Special thanks to Mark Froetschel and Robin.

Finally, special thanks to my family and my friends at UGA.

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CHAPTER 1

INTRODUCTION

The evaluations based on the 1st crop of daughters influence the sires impending usage in the artificial insemination (AI) system. Subsequent evaluations, based on 1st crop and additional 2nd crop daughters, could be different from initial evaluations because of increased effective daughter information. If the assumptions of BLUP are satisfied, the expectation is that the mean difference between initial and later evaluations should be close to zero. However, large changes in predictive transmitting abilities (PTA) are not uncommon. The sires with a large change in PTA from initial to later evaluations are prone to be eliminated from general usage in the AI system.

Large changes of PTA are of a major concern for dairy farmers and the AI industry. First, dairy farmers may lose confidence in the genetic evaluation system and also in the AI companies that merchandise the semen. Furthermore, the AI companies can mistakenly keep or cull a graduate from their progeny testing program based on PTA values. As result, semen sales could decline if public relations with dairy farmers deteriorate. Finally, the large changes of PTA can restrict a sire's regular usage in progeny testing programs, resulting in decreased genetic progress and increased genetic interval.

Despite the presence of many new traits in dairy cattle, the type (or final score) remains one of the most important traits in the industry. With regard to type traits, changes can occur due to reclassification. This implies that popular sires are put at a disadvantage when the 2nd crop of daughters, which have not yet been reclassified, enter the evaluation (Lohuis and Schaeffer, 1995). This disadvantage increases with more reclassifications. Although many researchers investigated the causes of changes in PTA milk, fat and protein from 1st to 2nd crop evaluations, there is very little information on changes in PTA for type (PTAT). Identifying factors responsible for changes in PTAT and investigating model alternatives to reduce PTA changes will be useful to the industry and dairy farmers.

The objectives of the present study are:

1. Identifying the factors responsible for changes in sires' PTAT from first to second crop evaluations.
2. Use this information to improve the genetic evaluation to minimize the percent of sires showing major changes in PTAT and to minimize the variation between 1st and 2nd crop sire PTAT trends.

CHAPTER 2

REVIEW OF LITERATURE

The stability and accuracy of genetic evaluations are the most desirable characteristics of genetic evaluation system. The accuracy of genetic evaluations depends on the amount of information available. The sire's initial evaluation depends only on information from the 1st crop daughters. However, subsequent evaluations based on 1st crop and additional 2nd crop daughter information will be different and more accurate than the initial evaluations because of increased effective daughter information. Except for changes due to added 2nd crop daughter information, changes in mean evaluation for groups of sires in the two evaluations should be small (Powell et al., 1997) and the prediction error variance should be close to zero. However, large changes in evaluations are not uncommon. Large changes in PTA, beyond the expected, may prevent a proven bull from being utilized. This will be disappointing, especially, for the AI companies as they incur large costs in progeny testing programs. Factors that might cause the changes in evaluations, besides additional information, include:

1. *Inaccurate 1st crop daughter information.*

Sires with inaccurate 1st crop daughter information may get high initial evaluations because of chance or positive sampling deviation. This initial evaluation does not reflect the sire's true genetic merit, which means that he could be used more heavily than he should. On the other hand, the sire's later evaluations, based on 1st crop and additional 2nd crop daughters, could often be disappointing due to more accurate information added from 2nd crop daughters. Some farmers will delay scoring their poorest daughters until they are mature enough to get the highest classification possible when the classifier first sees them. This is however more beneficial for marketing purposes than for breed improvement (Schaeffer, 1995).

2. Misidentification of parents or loss of pedigree information.

Missing pedigree information may cause underestimation of inbreeding and relationships. Missing pedigrees occur more in cows with no phenotypic records. This lack of pedigree and phenotypic data from maternal relatives may cause fluctuation in sire proofs (Zwald et al., 2005).

3. Base change.

The average population breeding value increases with positive selection in the population. It will influence the breeding value estimates. Nevertheless, increasing the population average decreases the animal's absolute breeding value. Therefore, adjusting the breeding values to a specific base is a good practice to account for the differences in population averages.

There have been many efforts to identify the factors responsible for fluctuations in sire proofs. These include:

1. Selection problems.
2. Differential mating of sires.
3. Preferential treatment of bulls, bull dams and daughters of some sires.
4. Heterogeneous herd variance.
5. Classifiers' choice.
6. Inappropriate adjustment factors.
7. Differences between registered and grade animals.
8. Regional genetic differences.

1. Selection problems

The usual assumption of randomness in sire selection procedures may not hold at all times. Non randomness in methods of sire sampling, evaluation and female selection could cause fluctuations in sire evaluations. Examining the methods of purchasing and sampling unproven sires would be helpful in validating the assumption of randomness in sire selection or sampling programs. According to Bolgiano et al. (1979), a few potential bulls will be mated to cows with high estimated transmitting abilities (ETAs) at the beginning of the sire sampling program. The semen of selected male calves, based on pedigree information, will then be distributed across herds. Those bulls returned to service, after their initial evaluations based on the daughters performance records, will produce a second crop of daughters and will be reevaluated.

Uniformity in sire selection and evaluation methods is vital to control fluctuations in sire proofs. However, selection forces such as parental selection, sequential selection, preferential treatment and misclassification or manipulation of contemporary groups will affect uniformity in sire selection practices. The field data would invariably be collected from herds where some form of artificial selection has been practiced for a long time (Schaeffer et al., 1998). So, the usual assumption of random sampling invoked for estimation and prediction is no longer valid (Henderson, 1984). A change in evaluation methods could also affect proof stability. Introduction of more accurate evaluation procedures could bring substantial changes in selection practices. The altered selection practices may cause imbalances in genetic merit of sires and dams. Lee et al., (1985) reported higher changes in the genetic merit of bulls compared to dams after introducing more accurate evaluation procedures in 1968.

Practicing female selection for a long time would also bring fluctuations in sire proofs. The initial high evaluation of young sires allows them to be used on elite cows. On the other hand, subsequent evaluations could often be disappointing. The use of complete pedigrees back to a base population of non selected, non related and non inbred animals (Sorensen and Kennedy, 1984; Kennedy and Sorensen, 1990) could reduce the bias due to female selection. Using all the available data on candidates for selection can also account for parental selection, provided the selection process and the distribution of selection criteria are known (Henderson, 1975; Fernando and Gianola 1990). Previous studies have indicated that there is no general statistical solution to completely account for selection problems (Schaeffer et al., 1998). However, the bias due to female selection was found to be greatly minimized by animal model evaluations because of their property of incorporating all possible relations while computing evaluations. In practice it is even harder to quantify the amount of parental selection so it would be advisable to allow randomness in sire sampling procedures to account for changes in sire evaluations.

2. Differential mating

The mates of sires should have the same average merit in order to estimate the sire's genetic potential accurately. If some sires were mated with superior cows while others had genetically inferior mates then daughter records would not accurately reflect the differences between their sires' genetic values. Bolgiano et al. (1979) observed that the problem bulls' (i.e. bulls with high initial evaluations that are dropped later) 1st crop daughter dams have higher estimated transmitting abilities (ETA) than the daughter dams of normal bulls (i.e. bulls with no observable change in evaluations). This is a result of mating problem bulls with superior cows. Their studies suggested withholding the identities of unproven sires, when the semen is originally distributed, to avoid the problem of differential mating. To minimize the bias due to differential mating, Schaeffer et al. (1978) suggested including the dams' final class classification effect in the model. However, unequal merit of mates would be partially accounted for by the animal model, thus fitting additional fixed effect with the dams' final class classification effect in animal model evaluations is not required. Several other researchers also reported the effectiveness of animal model in accounting for the differential mating of sires (Kuhn et al., 1994). Despite above reports, the preferential treatment given to the daughters and dams of certain sires beyond the effect of the dams' classification can still be a potential source of bias (Kuhn et al., 1994).

3. Preferential treatment

Popular opinion indicates that intentional preferential treatment occurs among US dairy cows. Preferential treatment can be described as any management practice that increases production and is applied to one or several cows but not to their contemporaries. This was identified as a potential source of bias in genetic evaluations based on contemporary comparison (Nicholson et al., 1978). Several researchers have suggested that animal model evaluations may also be biased by preferential treatment (Meinert and Pearson, 1992; Weigel et al., 1994; Kuhn et al., 1994; Kuhn and Freeman, 1995; Lohuis and Bagnato, 1998). As the percentage of related animals receiving preferential treatment increases, the animal effect becomes increasingly biased. This bias can either be from preferential treatment given to certain bulls, or to their daughters as well as their dams (Meinert and Pearson, 1992).

3.1 Preferential treatment to some daughters of bulls

Bolgiano et al., (1979) identified preferential treatment given to certain daughters of sires as a potential cause of a large drop in sire PTA. This drop in PTA was larger for those bulls that had high initial evaluations. The amount of preferential treatment given to certain daughters of bulls is proportional to herd size. In large herds, the biases will increase with the increase in the proportion of daughters receiving preferential treatment (Nicholson et al., 1978).

The sampling status of bulls also has some effect on the amount of preferential treatment given to his daughters. Daughters of AI sampled bulls might be treated more preferentially than daughters of non-AI sampled bulls. Meinert and Pearson (1992) reported a higher decrease in 2nd crop modified contemporary comparison (MCC) evaluations of non-AI sampled bulls than those of AI sampled bulls. This overestimation of the non-AI sampled bull's 1st crop evaluations was due to preferential treatment given to their initial progeny test daughters. The decline was greater for the non-AI sampled bulls born in recent years indicating a higher level of preferential treatment in recent years. Powell and Norman (2001) reported stable and unbiased evaluations for 'S' sampled bulls (i.e. bulls that were reported to have had semen distributed to a minimum of 40 herds and sampled by an organization that did not have self-interest in which particular bull had a successful sampling result). Conversely, the evaluations of 'O' sampled bulls (i.e. bulls that had not been reported as having been sampled at least 40 herds by 3 year of age) were unstable and biased. This might be due to the preferential management of early daughters of the 'O' sampled bulls. The amount of bias due to preferential treatment depends on the number of preferentially treated daughters of a sire. A maximum of 5-6% daughters of each sire can receive preferential treatment without a serious bias to the sire's PTA (Kuhn and Freeman, 1995).

Sometimes, herd mates will be treated more preferentially than newly purchased cows. Thus, the inclusion of the records of later herds in the model will cause difficulties when accounting for the preferential treatment of these cows. Another popular opinion is that preferential treatment is practiced in second or later proofs and is prompted by an outstanding first record (Nicholson et al., 1978). Restricting the data to only first available classification record of cows can estimate sire proofs more accurately than using later records (Nicholson et al., 1978; Wiggans and VanRaden, 1990).

In contrast to the above reports many breeders feel that the most recent classification record reflects the true value of a cow better than its initial classification record. Most recent classification records of cows, pre-adjusted for age and stage of lactation, were suggested for official genetic evaluation for conformation in Canadian Holsteins (Jamrozik and Schaeffer, 1988). This is because reclassified records for type in Canada cannot decrease. Contrary to these observations, Jamrozik and Schaeffer (1993) have stated that the inclusion of data from beginning of data collection to the present is usually needed in genetic studies to account for phenotypic and time trends properly.

3.2 Preferential treatment to potential bulls and bull dams

Financial incentives of selling embryos and semen have prompted some dairy breeders to give preferential treatment to bull dams and potential bulls. This has resulted in a bias in selection of bull dams. Thus, their sons' genetic evaluations will be overestimated due to inflated parent averages and the ultimate progeny test information will often be disappointing to the producers who milked the cows (Weigel et al., 1994; Cassell, 1996). Choosing bull dams from 1st crop heifers or allowing a bull to have a minimum of 30 daughters when bull mothers receive preferential treatment, will reduce the bias in evaluations (Kuhn and Freeman, 1995).

A degree of positive association was observed between the semen price and the amount of change in PTA. However, fitting fixed effects of semen price group in an animal model had no significant effect in improving the accuracy of evaluations (Teirney and Schaeffer, 1994). Kuhn et al. (1999), using simulated data, investigated the effectiveness of power transformation to phenotypic records, fitting a random preferential treatment effect to suspected records, and a two group mixture model to correct for preferential treatment in the genetic evaluation of US dairy cattle. They advocated fitting a random effect for preferential treatment in the model to reduce the bias, provided an appropriate variance for the preferential treatment effect was estimated. Usually, records with preferential treatment were typically identified only 45-60% of the time. However, research with field data cannot prove, quantify or estimate the impact of bias on overall genetic improvement (Weigel et al., 1994) because this preferential treatment can be identified only after the fact (Kuhn et al., 1994). Therefore, it is better avoiding preferential treatment than trying to statistically account for it.

4. Heterogeneous herd variances

Many current applications of BLUP genetic evaluations for economically important traits of dairy cattle assume constant variances across environments. Cows generally express all their records in a single herd so there will be heterogeneity of variances within herds. Many researchers reported the existence of heterogeneous variance for production and conformation traits (Boldman and Freeman, 1990; Smothers et al., 1993; Weigel et al., 1993). Henderson (1984) and Gianola (1986) demonstrated that differences in within subclass variance components could be accommodated if all appropriate variance components are known. However, it is rare to know all the variances appropriately. Consequently, using inappropriate variances could potentially bias genetic evaluations (Reverter et al., 1994).

The potential effect of heterogeneity of variance on genetic evaluation of sires and cows, and on selections based on such evaluations, is of a major concern to animal breeders. The rankings of sires would not be greatly affected by heterogeneity of variances if their daughters are randomly distributed across herds. However, the rankings of cows were greatly influenced by heterogeneity of variances (Togashi et al., 2004). Ignoring the heterogeneity of variance in computing cow evaluations will strongly favor high performers in high variable herds as opposed to low variable herds. If these high performing cows are chosen as dams of future AI bulls, biases are likely to appear in sire evaluations (Vinson, 1987). Hence, the performance of daughters in more variable herds will influence the eventual sire evaluation to a greater extent than the performance of daughters in less variable herds. Correcting for heterogeneity variance within herd cannot remove all bias in parent averages though a general improvement of bias and accuracy of breeding values can be expected (Van der Werf et al., 1994). Van Vleck (1964) and Purohit et al. (1973) found herd effects to represent only less than 10% of total variance. They concluded that there was no need to include herd effects in sire evaluation unless many sires had daughters in very few herds. This is in agreement with the findings of Weigel and Lawlor (1994), who reported that the evaluations of sires with daughters in many herds are unaffected by heterogeneous variance adjustment. The overall impact of adjustment of heterogeneous variance was small on sire evaluations but not on cow evaluations. However, if heritability also differs across herds the accuracy of evaluations will be reduced by the failure to account for such differences (Vinson, 1987).

Koots et al. (1994) investigated the presence of heterogeneous variance across herds for type classification records of Canadian Holsteins. Variance components and BLUP estimates for herds were obtained via maximum likelihood procedures by fitting phenotypic standard deviation of herd-round-classifier to a mixed model that included round, classifier and region as fixed effects, herd size as a covariate and herd as a random effect. Then the phenotypic data was standardized for the phenotypic standard deviation of herd-round-classifier. The results gave some evidence of heterogeneous variance across herds for all 28 conformation traits studied. However, standardization of the classification records was found to have very a minor effect on genetic evaluations.

Though the variation due to herd effect was small and insignificant, the variation due to herd-year interaction effect was found to be significant. Cow evaluations, which are typically based on within herd-year levels, may be more biased by differences in variation within herd-years. McEwen and Winkleman (1990) studied the expressions of sire proofs at various herd production levels and found that the herd-year level by sire proof interaction was highly significant for milk and fat yield.

Vinson et al. (1975) studied the effect of herd, classifier and their interaction on the variability of overall type score, score card ratings, (i.e., general appearance, body capacity, dairy character and mammary system) and 12 other descriptive traits scored in Holstein Friesian descriptive classification program. They found that the percent of variance due to herd by classifier interaction was more than that due to classifiers effect alone for all traits and herd effect alone for all descriptive traits. For final score, variance due to herds (13.8%) is greater than that due to herd-classifier interaction (5.9%) or classifier (2.6%) effect alone. Sires, however, commonly have daughters with many herd-years, herd-classifiers or herd-year-season-classifiers of different levels and therefore the bias to sire proofs would likely be small.

Besides heterogeneous variance adjustment, the variance of evaluations should be stable over time because heterogeneous variance adjustment does not force the variance of evaluations to be constant. Moreover, the variance of evaluations is affected by the variance of appraisals. To stabilize the variance of evaluations, a base period for variance has to be specified. This will reduce the effects of changes in the variability of the scores assigned. These variance components should be updated periodically either with base change or major changes in the evaluation system. The updated variance components would then improve the correspondence between the evaluation and the correct characteristics of appraisal dates (Wiggans et al., 2004).

5. Classifiers' choice

The final score of a cow is a combination of front end/capacity (20%), dairy strength (20%), rump (5%), feet and legs (15%) and udder (40%). For bulls, the final score is a composite of front end/capacity (40%), dairy strength (25%), rump (10%) and feet and (&) legs (25%). The US classification system classifies cows every year and allows for downgrading. From a statistical and genetic point of view, a classification system that allows for downgrading and classifies all cows each year is advantageous (Schaeffer et al., 1978). In contrast, the Canadian classification system does not permit the downgrading. When classifiers judge a young Canadian Holstein cow they are actually judging its conformation at maturity (Jamrozik and Schaeffer, 1988). Nonetheless, the accuracy of this criterion depends on how precise the classifiers are in judging the cows. Also, inexperienced classifiers tend to give extreme scores (Vinson et al., 1975). Moreover, in the US the classification system tends to be subjective (Schaeffer et al., 1978). Wilcox et al. (1962), using US data, showed that the correlation between appraisals given by two classifiers at the same time on the same cow was only 0.7, and between appraisals on the same cow at different times by the same classifier was 0.5. Hansen et al. (1969) also reported that the US cows were appraised higher at the beginning and the end of lactation than during lactation. Additionally, the evaluators tended to raise scores as their age increased. Using the latest record of cows would partially account for bias due to classifiers' choice.

6. Adjustment factors

Cassell et al. (1973) computed age adjustment factors for final score and other four score card categories using data on registered Holstein cows classified from 1967 to 1971. The Holstein Association used a two-step multiplicative approach to adjust type scores for age within parity and stage of lactation across parity. This two-step approach over-adjusted for age (Hayes and Mao, 1987) and under-adjusted for the stage of lactation (Funk et al., 1991). Bonaiti et al. (1993) pointed out that pre adjustment for age or parity effect may seriously affect the estimation of genetic trend. The score given to a cow should represent her present age and stage of lactation rather than its age at maturity. This would help to compute better age and stage adjustment factors.

7. Differences between registered and grade animals

Pedigrees of registered animals may be recorded fairly accurately over many generations but genetic evaluations also include grade animals with pedigrees that may trace back only one to two generations. These differences in known pedigree information, preferential feeding and management of registered cows might make them appear to be superior to grades within herds while overall, the grades are genetically similar to registered cows (Powell and Norman, 1986).

Although, registered cows produced significantly more milk and fat than grade cows with unidentified parents there was no difference between registered and sire identified grade cows. This might be due to use of similar AI sires in both registered and sire identified grade populations. However, most bulls had a mixture of registered and grade daughters so bias in sire summaries can be smaller and no important misrankings would occur due to differences in registry status.

8. Regional differences

The effect of location in the US was investigated and found to be unimportant (Tong et al., 1980; Funk et al., 1991). Increase in inter-regional reciprocal semen exchange accurately accounted for the genetic differences between regions so it is undesirable to include the effect of region of sire stud in a model for national evaluations.

Summary of literature review

Very few studies have been recently conducted on the potential source of bias in sire evaluations though many of them were identified in earlier studies. The present study aims to improve the genetic evaluation model by accounting for the above mentioned sources of bias thus, reducing the changes in genetic evaluations for PTA type from 1st to 2nd crop of daughters.

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CHAPTER 3

CHANGES IN GENETIC EVALUATIONS FROM 1ST TO 2ND CROP FOR FINAL SCORE IN HOLSTEINS [1]

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[1] V. Koduru, I. Misztal, S. Tsuruta, T. Lawlor. To be submitted to the Journal of Dairy Science.

Abstract

The purpose of this study was to investigate the changes of predictive transmitting abilities (PTAs) of Holstein sires for final score from 1st to 2nd crop of daughters. The PTAs were estimated from two datasets: D01 (records classified up to 2001) and D05 (records classified up to 2005). The PTA changes were calculated as difference between the evaluations based on D01 and D05. The PTAs were adjusted to a common genetic base of all evaluated cows born in 1995. The single trait animal model (ST) included the fixed effects of herd-year-season-classifier, age by year group at classification, stage of lactation at classification, registry status of animal and additive genetic and permanent environment random effects. Unknown parent groups (UPG) were defined based on every other birth year starting from 1972 to a year that contained at least 1000 unknown parents. Modifications to the ST model included using single record per cow, considering separate UPG for 1st and 2nd crop daughters, separate UPG for sires and dams, and using additional pedigrees for dams' with missing phenotypic records. Also, multiple trait model treated records of registered and grade cows as correlated traits. The mean PTA change, for all the sires, was close to zero in all the models analyzed. However, the estimated mean PTA change, for the selected 145 sires (i.e. sires with 40 to 100 first crop and ≥ 200 second crop daughters) was -0.33, -0.20, -0.13, -0.28 and -0.12 with ST, only first records, only last records, updated pedigrees and allowing separate UPG for sires and dams after updating pedigrees, respectively. The percentages of sires showing drops were reduced from 74.5% (with ST) to 57.3% by using only last records of cows; and to 56.4% by allowing separate UPG for sires and dams after updating the pedigrees. Though updating of the pedigrees alone was not effective, alternate UPG for sires together with additional pedigree is helpful in reducing the drops.

Keywords: Final score, Holstein, PTA

Introduction

Changes in sires' PTA from 1st to 2nd crop evaluation have been a major concern to the dairy industry. A sire's initial progeny evaluation, based on 1st crop daughters, should be an unbiased estimate of later evaluations based on 1st and additional 2nd crop daughters. Some changes in PTA are expected due to additional daughter information. Selective reporting of daughters and misidentification or lack of pedigree information could also result in larger changes than expected. Parental selection, female selection, non-randomness in sire sampling, evaluation procedures (Bolgiano, 1979), and preferential treatment practices can also cause bias in sire evaluations (Kuhn and Freeman, 1995). Parental selection can be partially accounted by using complete pedigrees (Kennedy and Sorensen, 1990) and data on all candidates for selection (Henderson, 1975). Although, animal model evaluations account for differential mating of sires, preferential treatment to daughters of bulls or to potential bulls and dams cannot be accounted for (Kuhn et al., 1994). Model fitting of random effect for preferential treatment was found ineffective in accounting for bias, since accurate estimation of variances for preferential treatment is not feasible (Kuhn et al., 1999). Generally, preferential treatment is practiced in 2nd or later proofs due to an outstanding 1st record. In these cases, bias due to preferential treatment can be reduced by using only first classification record of cows (Jamrozik and Schaeffer, 1988). However, quantifying the amount of bias with field data is very difficult (Weigel and Lawlor, 1994). With regard to type traits, changes can occur due to reclassification. This implies that popular bulls are put at a disadvantage when the 2nd crop of daughters, which have not yet been reclassified, enter the evaluation (Schaeffer and Lohuis, 1995). The disadvantage is greater if the re-classes are to higher scores only, as in Canada, and if the mates were re-classified more than the average. Improper accounting for heterogeneity of variances across subclasses, inaccurate age and stage of lactation adjustment factors, differences between registered and grade cows and variation among classifiers' choice could be other identified sources of bias (Schaeffer et al., 1978; Powell and Norman, 1986; Bonaiti et al., 1993; Togashi et al., 2004).

Although many studies investigated the causes of changes in PTA milk, fat and protein from 1st to 2nd crop evaluations, few studies looked at changes in PTA for type (PTAT). The objectives of the present study are to identify factors responsible for large changes in sires' PTAT from 1st to 2nd crop evaluations, and to use this information to improve genetic evaluation.

Materials and Methods

Data

Conformation final scores of Holsteins were obtained from the Holstein Association USA, Inc. PTAs were estimated from two datasets: D01 (final score records classified up to 2001) and D05 (records classified up to 2005). D01 comprised 7.7 million records from 4.6 million cows and D05 comprised 8.4 million records from 5.1 million cows. Figure 3.1 illustrate the distribution of records as a function of year of classification. There are fewer of records in most recent years of classification because very few animals had a chance to reclassify. The percentage of grade cows has increased gradually from 12% in 1980 to 37% in 1990. The percentage of records from grade cows also increased over the same period to 40% in 2005 (Figure 3.1). Figure 3.2 shows the distribution of mean final score (of all records, of records from registered cows, of records from grade cows) by year of classification. The mean final score was maximum (80.1 ± 4.8) in 1973, minimum (78.1 ± 3.7) in 1994 and the average was 79.2 ± 4.4. Registered cows had a higher mean final score (80.02 ± 4.08) than grade cows (75.98 ± 3.83) across all classification years.

Pedigrees

Table 3.1 illustrates characteristics of the pedigree files used with D01 and D05. The pedigree file of D01 consisted of 5,993,207 animals and that of D05 included 6,606,175 animals. In the last pedigrees, 4,082,433 had both parents known and 1,366,322 had neither parents known. Of 2,889,071 dams in D05, only 1,389,893 had both parents known, 134,821 had only sire known and 1,364,340 had neither parent known. Tracing the pedigrees of dams with missing parentage added 892,546 pedigrees to the pedigree file of D01 and 955,672 to that of D05 (Table 3.1). Of the 1,364,340 dams that had neither parents known (in the pedigree file of D05) 1,250,332 acquired both parents information by updating the pedigrees (Table 3.2).

Statistical analysis

I. Variance component estimation

Variance components were estimated from three subsets of D05. Subset A included final score records classified during 1993-96; subset B during 1997-2000; and, subset C during 2001-04. Single trait (ST) and multiple trait (MT) animal models were used to estimate variances. The standard (ST) model was defined as

$$Y_{ijklmn} = HYSC_i + Age_j + S_k + R_l + a_m + p_m + e_{ijklmn}$$

where, $HYSC_i$ = fixed effect of management group (herd-year-season-classifier) i, Age_j = fixed effect of age x year group at classification j; S_k = fixed effect of stage of lactation at classification k; R_l = fixed effect of registry status (i.e., l=1 for registered animals and 2 for grade animals); a_m = additive genetic random effect of animal m; p_m = random permanent environment effect of cow m. Unknown parent groups (UPG) were defined based on every other birth year starting from 1972 to a year that contained at least 1000 unknown parents. Table 3.3 shows the total numbers of dams and sires with UPG starting from birth year 1972. Updating pedigrees (for

D05) reduced the dams replaced by UPG from 956,455 to 115,187 and increased the sires replaced by UPG from 33 to 4,547.

A MT model that considered the final scores of registered and grade cows as two separate but correlated traits was fit to the data. Each trait has the same effect as the ST model except that the registry status effect was eliminated. Adjustment for heterogeneity of variances within management group was also considered in the models as in Weigel et al., (1994).

II. Prediction of breeding values

In the ST model, the variance ratios to additive genetic and permanent environment effects were set to 1.6 and 2.5, respectively; this corresponds to a heritability of 0.31 and a repeatability of 0.80. Modifications to the ST model included:

1) Separate UPG for 1st and 2nd crop of daughters (SEPUPG).
2) Separate UPG for sires and dams (SEPUPG-SD).
3) Restricting the records to first (ST-FCL) or last (ST-LCL).
4) Inclusion of additional pedigrees for dams with missing parentage (ST-PED).
5) Additional pedigrees and separate UPG for sires and dams (ST-PED-SUPG-SD).
6) Additional pedigrees and using only first (ST-PED-FCL) or last (ST-PED-LCL) records.
7) Applying a multi-trait model (MT) assuming final score of registered and grade cows are two separate correlated traits.

Sires born in recent years were expected to have their initial evaluation, based on 1st crop daughters only, by 2001 and those returned to service were expected to have their later evaluations, based on 1st and additional 2nd crop daughters, by 2005. Thus, for common sires in D01 and D05, the PTAs computed using D01 were considered 1st crop evaluations (PTA-01) and those predicted using D05 were 2nd crop evaluations (PTA-05). These sires were defined as those with 40 to 100 daughters classified by 2001 and ≥ 200 daughters classified by 2005. All PTAs were adjusted to the genetic base of all evaluated cows born in 1995 and compared for stability of genetic evaluations from 1st to 2nd crop evaluation. PTA change was calculated as the difference between base adjusted PTA-01 and PTA-05. Correlations between Parent average (PA) and PTA were calculated by sire birth year.

Results and Discussion

I. Estimates of (Co) variances and heritability

Table 3.4 shows the variance components estimated with the ST model using the three subsets of data. The variation between variance components was significant between subset A & C but not between A & B and B & C. Additive genetic variance estimates decreased over time from 1993 to 2004. Additive genetic variance estimated from subset A was higher (4.2) than estimates from subset B (4.0) and subset C (3.3). A larger decrease was observed from 1997 to 2004 than from 1993 to 1997. This decrease may be due to selection and increased numbers of grade cows, which have limited pedigree information in recent years, as described by Tsuruta et al., (2002). Sorensen et al., (2001) also observed a similar pattern in additive genetic variance in recent years and reported that increased inbreeding and linkage disequilibrium are responsible for the observed downward trend in additive genetic variance. The reduction in the additive genetic variance might also be due to increased selection pressure on final score or other correlated traits in recent years (Tsuruta et al., 2004).

Estimates of the residual variance decreased from subset A to subset C. Permanent environmental variance estimated from subset C is higher than from the other two subsets of data. Heritability estimates from subsets A and B were similar (0.30) but were reduced (0.26) in subset C. The differences between variances estimated from different subsets of data may also be due to changes in the structure of field data, i.e. changing the definition of final scores or changes in base definition.

Table 3.5 shows (co) variance components estimated with the MT model. Changes in the estimates of variance components across the three subsets of data were similar to those observed with the ST model. The additive genetic variances of registered cows were higher. This may be due to more pedigree information available and better accuracy of recording. However, the estimated residual and permanent environment variances of registered cows were lower in all the three time periods. The lower residual variance for registered cows might be due to better management. In the end, the heritability of final score for registered cows is greater than for grade cows across the three subsets of data. Repeatability estimates of registered and grade cows were similar over time. The genetic correlations between registered and grade cows was high (0.77) and constant over time. Even though the variances altered over time, the variances estimated from subset B are similar to those reported in the literature. Subset B also represents the most recent data common to both D01 and D05. Hence, the variances estimated from subset B (i.e. 1997-2000) were utilized in the present study.

II. Summary of predicted transmitting abilities (PTAs)

PTA changes were calculated for two groups of sires: 'ALL' includes all the sires with daughters in both D01 and D05; and, 'SELECT' comprise 145 sires with 40 to 100 daughters in D01 and ≥200 daughters in D05. For ALL sires, means and standard deviations of the base adjusted PTA-01 and PTA-05, for all models, are summarized in Table 3.6. The correlations between PTA-01 and PTA-05 ($r_{01,05}$) are also presented in Table 3.6. For sires with no change in the number of progeny from the 1st to 2nd crop evaluations, the mean PTA change was close to zero. Only a few sires had more daughters added in 2nd crop evaluations so the correlation between PTA-01 and PTA-05 was close to 1.0 in all the models analyzed. For SELECT sires, the means and standard deviations of PTA-01 & PTA-05 and $r_{01,05}$ are also presented in Table 3.6. The correlation, between PTA-01 and PTA-05, was 0.77 in the ST model and increased to 0.82 in the ST-PED-SUPG-SD model.

III. Summary of PTA type changes

Table 3.7 summarizes means and standard deviations of changes in sire PTA from 1st to 2nd crop. For ALL sires, the mean PTA change ranges from -0.03 to 0.06 among different models analyzed.

For SELECT sires, the PTA change ranged from -1.77 to 0.65 in the ST model with a mean PTA change of -0.33 ± 0.04. As demonstrated in Figure 3.3, the distribution of PTA changes for SELECT sires, with ST, is negatively skewed. Adding separate UPG to 2nd crop daughters (SEPUPG) increased the mean changes to -0.38 ± 0.04. Adding separate UPG for sires (SEPUPG-SD) slightly reduced the changes to -0.29 ± 0.04. Separate UPG for sires had very few (33) contributing animals with sire missing but dam present (Table 3.3). Restricting the records to only first classification records of cows (ST-FCL) reduced the mean PTA change to -0.20 ± 0.03. The decrease is mainly due to increased merit of all the sires, including the old sires. This reduced the merit of dams of 2nd crop daughters and increased the merit of 2nd crop evaluations of sires. When only the last records were used (ST-LCL), the mean PTA change was further reduced to -0.13 ± 0.04. Later records are, on average, higher than first. Only 1st crop will have later records when 2nd crop is coming resulting in inflated 2nd crop evaluations.

Inclusion of additional pedigrees for dams with missing parentage (ST-PED) reduced the drops (-0.28 ± 0.04) very little compared to ST. Allowing separate UPG for sires and dams together with additional pedigrees (ST-PED-SUPG-SD) greatly reduced the mean PTA change to

-0.12 ± 0.03. Addition of pedigrees increased the number of sires contributing to UPG from 33 to 4,547 (in D05) and allowed more accurate estimation of genetic groups for sires (Table 3.3). Figure 3.4 shows less negatively skewed distribution of PTA changes estimated with ST-PED-SUPG-SD than those of with ST model. Because most of UPG contributions for sires are for dams of test cows, these UPG act as proxy for average merit of dams of test bulls.

Results of the MT model showed that the mean PTA change was larger for registered cows (-0.41 ± 0.04) than for grade cows (-0.24 ± 0.03), although the changes are large. Smaller changes in grade cows PTA could be due to lower additive genetic variances in grades.

IV. Percentage of sires showing PTA changes

The percentage distributions of the SELECT sires, divided into three categories according to PTA change, are given in Table 3.8. The percentage of sires showing drops were 74.5% with the ST model, of which 27.6% were showing a change between -1 to -0.5 and 6.9 % showing change > -1. The percentage of sires showing drops was 78.6 % when allowing separate UPG for 2nd crop daughters (SEPUPG) and was slightly reduced (72.4%) when allowing separate UPG for sires (SEPUPG-SD). This small variation in percentage may be due to random chance as there is no observable difference between parent averages of these sires among the above three models. Using only first classification records of cows (ST-FCL) reduced the percentage of sires showing drops to 64.8% of which, only 20.7% were showing a drop of high magnitude i.e. below -0.5. Considering only the most recent classification records of cows (ST-LCL) further reduced the percentage of sires showing drops beyond -0.5 to 17.3%. The changes with the MT model were similar as in the ST model, suggesting minor influence of grade status on PTA changes.

Using additional pedigrees (ST-PED) slightly reduced the percentage of sires showing drops from 74.5% to 72.1%, of which 32.0% were showing a change below -0.5. Only a slight improvement was possibly due to low connectivity through those dams and possibly larger misidentifications. The percentage of sires showing changes below -0.5 was reduced to 17.7% by ST-PED-LCL and 17.0% by ST-PED-FCL. The accuracy of evaluation methods based on first classification records only depends on how accurate the classifiers are in judging a cow at a young age. Restricting data to only the most recent classification reduces the drops but retains bias in 2nd crop and may cause more bias than actually reducing. Using single records per cow would also reduce the participation in the classification program.

The percentage of sires showing drops was smallest (56.4%) with separate UPG for sires and dams together with additional pedigrees (ST-PED-SUPG-SD). Only 12.2% of sires showed a change below -0.5. Correlations between parent average (PA) and PTA for sires, born after 1991, are shown in Figure 3.5. Correlations were higher with the ST-PED-SUPG-SD model compared to the ST model. Compared to the other models the ST-PED-SUPG-SD model had a lower mean PTA change of -0.12, a smaller percent to sires showing drops (56.4%) and a high correlation between PA and PTA (0.745).

Conclusions

Large changes in sire PTA type for final score were observed from 1st to 2nd crop evaluations especially for sires born in recent years. Drops were caused indirectly by increased fraction of grade cows and subsequently inadequate accounting for merit of mates. Drops are reduced by allowing separate UPG for sire and dams along with additional pedigrees for dams, and also by using single record per cow. However, drops are not reduced by considering separate UPG for 1st and 2nd crop daughters, additional pedigrees alone and by considering differences in registered and grade animals. Use of the first records reduces the drops but also the accuracy of evaluations. Using only the last records reduces the drops but causes bias in the second crop.

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Table 3.1: Characteristics of regular and updated pedigrees of D01[1] and D05[2] as used in the genetic analyses.

	Total #	***# of parents known***			
		Both	**Sire only**	**Dam only**	**Both unknown**
Regular pedigree					
		D01			
Animals	5,993,207	3,742,249	991,273	268	1,259,417
Sires	177,638	174,319	1,072	268	1,965
Dams	2,640,736	1,271,700	111,569	0	1,257,452
		D05			
Animals	6,606,175	4,082,433	1,157,141	279	1,366,322
Sires	189,003	185,610	1,117	279	1,982
Dams	2,889,071	1,389,893	134,821	0	1,364,340
Updated pedigree					
		D01			
Animals	6,885,753	5,704,276	1,080,000	2,786	98,691
Sires	271,342	267,223	188	4	3,927
Dams	3,628,177	3,319,152	211,479	2,782	94,764
		D05			
Animals	7,561,587	6,171,764	1,260,822	6,010	122,991
Sires	285,850	280,758	233	4	4,855
Dams	3,961,039	3,585,311	251,586	6,006	118,136

[1] D01: records classified up to 2001

[2] D05: records classified up to 2005

Table 3.2: Number of dams and sires with different classes of updated parent information with the additional pedigree files of D01[1] and D05[2]

# of dams		***# of sires***		***Change in known pedigree info from***		
D01	***D05***	***D01***	***D05***	***Regular***	**=>**	***Updated pedigree file***
491	491	925	927	Only sire	**=>**	Both
0	0	254	269	Only dam	**=>**	Both
1,159,847	1,250,332	1,818	1,833	None	**=>**	Both
84,523	96,914	0	0	None	**=>**	Only sire
2,443	4,836	0	0	None	**=>**	Only dam

[1] D01: records classified up to 2001
[2] D05: records classified up to 2005

Table 3.3: Number of sires and cows occurring as parents but without pedigree information in regular and updated pedigree files of D01[1] and D05[2]

	Regular pedigree			**Updated pedigree**	
	D01	***D05***		***D01***	***D05***
Dams[*]	849,628	956,455		91,924	115,187
Sires[**]	24	33		3,628	4,547

[*] Dams: cows occurring as parents but without pedigree information

[**] Sires: sires occurring as parents but without pedigree information

[1] D01: records classified up to 2001

[2] D05: records classified up to 2005

Table 3.4: Estimates of variance components from single trait models

Parameter[*]	**Subset A**[1]	**Subset B**[2]	**Subset C**[3]
$\sigma^2{}_a$	4.20	4.00	3.30
$\sigma^2 p$	6.30	6.20	7.10
$\sigma^2 e$	2.80	2.50	2.30
h^2	0.31	0.31	0.26
r^2	0.79	0.80	0.82

[*] $\sigma^2{}_a$: additive genetic variance; $\sigma^2 p$: permanent environment effect variance; $\sigma^2 e$: random residual variance; h^2 : heritability (%); r^2 : repeatability(%)

[1] Subset A: Subset of whole data with records classified from 1993 to 1996

[2] Subset B: Subset of whole data with records classified from 1997 to 2000

[3] Subset C: Subset of whole data with records classified from 2001 to 2004

Table 3.5: Estimates of (co) variances from multiple trait animal models

Parameter*	**Animal type**	**Subset A[1]**		**Subset B[2]**		**Subset C[3]**	
		Reg.	**Grade**	**Reg.**	**Grade**	**Reg.**	**Grade**
σ^2_a	**Reg.**	4.44	2.80	4.24	2.72	3.72	2.41
	Grade	2.80	3.25	2.72	2.92	2.41	2.65
$\sigma^2 p$		6.02	7.21	5.51	7.99	5.97	8.90
$\sigma^2 e$		2.81	3.55	2.51	2.81	2.32	2.47
h^2		0.33	0.23	0.35	0.21	0.31	0.19
r^2		0.79	0.75	0.80	0.80	0.81	0.82
$\mathbf{r}_{(\mathbf{reg,grade})}$		0.74		0.77		0.77	

* σ^2_a : additive genetic variance; $\sigma^2 p$: permanent environment effect variance;
$\sigma^2 e$: random residual variance; h^2 : heritability (%); r^2 : repeatability(%)

[1] Subset A: Subset of whole data with records classified from 1993 to 1996

[2] Subset B: Subset of whole data with records classified from 1997 to 2000

[3] Subset C: Subset of whole data with records classified from 2001 to 2004

Table 3.6: Statistics of PTA for two datasets and several models

Animal Models[*]	**ALL (N=177451)**[**]		**SELECT (N=145)**[**]		
	MPTA-01[1]	**MPTA-05**[2]	**MPTA-01**[1]	**MPTA-05**[2]	$\mathbf{r}_{(01,05)}$[3]
ST	-1.29 ± 0.003	-1.32 ± 0.003	1.23 ± 0.06	0.90 ± 0.05	0.77
SEPUPG	-1.29 ± 0.003	-1.33 ± 0.003	1.2 ± 0.06	0.89 ± 0.05	0.77
SEPUPG-SD	-1.31 ± 0.003	-1.34 ± 0.003	1.28 ± 0.06	0.99 ± 0.05	0.78
ST-FCL	-1.20 ± 0.002	-1.19 ± 0.002	1.27 ± 0.06	1.06 ± 0.06	0.81
ST-LCL	-1.33 ± 0.002	-1.23 ± 0.002	1.16 ± 0.06	1.03 ± 0.06	0.80
ST-PED	-1.61 ± 0.002	-1.61 ± 0.002	1.32 ± 0.06	1.04 ± 0.05	0.78
ST-PED-SUPG-SD	-1.69 ± 0.002	-1.67 ± 0.002	1.41 ± 0.06	1.29 ± 0.05	0.82
ST-PED-FCL	-1.51 ± 0.002	-1.47 ± 0.002	1.38 ± 0.06	1.25 ± 0.06	0.82
ST-PED-LCL	-1.56 ± 0.002	-1.53 ± 0.002	1.39 ± 0.06	1.21 ± 0.06	0.81
MT Reg.	-1.54 ± 0.003	-1.58 ± 0.003	1.12 ± 0.06	0.71 ± 0.06	0.75
Grade	-0.60 ± 0.001	-0.56 ± 0.001	1.08 ± 0.05	0.84 ± 0.05	0.80

[*] ST: single trait repeatability animal model; SEPUPG: ST with separate UPG for 1st and 2nd crop daughters; SEPUPG-SD: ST with separate UPG for sires and dams; ST-FCL: ST with only 1st classification record of cow; ST-LCL: ST with only last classification record of cows; ST-PED: ST with additional pedigree; ST-PED-SUPG-SD: ST-PED with separate UPG for sire and dams; ST-PED-FCL: ST-PED with only 1st classification record of cows; ST-PED-LCL: ST-PED with only latest classification record of cows; MT: Multiple trait animal model

[**] ALL: all the sires with daughters in both D01 and D05; SELECT: sires with 40 to 100 daughters classified by 2001 (D01) and ≥200 daughters classified by 2005 (D05)

[1] MPTA-01: average 1st crop PTAs of sires

[2] MPTA-05: average 2nd crop PTAs of sires

[3] $r_{(01,05)}$: correlation between 1st crop and 2nd crop PTAs

Table 3.7: Estimates of PTA changes from 1st to 2nd crop evaluations for several models

Animal Models[*]	ALL (N=177451)[**]				SELECT (N=145)[**]		
	Mean	**Min**	**Max**		**Mean**	**Min**	**Max**
ST	-0.03 ± 0.0001	-1.77	2.19		-0.33 ± 0.04	-1.77	0.65
SEPUPG	-0.04 ± 0.0001	-1.82	2.19		-0.38 ± 0.04	-1.82	0.60
SEPUPG-SD	-0.03 ± 0.0001	-1.72	2.27		-0.29 ± 0.04	-1.72	0.73
ST-FCL	0.00 ± 0.0001	-1.66	2.23		-0.20 ± 0.03	-1.41	0.85
ST-LCL	0.10 ± 0.0001	-1.55	2.29		-0.13 ± 0.04	-1.40	0.88
ST-PED	0.00 ± 0.0001	-1.78	3.85		-0.28 ± 0.04	-1.78	0.65
ST-PED-SUPG-SD	0.03 ± 0.0001	-2.14	4.29		-0.12 ± 0.03	-1.47	0.81
ST-PED-FCL	0.04 ± 0.0001	-2.46	2.63		-0.14 ± 0.03	-1.29	0.85
ST-PED-LCL	0.02 ± 0.0001	-2.67	2.18		-0.18 ± 0.03	-1.46	0.77
MT Reg.	-0.04 ± 0.0001	-1.86	5.85		-0.40 ± 0.04	-1.85	0.78
Grade	0.04 ± 0.0001	-1.54	1.85		-0.24 ± 0.03	-1.39	0.58

[*] ST: single trait repeatability animal model; SEPUPG: ST with separate UPG for 1st and 2nd crop daughters; SEPUPG-SD: ST with separate UPG for sires and dams; ST-FCL: ST with only 1st classification record of cow; ST-LCL: ST with only last classification record of cows; ST-PED: ST with additional pedigree; ST-PED-SUPG-SD: ST-PED with separate UPG for sire and dams; ST-PED-FCL: ST-PED with only 1st classification record of cows; ST-PED-LCL: ST-PED with only latest classification record of cows; MT: Multiple trait animal model

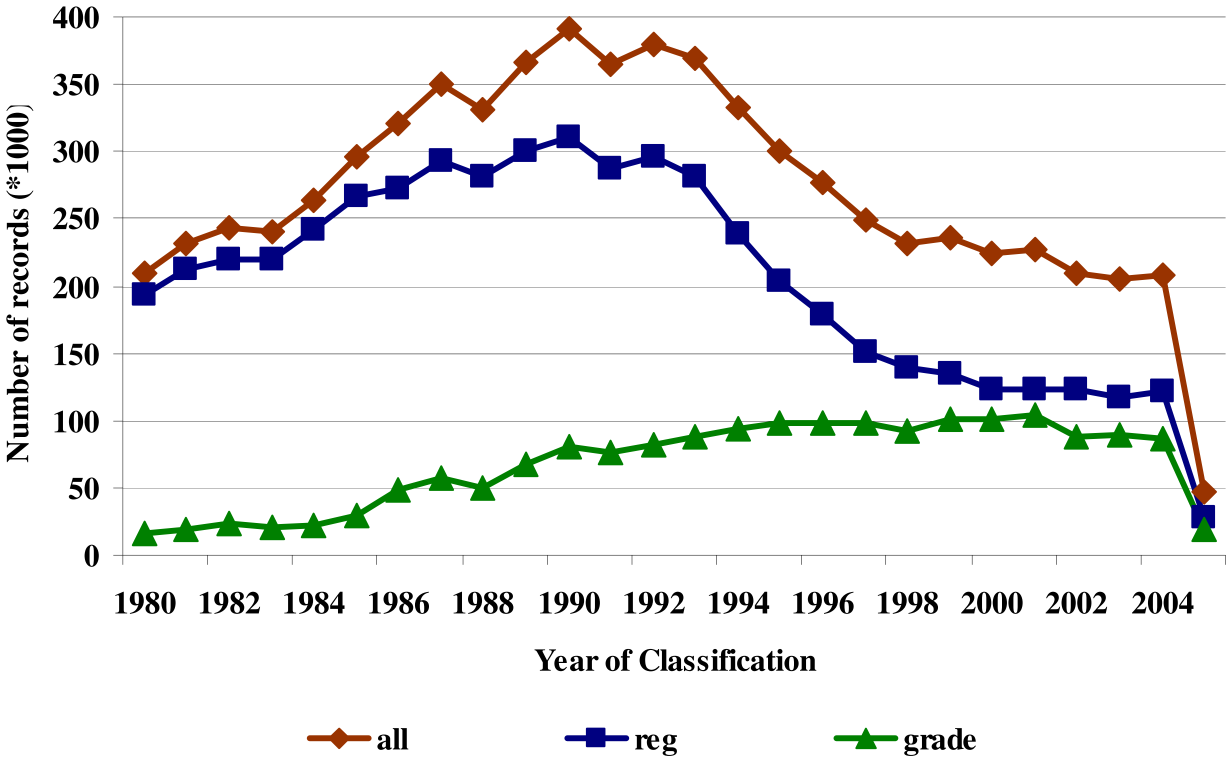
[**] ALL: all the sires with daughters in both D01 and D05; SELECT: sires with 40 to 100 daughters classified by 2001 (D01) and ≥200 daughters classified by 2005 (D05)

Table 3.8: Percentage of SELECT* sires (N=145) showing drop in PTA from 1st to 2nd crop for different models

Animal models**[**]**	***% Sires Showing drops between***			
	0 to -0.5	**-0.5 to -1**	**> -1**	**Total**
ST	40.0	27.6	6.9	74.5
SEPUPG	40.7	30.3	7.6	78.6
SEPUPG-SD	41.4	24.8	6.2	72.4
ST-FCL	44.1	16.6	4.1	64.8
ST-LCL	40.0	14.5	2.8	57.3
ST-PED	40.1	25.9	6.1	72.1
ST-PED-SUPG-SD	44.2	8.8	3.4	56.4
ST-PED-FCL	42.2	13.6	3.4	59.2
ST-PED-LCL	45.6	13.6	4.1	63.3
MT Reg.	42.8	24.8	11.7	79.3
Grade	46.9	20.0	3.5	70.4

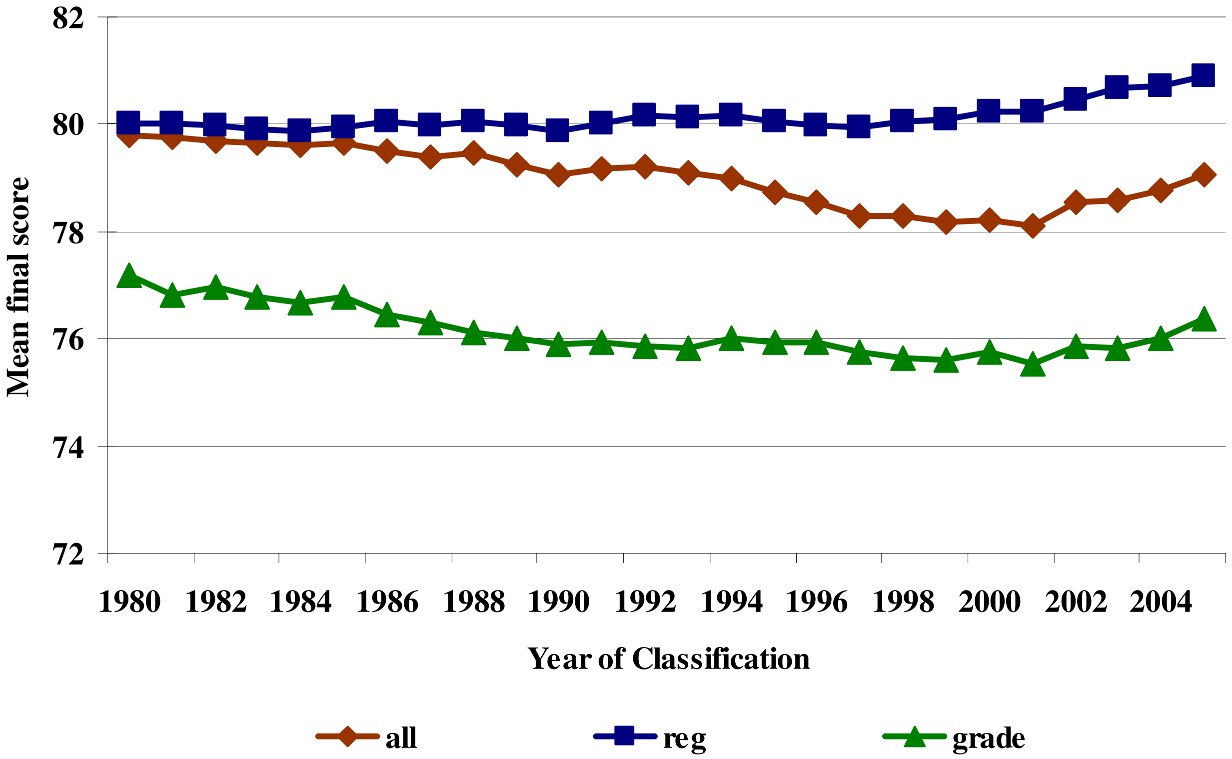
[*] SELECT: sires with 40 to 100 daughters classified by 2001 (D01) and ≥200 daughters classified by 2005 (D05)

[**] ST: single trait repeatability animal model; SEPUPG: ST with separate UPG for 1st and 2nd crop daughters; SEPUPG-SD: ST with separate UPG for sires and dams; ST-FCL: ST with only 1st classification record of cow; ST-LCL: ST with only last classification record of cows; ST-PED: ST with additional pedigree; ST-PED-SUPG-SD: ST-PED with separate UPG for sire and dams; ST-PED-FCL: ST-PED with only 1st classification record of cows; ST-PED-LCL: ST-PED with only latest classification record of cows; MT: Multiple trait animal model



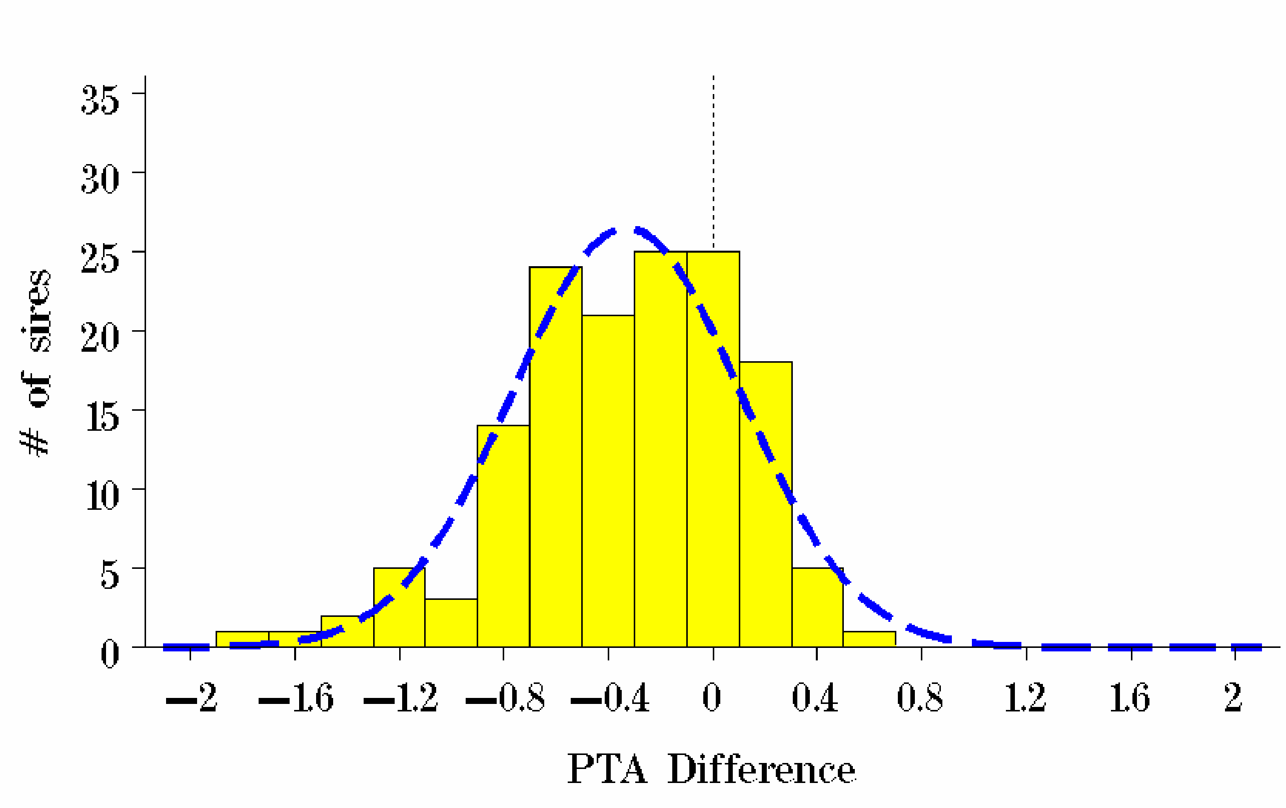
[*]all: all the records; reg: records from registered cows; grade: records from grade cows

Figure 3.1: Distribution of number of records by classification year



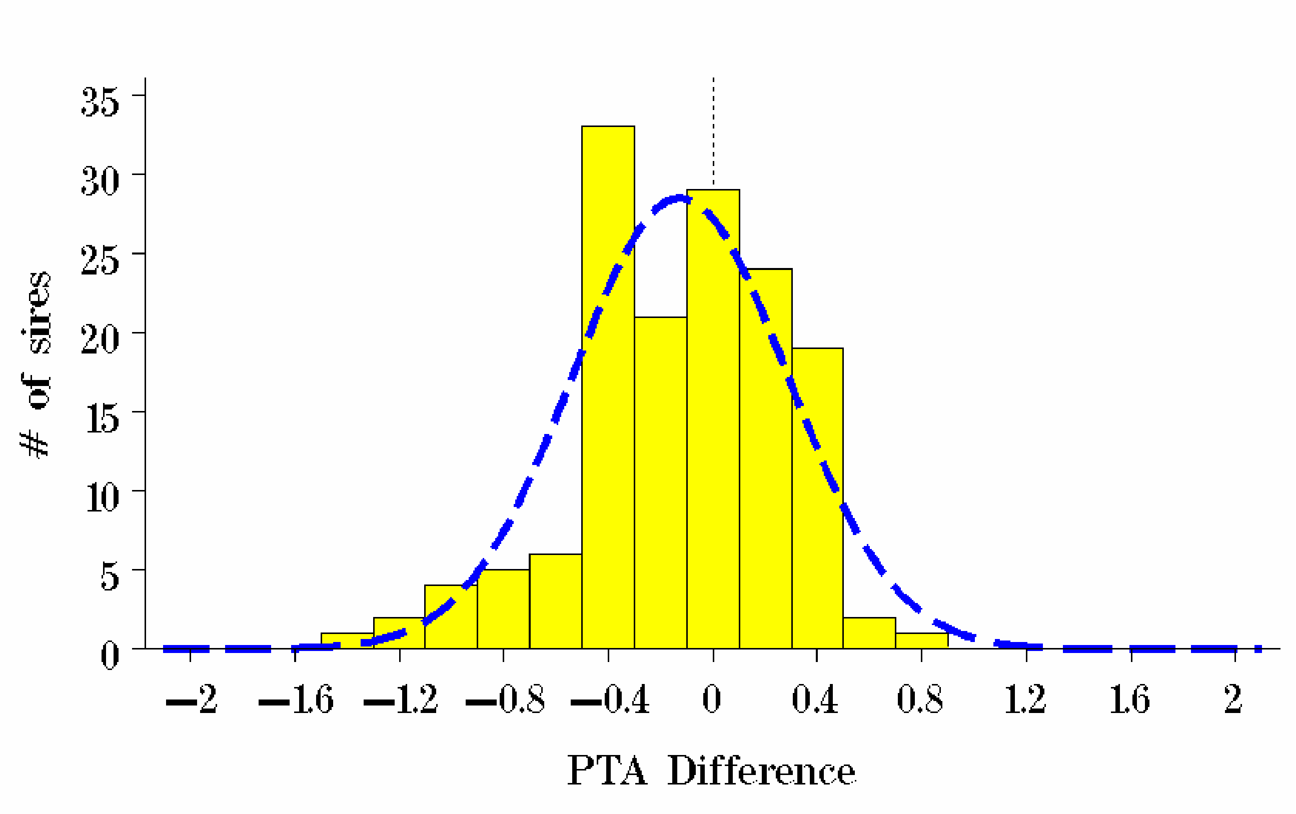
*all: overall mean final score; reg: mean final score of records from registered cows; grade: mean final score of records from grade cows

Figure 3.2: Distribution of mean final scores by classification year



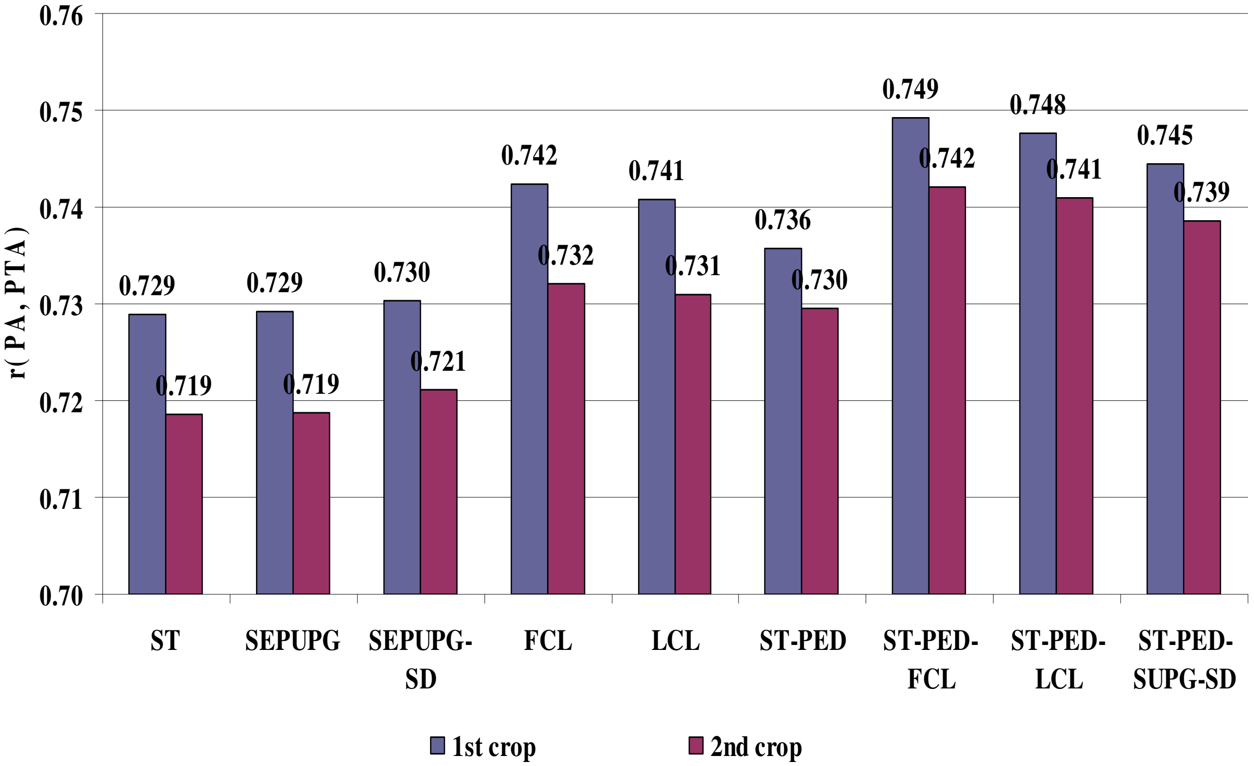
*PTA Difference: difference between 1st crop and 2nd crop predictive transmitting abilities (PTAs)
[1]SELECT: sires with 40 to 100 daughters classified by 2001 and ≥200 classified by 2005
[2]ST: single trait model

Figure 3.3: Distribution of PTA changes for SELECT[1] sires – ST[2]



[*] PTA Difference: difference between 1st crop and 2nd crop predictive transmitting abilities (PTAs)
[1] SELECT: sires with 40 to 100 daughters classified by 2001 and ≥200 classified by 2005
[2] ST-PED-SUPG-SD: single trait model with additional pedigrees and separate UPG for sire and dams

Figure 3.4: Distribution of PTA changes for SELECT[1] sires - ST-PED-SUPG-SD[2]



*r(PA,PTA): correlation between parent average (PA) and PTAs; 1st crop: evaluations based on records classified up to 2001; 2nd crop: evaluations based on records classified up to 2005; ST: single trait repeatability animal model; SEPUPG: ST with separate UPG for 1st and 2nd crop daughters; SEPUPG-SD: ST with separate UPG for sires and dams; ST-FCL: ST with only 1st classification record of cow; ST-LCL: ST with only last classification record of cows; ST-PED: ST with additional pedigree; ST-PED-SUPG-SD: ST-PED with separate UPG for sire and dams; ST-PED-FCL: ST-PED with only 1st classification record of cows; ST-PED-LCL: ST-PED with only latest classification record of cows; MT: Multiple trait animal model

Figure 3.5: Correlation between PTA and PA for all sires born after 1991, multiple models

CHAPTER 4

TRENDS IN 1ST AND 2ND CROP PTA AND MENDELIAN SAMPLING FOR FINAL SCORE IN HOLSTEINS [1]

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[1] V. Koduru, I. Misztal, S. Tsuruta, T. Lawlor. To be submitted to Livestock Prod. Sci.

Abstract

The purpose of this study was to analyze trends in predicted transmitting abilities (PTAs), average and standard deviation (SD) of mendelian sampling (MS) estimates for final score from 1st to 2nd crop of daughters for Holstein sires. Data included 8.4 million final scores from 5.1 million cows. The data was divided into two overlapping subsets: records classified up to 2001 (D01) and records classified up to 2005 (D05). The standard pedigree included 6.6 million animals, and an additional 1 million pedigrees were available for dams without records. A single trait animal model (ST) included the fixed effects of herd-year-season-classifier, age by year group at classification, stage of lactation at classification, registry status of animal; additive genetic and permanent environment random effects. Unknown parent groups (UPG) were defined based on every other birth year starting from 1972 to a year that contained at least 1000 unknown parents. Alternative UPG were defined separately for sires and cows by animal birth year. PTAs were computed for both subsets, standard and additional pedigrees, and regular and alternative UPG. All PTA were adjusted to a common genetic base of all evaluated cows born in 1995. A set of sires was identified that had a first crop of daughters by 2001 and the second crop by 2005. In the basic ST model, the trend for sires based on D01 was slightly superior for sires born in 1991-97 relative to D05. There was a slight decrease for cows born in 1998-99. With additional pedigrees, the inflation for sires was smaller while the trend was larger. With alternative UPG, the trend was even higher while the difference decreased further. With ST the trend for SD of MS estimates was fluctuating; the fluctuation disappeared with additional progeny and refined UPG. The genetic evaluation requires a balance of the size of pedigree and appropriately defined UPG.

Keywords: Final score, Holstein, PTA trends

Introduction

Genetic trends define the future of breed improvement (Lee et al., 1985). Monitoring genetic trends help determine the effectiveness of breeding programs (Hintz et al., 1978) and, indirectly, of genetic evaluation systems. Significant differences in the estimates of genetic trends obtained with older and newer datasets would indicate a bias in the sire evaluation system (Bonaiti et al., 1993; Biffani et al., 2001). Other indicators in identifying the source of bias are trends in the average and standard deviation (SD) of mendelian sampling (MS) estimates (i.e. difference between animals' parent average (PA) and its own PTA) (Van Doormaal and Miglior, 2000; Lidauer et al., 2005). Unbiased evaluation is expected to have an average MS of zero and not any trends over time in the SD of MS estimates (Van Doormaal and Miglior, 2000). The treatment and definition of phantom groups were found to be sensitive on multiple-across-country-evaluation (MACE) results (Fikse, 2003; Van der Linde et al., 2005). Koduru et al. (2006) investigated the drops of PTA for final score for Holstein sires from 1st to 2nd crop. They found that those drops could be minimized by applying additional pedigrees and refining the definition of unknown parent groups. The purpose of the present study was to investigate the impact of such changes on estimates of genetic trends with focus on change over 4 years, a period between the arrivals of 1st to 2nd crop daughters for sires born in recent years.

Materials and Methods

Data and pedigree

Conformation final scores of Holsteins were obtained from the Holstein Association USA, Inc. PTAs were estimated from two datasets: D01 (final score records classified up to 2001) and D05 (records classified up to 2005). D01 included 7.7 million records from 4.6 million cows and D05 included 8.4 million records from 5.1 million cows. The regular pedigree file, used with

D05, consisted of 6,606,175 animals, including 189,003 sires and 2,889,071 dams. Of these dams, 134,821 had only sire known and 1,364,340 had neither parent known. Tracing of the pedigrees of dams with missing parentage added 0.9 million more pedigrees to the regular pedigree file of D01 and 1 million to that of D05. The additional pedigrees of D05 reduced the number of dams without a pedigree from 956,455 to 115,187 and increased the number of sires without a pedigree from 33 to 4,547.

Statistical analysis

A single trait (ST) repeatability animal model included the fixed effects of management group (herd-year-season-classifier), age x year group at classification, stage of lactation at classification and registry status; plus, additive genetic and permanent environment random effects. Modifications to the ST model included:

(i) Inclusion of additional pedigrees for dams with missing parentage (ST-PED).

(ii) Additional pedigrees and separate UPG for sires and dams (ST-PED-SUPG).

Unknown parent groups (UPG) were defined based on every other birth year starting from 1972 to a year that contained at least 1000 unknown parents. PTAs were computed from both D01 and D05 datasets. Sires born in recent years were expected to have their initial evaluation, based on 1st crop daughters only, by 2001 and those sires which returned to service were expected to have later evaluations, based on 1st and additional 2nd crop daughters, by 2005. Thus, for common sires in D01 & D05 the PTAs computed using D01 were considered 1st crop evaluations and those predicted using D05 were 2nd crop evaluations. The PTAs were adjusted to the genetic base of all evaluated cows born in 1995. For animals with both parents known, the MS estimates were calculated as the difference between a sire's parent average and its own PTA. For sires and dams replaced by genetic groups the MS would be equal to zero if neither parent was known; and equal to difference between PA and its own PTA, if some other UPGs were assigned as parents of these animals. Yearly PTA trends were derived by comparing the average PTAs, by birth year, for sires with ≥ 10 daughters, cows with records and all dams. Trends in average and SD of MS estimates were also estimated as that of genetic trends. Mean PTA (or MS) difference was calculated as the difference between PTA (or MS) estimates from D01 and D05.

Results and Discussion

Sire PTA and average MS trends, computed from D01 with all 3 models (ST, ST-PED, ST-PED-SUPG), by sire birth year, are in Table 4.1 and those computed from D05 are in Table 4.2. From 1985 to 1997 the overall 1st crop mean PTA trend (i.e. trend computed from D01) was 0.04, 0.14 and 0.17 with the ST, ST-PED and ST-PED-SUPG models, respectively (Table 4.1). The overall 2nd crop mean PTA trend (i.e. trend computed from D05) was 0.12, 0.28 and 0.36 with ST, ST-PED and ST-PED-SUPG, respectively (Table 4.2). Only minor differences between models in either dataset were observed for average MS estimates.

Figure 4.1 illustrates the positive trend of 1st and 2nd crop PTAs, computed with ST, for sires, dams and cows. There is an observable difference between trends of sire PTAs from D01 to D05, especially for sires born after 1992, but not for cows and dams. Overall, from 1985 to 1997, the average PTA difference between D01 and D05 trends was -0.06. The slight upward trend in sire PTAs after 1999 and slight downward trend in cow PTAs after 1998 could be due to the smaller number of sires (788) and dams (5213) available. The trends in average and SD of MS estimates would support the existence of bias for sires (Van Doormaal and Miglior, 2000; Lidauer et al., 2005). Trends in average and SD of MS estimates, computed with the ST model, are presented in Figures 4.2 and 4.3, respectively. Average MS was close to zero for cows and there is no observable trend in average or SD of MS. For sires born after 1992, the 2nd crop average MS was higher than that of 1st crop and the trend in SD of MS was not flat, indicating bias in evaluations of sires born in recent years.

Treatment and configuration of genetic groups found to have significant effect on sires' PTA estimates (Fikse, 2003; Van der Linde et al., 2005). Trends in 1st and 2nd crop PTAs of UPG are illustrated in Figure 4.4. The 1st crop PTAs of UPG, computed with ST, were lower than 2nd crop PTAs. These differences were minimized with ST-PED. The sires and dams replaced by genetic groups are expected to have identical trend over time as they are considered to be from the base population. The PTA trends of these sires and dams, computed with ST, are not identical (Figure 4.5); indicating some differences between genetic groups of sires and dams. Trends in average MS of these sires also show some fluctuations. This could be due to the small number (33) of sires replaced by UPG available to estimate genetic trends. Conversely for the dams, the 1st crop and 2nd crop trends in average MS were identical and their average MS estimates were close to zero (Figure 4.6).

Sire's PTA trends, computed with all 3 models using both D01 and D05, are presented in Figure 4.7. For sires born from 1985 to recent years, the high mean PTA difference (-0.06), with the ST model, was reduced to -0.02 after including additional pedigrees (ST-PED) and practically eliminated with the ST-PED-SUPG model. PTAs of sire UPG (both 1st and 2nd crop) were higher than that of dam UPG (Figure 4.8). Subsequently the 1st and 2nd crop trends of sires and dams replaced by genetic groups are identical (Figure 4.9). The average MS estimates of these sires and dams were also close to zero (Figure 4.10).

While the average MS for cows and sires is close to zero, there are some fluctuations, especially in recent years. This could be due to other factors, such as preferential treatment of 1st crop daughters, selective reporting, or incomplete data from the last years.

Conclusions

Differences in trends of sire PTA type for final score were observed from 1st to 2nd crop evaluations especially, for the sires born after 1991. These differences were reduced by allowing separate UPG for sire and dams in addition to including additional pedigrees for dams. Including additional pedigrees alone was not significant.

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Table 4.1: Trends in average 1st crop sire PTAs[1] and average MS[2] by sire birth year (YOB) for several models[3]

Sire YOB	**# of sires**	**Mean 1ST crop PTAs**				**Mean 1ST crop MS estimates**		
		ST	**ST-PED**	**ST-PED-SUPG**		**ST**	**ST-PED**	**ST-PED-SUPG**
1985	1373	-0.61	-0.51	-0.53		0.09	0.09	0.09
1986	1482	-0.54	-0.45	-0.48		0.07	0.08	0.09
1987	1454	-0.44	-0.34	-0.37		0.07	0.07	0.08
1988	1473	-0.41	-0.31	-0.35		0.07	0.06	0.08
1989	1547	-0.14	-0.04	-0.07		0.08	0.09	0.09
1990	1575	0.00	0.11	0.08		0.10	0.10	0.10
1991	1555	0.11	0.22	0.22		0.08	0.09	0.09
1992	1652	0.10	0.21	0.23		0.11	0.11	0.10
1993	1543	0.19	0.30	0.35		0.10	0.11	0.09
1994	1490	0.35	0.46	0.54		0.11	0.12	0.09
1995	1452	0.49	0.59	0.71		0.11	0.13	0.10
1996	1325	0.60	0.70	0.85		0.10	0.11	0.09
1997	555	0.77	0.89	1.04		0.03	0.04	0.03

[1] PTA: predictive transmitting ability

[2] MS: mendelian sampling estimates

[3] ST: single trait repeatability animal model; ST-PED: ST with additional pedigree; ST-PED-SUPG: ST-PED with separate UPG for sires and dams

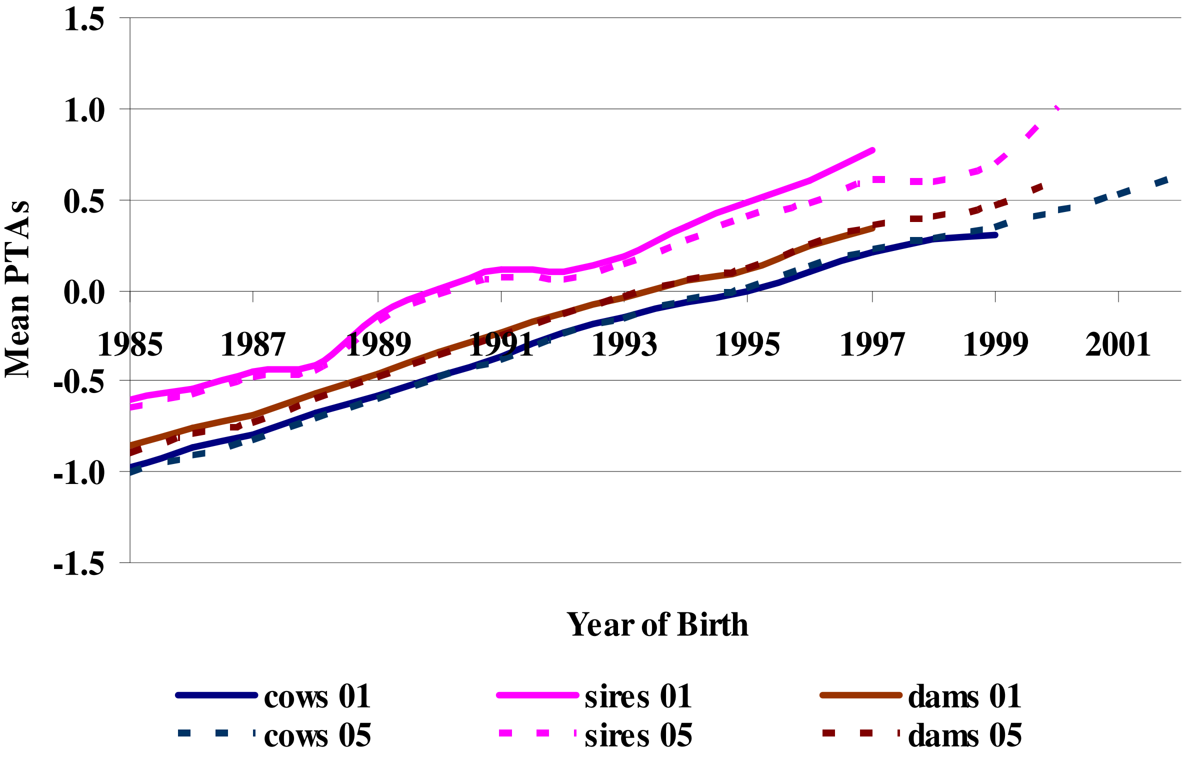
Table 4.2**:** Trends in average 2nd crop sire PTAs[1] and average MS[2] by sire birth year (YOB) for several models[3]

Sire YOB	**# of sires**	**Mean 2nd crop PTAs**				**Mean 2nd crop MS estimates**		
		ST	**ST-PED**	**ST-PED-SUPG**		**ST**	**ST-PED**	**ST-PED-SUPG**
1985	1374	-0.65	-0.53	-0.51		0.09	0.08	0.09
1986	1483	-0.58	-0.46	-0.46		0.07	0.07	0.09
1987	1455	-0.48	-0.33	-0.35		0.06	0.06	0.08
1988	1475	-0.44	-0.31	-0.33		0.07	0.06	0.08
1989	1553	-0.17	-0.03	-0.05		0.08	0.08	0.09
1990	1578	-0.03	0.12	0.11		0.10	0.10	0.10
1991	1563	0.07	0.23	0.24		0.09	0.09	0.08
1992	1668	0.05	0.22	0.25		0.11	0.10	0.09
1993	1571	0.13	0.32	0.37		0.11	0.11	0.08
1994	1529	0.27	0.44	0.53		0.13	0.13	0.10
1995	1528	0.40	0.57	0.69		0.13	0.14	0.11
1996	1452	0.47	0.64	0.79		0.13	0.14	0.11
1997	1398	0.61	0.78	0.96		0.10	0.12	0.10
1998	1438	0.59	0.75	0.96		0.08	0.10	0.07
1999	1257	0.70	0.86	1.09		0.06	0.08	0.06
2000	788	1.01	1.17	1.42		0.05	0.07	0.06

[1] PTA: predictive transmitting ability

[2] MS: mendelian sampling estimates

[3] ST: single trait repeatability animal model; ST-PED: ST with additional pedigree; ST-PED-SUPG: ST-PED with separate UPG for sires and dams

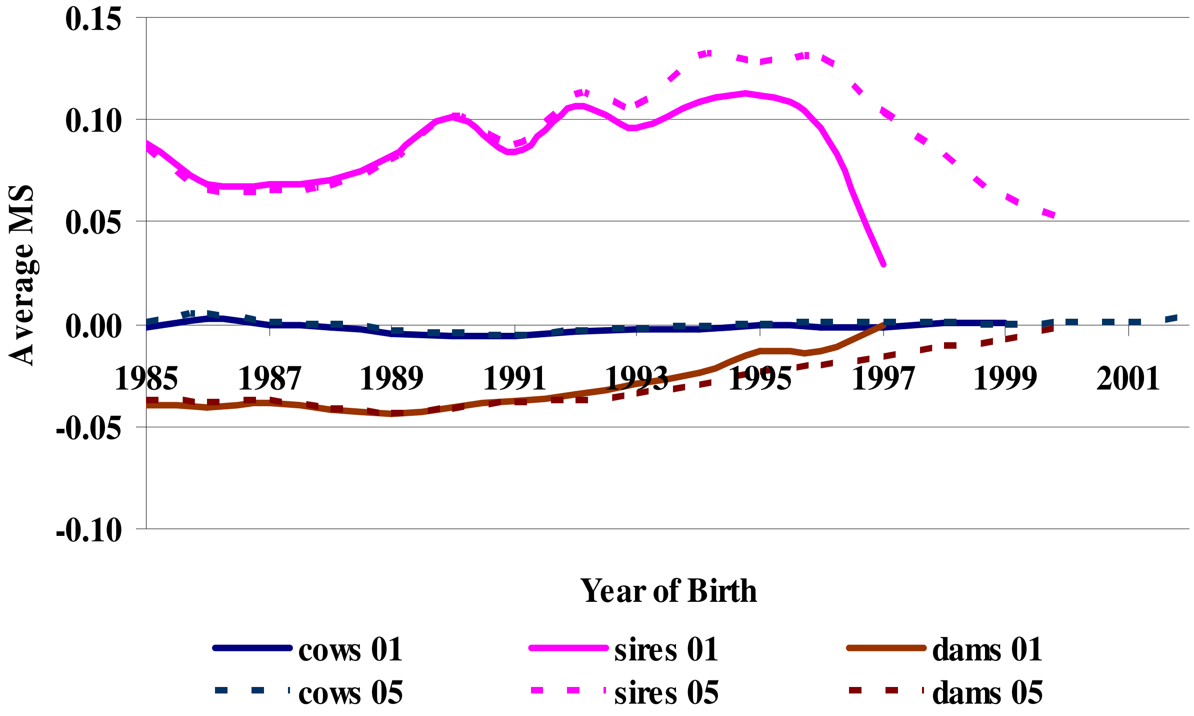


*cows01: cow 1st crop evaluations; sire01: sire 1st crop evaluations; dams01: dams 1st crop evaluations; cows05: cows 2nd crop evaluations; sire05: sires 2nd crop evaluations; dams05: dams 2nd crop evaluations; PTAs: predictive transmitting abilities; ST: single trait model

[1]sires: sires with ≥ 10 daughters

[2]cows: cows with final score records

Figure 4.1: Trends in PTAs of sires[1], dams and cows[2] – ST

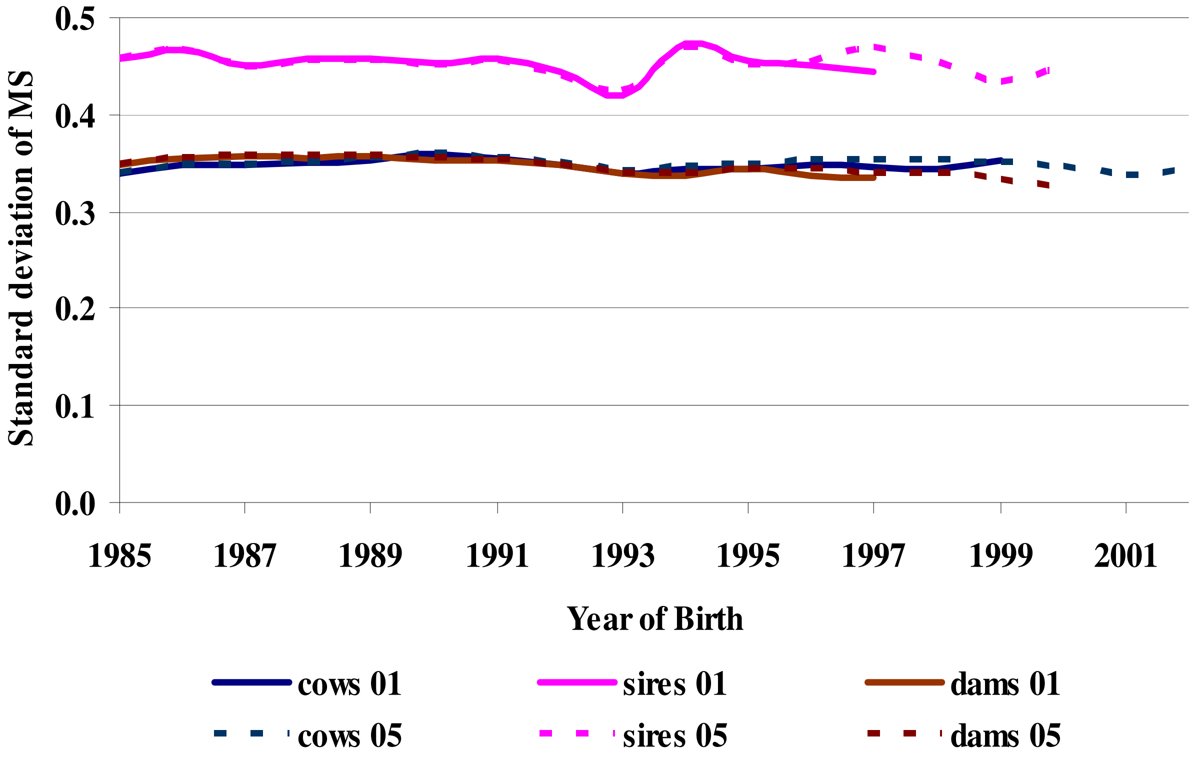


*MS: mendelian sampling estimates; cows01: cow 1st crop evaluations; sire01: sire 1st crop evaluations; dams01: dams 1st crop evaluations; cows05: cows 2nd crop evaluations; sire05: sires 2nd crop evaluations; dams05: dams 2nd crop evaluations; ST: single trait model.

[1] sires: sires with ≥ 10 daughters

[2] cows: cows with final score records

Figure 4.2: Trends in average MS of sires[1], dams and cows[2] – ST

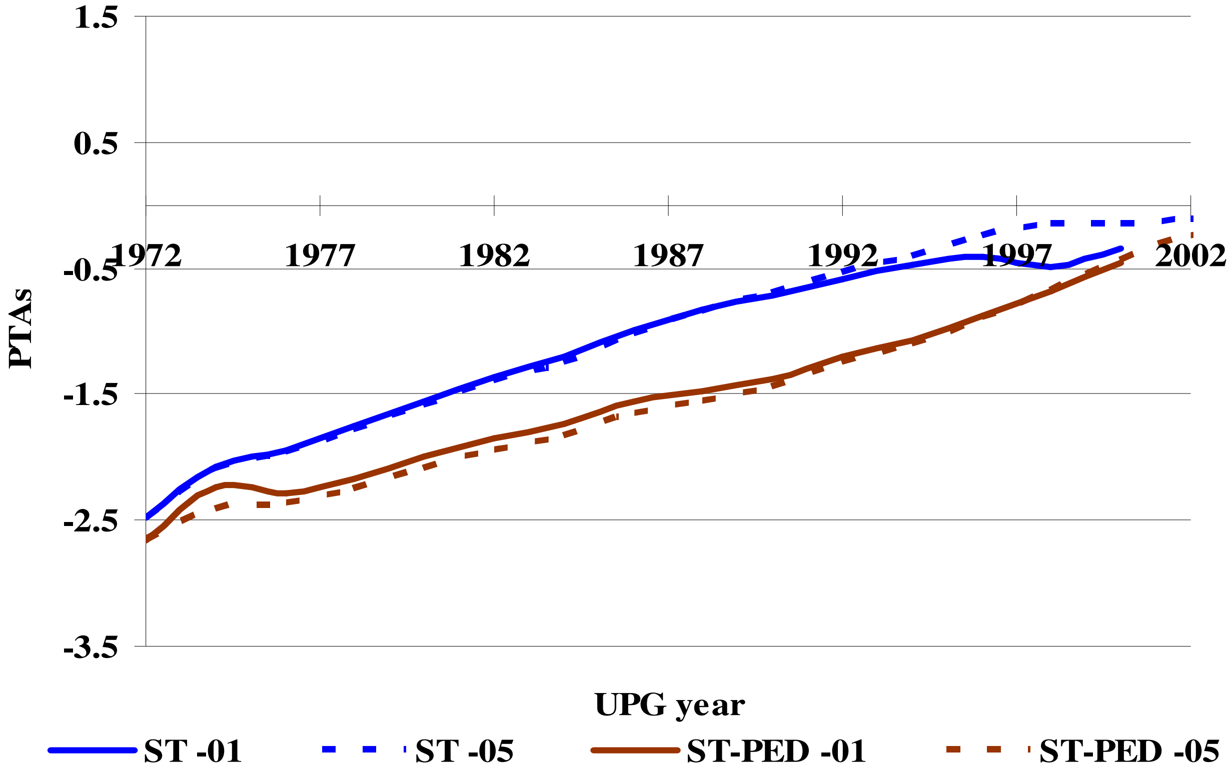


*MS: mendelian sampling estimates; cows01: cow 1st crop evaluations; sire01: sire 1st crop evaluations; dams01: dams 1st crop evaluations; cows05: cows 2nd crop evaluations; sire05: sires 2nd crop evaluations; dams05: dams 2nd crop evaluations; SD: standard deviation; ST: single trait model

[1] sires: sires with ≥ 10 daughters

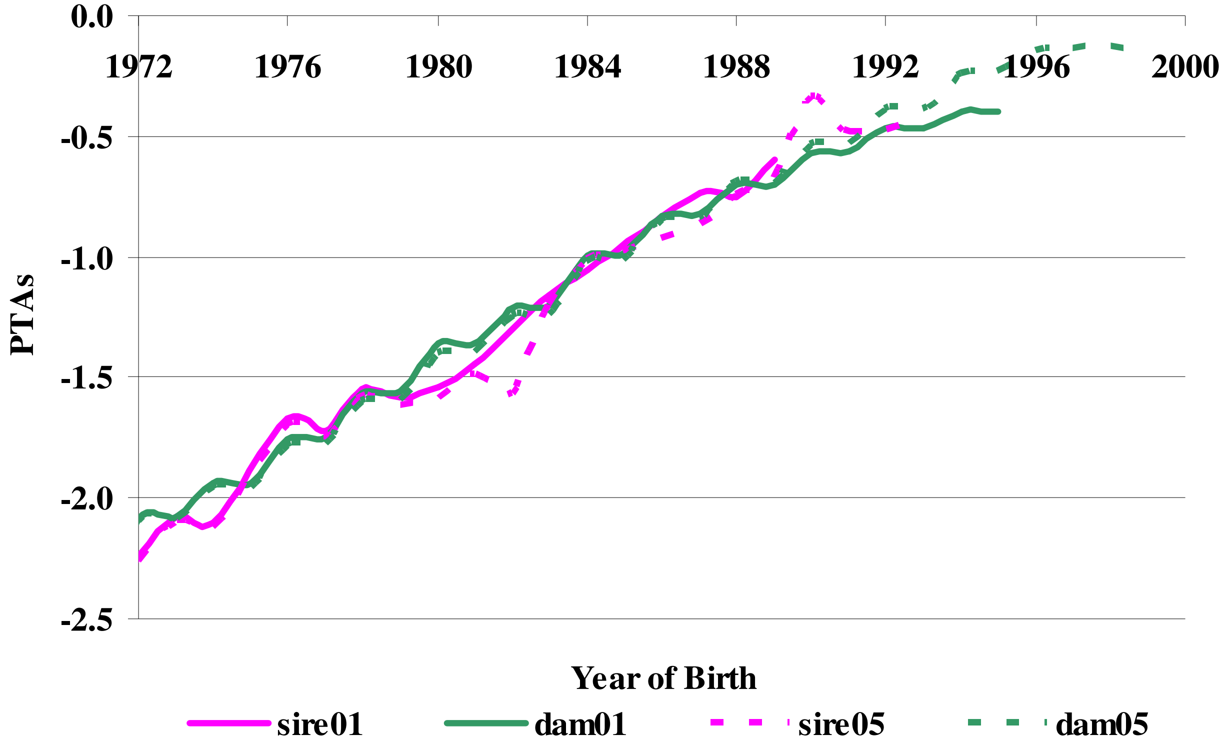
[2] cows: cows with final score records

Figure 4.3: Trends in SD of MS of sires[1], dams and cows[2] – ST



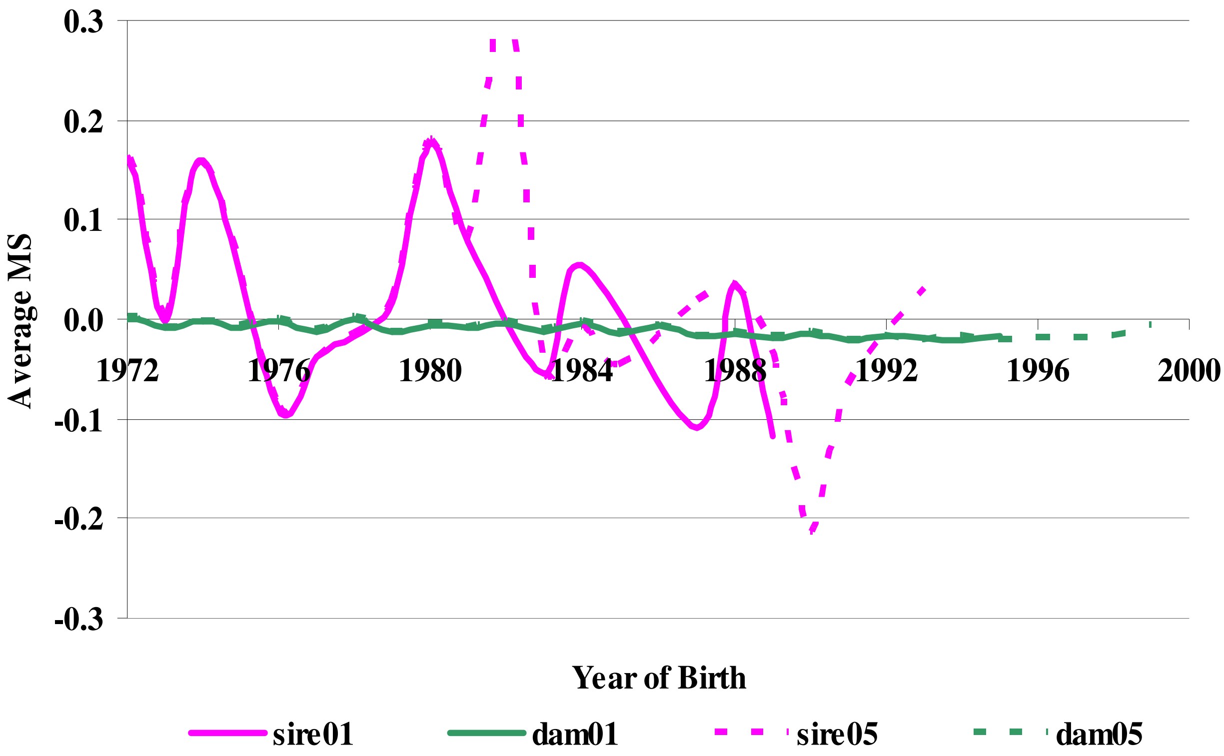
*ST -01: 1st crop PTAs of UPGs – ST model; ST -05: 2nd crop PTAs of UPGs –ST model; ST-PED -01: 1st crop PTAs of UPGs – ST-PED model; ST-PED -05: 2nd crop PTAs of UPGs – ST-PED model; UPG: unknown parent groups; ST: single trait model; ST-PED: single trait model with additional pedigrees.

Figure 4.4: Trends in PTAs of UPG: ST and ST-PED



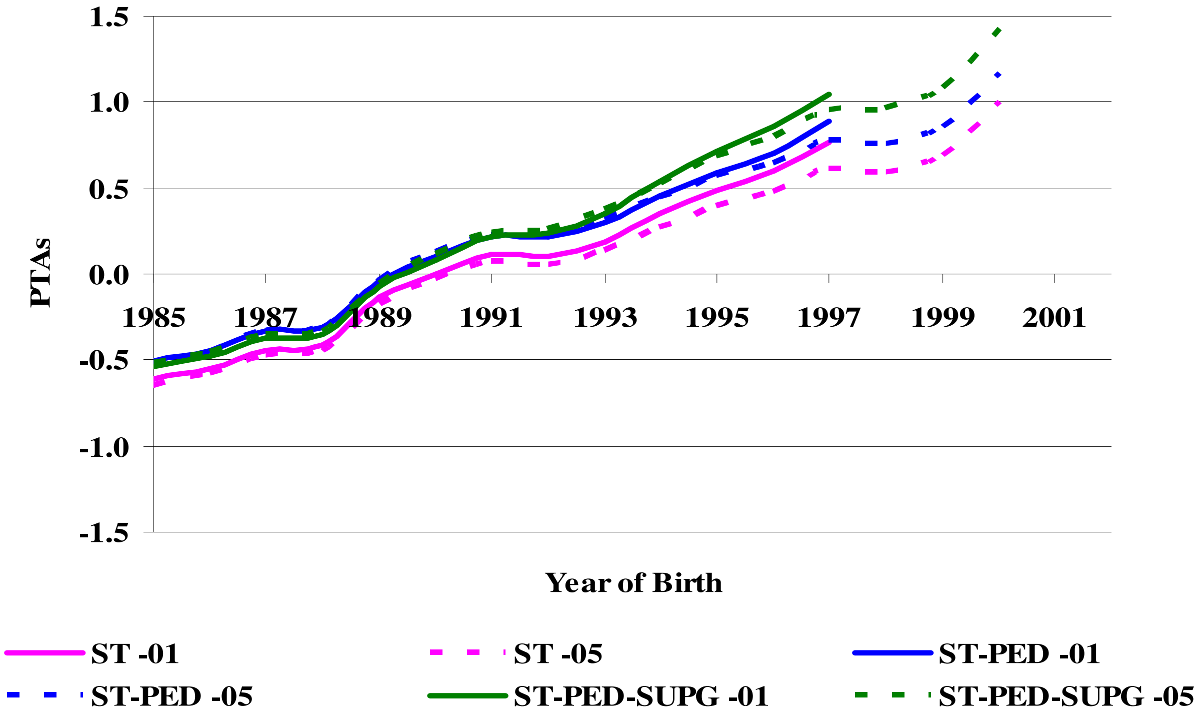
*sire01: sire 1st crop evaluations; dams01: dams 1st crop evaluations; sire05: sires 2nd crop evaluations; dams05: dams 2nd crop evaluations; PTAs: predictive transmitting abilities; UPG: unknown parent groups; ST: single trait model

Figure 4.5: Trends in PTAs of sires and cows occurring as parents but without pedigree – ST



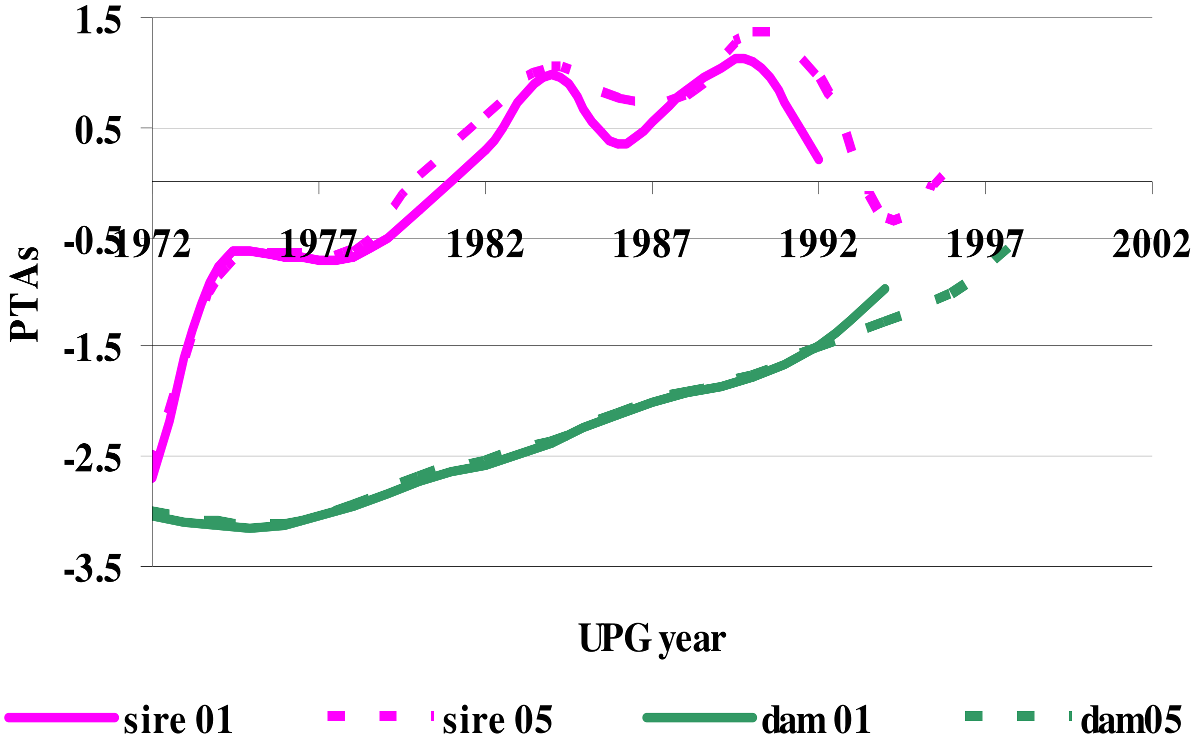
[*] MS: mendelian sampling estimates; sire01: sire 1st crop evaluations; dams01: dams 1st crop evaluations; sire05: sires 2nd crop evaluations; dams05: dams 2nd crop evaluations; PTAs: predictive transmitting abilities; UPGs: unknown parent groups; ST: single trait model

Figure 4.6: Trends in average MS of sires and cows occurring as parents but without pedigree – ST



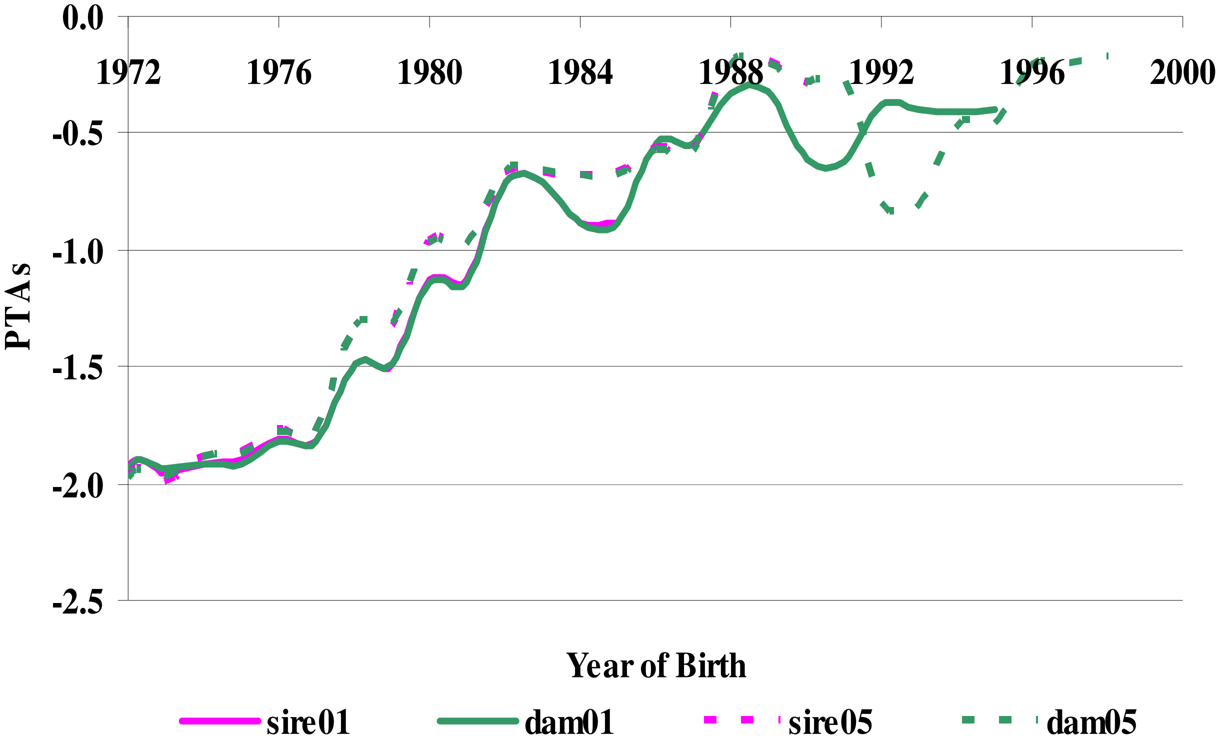
*ST -01: 1st crop evaluations with single trait model; ST-05: 2nd crop evaluations with ST model; ST-PED-01: 1st crop evaluations with ST model with additional pedigrees; ST-PED-05: 2nd crop evaluations with ST-PED; ST-PED-SUPG -01: 1st crop evaluations from ST-PED model with separate UPG for sires and dams. PTAs: predictive transmitting abilities; UPGs: unknown parent groups.

Figure 4.7: Trends in sire's 1st and 2nd crop PTAs – comparison of all 3 models



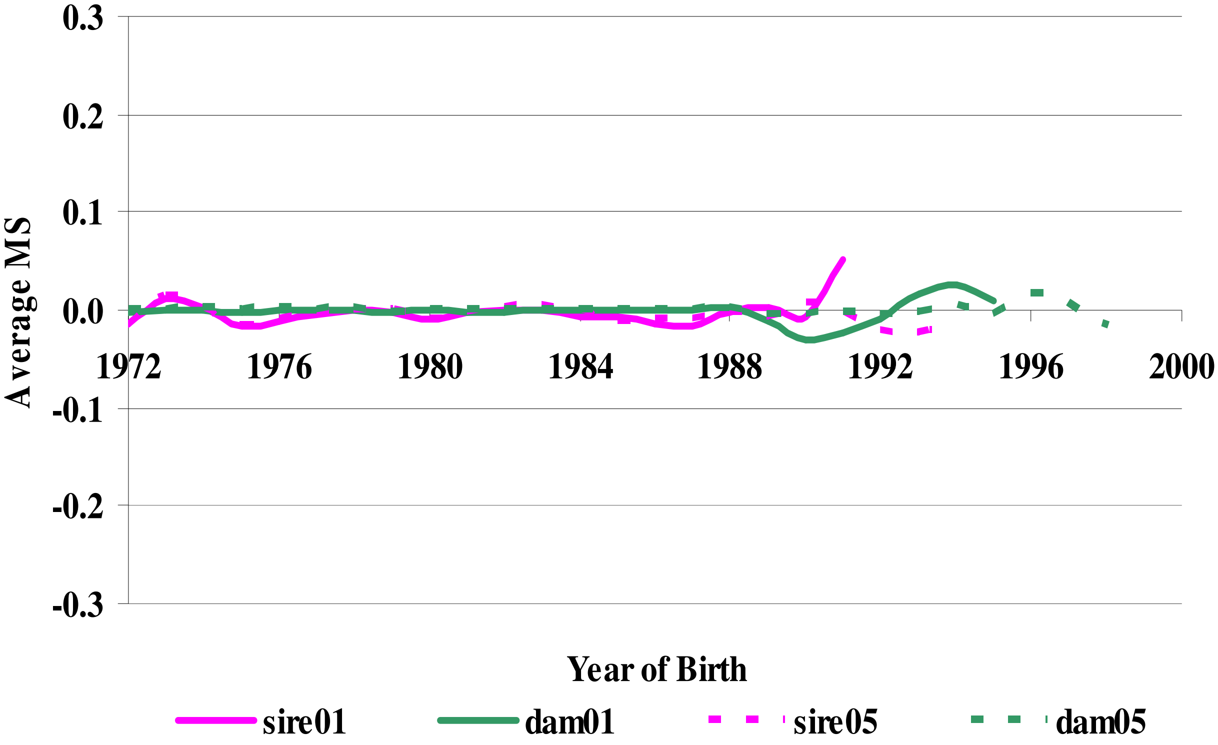
*sire01: 1st crop PTAs of sire UPGs; dam01: 1st crop PTAs of dam UPGs; sire05: 2nd crop PTAs of sire UPGs; dam05: 2nd crop 1st crop PTAs of dam UPGs; UPG: unknown parent groups; ST-PED-SUPG: single trait model with additional pedigrees and separate UPG for sires and dams.

Figure 4.8: Trends in sire and dam UPG PTAs: ST-PED-SUPG



*sire01: 1st crop evaluations of sires with UPG; dam01: 1st crop evaluations of dams with UPG; sire05: 2nd crop evaluations of sires with UPG; dam05: 2nd crop evaluations of dams with UPG; PTAs: predictive transmitting abilities; UPG: unknown parent groups; ST-PED-SUPG: single trait model with additional pedigrees and separate UPG for sires and dams.

Figure 4.9: Trends in PTAs of sires and cows occurring as parents but without pedigree: ST-PED-SUPG



*sire01: 1st crop evaluations of sires with UPG; dam01: 1st crop evaluations of dams with UPG; sire05: 2nd crop evaluations of sires with UPG; dam05: 2nd crop evaluations of dams with UPG; MS: mendelian sampling estimates; UPG: unknown parent groups; ST-PED-SUPG: single trait model with additional pedigrees and separate UPG for sires and dams.

Figure 4.10: Trends in average MS of sires and cows occurring as parents but without pedigree: ST-PED-SUPG

CHAPTER 5

CONCLUSIONS

Large changes in predictive transmitting abilities (PTA) for final score were observed from 1st to 2nd crop evaluations for Holstein sires, especially for the sires born in recent years. These large changes in PTA are of a major concern for dairy farmers and artificial insemination (AI) industry. The stability of genetic evaluations improves dairy farmer's confidence on genetic evaluation system and also on AI companies that merchandises the semen.

PTA changes were reduced by allowing separate unknown parent groups (UPG) for sires and dams along with additional pedigrees for dams, and also by using single record per cow. However, drops are not reduced by considering separate UPG for 1st and 2nd crop daughters, additional pedigrees alone and by considering differences in registered and grade animals.

Trends in sire PTAs, average and standard deviation (SD) of mendelian sampling (MS) estimates were also observed. Mean PTA differences between 1st and 2nd crop trends are reduced by allowing separate UPG for sire and dams along with additional pedigrees for dams. This could be due to accounting for the differences between genetic groups.

A model that uses additional pedigrees and allows separate UPG for sire and dam would account for large changes in sires' PTA for final score and also stabilizes the PTA trends from 1st to 2nd crop.