The Effect of Inbreeding in Dairy Cattle: Effects of Genomic Versus Non-Genomic Predictions

A Senior Project

presented to

the Faculty of the Dairy Science Department

California Polytechnic State University, San Luis Obispo

In Partial Fulfillment

of the Requirements for the Degree

Bachelor of Dairy Science

by

Michelle Gabrielle Khal

March, 2013

Acknowledgments

This project would not have been possible if I had not had the help and support from many people. I would first like to thank my parents who have given me this opportunity to attend such an outstanding college and have supported me throughout my education here at Cal Poly. Their continuous push and motivation has driven me to achieve the goals that I desire. Second, I would like to thank my senior project supervisor, Dr. Bruce Golden. Without his guidance I would not have been able to succeed in finishing this project. His experience and knowledge in this field made this experience more enjoyable in conducting. I would also like to express my gratification towards Joey Airoso who allowed me to use his registered herd of Holstein heifers in conduction this study. I would also like to thank Pfizer Animal Genetics and USA Holstein Association in aiding me in the test results that made this experiment possible.

Abstract

The objective of this project was to examine the relationship between the genomic value inbreeding coefficient and the pedigree value inbreeding coefficient. Hair samples were collected from 50 registered Holstein heifers from Airosa Dairy Tipton, California. The 50 hair samples were sent to Pfizer Animal Genetics for the genomic inbreeding values. DNA was extracted from the hair sample and ran through a low-density DNA SNP marker. Two values were computed from the genomic test; the future inbreeding value and the individual inbreeding value. The registered identification numbers of each of the heifers was also sent to the United States Holstein Association to obtain the pedigree inbreeding coefficient. Both the averages and standard deviations were computed for the three inbreeding values. Deviations were computed between the three inbreeding coefficients to examine how closely related the coefficients were. The standard deviation of the genomic individual inbreeding coefficient was greater than the pedigree coefficient. The standard deviation value computed from the pedigree was 1.8 percent and the genomic value for the individual inbreeding value was 2.4 percent. The average of the inbreeding coefficients resulted in the pedigree value being greater than the individual genomic value. Correlations were computed between the three inbreeding coefficients. When looking at the correlation between the production traits and inbreeding coefficient, the pedigree and individual inbreeding values favorably correlated to the type traits The correlation of the future inbreeding value indicated that the superior animals in the herd were more closely related to the population with the exception of the SCS trait.

Key Words: standard deviation, inbreeding coefficient, single nucleotide polymorphism, correlation

Table of Contents

List of Figures

.

INTRODUCTION

The effects of inbreeding can be controlled from two sources, the population as a whole, and then from an individual animal level. It is evident that both a genomic and pedigree based value can be calculated. With the availability of PTA scores and inbreeding values the correlation between the different values can generate information about animals. Dairymen all over the world seek for ways to improve their herds genetically to increase their milk production. With the knowledge of the values significance, the famers could potentially benefit by being able to increase the animals' genetic value in their herds. Dairymen would gain further knowledge of the useful type traits that would further benefit the production of the herd.

The objective of this study was to determine if there was a difference between pedigree inbreeding values versus the genomic inbreeding values and furthermore, if those particular values had any effect on production traits in dairy cows.

LITERATURE REVIEW

Inbreeding occurs in most all populations to some extent, the effects of inbreeding in dairy cattle are disregarded for genetic evaluation (Wiggans etal., 1995). Inbreeding results from the mating of parents who are closely related genetically (Merriam Webster Dictionary). Inbreeding in dairy cattle reduces the phenotypic performance (inbreeding depression) (Wiggans et al., 1995). A goal for all dairymen is breeding cows for superior genetics and production traits. With this goal in mind, inbreeding often occurs. Dairymen pick particular bulls that on record are shown to produce the best quality they desire in a particular cow. Through the advancement of reproduction technologies such as AI, dairy farmers around the world are able to improve the genetic quality of their stock. To calculate the inbreeding coefficient there are two different methods used to achieve this goal. The first is the older method, where a calculation was done through the use of an animal's pedigree. The second method is the newer method, where the concept still stays true just using a different means, through the use of DNA markers to gain further information on the animals.

Pedigree Based Genetics

The ability to calculate the coefficients of inbreeding has been around for some time. Initially, the relationship between animals was calculated through the use of an animal's ancestry line. The most commonly used measure of relationships would be the additive relationship calculation. This relationship measures the amount of like genes that two animals share. With this knowledge, one can then predict how reliable one of the relative's records will be to further predict the genetic value of the other animal. When using pedigree based relationships to determine the inbreeding coefficient of an animal, it is calculated by

taking one-half of the genes from each parent (Van Vleck et al., 1989). For example, if a dam (A) and a sire (B) have a calf (C), the calf would have 50 percent of its genes from the dam and 50 percent of its genes from the sire. When the F1 offspring (C) of the two parent progeny mates with another individual (F), the F2 generation would be related to each grandparent-grandprogeny (A and B) by 25 percent. This process of halving the genes from each progeny only holds true of the mating individuals are unrelated to one another (Van Vleck, et al., 1989). Diagrams of the relationships between unrelated ancestors are shown below (Fig. 1).

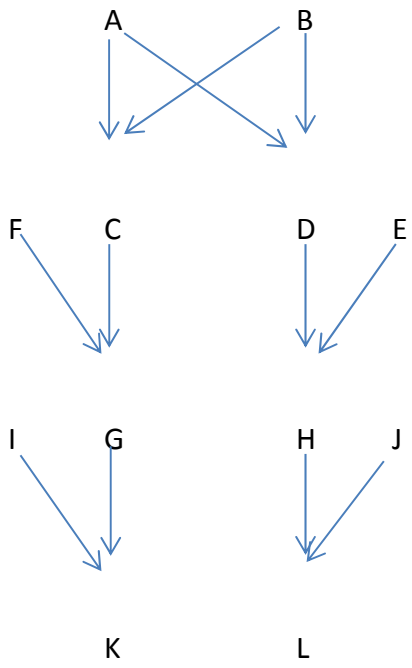

Figure 1. (Redrawn from Van Vleck, et al., 1989) an example of common relationships of unrelated ancestors by using arrow pedigrees.

If however, there are ancestors that are related to one another, a minor calculation must be executed before the main calculation can be calculated. A calculation of first must be made by using the common ancestors of the (G) and (H) to determine what we will call FI. Then the answer calculated would then be incorporated to find the total inbreeding. The

reason FI needs to be calculated is because it is the only common ancestor between (O and P). To calculate FI determine the amount common ancestor of parents (G) and (H). You would do this by taking the number of paths it takes to get back to each parent (A) and (B) which can then be multiplied by (1 + FA). The number of paths it takes to get to (A) is $G^{-1}D^{-2}A^{-3}E^{-4}H$ which is then applied to (1/2)n+1. The total is 1/32. The calculation is plugged into (1 + FA) resulting in 1/32. The same process as done above is executed for (B). The number of paths is $G^{-1}D^{-2}B^{-3}E^{-4}H$, which is then applied to same equation to get 1/32, again inserted into equation (1/2)n+1 to result in 1/32. The two calculations are added, to result in 1/16. Therefore, $F_I = \Sigma [(1/2)^{n+1}(1 + F_A)]$ results in 6.25%. The main part of the calculation is then computed to find FQ. The same process as before applies. Determine the number of common ancestors to (I) and (J). The paths for (I) is $O^{-1}L^{-2}I^{-3}M^{-4}P$, inserted into equation (1/2)n+1 which results in 0.03125. Plug that answer into (1+FA) to result in 0.03220. Same procedure for (J), paths are $O^{-1}L^{-2}J^{-3}M^{-4}P$, insert into the equation (1/2)n+1. Results in 0.03125 and then plug into (1+FA) to get 0.03125. The two results 0.3220 and 0.03125 are added to get 0.06445. This answer is then put into the equation $F_Q = \Sigma[(1/2)^{n+1} (1 + F_A)]$ and results FQ being 6.45 %. The paths to determine this percentage can be followed below in Fig 2.

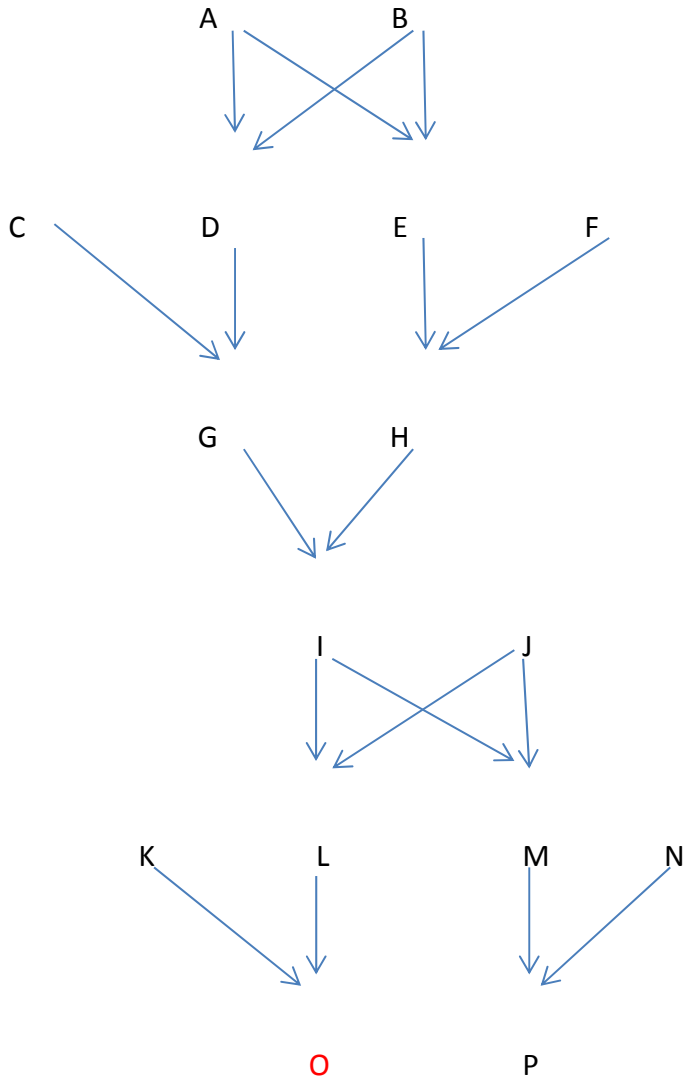

Figure 2. Example of common relationship with related ancestors shown by using arrow pedigrees.

Genomic Inbreeding Coefficients

The second method that is used to compute the Inbreeding Coefficient is the use of genomics. When discussing the genomic aspect of inbreeding coefficients it is important to understand what genomic is referring to. Genomic is the technological use of molecular biology and genetics to the genetic mapping and DNA sequencing of sets of genes (Merriam

Webster Dictionary). The SNP markers are used to predict breeding values of candidates for genomic values (Guo et al., 2010). The mapping of these genes can occur on a low –density DNA marker or a high-density maker. A higher marker density should result in better results because the makers are present in stronger linkage disequilibrium. This stronger linkage results in the genes positively affecting the desired trait (Su et al., 2012).

Genomic Prediction

Genomic prediction is a fairly new technique in animal breeding. When determining the genomic prediction, genome-wide dense markers are used to predict genetic values of animals (Meuwissen et al., 2001). One of the major goals in genomic selection has been the ability to increase the accuracy of the prediction of breeding values in dairy cattle (Karoui et al., 2012). The reliability of genomic estimated breeding value (GEBV) depends on the accuracy of estimated marker effects, which then relies on the information of variables in the reference data (Guo, et al. 2010). Currently, genomic evaluations are calculated with a multiple-step procedure (VanRaden, 2008; Hayes et al., 2009; Aguilar et al., 2010). A typical evaluation requires a total of four different processes, the first being a traditional evaluation with an animal model. The second procedure is an extraction of pseudo-observations such as de-regressed evaluations or daughter deviation (DD). The third procedure usually uses a simple sire model to estimate the genomic effects for genotyped animals. The fourth procedure might possibly set the genomic index with traditional parent averages (PA) and EBV (Hayes et al., 2009; Aguilar, 2010).

SNP

A useful aspect of genetic inbreeding calculations requires a good understanding of the process. One of the terms that continually show up while discussing inbreeding is SNP, which stands for single nucleotide polymorphism. A SNP occurs when a genetic variation occurs in the Deoxyribonucleic acid (DNA) sequence that occurs when a single nucleotide in a genome is altered. With the availability of SNP for livestock it is advancing the research on whole genome-selection (Vasquez et al., 2010). When computing genomic predictions in dairy cattle on the most commonly used methods is a medium-density SNP chip with approximately 54,000 markers is used (Su et al., 2012). Recently a new method had been discovered. A high-density (HD) SNP chip with approximately 777,000 markers was released (Matukumali et al., 2011.; Su et al., 2012). SNP-effect variances depend upon the number of markers. Therefore, the more markers there are, the smaller the variance (Su et al., 2012).

Holstein Cattle

The first national single-step, full-information (phenotype, pedigree, marker genotype) genetic evaluation was developed for final score of US Holsteins (Aguilar, et al. 2010). A total of four analyses were completed to see what method would result in the best methodology. The first analysis used only a pedigree-based relationship matrix. The second analysis used a relationship matrix based on both pedigree and genomic information (single-step approach). The third analysis used the complete data set and only the pedigree-based relationship matrix. The fourth analysis used predictions from the first analysis and prediction using a genomic based matrix to obtain genetic evaluation which is a multiple-step approach (Aguilar et al., 2010). It was concluded in that experiment that the single-step

approach such as the full genomic and pedigree evaluations were "as good as those obtained with the multiple-step approach in terms of accuracy and bias." (Aguilar et al., 2010) The study even went as far to say that the single-step approach had advantages in its simplicity and should increase in the future due to animals being preselected based on genotypes (Aguilar et al., 2010). Another genomic selection experiment was conducted in 2008 on US Holsteins by USDA-ARS Animal Improvement Programs Laboratory based on a multi-step procedure to create genomic predictions (VanRaden, 2008; Tsuruta et al., 2011). The computations for these genomic predictions dealt with several genomic relationship matrices that assumed different allele frequencies (Tsuruta, et al., 2011). The final result concluded that single-trait modes would increase the accuracy for genomic evaluation and would not increase computational time, compared to an increase in computational costs that was seen in a multiple-trait model (Tsuruta et al., 2011).

Artificial Insemination

A particular influence that increases the inbreeding coefficients is the implementation of artificial insemination (AI). AI advancement has been around for some 75 years and still continuing strong (Vishwanath, 2003). AI can constitute as being one of the strongest tools to aid in the reproduction of livestock, especially in dairy cattle. Dairymen all over the world have the ability to advance their herds genetically with the use of two methods. First, by preselecting the top genetic merit bulls and secondly, the ability to select calves of high breeding merit as replacements (Vishwanath, 2003). With these two capabilities the herds have genetically improved worldwide. Semen selling companies have also made it extremely easy in the ability to obtain genetic merit bulls semen with desired traits. According to the World Wide Sires website in the US alone, 1,300 Holstein bulls go through progeny testing

through the AI industry. Through the use of a semen company, the bull proof is available along with the pedigrees. With this type of technology AI has helped to establish favorable genes amongst the dairy cattle population. However, also with the high in demand use of AI comes along the room for greater Inbreeding cases.

METHODS AND MATERIALS

Data Collection

Data for this project were collected from Airosa Dairy in Tipton, California during the winter of 2011. This farming operation has about 2,600 registered milking cows. These cows are milked three times a day with a rolling herd average of about 28,000 pounds of milk. The owner farms 1,600 acres of farmland which allows them to grow about 90 percent of the forages that they feed to their cows. The operating software system that the owner uses on the dairy is DairyComp 300 which allows for an accurate record keeping of all livestock.

Hair sampling cards were provided by Pfizer Animal Genetics, which allowed for 50 hair samples to be sent in. The hair samples were taken from 50 registered Holsteins from the Airosa Dairy. The hair samples were collected from the tail switch hairs Holstein heifers and directly placed in between the sample cards to ensure no further contamination. Approximately 20-40 hair follicles were needed in order to ensure a sufficient amount of hair was available. The hair samples were completely enclosed. Individual sample cards were provided for each heifer. After directly placing the hair sample into the collection card, individualized identification numbers were applied to each card. Along with Pfizer's identification number each animals tag numbered was also written on the card in the space provided. Another critical aspect that was needed along with the collected hair samples is the order form provided by Pfizer.

Data Processing

After the hair samples were collected and correctly labeled, they were sent to the Pfizer Animal Genetics laboratory located in Kalamazoo, Michigan. After obtaining the hair samples, Pfizer took them and extracted the DNA. The program that was used for the dairy genomics was CLARIFIDE®.

Pfizer Animal Genetics offers this state of the art genomic 6,909 SNP DNA-marker panel specifically for dairy cattle. The DNA marker that is used is a low-density marker panel after having extracted the DNA they take the genotypes, which were then used as DNA markers. This DNA-marker panel allows for the ability to optimize selection and dairy and management of dairy replacement heifers for breeds including, Brown Swiss, Holstein, and Jerseys. Using CLARIFIDE, Pfizer is able to generate 30 health, production, and type traits computed by USDA AIPL. Along with all the traits, a total of nine composite indexes were made to allow for long-term production profitability's and capabilities. The results from CLARIFIDE were reported as genomic predicted transmitting ability (GPTA). Included in the report was the genomically computed inbreeding value. There were two inbreeding values computed through the system, individual inbreeding coefficient and future inbreeding coefficient. The reports generated from Pfizer Animal Genetics was compiled into an easy accessible excel spreadsheet (Fig. 3).

On-farm ID (Herd Management #)	Official ID (Registration #, USDA AIN, Calfhood Vaccination #)	AIPL #	Birth Date	Sex
14027	USA000069554706		2010/05/14	F
14033	USA000069554712		2010/05/15	F
14049	USA000069554728		2010/05/19	F
14064	USA000069554743		2010/05/23	F
14066	USA000069554745		2010/05/24	F
14073	USA000069554752		2010/05/25	F
14075	USA000069554754		2010/05/29	F
14081	USA000069554760		2010/06/01	F
14096	USA000069554775		2010/06/03	F

Figure 3. Snapshot of excel spreadsheet generated by Pfizer with some of the data from this experiment..

For this experiment alone only a small portion of the data that was generated was needed. However, the dairymen whose herd was used for this experiment were able to use this excel spreadsheet to gain knowledge to further advance his herd gnomically.

HOLSTEIN ASSOCIATION USA

To further gain information about the Holstein heifers a list of the heifers register identification was sent to one of the representatives at the Holstein Association USA. The animals register id was the only information that was needed to obtain the information. The Holstein USA Association was able to provide the genetic results for the individual registered Holstein heifers. The information that was provided was the traditional inbreeding values and PTA values of NM$, Milk, Fat, Protein, Productive Life, and Somatic Cell Score.. The inbreeding coefficient that is calculated comes from the pedigree of each individual heifer. The pedigree inbreeding value is considered the traditional value. The other information that was provided by the Holstein USA Association was PTA scores for each of the heifers. The majority of these trait values included genomic information that was provided prior to December.

RESULTS and DISCUSSION

GENOMIC INBREEDING

Two separate values were calculated from the genomic information for the inbreeding purposes. The genomic calculations were computed through the use of the CLARIFIDE test. The two types of genomic inbreeding results were genomic individual inbreeding and the second was genomic future inbreeding. The individual inbreeding value is measured differently from that of a pedigree calculation. The value for individual inbreeding comes from the percentage of genes in common and the actual homozygosity. When looking at the results from the test. The most common percent of individual inbreeding values came from the three, four, and five percent inbreeding (Figure 4).

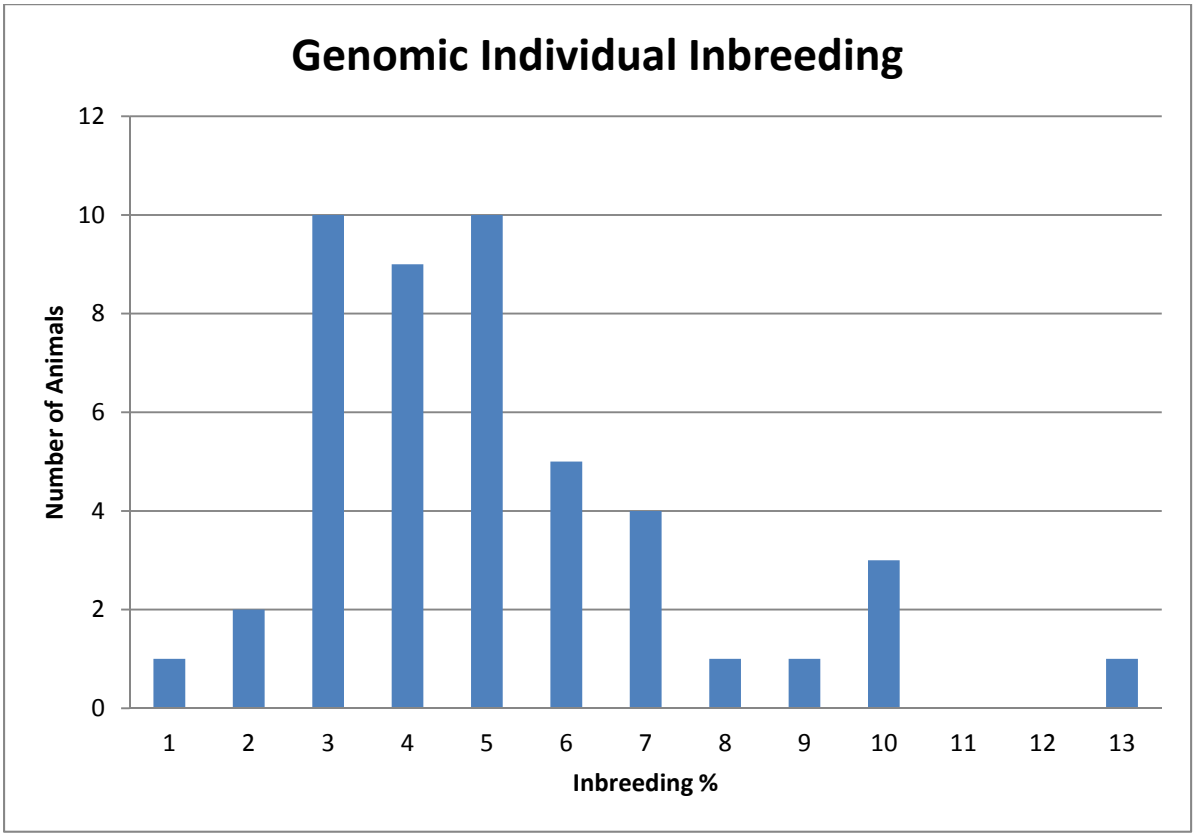

Figure 4. The number of animals Genomic Individual Inbreeding percent.

The second value that comes as a result of the CLARIFIDE test is the future inbreeding. This value is different from that of the first because it uses the information from genotyped animals from the last ten years to indicate a value of inbreeding. This value is derived from the assumption that if an animal is mated at random the value would indicate the level of inbreeding the progeny will contribute to the population.

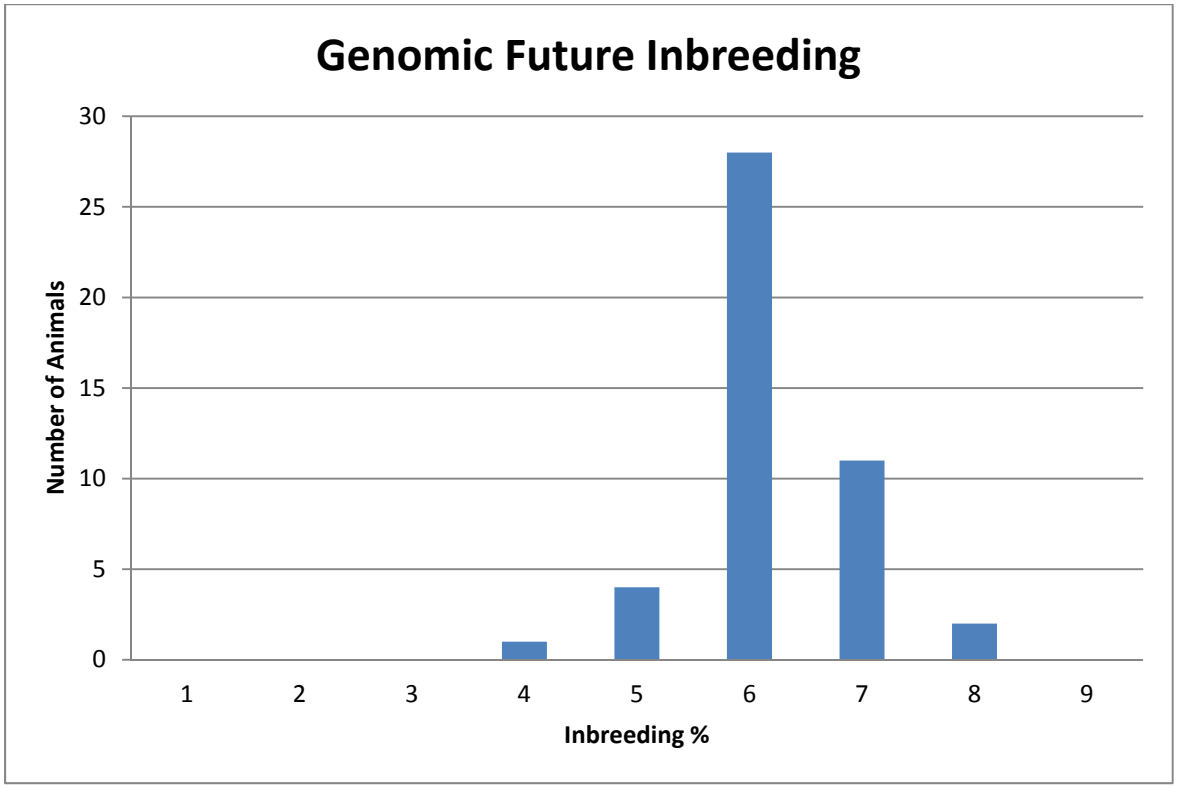

Figure 5. The number of animlas Genomic Future Inbreeding percent.

Looking at the future genomic values the animals with higher inbreeding coefficients could be seen as the having more genes in common with the greater population. Higher inbreeding value could mean higher frequency genes in the greater population. The animals with lower future inbreeding values could be seen as less related to the population at large.

PEDIGREE INBREEDING

A third type of inbreeding was calculated to conduct this experiment. A pedigree inbreeding value was computed for the Holsteins. The pedigree inbreeding values were determined with the use of the animals' pedigrees. The information of the traditional inbreeding coefficients was provided by the Holstein Association USA. Of the 50 heifers that were used for this study 25 of them had an inbreeding of about six percent or higher.

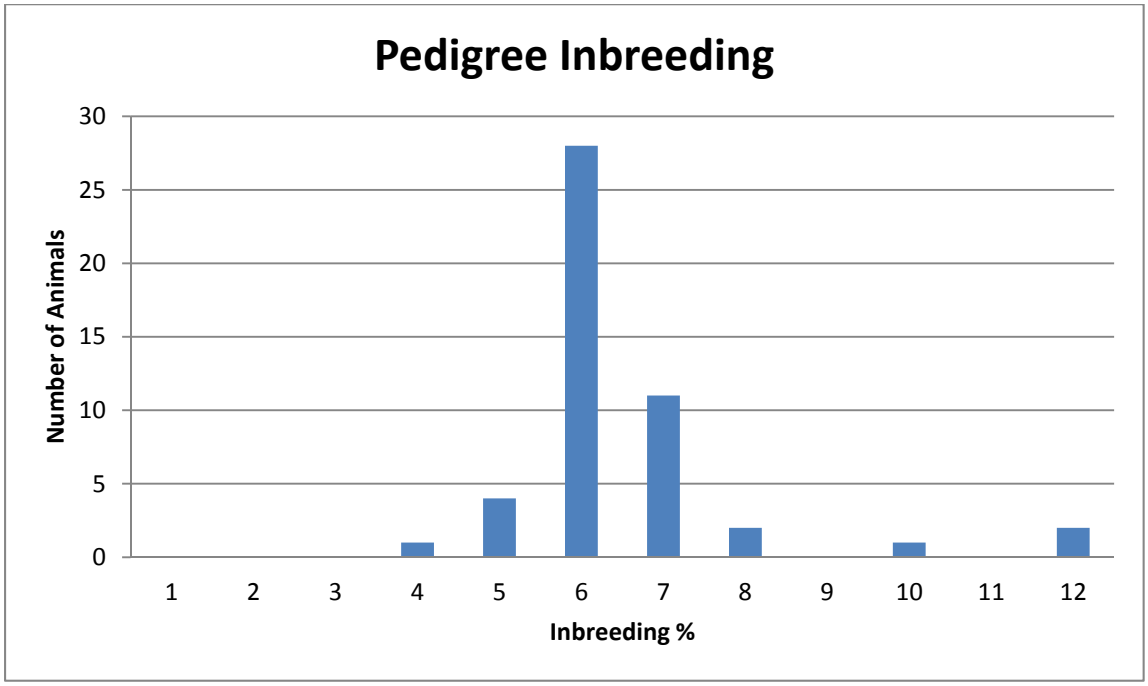

Figure 6. The number of animals Pedigree Inbreeding percent.

.

COMPARING INBREEDING COEFFICIENTS

The three averages future, pedigree, and individual inbreeding values were compared. The average of pedigree based values were higher than the Genomic Individual value (Figure 7). The pedigree average among the 50 heifers was 6.1% compared to the genomic individual average 5.5%. This was as anticipated. The maximum pedigree inbreeding coefficient

observed among the animals in the data was 12.3% compared to the individual genomic coefficient of 13.6%. This may indicate that selection favored animals with mendelian samples that resulted in lower genomic inbreeding.

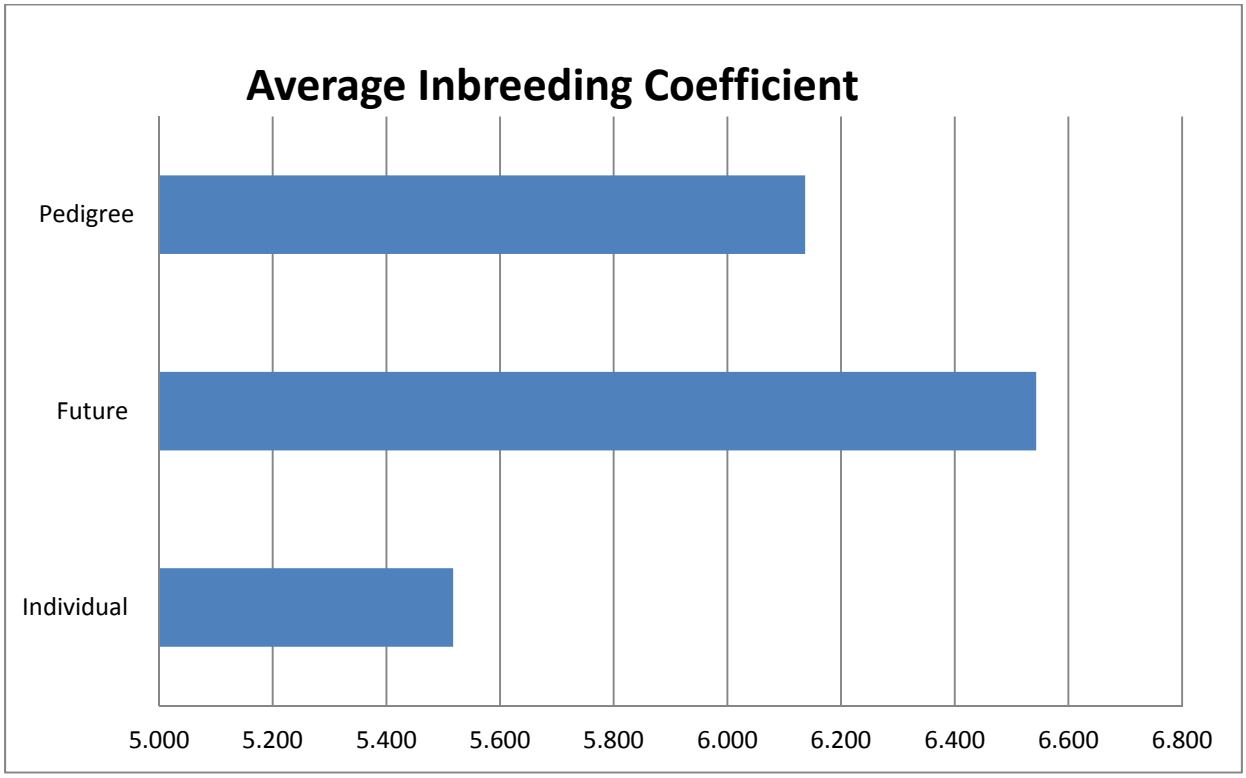

Figure 7. Average of inbreeding Coefficients.

What this could mean is that Dairy Producers as a whole tend to gravitate towards low inbreeding animals because low inbreeding Holsteins tend to be overall healthier than a higher inbreed animal. Thus, the more animals were less favored which decreased the genomic individual inbreeding coefficient. The correlation computed between the inbreeding values helped to support the idea of higher inbreeding animals to be less favored (Figure 8). The correlation between the individual values and pedigree values were low at 0.43%.

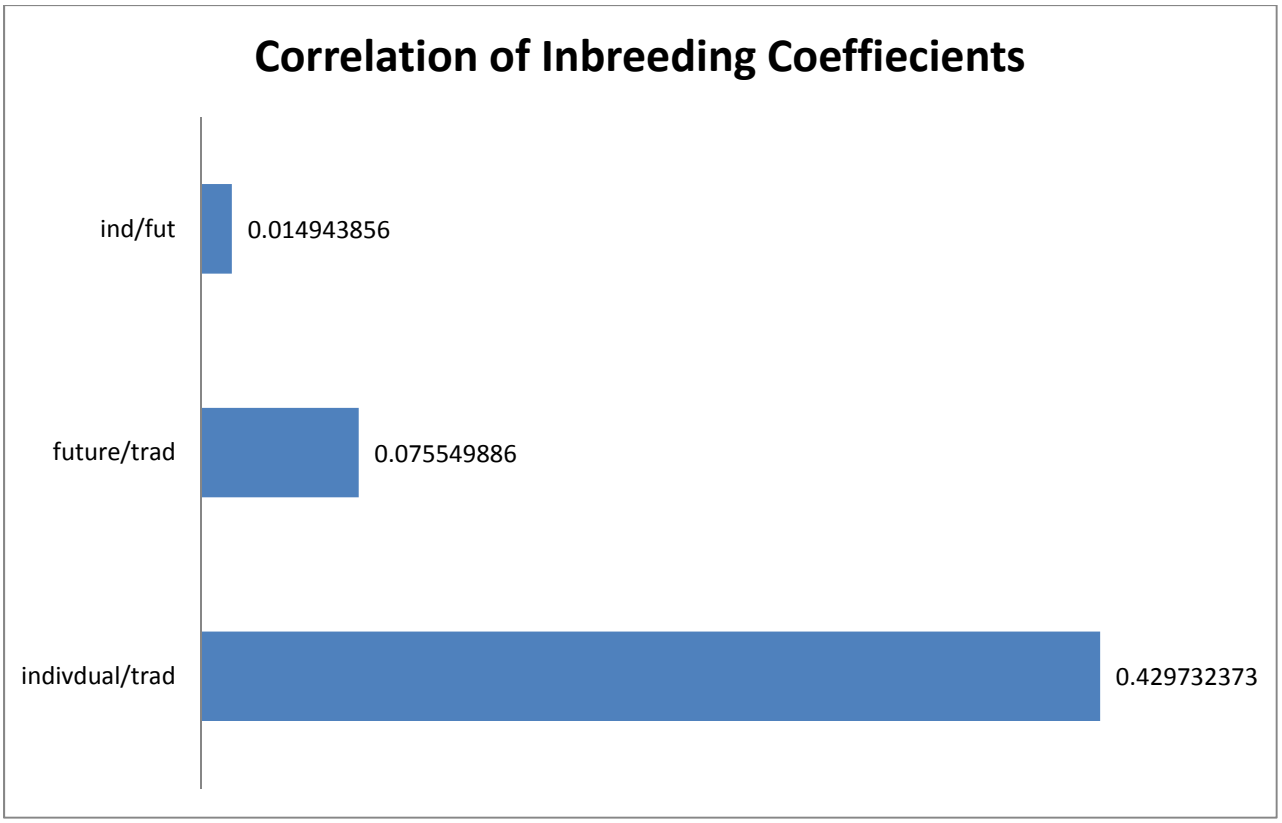

Figure 8. Correlation between Inbreeding Coefficients.

Three correlation calculations were computed between the different inbreeding coefficient values to determine the direct relationship amongst them. The coefficient that is the closest is the individual/traditional correlation.

When comparing the individual inbreeding coefficient to the future inbreeding coefficient the values vary between each heifer. In some instances the Individual value is higher than the future value, which represents the value the progeny would contribute if the animal were to randomly mated in the population Future values might be lower because those particular traits that were being picked are different to the present day traits. The traits that were once popular may not be the future desired traits. However, those particular genes that were not desired then could be considered a desired quality in a future offspring.

PTA's

Holstein USA computed PTA scores for the 50 Registered Holsteins. Pfizer determined the PTA values at a genomic level. For the purpose of this experiment only a few of the type traits were utilized. The traits that were utilized were Net Merritt $ (NM$), PTA milk yield (PTA MILK), PTA Fat, PTA Protein (PTA PRO), PTA Production Life (PTA PL), and PTA Somatic Cell Score (PTA SCS). Holstein USA genetically scored the PTA for each individual trait. To determine if the results from Holstein USA had any genomic information included in the calculations the reliability production column was used. If the values in the reliability production column resulted in a value greater than 70% than the values included genomic results. Any heifer that had genomic results from before December 2012, the information would include the genomic results. The calves that had not been genomically calculated after December would have only traditional PTAs and the reliability would be in the 30% range. After having gained this knowledge, it was determined that only one heifer had been done after December and had a reliability production of 10. The average of the Real Prod including the heifer with the Real Prod of 10 was 73.93 versus the average without the heifer with the Real Prod of 10 was 75.35.

The NM$ value expressed the expected lifetime profit of a female compared to the breed base. The traits that are utilized in determining how the heifer will profit are economically relevant traits. The overall traits that are chosen are related to yield health, longevity, and calving ease. All of these traits compiled result in a profitable heifer. More specifically, the traits that are included in the NM$ index include fat, protein yield, and production life.

PTA MILK, PTA FAT, and PTA PRO were other main traits that were involved in the experiment. All three of these type traits were based off a 305-day lactation period. PTA MILK is a value that represents the genetic difference in total pounds of milk produced. PTA FAT is the genetic difference in the quantity of milk fat also produced. The same is applicable for the PTA PRO, the value is a result of the difference in protein in the lactation period.

PTA Productive Life (PTA PL) and PTA Somatic Cell Score (PTA SCS) were examined. The PTA PL evaluates a heifers' genetic ability to stay in a herd and accounts for characteristics that make a cow more sustainable for a dairy operation. This value determines how much milk the heifer would be expected to produce relative to the breed average.

The average of each of the PTA was calculated to determine what the average for each type trait in the Registered Herd. As you can see below in fig. 7 the averages were as following.

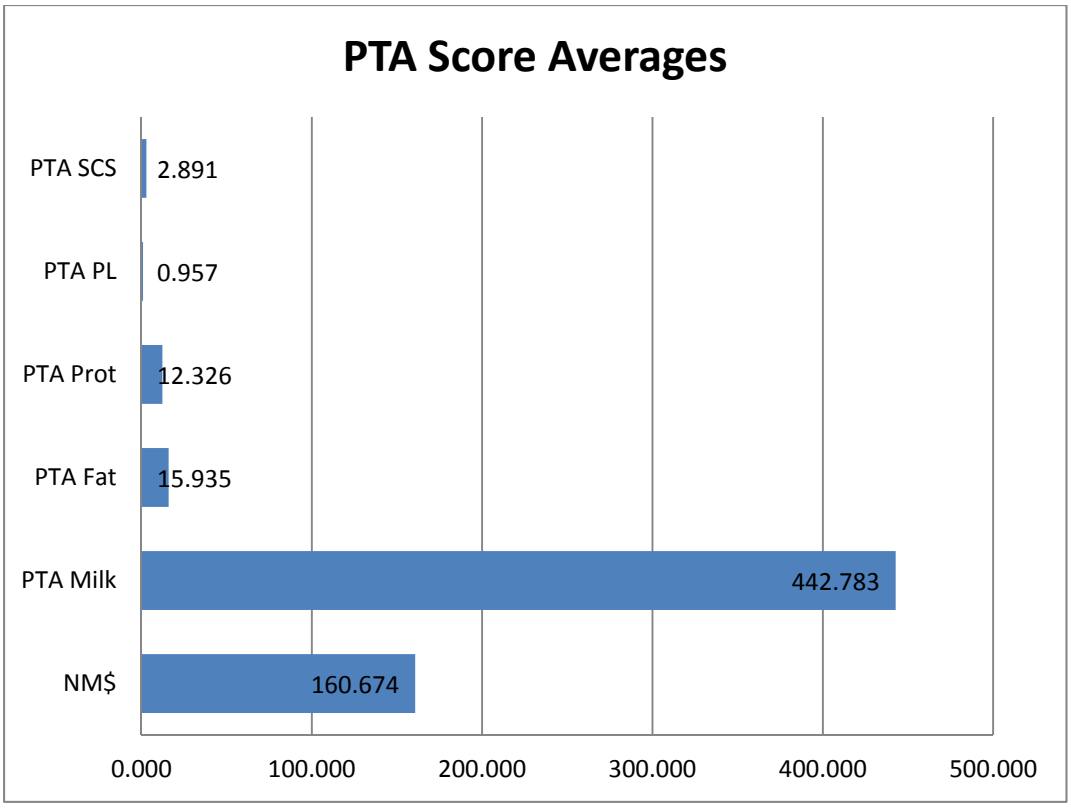

Figure 9. Average PTA for each type trait examined.

The PTAs played an important part of the experiment. Each PTA was individually compared to all three of the inbreeding results; Future Inbreeding, Individual Inbreeding, and the Traditional Inbreeding Coefficient. Each trait was compared to all three of the inbreeding coefficients to determine how inbreeding affects different type traits. The correlation was also derived from the Inbreeding Difference (F DIFF).The difference between the Individual Inbreeding and Traditional Inbreeding coefficient was taken to calculate F DIFF. After computing the F DIFF, the value was too correlated to each type trait.

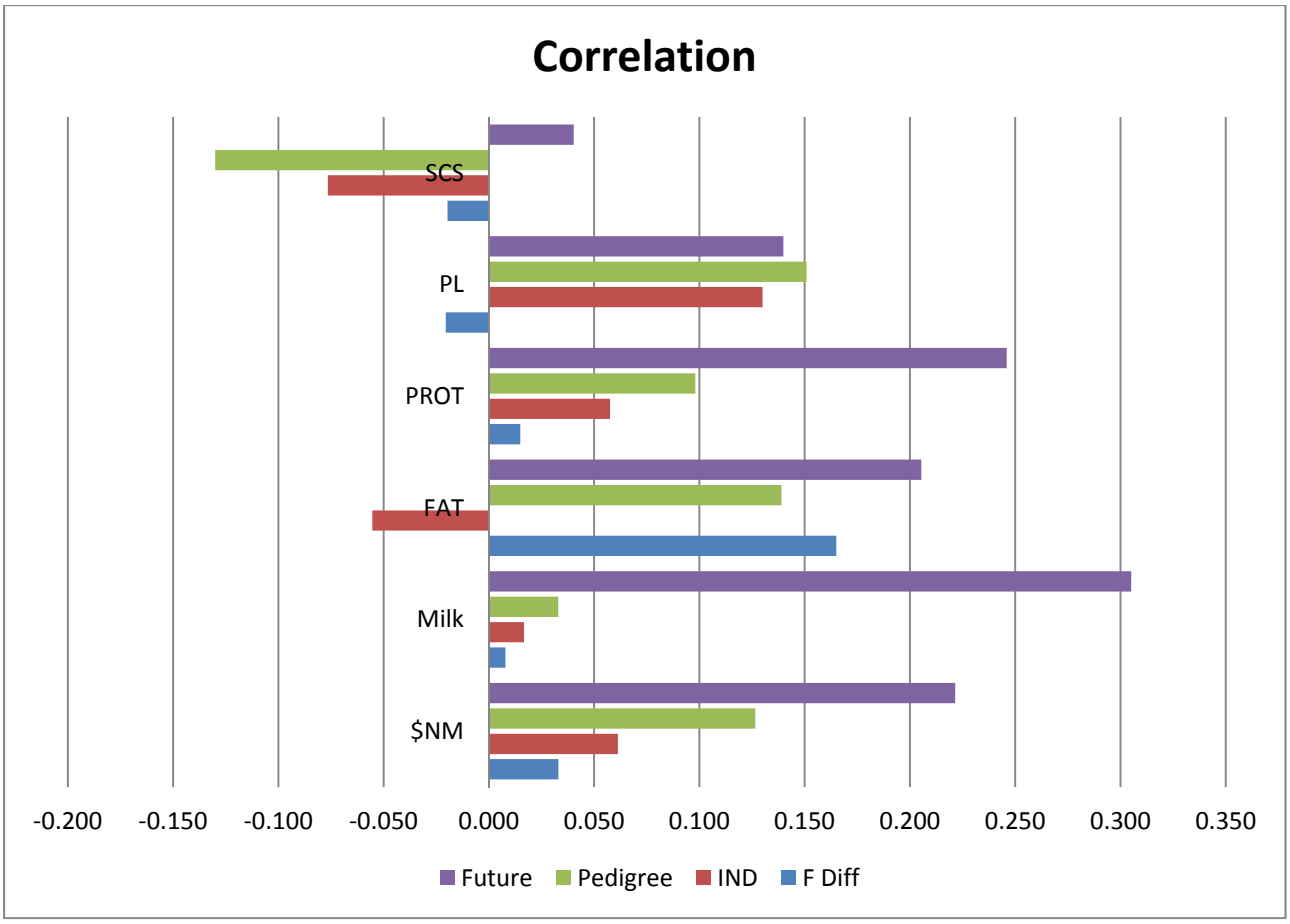

Figure 10. The correlation between the production traits and Inbreeding Coefficients.

The analytical method used to produce PTA may not have separated the inbreeding effects from breeding values cleanly. However, the pedigree and individual inbreeding favorably correlated to PTA. It is likely that the effects of selection for superior animals increased inbreeding. Additionally, the correlation of PTAs with future inbreeding indicated that the superior animals in the herd were those animals that were more closely related to the population with the exception of the SCS.

CONCLUSION

After looking at the results, it was apparent that there is a correlation between the inbreeding coefficients. The correlation between the genomic individual inbreeding coefficient and the pedigree value was significant because the pedigree value was greater than the genomic value calculated. The pedigree value was greater which exhibits that dairy men are picking heifers that are prone to be fit. These heifers lead to live longer, healthier lives. By avoiding large inbreeding coefficients in progeny through the control of mating it will control the depression of the animals' fitness traits. This notion also explains why the genomic value is lower than the traditional value, the genes that lead toward healthier animals are less gnomically inbreed, which results in an inbreeding depression.

When looking at the correlation between the production traits and inbreeding coefficient, the pedigree and individual inbreeding values favorably correlated to the type traits. The correlation of the future inbreeding value indicated that the superior animals in the herd were more closely related to the population with the exception of the SCS trait.

References

Aguilar, I., I. Misztal, D. L. Joshnson,A. Legarra, S. Tsuruta, and t. J. Lawlor. 2010. Hot topic: a unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of a Holstein final score. J. Dairy Sci. 93:743-752.

Golden, B.L., J. Garrick, S. Newman, and R. M. Enns. 2000. A framework for the next generation of EPD. Proc. Beef Improv. Fed. 32nd Ann. Res. Symp. Annu. Meet. 32:2-13.

Guo, J., M. S. Lund., Y. Zhang, and G. Su. 2010. Comparision between genomic predictions using daughter yield deviation and concentional estimated breeding value as respose variables. J. Anim. Breed Genet. ISSN 0931-2668.

Hayes, B. J., P. J. Bowman, A. J. Chamberlain, and M. E. Goddard. 2008. Invitited review: genomic selection in dairy cattle: progress and challenges. J. Dairy Sci. 92:433-443.

Karoui, S., M. J. Carabano, C. Diaz, A. Legarra.2012. Joint genomic evaluation of French dairy cattle breeds using multiple-trait models. Genetics Selection Evolution. 44:39.

Matukumalli, L. K., S. Schroeder, S. K. DeNise, T. Sonstegard, C. T. Lawley, N. Georges, W. Coppieters, K. Gietzedn, J. F. Medrano, G. Rincon, D. Lince, A. Eggen, L. Glaser, G. Cam, and C. Van Tasel. 2011. Analyzing LdD blocks and CNV segments in cattle: Novel genomic features identified using the BovineHD Beadchip. Pub. No. 370-2011-002. Illumina Inc., San Diego, CA.

Sue, G., R. F. Brondum, P. Ma, B. Guldbrandsten, G. P. Aamand, and M. S. Lund. 2012. Comparison of genomic predications using medium-density, (54,000) and high-

denisty (777,000) single nucleotide polymorphism marker panels in Nordic Holstein and Red dairy cattlr population. J. Dairy Sci. 95:4657-4665.

VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. J. Dairy Sci. 91:4414-4423.

Van Vleck, D. L., J. E. Pollak, and B. E. A. Oltenacu. 1993. Genetics for the Animal Sciences. Genetic. W. H. Freeman and Company.

Vazquez, A. I., G. J. M. Rosa, K. A. Weigel, G. de los Campos, D. Gianola, and D. B. Allison. 2010. Predictive yield deviation and conventionality of subsets of single nucleotide polymorphisms with and without parent average in US Holsteins. J. Dairy Sci. 93:5942-5949.

Vishwanath, R. 2003. Artificial insemination: the state of the art. Theriogenology. 571-584.

Wiggans, G. R., and P. M. VanRaden. 1995. Calculations and use of inbreeding coefficients for genetic evaluation of United States dairy cattle. J. Dairy Sci. 78:1584-1590.