CHANGES IN GENETIC TRENDS AND HERD STATISTICS FOR DAIRY CATTLE IN THE U.S.

by

FIONA LOUISE GUINAN

(Under the Direction of Daniela Lourenco)

ABSTRACT

The use of genomic information in United States (U.S.) dairy cattle evaluations has rapidly increased the rate of genetic gain for several important economic traits. The direction of this gain has not been documented completely and the purpose of this study is to address assumptions of the genetic improvement of U.S. dairy cattle. Gain is expected in heavily selected traits, but determining how the estimated breeding values are used needs to be analyzed. Progress was measured to address assumptions and review the use of genomics in all dairy cattle breeds. Benchmarking dairy cow production records is a resource utilized and referenced widely in the dairy industry (loan purposes, research, extension specialists). Dairy cow population and production statistics are of interest to the industry on a state and national level as indicators of progress. Performance metrics were calculated to increase interaction and accessibility to descriptive statistics in the National Cooperator Database.

INDEX WORDS: Genomic selection, Genetic trends, Colored breeds, Dairy Herd Improvement, Milk recording

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DEDICATION

To all of my family, near and far.

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To everyone who has been there each step of the way, thank you.

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CHAPTER 1

INTRODUCTION

Genetic trends indicate the level of progress and direction of genetic improvement in a population. The inclusion of genomic information accelerated the rate of genetic gain in the Holstein breed in the United States (US). Limited literature is available in the US reviewing the direction genetic trends are taking in colored breeds (Ayrshire, Brown Swiss, Guernsey, and Jersey). Assumptions and theories are widely available regarding expected gain and inbreeding measures. If genetic trends are not presenting as expected, evaluation methodology and selection indices may need to be reevaluated. Another benchmarking method used widely by the industry are descriptive statistics on the National Cooperator Database managed by the Council on Dairy Cattle Breeding (CDCB; Bowie, MD). Distinguishing geographical regions of US dairies and how these statistics reflect the overall market structure is vital for producers and industry stakeholders. Developing decision support tools utilizing the large database owned by producers adds value back to the data owners while reflecting phenotypic trends in the population.

The objective of this thesis was to investigate the genetic trends of all breeds receiving a genomic evaluation in the US dairy industry and provide cow census information from milk recording herds through the National Dairy Herd Information Association (DHIA; Fitchburg, Wisconsin). In Chapter 2 a literature review is presented. Chapter 3 presents results and discussion of the study to investigate changes in genetic trends in US dairy cattle since 1975. In chapter 4, results and discussion of cow census data from DHI cows are outlined. General conclusions of this thesis are presented in Chapter 5.

CHAPTER 2

LITERATURE REVIEW

Herd improvement can be tracked through numerous approaches, including routine monitoring of genetic trends and farmer usage of various tools and technologies (Newton et al., 2021). Many different methods were tested at this time, and a study by Edwards (1932) compared five different indices and concluded that the simple daughter average was the best at that time. From early 1900 until the 1960s, genetic evaluations of dairy bulls were solely based on daughter averages or daughter dam comparisons. After this, the Herdmate Comparison Method was used (Norman et al., 1976). The Modified Contemporary Comparison (MCC; Norman et al., 1976), the first across herd evaluation, was used from 1974 to 1989. The MCC had several advantages such as accounting for the genetic merit of the competition (contemporaries), weighting all information according to the inverse of its expected variance, and incorporating the genetic merit of the ancestors. The genetic evaluation system for dairy animals in the United States now applies an animal model to produce evaluations that are used to achieve a high rate of genetic progress. The system is updated frequently to meet the needs of the US dairy industry and to exploit advances in computer technology and evaluation methodology (Wiggans, 1997). The animal model was first implemented in July 1989 and allowed simultaneous genetic evaluation of bulls and cows with all relationships included (Wiggans, 1989).

One way to enhance the annual genetic progress is using information from single nucleotide polymorphisms (SNP; Meuwissen et al., 2001). Genomic selection is highly efficient for sex-limited traits and traits with low heritability, such as fertility. Animals can be genotyped at birth; therefore, parents of the next generation can be selected at a much younger age (Hutchison et al., 2014). The official United States Department of Agriculture (USDA) genomic evaluations were first released in January 2009 for Holsteins and Jerseys, August 2009 for Brown Swiss, April 2013 for Ayrshires, and April 2016 for Guernseys (Wiggans et al., 2017). Before the genotyping of animals to calculate breeding values, producers relied on phenotypic and pedigree data alone to predict future animal performance. Once genotyping of animals became affordable in late 2010, the number of dairy cattle genotyped increased exponentially. To utilize this new information, the multistep method was developed to incorporate genomic information into evaluations (VanRaden, 2008). This was a novel idea and the US was the first to implement such a procedure. New computer algorithms and programs were needed to incorporate genomic data into genetic evaluations and to process the rapidly expanding numbers of genotyped animals (VanRaden, 2008).

Genomic evaluations in the US follow the Multistep method presented by VanRaden (2008) and VanRaden et al (2009). In this method, best linear unbiased prediction (BLUP) is used to derive deregressed proofs, which are then used as dependent variables in a model to estimate SNP effects. Genomic (G) predicted transmitting abilities (PTA) are obtained as weighted sums of SNP estimated effects times the number of reference alleles and combined with parent averages adjusted for the portion due to genotyped animals to avoid double counting. This method is particularly appropriate when phenotypic and genomic data have separate ownership, and it is well accepted by the dairy industry (Cesarani et al., 2021).

The Multistep method was developed when genotyping was performed almost exclusively on bulls, and genomic selection was yet to be widespread. When genotyping was extended to a large number of females, modifications were developed to reduce bias in genomic estimated breeding values (GEBV; Wiggans et al., 2011). An alternative to the Multistep procedure is single-step genomic BLUP (ssGBLUP) that utilizes phenotypic, pedigree, and genomic information (Legarra et al., 2009; Misztal et al., 2009; Christensen and Lund, 2010). This method is an extension of traditional BLUP, where the inverse of the pedigree relationship matrix ($\mathbf{A^{-1}}$) is replaced by $\mathbf{H}^{-1}$, the inverse of the realized relationship matrix (Aguilar et al., 2010). The $\mathbf{H}^{-1}$ is comprised of both genomic and pedigree relationships. Two main factors determine the accuracy of genomic selection: the size of the reference population (Meuwissen et al., 2001) and the relationship between the reference population and the predicted animals (Pszczola et al., 2012). Recent studies from the University of Georgia (UGA) have shown the challenges associated with the smaller reference populations in the colored breeds (Cesarani et al., 2021).

Genomic selection is now widely practiced across the livestock industry. Currently, there are 5,456,744 total genotypes in the National Cooperator Database and approximately 1 million animals are genotyped each year. Recently, the American Angus Association (AAA; Saint Joseph, MO) reached a milestone of 1 million genotypes (Reep, 2021). Over 100,000 animals per line are genotyped for some pig and broiler breeding companies (Misztal, 2020).

The current literature (Garcia-Ruiz et al., 2016) demonstrates the uptake of genomics in the US for the Holstein breed, as Holstein is the most prevalent breed (Guinan et al., 2019). Garcia-Ruiz et al. (2016) observed huge improvements for lowly heritable traits such as productive life and daughter pregnancy rate. This study was carried out 6 years after the first official genomic evaluation was released. Previously, the four-path model was chosen for similar analyses (Garcia-Ruiz et al., 2016; Van Tassell et al., 1991; Hagan et al., 2021), but since then, Dechow et al. (2018) published work that showed the four-path selection model was derived for a closed population and a genetic lag model works better to determine genetic progress. We decided to use the genetic lag model, as the four-path selection model does not represent what is actually occurring in dairy cattle herds. The latter model is representative of elite status herds and not commercial herds and predicts a higher rate of genetic progress in elite herds that provide artificial insemination (AI) sires. However, commercial farms using AI sires from other herds are not closed, breaking this assumption.

Another alternative to calculating genetic trends was presented by Doublet et al. (2019) that uses a delta variable to explain the effect of genomic selection. Historically, in Australia, Jersey cattle exhibit a lower genetic gain than expected; some reasons for this include the smaller population and slower uptake of young genomic bulls (Scott et al., 2021). In the US, this is not the case for Jersey sires and dams. Genomic selection has been rapidly adopted by the US dairy industry since GPTA were officially published for young bulls in 2009. Bulls are selected based on GPTA before they have a traditional PTA based on daughter performance records. Genomic selection has had a positive effect on recent genetic gain because of a shortened generation interval from intensive use of young bulls (García-Ruiz et al., 2016; Wiggans et al., 2017). In 2012, More than 50% of all AI matings used genotyped, young bulls (Hutchison et al., 2014), and this percentage increased to 73% in 2020 (Wiggans, 2021).

Understanding whether genomic selection has been effective or not is an essential question for both industry and academia (Abdollahi-Arpanahi et al., 2021). A recent study found that genomic selection has increased genetic gain and reduced genetic diversity in both bulls and cows in Australia (Scott et al., 2021). Their findings were similar to that of Garcia-Ruiz et al. (2016). Lozada-Soto et al. (2021) showed that the generation interval has declined from 5.15 years in sires pre-genomic selection to 4.88 years and 5.43 to 4.55 for dams. Scott et al. (2021) showed that since 2009, there has been a considerable decrease in the mean age of sires for Holsteins in both genomic information nucleus herds and national herds, as in 2017 it was 5.4 and 5.7 years respectively. Brito et al. (2021) showed that there is a reduction in genetic diversity and a deterioration of key biological mechanisms as a result of a massive increase in milk productivity in a limited number of breeds. In France, Doublet et al. (2019) observed an increased loss of genetic diversity for Holstein, but not for Montbeliarde and Normande bulls.

Genetic trend validation can be used to verify the breeding values used in genetic trend calculations. This method of validation compares trends estimated from first-lactation records with trends from all lactation records and if there is a significant difference, the trend is not validated (Boichard et al., 1994). The main purpose of investigating genetic trends is to verify whether selection is effective and whether there is an agreement with phenotypic trends (Abdollahi-Arpanahi et al., 2021). In the genomic era, genotypes are valuable if combined with phenotypes (Coffey, 2020). The reduced price of genotyping has led to the majority of young bulls and many females being genotyped. Therefore, the limiting factor for future evaluations of new traits of economic importance is now phenotypes (Coffey, 2020). However, the quality of any genomic breeding value estimation strongly depends on the number of phenotyped animals and the observed heritability of the used phenotypes (Daetwyler et al., 2008).

Milk recording began nationally in the US in 1906 (Voelker, 1981). Participation in milk-recording programs that provide data for national genetic evaluations of dairy cattle in the United States is voluntary, but the effectiveness of the evaluation system increases with the number of herds that contribute data (Hare, 2004). Methods used to test samples and incorporate the resulting observations into genetic improvement and herd management systems have been validated in the scientific literature for many years (McCaffree et al., 1974). Data collection on farms and determination of milk components is currently managed by 26 DHI affiliates. Geographical coverage by individual affiliates ranges from a county to several states. Data flows from the DHI affiliates to the Dairy Records Processing Centers for formatting. Four processing centers prepare reports for producers and forward data to the CDCB, for use in the calculation of genetic evaluations and benchmarking statistics and in turn, these descriptive statistics are used for strategic decision making.

The milk-recording program has evolved as cost pressures have forced dairy producers to become more efficient and as herd size has increased. National milk recording systems are the bedrock of the US dairy genetic improvement programs (Cole et al., 2021). To maintain the numbers of cows and farms that participate in milk recording, considerable flexibility has been allowed in data collection, which varies by the amount of supervision provided by the DHI affiliate, the amount of component sampling, and the frequency of milk recording (Wiggans, 1997).

Current documentation of DHI records consists of 'K Reports'. These reports cover participation, standardized lactation averages, herd averages, test-day somatic cell scores, reproductive status, reasons cows leave the herd, and breed composition statistics. Extending current monitoring of herd improvement to include regular illustrations of the value of the tools that underpin herd improvement is important for fostering the uptake of new or improved tools as they are released to the industry (Newton et al., 2021). Management plays a key role in the genetic improvement of livestock, and to ensure producers can track this, an interactive decision support tool is necessary to share information in an easily accessible way.

Electronic milk recording is used for some herds to record daily milk weights. An average of these weights is reported as the test-day milk yield. Dairy producers can arrange for a wide range of data collection schedules. For example, they can alternate supervised and unsupervised tests (Wiggans 1997). Unsupervised data are included if the herd meets additional restrictions. Supplementary restrictions imposed on those data include limits on the proportion of the herd with missing identification, the difference between milk shipped and the sum of the test-day weights, and the number of outliers (Wiggans, 1997).

On January 1, 1997, about 4.5 of the 9.3 million cows in the United States were enrolled in test plans of the National Cooperative DHI Program (Wiggans, 1997). Due to edits and data restrictions, not all cows meet the requirements to contribute to genetic evaluations. Approximately 55% of DHI cows contributed data to genetic evaluations in 1997.

National and international genetic evaluation systems rely on the participation of producers for herd management data (Hare et al., 2004). The percentage of US cows enrolled in DHI programs was reported each year by the USDA Animal Improvement Programs Laboratory (AIPL). The International Committee for Animal Recording (2015) annually reports on the situation of milk recording for its member countries. For countries that participated in international genetic evaluations for production traits during 2020, percentages of cows that were milk-recorded ranged from 6.1% for Tunisia to 100% for Iceland and Romania (International Committee for Animal Recording, 2020). The duration of herd participation in DHI testing varied geographically and tended to increase over time from 1960 through 2002. Herds in the northeastern and Mideastern US tended to remain on test longest during recent years; the shortest time on test occurred in the southeast (Hare et al., 2004). Sampling month is known to affect sample day Somatic Cell Score (SCS). Kennedy et al. (1982) reported the lowest sample day SCS during May and the highest SCS during December for cows in Quebec, Canada. Improved sire identification will increase the percentage of records being used in genetic evaluations (Meinert and Norman, 1994).

Newton et al. (2021) demonstrated the value of herd improvement in the Australian dairy industry where improvements in genetic gain are predominantly due to genomics and extension. The use of extension in countries like Ireland, Australia, and New Zealand has been paramount to increasing genetic gain at a national level. An ongoing challenge within milk recording is the uptake in robotic milking machines and multiple sources of data. In Australia, the number of herds participating in milk recording has declined from 48% to 29% between 2005-2006 and 2016-2017.

Newton et al. (2021) also reported that results from a 15-month producer survey indicated that incorporating herd testing into businesses was seen as a risk reduction tool, and resulted in more confident decision making. Another big incentive for producing these reports is cows sold with herd test records received higher prices, and one participant noted that this information was used as the criterion for a bank loan. An example of driving profit associated with herd record-keeping is AngusLink used by the AAA to drive genetic progress and add value back to the producer. Currently, the national performance metrics are being used in this way in the US, but perhaps not to their full potential. Data-driven decision support tools are aimed to help dairy farmers improve their decision-making, environmental stewardship, and economic performance (Cabrera, 2018). It is important to update these statistics as objectives and assumptions change over time.

Adding value back to herd testing is vital to maintain support in the NDHIA. Confident, informed decision-making and risk reduction are key components of the use of these reports. Benchmarking statistics have been demonstrated to be used in other areas of farm performance like irrigated feed utilization (Newton et al., 2021). Researchers in the environmental sciences have found that despite the availability of scientific knowledge, relatively little science is used by practitioners (Dicks et al., 2014). Thus, there is a need to find a way of linking science and practice better, and decision support systems (DSS) are a suggested solution (Rose et al., 2018).

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CHAPTER 3

CHANGES IN GENETIC TRENDS FOR DAIRY CATTLE IN THE U.S.[1]

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ABSTRACT

Genomic selection increases accuracy and decreases generation interval, accelerating genetic changes in populations. Assumptions of genetic improvement must be addressed to quantify the direction of change. Genetic trends of US dairy cattle breeds were examined to determine the genetic gain since the implementation of genomic evaluations in 2009. Breeds included Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holstein (HO), and Jersey (JE), which were characterized by the evaluation breed the animal received. Mean Predicted Breeding Values (PBV) were analyzed per year to calculate genetic trends for bulls and cows. The data set contained 154,602 bulls and 27,802,645 cows born since 1975. Breakpoints were estimated using linear regression, and nonlinear regression was used to fit the piecewise model for the small sample number in some years. Generation intervals and inbreeding levels were also investigated since 1975. Milk, fat, protein, Somatic Cell Score (SCS), Productive Life (PL), Daughter Pregnancy Rate (DPR), and Livability (LIV) PBV were documented. The number of bulls obtaining genomic evaluations has increased 75% since 2010, and in 2017, 100% of bulls in this dataset were genotyped. Genotyped cows have increased 20% in the same period. Overall, production traits have increased steadily over time as expected. Holstein and Jersey have benefited most from genomics, with up to almost a 6-fold increase in genetic gain. Due to the low number of observations, trends for AY, BS, and GU are difficult to infer from. Trends in fertility are most substantial – most breeds are trending downwards, DPR for JE has been decreasing steadily since 1975 for bulls and cows. Levels of genomic inbreeding coefficients are increasing at an alarming rate in HO bulls and cows. In 2017, genomic inbreeding levels were at 12.64% for bulls and 8.82% for cows. A suggestion to control this is to apply a negative weight (genomic inbreeding coefficient) to the selection index of bulls with high genomic inbreeding levels. The number of

colored breed bulls in the U.S. is currently at a very low level, and this number will only increase with a market incentive or with additional breed association involvement. Increased education and extension could be beneficial to increase knowledge about inbreeding levels, use of genomics and genetic improvement, and diversity in the genomic selection era.

INTRODUCTION

Official genomic evaluations for dairy cattle in the United States were released in 2009 for Holstein (HO), Jersey (JE), and Brown Swiss (BS), 2013 for Ayrshire (AY), and 2016 for Guernsey (GU) (Wiggans et al., 2017). Those evaluations comprise multibreed BLUP followed by single-breed estimation of SNP effects. Genomic PTAs are obtained as the combination of direct genomic value based on markers and parent average. Since the implementation of genomic selection (GS) in the US, it has been documented that genetic trends have changed significantly for the HO breed (Garcia-Ruiz et al., 2016). Genetic trends measure the success or failure of a breeding program and are needed to justify the usefulness of genetic evaluations and, therefore, the rationale behind using new methodologies (Grosu, 2013). Milk, fat, and protein yield have increased remarkably alongside the uptake of genotyping in the dairy industry. Since 2009, the genetic improvement in countries like the US with advanced dairy industries has predominantly relied on genomic selection (Scott et al., 2021).

There are currently over five million genotyped animals in the US evaluation system (https://queries.uscdcb.com/Genotype/cur_ctry.html), but the uptake of genotyping is not even across breeds. As of October 2021, the number of genotyped AY, BS, GU, HO, and JE is 14.7K, 63.8K, 7.4K, 4.9M, and 623K, respectively. The increase in reliability of genomic PTA depends on the number of genotyped animals (VanRanden et al., 2009), trait heritability (Hidalgo et al., 2021), phenotype availability (Mulder., 2017), and how the genomic information is used (Scott et al., 2021). Increased reliability and a reduction in generation interval (GI) are known for driving the accelerated rates of genetic gain under GS. Garcia-Ruiz et al. (2016) showed that GI for sires and dams of HO bulls in the US decreased from 7 and 4 years, respectively, to 2.5 years after the implementation of GS. This enabled an annual increase in genetic gain for US HO of up to twofold for production traits and fourfold for traits with low heritability as fertility and productive life. As HO is the predominant breed in the U.S. and makes up 81.4% of the national breed composition in 2018 (Guinan et al., 2019), it is no surprise that the improvements after GS are evident in this breed. Nonetheless, this may not be the reality for all dairy breeds.

The improvement in genetic trends for all breeds has been documented and is available at https://queries.uscdcb.com/eval/summary/trend.cfm for traditionally evaluated animals. However, there is little evidence/documentation of the improvement and changes in colored breeds (i.e., AY, BS, GU, and JE) in the US since the introduction of genomic evaluations. Reviewing the assumptions of genetic progress since the introduction of genomics is crucial for advising breed associations and non-academic stakeholders on how to utilize this technology moving forward. Therefore, the main purpose of this study was to investigate genetic trends in the five breeds receiving genomic evaluations for production, fertility, longevity, and health traits. We further investigated changes in generation intervals and inbreeding levels for those breeds.

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MATERIALS AND METHODS

Animal Care and Use Committee approval was not needed as data were obtained from preexisting databases.

Data

The data for this study were extracted from the National Cooperator Database maintained by the Council on Dairy Cattle Breeding (CDCB) in Bowie, Maryland. The data included (Genomic) Predicted Transmitting Abilities (PTAs) of bulls and cows born since 1975 that incorporated pedigree, phenotypic and genomic (when available) data from the August 2021 official evaluation with the latest lifetime net merit (NM$) index update (VanRaden et al., 2021). Phenotypic data is collected on farms as part of routine herd management by the National Dairy Herd Information Association (NDHIA).

For an animal to be included in the analyses, the IDs required a USA, CAN, or 840 identification code to illustrate the progress in North America. Cows without sire information were removed. Minimum reliability for Milk PTA was 9%, and if Milk PTA was missing, the record was deleted. The genetic base year was 2015 (Norman et al., 2020), meaning that EBV for all milking cows born in 2015 were set to 0. Each breed is on an individual base (i.e., within-breed base); therefore, individual plots are not directly comparable. Breed code was based on the one the animals received in the August 2021 evaluation, which reflects the breed base representation (BBR). Evaluation breed codes include AY, BS, GU, HO, and JE.

We analyzed milk, fat, and protein yield, somatic cell score (SCS), productive life (PL), daughter pregnancy rate (DPR), livability (LIV), and health traits (when available). These traits were selected based on their weight in the most recent update of the NM$ index (VanRaden et al., 2021). Data were restricted to ≥10 daughters per bull, and a weighted average for bulls was calculated. No bulls with less than 10 daughters were included in the genetic trends as they do not substantially contribute to the genetic trends. Cows had to have at least one calf (Masuda et al., 2018), but their PTAs were not weighted by progeny size. Additionally, the cows must have an evaluation and their milk, fat, and protein records contribute to the sire evaluation. After applying the above filters, predicted breeding values (PBV) were calculated by multiplying the stored (G) PTA by two. Only PBV from bulls born from 1975 up to 2017 and cows up to 2019 were used for plotting genetic trends to highlight the progress made with multiple genetic evaluation methodologies. Pedigree inbreeding levels were calculated using inbreeding coefficients with the same data. Genomic inbreeding levels were limited to genotyped animals with genomic inbreeding coefficients.

Generation intervals (GI) were calculated using the same edits and were divided into dams of bulls, sires of bulls, sires of cows, and dams of cows. To stratify by breed, both parents and animals must have the same breed code. Additionally, pedigree information was determined. GI was limited to where the breed of both parents was known. Generation interval equals animal birth date minus parent birth date divided by 365.25 and dam age must be greater than 1.

Model and Analysis

In previous studies (Garcia-Ruiz et al., 2016, Van Tassell et al., 1991 and Hagan et al., 2021), the four-path selection model was used to calculate genetic trends using selection differentials. Research by Dechow et al., (2018) has shown that the four-path selection model was derived for a closed population, however, through the use of artificial insemination commercial herds are not in fact closed. The authors demonstrated that by tracing the transmission of genetic merit from parents to offspring, the rate of genetic progress in commercial dairy farms is expected to be the same as that in the genetic nucleus. Thus, we generated genetic trends based on bull and cow contributions to genetic improvement.

Statistical Analysis Software (SAS) was used to calculate genetic trends, inbreeding levels, and generation intervals. Average PBV inbreeding and generation intervals per year were calculated using PROC MEANS. The PROC REG was used to create a linear model to estimate the breakpoints (priors) to be included in PROC NLIN to fit the best line between the breakpoints. The breakpoints were estimated every five years. This aided in plotting the colored breeds' genetic trends when data were limited and based on only a few observations in a given year. Finally, PROC GPLOT and PROC SGPLOT were used to plot the data over time.

RESULTS AND DISCUSSION

In this study, we investigated genetic trends for AY, BS, GU, HO, and JE to identify the rates of genetic gain since genomic selection was implemented for these breeds. Genomic evaluations in the US officially started in January 2009 for HO and JE, in August 2009 for BS, in April 2013 for AY, and in April 2016 for GU (Wiggans et al., 2017). Trends were explored from 1975 to 2017; therefore, most of the progress achieved for GU is expected to be under traditional selection. To better understand the data and the genotyping uptake in these five breeds, we provide descriptive statistics for each breed before examining individual trends.

Descriptive Statistics

Since 1975, there have been 154,602 bulls with at least 10 daughters with milk records in the US evaluation system, as shown in Table 3.1. Of those bulls, AY, BS, and GU make up less than 2%, whereas HO and JE represent 86.97% and 8.13%, respectively. Interestingly, BS proportionally has the most genotyped bulls (Table 3.2). This is a result of the European Brown Swiss Federation Intergenomics project, which established an international database of genotypes for the Brown Swiss populations. As seen in the frequency distribution in Figure 3.1, the number of bulls genotyped has been increasing rapidly per year. In 2005, slightly more than half of the bulls were genotyped, and in 2017 all bulls were genomically tested. Although the number of genotyped cows has increased throughout the years, they still represented only 19.98% of the total cows born in 2017 (Figure 3.2). Proportionally, the JE breed has genotyped the most cows (8.73%); however, the proportion of cows genotyped is still a stark contrast to the bulls (overall 4.62% versus 24.06%). This is due to the widespread use of bulls and the biological limitation that makes cows have fewer daughters per year. Among all the cows, HO represents the largest proportion and AY is the least represented breed (Table 3.1).

Genetic trends

Milk, Fat, and Protein

The most apparent improvement across all traits was observed for production. Since milk historically received so much emphasis in the selection indexes (52% in 1971) and producers were primarily paid for increased production, this is no surprise. Breeding objectives of dairy industries around the world have been evolving over the years towards functional traits and away from production traits (Miglior et al., 2005).

Overall, genetic trends for milk, fat, and protein were similar for both bulls and cows across all the breeds (Figures 3.3-3.12). This is partially due to the high genetic correlations between the three yield traits. Tsuruta et al. (2004) reported milk-fat genetic correlations to range from 0.48 – 0.69 and milk-protein from 0.82 – 0.87. Milk, fat, and protein PBV for AY bulls show a steady increase (Figure 3.3). Interestingly, the rate of genetic improvement for production traits accelerated in 2009, even though AY did not receive a genomic evaluation until 2013. This is due to producers genotyping the best AY bulls once genomic evaluations were released for HO and JE in 2009, which impacted all the traits. Ayrshire bulls born in 2016 had PBV of 907.67 kg for milk, 48.12 kg fat, and 33.18 kg protein, whereas the ones born in 2012 (i.e., before GS) had PBV of 214.22 kg, 14.95 kg, and 10.44 kg, in the same order. A similar trend is evident for the AY cows.

In 2006, PBV for milk, fat, and protein for AY cows became positive (Figure 3.8). This again highlights the impact of genotyping bulls that were being used when genomic evaluations were initially released.

Genetic trends for BS bulls and cows are comparable, moving upward, especially since 2009 when BS received genomic evaluations. This was also the point where milk and fat PBV became positive (Figures 3.4 and 3.9). Protein was a couple of years behind in 2011, probably because of the lower emphasis in the NM$ at that time. As GU only began receiving genomic evaluations in 2016, and in the dataset, we only have bulls with at least 10 daughters up to 2016, the inference to be made from this trend regarding the use of genomics is limited (Figure 3.5). However, since 1975, there has been a significant increase in milk, fat, and protein production for GU bulls. As our GU cow dataset extends to 2019, we see an increase in PBV for the yield traits since 2009 (Figure 3.10). This infers that the best GU were genotyped before receiving a genomic evaluation.

Due to the large number of HO bulls and cows, the trends are more defined. HO bulls have potentially made the most progress in the evaluated time period. In 1975, the mean PBV for milk yield was -2,720.65 kg; in 2017, this statistic is 811.26 kg. A sharper increase is evident for fat and protein yields since implementing HO genomic evaluations in 2009 (Figure 3.6). Similarly, milk, fat, and protein PBV have increased substantially over time for HO cows (Figure 3.11). In 2017, JE bulls had average milk, fat, and protein PBV of 358.27, 21.66, and 18.9 kg. Compared to 2009, this is an increase of 908.77 kg, 40.04 kg, and 35.58 kg, respectively. Despite not receiving any emphasis in the Jersey Performance Index, milk has also increased over time for both bulls and cows (Figures 3.7 and 3.12).

Somatic Cell Score

Genetic evaluations for somatic cell score (SCS) were published by the Animal Improvement Programs Laboratory (AIPL) in 1994. This resulted in favorable changes in SCS that had previously been due to selection for high milk yields; however, it took 8 years for this to be evident (Norman et al., 2016). In our study, due to the low number of bulls with daughters with SCS records, the trend is almost nonexistent in the AY bulls, and therefore, inferences are not relevant (Figure 3.3). With AY cows (Figure 3.8), a steady increase in SCS is apparent until 2011 (6.04). After this point, a downward trend is visible, which is favorable. More progress is being made with AY cows in SCS. For BS bulls (Figure 3.4), SCS has increased over time, although we see an overall downward trend since 2006. The scale of this graph is relevant. Although there is a trend, the graph ranges from 5.68 to 6.1, showing an approximately 0.4 increase from 1975 to 2017. We see a gradual increase in SCS PBV for cows until 2012, with a substantial decline after that (Figure 3.9). Trends of SCS for GU bulls (Figure 3.5) increased from 1975 until 2011, where we see a steep decrease until 2016 (5.86). A similar trend is visible for cows in Figure 3.10 – SCS has decreased since 2011, indicating that the best performing GU cows were genotyped before receiving a genomic evaluation.

In 1994, SCS was implemented into the NM$. It often takes about 6 years for the trend to start changing in the desired direction after implementing a new trait in a selection index. The SCS trend for HO gradually increased from 1975 to 2000; however, since 2000 it has been on a steady downward trend (Figure 3.6). Thus, highlighting the usefulness of incorporating new traits into the NM$. Even though it is a slight decrease, proportionally, the mean PBV decreased by 0.58 percent. The SCS trend for HO cows is a little more delayed than the HO bulls (Figures 3.11 and 3.6, respectively). Since 2005, HO cows have consistently decreased the PBV for SCS. No evident trend changes were observed for this trait after the implementation of GS; nonetheless, it is hard to assert from the trends how much of the gain observed from 2009 to 2017 is free of genomics. In 2010, SCS received its highest weight in the Jersey Performance Index (JPI), which is 6.0%. Since 2011, there has been a downward trend in SCS for JE bulls (5.91 in 2017) (Figure 3.7). Up until this point, SCS PBV were increasing. Conversely, in JE cows, SCS has remained constant since 2010, as seen in Figure 3.12.

Productive Life

Productive life (PL) measures a cow's ability to stay alive on the farm while producing milk and is measured in months. Genetic evaluations for PL were first published by AIPL in 1994. Although cows have been directly selected for longer productive lives, management decisions have shortened cows' actual tenure in the milking herd (Norman et al., 2019). The PBV for productive life has increased steadily for AY bulls over the past 41 years, from -8.77 months in 1975 to 0.98 months in 2016 (Figure 3.3). The AY cows have had much more progress in PL, with an average PBV for PL in 1975 of -2.46 to 4.71 in 2019, again becoming a positive PBV in 2005 (Figure 3.8).

In 2011, we saw a positive PL PBV for BS bulls. Since 2011, the genetic trend has been positive and with a steep slope. Productive life has increased 8.37 months since 1975 for BS bulls (Figure 3.4). Similarly, with BS cows, PL has been gradually increasing over time (Figure 3.9). Since 1999 there has been a consistent increase in mean PBV per year for PL. This trait has also been consistently increasing over time for GU bulls. From a low of -9.75 months in 1975 to 3 months PBV in 2016 (Figure 3.5). For GU cows, PL declined from 1975 until 1986. Since then, it has increased to 3 months of extra productive life in 2019 (Figure 3.10). About 6 years after PL was introduced to the genetic evaluation, we started to see an increase in PBV for HO bulls and cows (Figures 3.6 and 3.11). Productive life has increased by 15 months for HO bulls and 6 months for HO cows since 1975. Jersey bulls' PL averaged -11.42 months in 1975 6.07 months in 2017(Figure 3.7). For JE cows, PL declined from 1975 to 1980 and has been increasing steadily since then to reach an average of 2.8 months in 2018 (Figure 3.12).

Daughter Pregnancy Rate

Genetic evaluations for DPR were introduced in the United States in February of 2003 to improve reproductive performance (VanRaden et al., 2004). DPR had not been focused on for a large portion of history due to its low heritability (0.04), despite research showing unfavorable genetic correlations between yield and fertility (VanRaden et al., 2004). The same authors showed that from 1960 to 2000, PTA for DPR decreased for bulls in all breeds, including Milking Shorthorn

The DPR for AY bulls has been reducing since 1975 and over this period declined from 12.39% to -0.18% in 2016 (Figure 3.3). Alternatively, AY cows began increasing in 2005 through 2010, and a downward trend is seen (Figure 3.8). Although the AY cows' PBV for DPR trended downwards, it is not a negative PBV, as we see with the bulls. Average PBV for this trait has been decreasing since 1975 for BS bulls (Figure 3.4). Since 1975, DPR has drastically dropped 19.2 percentage points to -3.6% in 2017. Similarly, BS cow's fertility declined to 1.36% in 2019 (Figure 3.9). The DPR has increased since 2010 for GU bulls from -1% to 1% in 2016, indicating an increase in fertility (Figure 3.5). For cows, DPR started at 17.48% in 1975 and declined to 0.55% in 2010, remaining approximately at this level ever since (Figure 3.10).

Although there has been a steep decline of -13.55 percentage points in DPR for HO bulls from 1975 to 2008, minor improvements have been made since then (Figure 3.6). The DPR is trending upward since its weight in the NM$ increased in 2006. For cows, we see a slightly different trend (Figure 3.11). Between 1975 and 2010, DPR decreased from 15.54% to 0.25%.

This is an alarming rate, and efforts must be increased to change this trend. HO DPR PBV have remained centered around 0 since 2010. For JE bulls and cows, DPR has decreased steadily since 1975. There was a 13.98 and 17.97 percentage point reduction in DPR for JE cattle, respectively, for these 44 years (Figures 3.7 and 3.12).

Livability

Genetic evaluations for livability (LIV) were first computed in 2016 to improve the cow's ability to stay alive while in the milking herd (Wright et al., 2016), which is an indirect measure of mortality. Currently, LIV receives 4.4% relative emphasis in the NM$ selection index. PTA LIV is expressed as a probability value of a lactation not ending in death or on-farm euthanasia (https://queries.uscdcb.com/reference/Form_GE_Livability_1608.pdf). Due to the low number of AY bulls with daughters with greater than 10 records for LIV, there is no clear trend (Figure 3.3). For AY cows (Figure 3.8), we see a downward trend in LIV since the beginning of genomic evaluations in 2013, perhaps because LIV was introduced into the evaluation system in August 2016. Livability in BS bulls decreased over time and has had a negative PBV since 2014 (Figure 3.4). The mean PBV for LIV in BS bulls in 2016 is 0.86. This trend is influenced by the fact that the 2017 average is based on only one observation. We see a similar downward trend for BS cows but not a negative PBV at any time, although, since 2009, there has been a clear downward trend (Figure 3.9). LIV has been increasing since 2011 for GU bulls (Figure 3.5), despite a considerable reduction between 1975 and 2015 of 11.43 percentage points. GU cows have also decreased LIV since 1975, from a starting point of 17.48%. However, since 2012 this trend has remained positive and is slowly increasing over time (Figure 3.10).

Livability was incorporated into the NM$ in 2017; however, since 2000 there has been a positive increase in HO bull LIV PBV after a steady trend since 1980 (Figure 3.6). This could be due to the inclusion of productive life into the index in 1994, as livability is one of the traits that make up PL. A much smoother trend is evident in the cows due to the higher number of observations per year (Figure 3.11). Livability has increased in JE bulls since 2000 (Figure 3.7) and JE cows since 2007 (Figure 3.12). Currently, the mean PBV LIV for JE bulls is 1.73 and for cows is 0.57. Although LIV was added to the JPI in 2017, the trend started to improve a decade earlier, probably due to the inclusion of PL in 2002.

Pedigree & Genomic Inbreeding

Inbreeding is defined as the probability that two random alleles at the same locus from two uniting gametes are identical by descent from a common ancestor (Malécot, 1948). As the level of pedigree errors and missingness can be considerable in dairy populations, the genomic information can more precisely estimate the inbreeding levels (Howard et al., 2017). Pedigree and genomic inbreeding coefficients were analyzed for bulls and cows in this dataset. Previous studies (Garcia-Ruiz et al., 2016 and Forutran et al., 2018) have shown an increase in pedigree and genomic inbreeding in HO. Rates of inbreeding in recent years correspond closely to rates of genetic progress, which tend to be highest in the Jersey and Holstein breeds. The GS was expected to reduce the rate of inbreeding and increase genetic gain per generation simultaneously (Doublet et al., 2019). Many studies have found that the reality may be different (Scott et al., 2021).

The use of young animals as sires and dams substantially increased the rate of inbreeding per generation, which is caused by the lower accuracy of selection when young animals are selected as parents, leading to more weight on parent-average EBV and therefore more co-selection of sibs (De Roos et al., 2011). Inbreeding is currently controlled in the population by adjusting the EBV for inbreeding of future progeny. The rate of inbreeding per year is much higher with genomics because of the shorter generation interval (De Roos et al., 2011). Research by

González-Recio et al. (2007) showed that cows with higher inbreeding coefficients had impaired fertility. Similarly, a study from Ireland (Mc Parland et al., 2007) showed that higher rates of inbreeding had a deleterious effect on fertility. Previous studies (Pryce et al., 2012) predicted that the rate of inbreeding would be lower per generation in genomic breeding programs than in progeny testing and that shorter generation intervals would be responsible for higher rates of inbreeding per year.

From 2000 to 2008, pedigree inbreeding increased 1.09% yearly for HO bulls. Since 2009, it is increasing by 4.7%. For JE bulls, pedigree inbreeding went from 0.07 % yearly to 5.03% in the same period. BS bulls changed from 1.45% to 10.17% and AY bulls have continued to decline at -0.25% to -6.42% every year between 2009 and 2012, and 2013 and 2016, respectively. GU bulls were excluded as evaluations have not been available long enough for calculations. From 1998 to 2008, pedigree inbreeding increased 2.76% yearly for HO cows. Since 2009, it is increasing by 4%. For JE cows, pedigree inbreeding went from 2.27% yearly to 2.06% in the same period (Figure 3.13). Brown Swiss cows changed from 2.34% to -0.47% and AY cows have continued to decline at -5.19% to -5.21% every year. GU cows increased 1.44% between 2013 and 2016 and have declined 0.52% annually between 2016 and 2019.

From 2000 to 2008, genomic inbreeding increased by 0.88% yearly for HO bulls. Since 2009, it is increasing by 6.87% yearly. For JE bulls, genomic inbreeding went from -2.42 % yearly to 4.5% in the same period. Brown Swiss bulls changed from 0.25% to 13.25% and AY bulls have continued to decline at -1.44% to –16.12% on a yearly basis3 years pre and post-genomic evaluations. GU bulls were excluded as evaluations have not been available long enough for calculations. From 1998 to 2008, genomic inbreeding increased 0.49% yearly for HO cows. Since 2009, it is increasing by 6.88% yearly. For JE cows, genomic inbreeding went from -2.65% yearly to 3.34% in the same period. Brown Swiss cows changed from -0.35% to 1.79% and AY cows decreased 10% yearly between 2006 and 2012 and declined -34.19% between 2013 and 2019. GU cows increased 8.39% between 2013 and 2016 and have increased 5.65% annually between 2016 and 2019.

Bull Inbreeding

Pedigree inbreeding in AY bulls has increased since 1975 from 2.13% to 5.23% in 2016. For BS bulls, the pedigree inbreeding level was 7.63% in 2016. Guernsey bulls have increased pedigree inbreeding from 0.77% in 1975 to 6.67% in 2016 (Figure 3.14). The breed with the highest level of inbreeding in 2017 was HO at 10.62% (Figure 3.14), whereas the acceptable level may be around 6.25% (J.B. Cole, URUS, Madison, WI, personal communication). Pedigree inbreeding for JE bulls was higher than genomic breeding, at 8.92% in 2017. This indicates that the breed association has successfully implemented genomic selection as it was intended to be used. Due to the low number of genotyped bulls per year, genomic inbreeding trends cannot be inferred for AY and GU bulls (Figure 3.14). The level of genomic inbreeding for BS bulls in 2016 was extremely high (16.1%); however, it was only one observation and not an average. For HO bulls, the level of genomic inbreeding was 12.73% in 2017, which indicates it would be proper to update GPTA with the genomic inbreeding coefficient. As seen in Figure 3.14, the JE genomic inbreeding levels average at 7.22% in 2017, slightly less than the pedigree inbreeding levels.

Cow Inbreeding

Similarly, genomic inbreeding trends for AY and GU cows cannot be inferred due to the low number of observations per year. Although bulls born prior to receiving genomic evaluations were genotyped, this is not the case with cows. This is obviously due to the lower number of offspring per year and the higher cost of genotyping at that time. Pedigree inbreeding in AY cows (Figure

3.14) has decreased since 2003, and the mean in 2019 was 1.66%. For BS, this increased from 0.62% to 4.49% in 2019 (Figure 3.14). Guernsey cows have shown a slow increase in pedigree inbreeding levels since 1975, reaching 6.72% in 2019 (Figure 3.14). HO cows averaged at 7.66% in 2019 and JE cows are at 7.34% (Figures 3.14). Genomic inbreeding trends for BS cows only began in 1990 when the nonlinear regression was applied to the data. Again, because of the low number of observations, the linear regression would not accurately fit the trend before this time. Genomic inbreeding has increased steadily since 2009 for BS cows (6.67 – 7.82%). A similar trend is evident for HO and JE cows before 1990. The average genomic inbreeding for HO and JE cows in 2019 was 9.1% and 6.39%, respectively (Figure 3.14). Fortunately, the genomic inbreeding levels can be controlled by incorporating this information into the GPTA calculation.

Generation Interval

Genomic selection has allowed producers to select animals at a much younger age while simultaneously increasing the accuracy of prediction, which led to a much shorter generation interval. Breeders can accelerate rates of improvement through low generation intervals based on the breeder’s equation (Lush, 1937); however, there is a biological limitation in ruminants. Because of biological advantages in reproductive characteristics, high rates of genetic change are possible in fish, pigs, and poultry (Simm et al., 2020). Hagan et al. (2020) showed the reduction in generation intervals in Canada for AY, BS, HO, and JE cows since 1980 through the four-path selection model. Progress toward a decreased generation interval was slower for BS and AY compared to JE and especially HO.

In 1975, the average age of U.S. HO sires of bulls when offspring were born was 9.4 years, whereas, in 2017, it was 2.2 years (Figure 3.15). For JE, there are similar patterns, although not as low as for HO (9.8 – 3.1 years). Brown Swiss have also made progress in generation intervals from

2009 – 2016 (-3.1 years); however, very little progress has been made for AY and GU since 1975, probably because of the later implementation of genomics and the smaller number of genotyped selected candidates compared to the other breeds. For cows, the reduction in generation interval has been somewhat slower. For sires of HO cows, generation interval has decreased from approximately 6.9 years in 2009 to 4 years in 2019. Jersey and BS also saw a reduction in the sire generation interval of 2.4 and 2.7 years since 2009. Again, generation intervals for the parents of AY and GU cows have not decreased significantly since 1975 (Figure 3.15). Perhaps this is an area AY and GU breeds could benefit significantly from genomic technologies. Incentives could encourage data collection, genotyping, and the widespread use of young genomic bulls and heifers.

General observations

Significant improvements have been reached since the implementation of genomic evaluations in the US in 2009. Bulls are making more progress than cows as bulls have more progeny, and a great proportion of bulls (68%) are genotyped versus cows (5%) since 1975. Fat yield increased almost 6-fold for HO bulls between 2009 and 2017, while PL increased 4.2-fold (Figure 3.13). In comparison, HO cows have increased 1-fold for the same traits between 2009 and 2019. In the same periods, JE bulls have increased LIV 64%, while JE cows have increased 16.49% yearly. Because of the increased use of young genotyped bulls and heifers, a decrease in generation interval followed the implementation of GS for all breeds, except AY and GU. The generation interval before and after GS changed from 7.1 to 2.2 years in HO, 7.3 to 3.1 in JE, 8.4 to 5.2 in BS, and 7.6 to 5.3 in AY for sires of bulls (Figure 3.15). For dams of bulls, the GI before and after GS changed from 4 to 2.1 for HO, 5.2 to 2.6 years for JE, 5.8 to 3.9 for BS, and 5.6 to 4.5 years for Ayrshire (Figure 3.15). The generation interval before and after GS changed from 6.9 to 4 years in HO, 6.4 to 4.0 in JE, 7.29 to 4.58 in BS, and 9 to 7.5 in AY for sires of cows (Figure

3.15). For dams of cows, the GI before and after GS changed from 3.8 to 3.1 for HO, 3.6 to 3 years for JE, 4.3 to 3.6 for BS, and 4.1 to 3.6 years for Ayrshire (Figure 3.15). As genomic evaluations were only released for GU in 2016, it is too early to see the benefits as clearly as in other breeds, and this should be reviewed in the next five years. Applying a negative weight to inbreeding in the net merit could result in an increased ranking of colored breed bulls in North America. More focus on communication between geneticists and producers on how to use GPTA can help to control inbreeding levels. Progress for smaller breeds will need to be continually monitored to assess the level of genetic progress and to measure the level of genetic gain ten years post-genomic evaluations.

CONCLUSIONS

This research provides benchmarks for breed associations to evaluate the updates in genetic evaluations methodology in the genomics era. Genomic information has mainly benefitted Holstein and Jersey because the implementation of GS for these two breeds happened as early as 2009. Another reason is that HO and JE have larger reference populations and more refined selection indexes. However, it does not mean the other breeds are not benefiting from GS. In the short years investigated, there is success in the majority of traits for the colored breeds. Colored breeds in the US could significantly benefit from genotyping and phenotyping more of the population and increasing the adoption of genomic methods. This study should be updated in another five years to give these breeds further opportunity to develop.

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TABLES

Table 3.1. Number of bulls and cows by breed.

Breed Evaluation	Bulls		Cows	
	Frequency	Percentage	Frequency	Percentage
AY	2,107	1.36	137,962	0.5
BS	2,803	1.81	243,936	0.88
GU	2,662	1.72	142,992	0.51
HO	134,461	86.97	24,877,547	89.48
JE	12,569	8.13	2,400,208	8.63
Total	154,602	100	27802645	100

Table 3.2. Proportion of genotyped and non-genotyped bulls and cows born from 1975.

Animals	Genotyping status	Breed Evaluation					Total (%)	Total (No.)
		AY	BS	GU	HO	JE		
Bulls	Non-genotyped (%)	62.32	57.97	85.31	77.75	60.82	75.94	117,403
	Genotyped (%)	37.68	42.03	14.69	22.25	39.18	24.06	37,199
Cows	Non-genotyped (%)	99.48	97.48	98.46	95.72	91.27	95.38	26,518,215
	Genotyped (%)	0.52	2.52	1.5	4.28	8.73	4.62	1,284,430

FIGURES

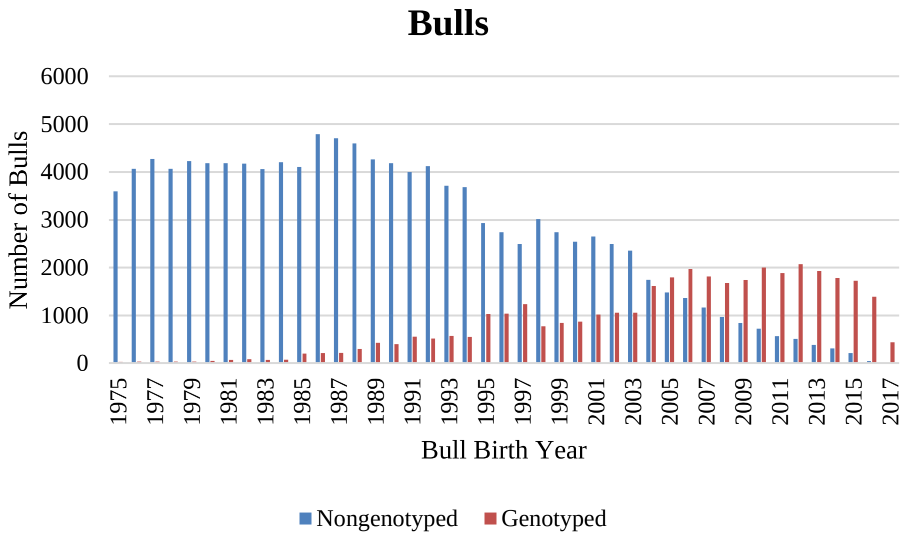


Figure 3.1. Number of genotyped and non-genotyped bulls since 1975.

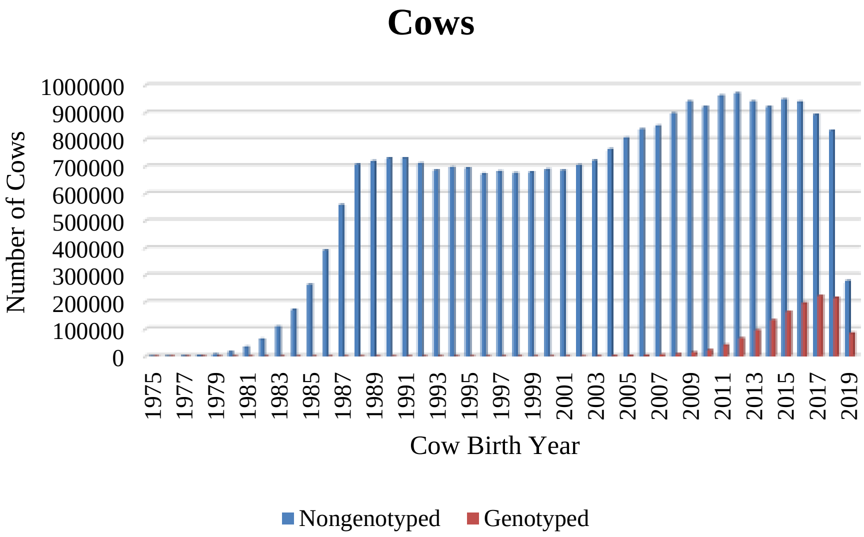
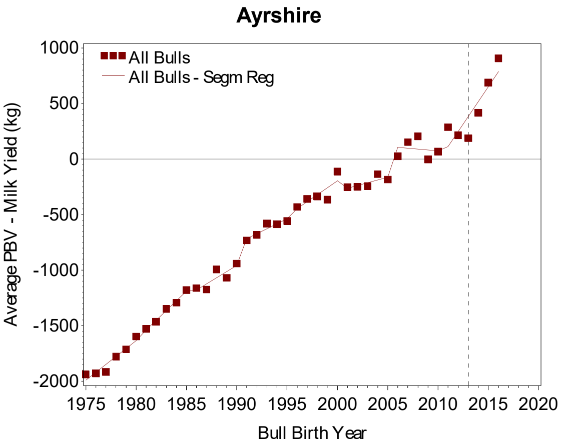


Figure 3.2. Number of genotyped and non-genotyped cows since 1975.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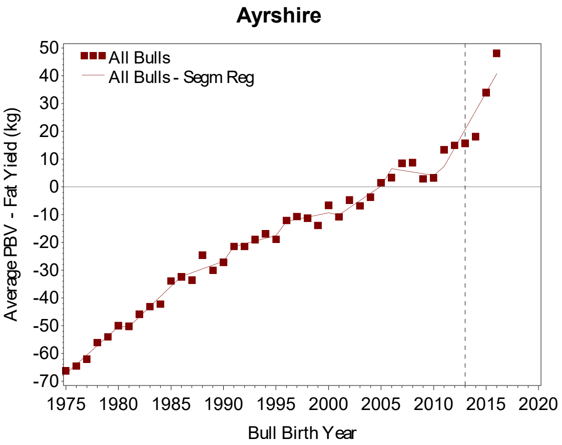
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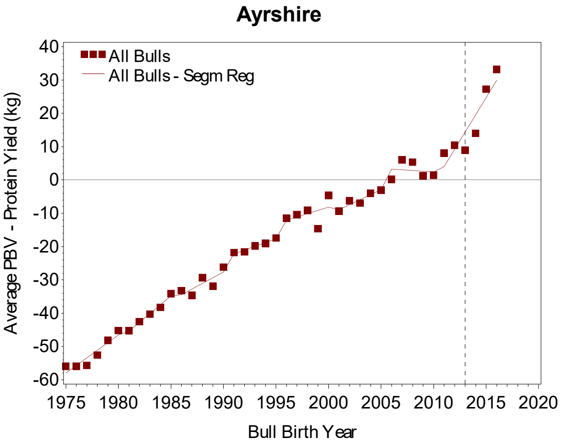
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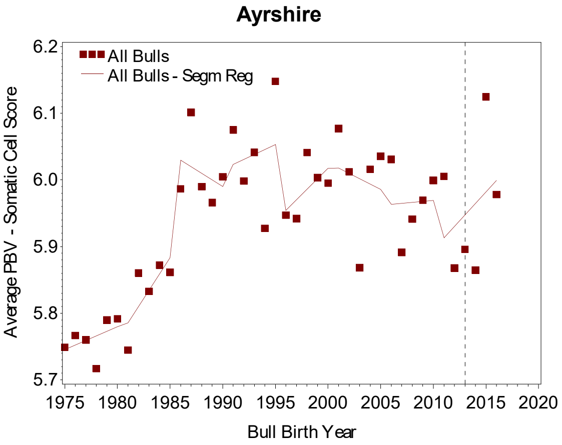
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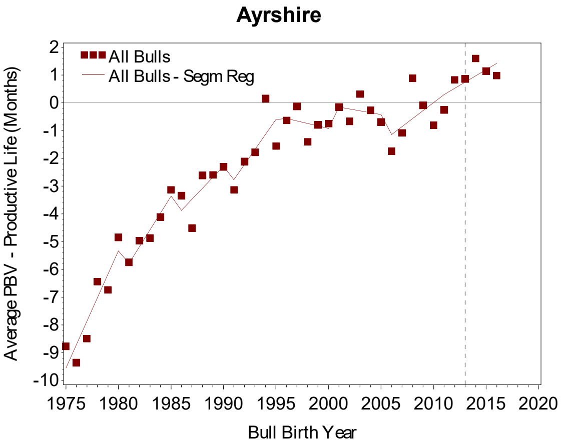
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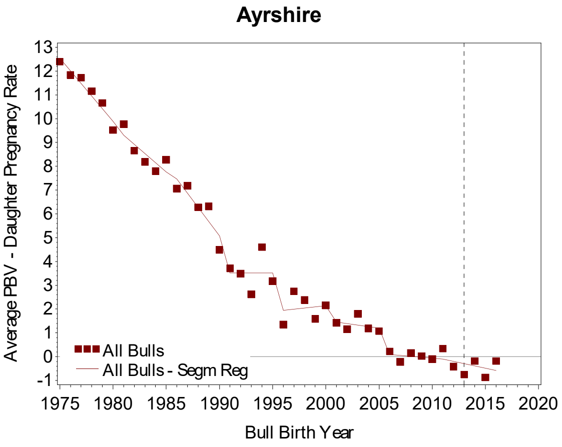
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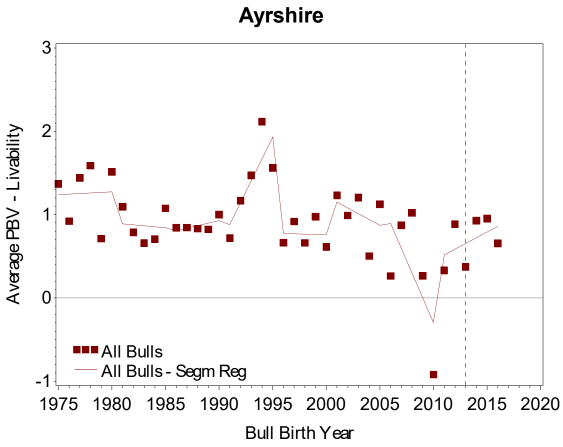
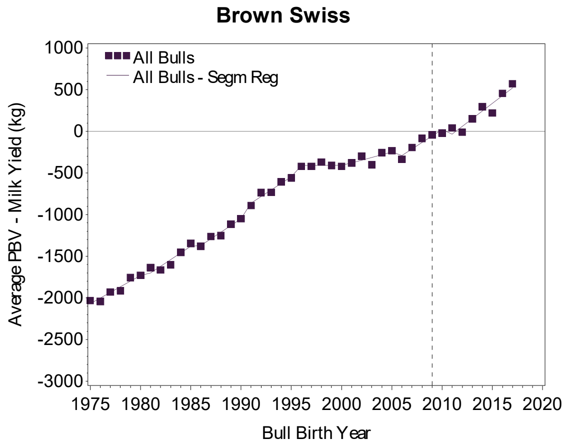
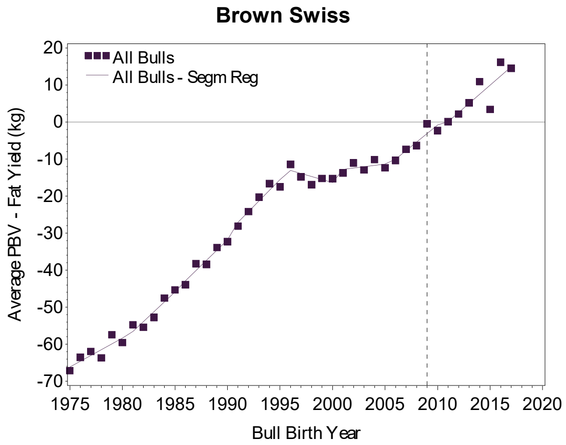
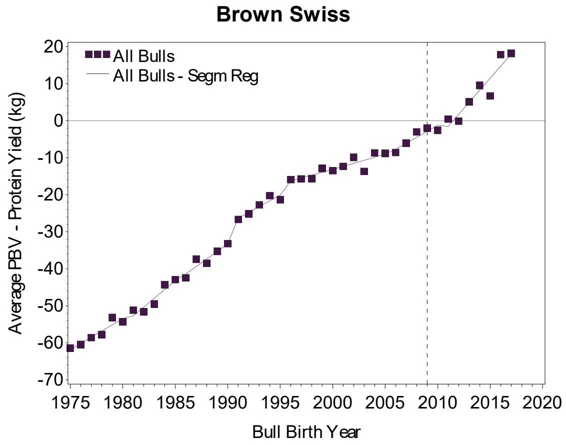
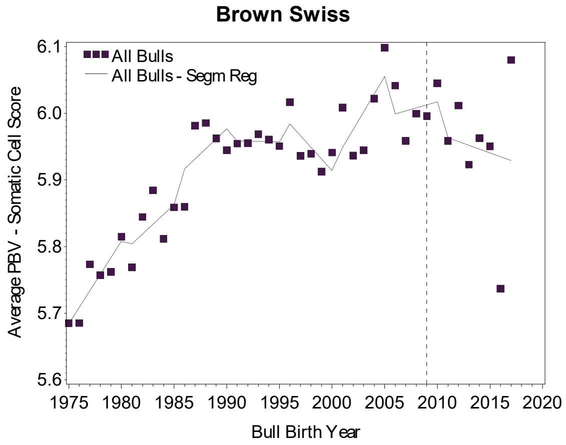


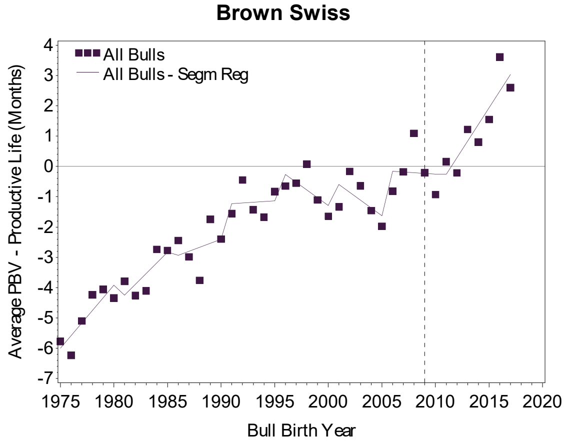
Figure 3.3. Estimates of genetic change per year from segmented regressions of PBV on birth year for AY bulls for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.

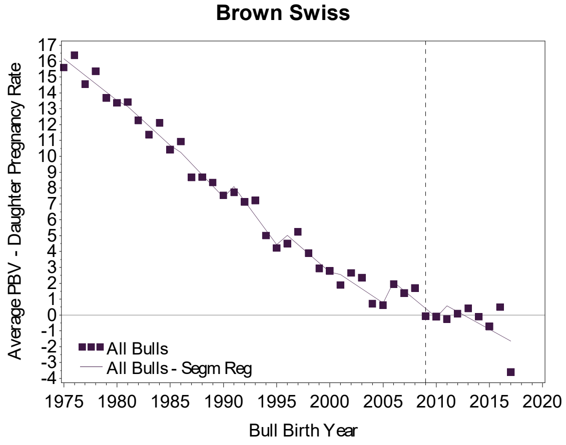

Brown Swiss
All Bulls
All Bulls - Segm Reg
Average PBV - Milk Yield (kg)
1000
500
0
-500
-1000
-1500
-2000
-2500
-3000
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Bull Birth Year


Brown Swiss
All Bulls
All Bulls - Segm Reg
Average PBV - Fat Yield (kg)
20
10
0
-10
-20
-30
-40
-50
-60
-70
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Bull Birth Year


Brown Swiss
All Bulls
All Bulls - Segm Reg
Average PBV - Protein Yield (kg)
20
10
0
-10
-20
-30
-40
-50
-60
-70
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Bull Birth Year


Brown Swiss
All Bulls
All Bulls - Segm Reg
Average PBV - Somatic Cell Score
6.1
6.0
5.9
5.8
5.7
5.6
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Bull Birth Year


Brown Swiss
All Bulls
All Bulls - Segm Reg
Average PBV - Productive Life (Months)
4
3
2
1
0
-1
-2
-3
-4
-5
-6
-7
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Bull Birth Year


Brown Swiss
All Bulls
All Bulls - Segm Reg
Average PBV - Daughter Pregnancy Rate
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
-1
-2
-3
-4
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Bull Birth Year

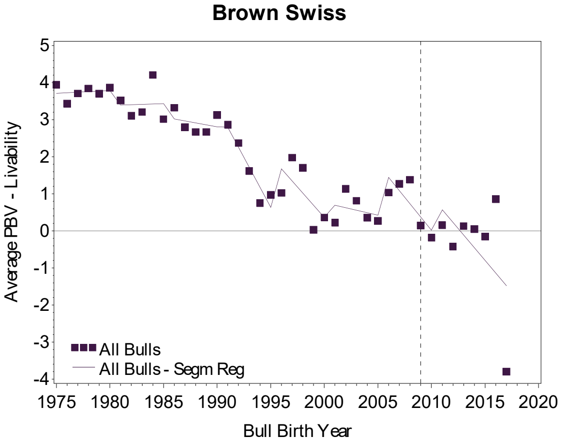
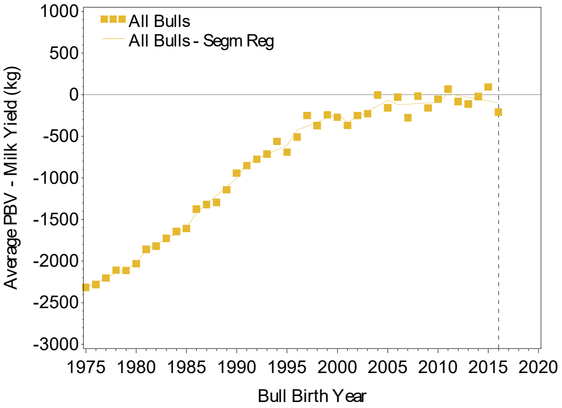


Figure 3.4. Estimates of genetic change per year from segmented regressions of PBV on birth year for BS bulls for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.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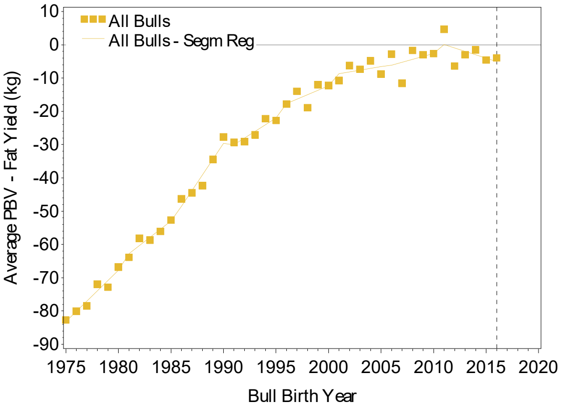
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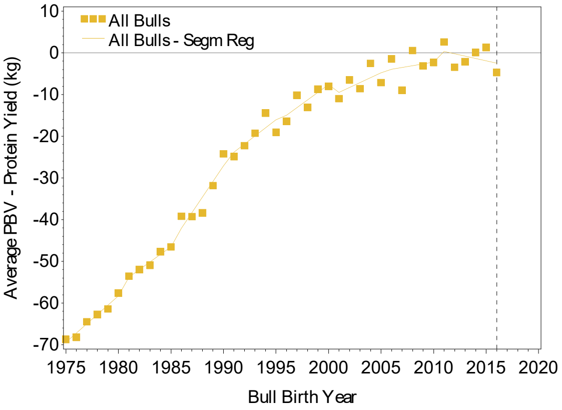
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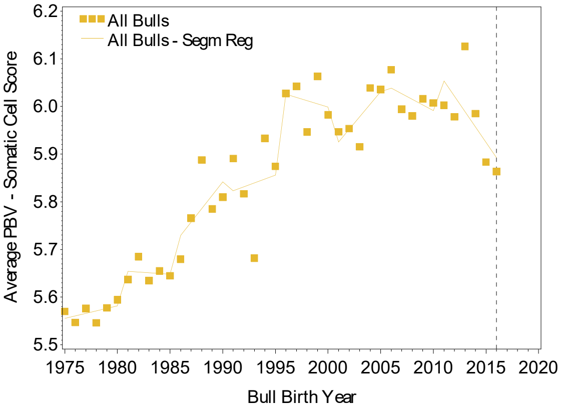
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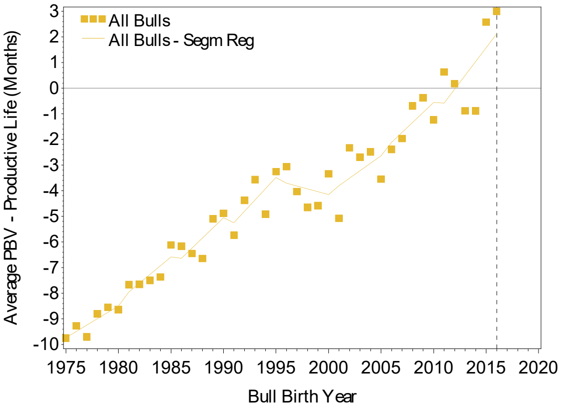
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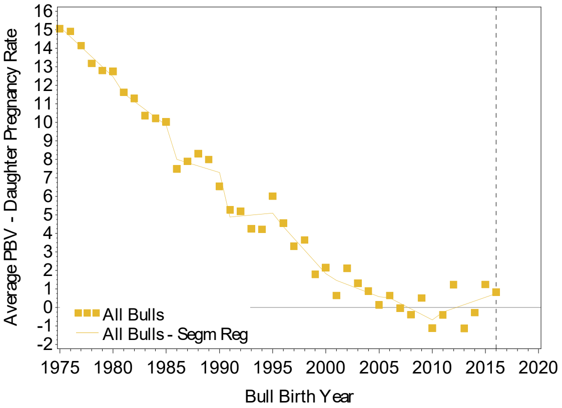

Guernsey

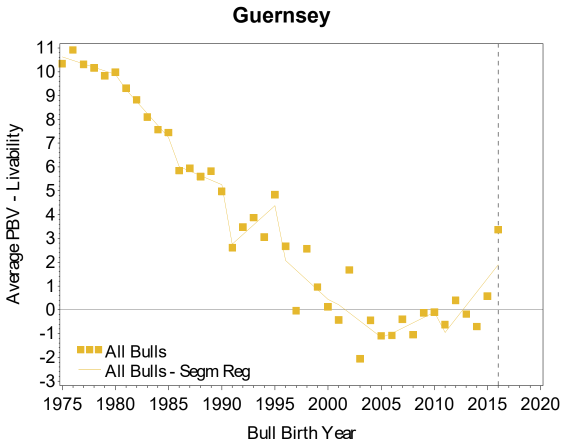
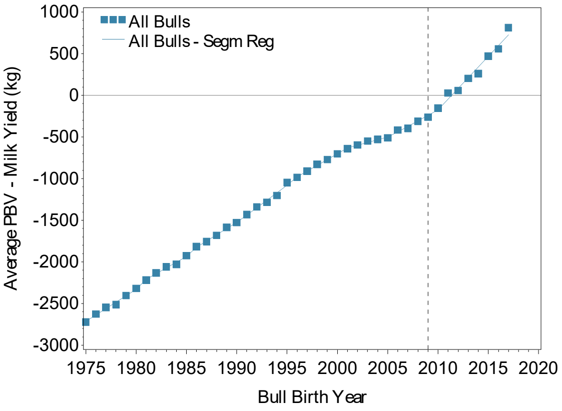
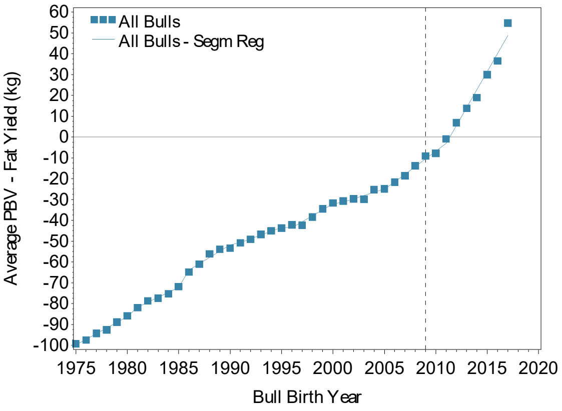


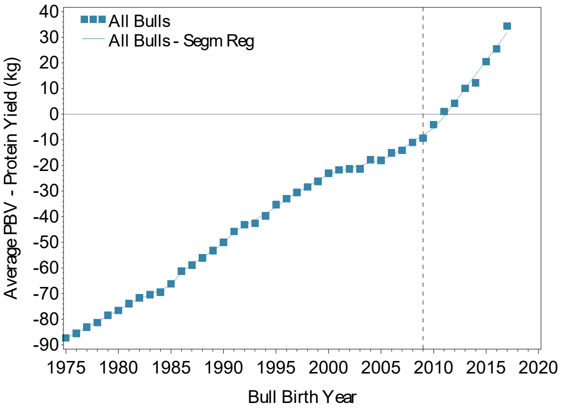
Figure 3.5. Estimates of genetic change per year from segmented regressions of PBV on birth year for GU bulls for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.



Holstein



Holstein



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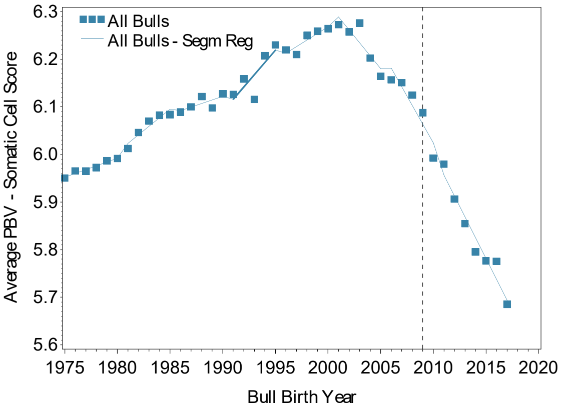

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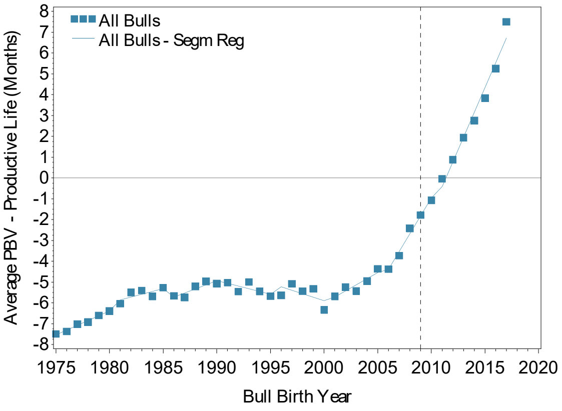

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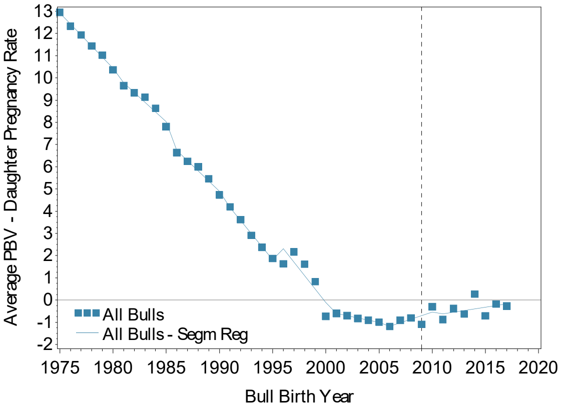

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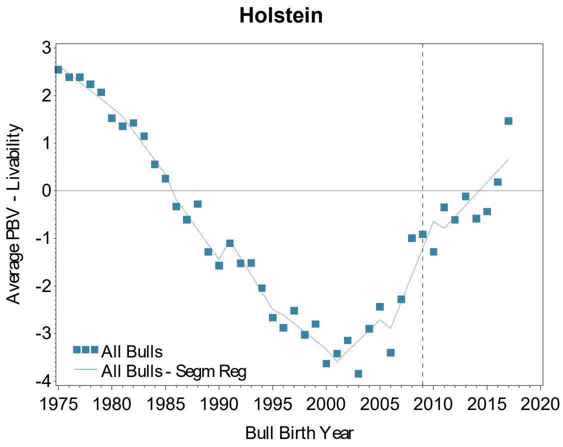
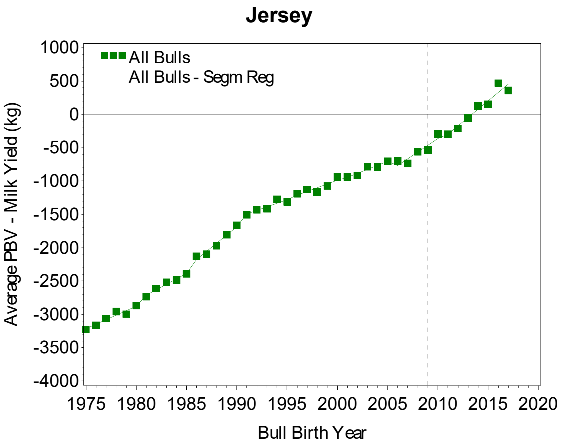


Figure 3.6. Estimates of genetic change per year from segmented regressions of PBV on birth year for HO bulls for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.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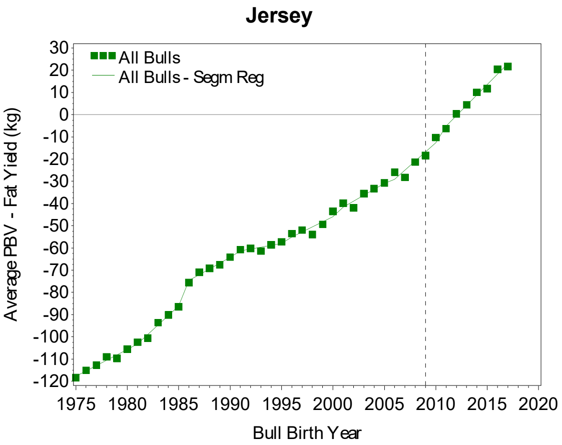
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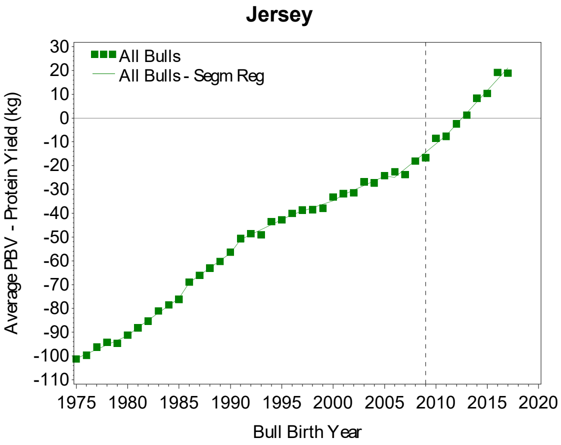
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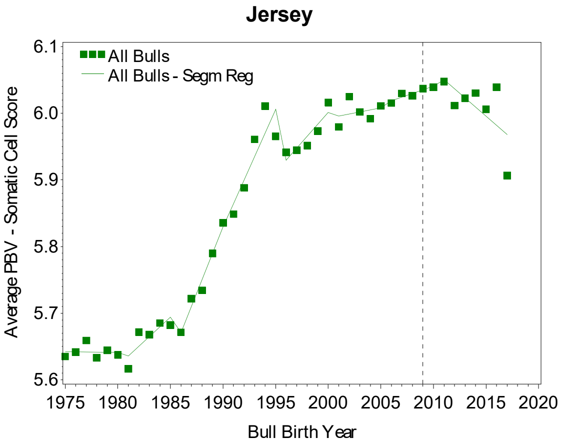
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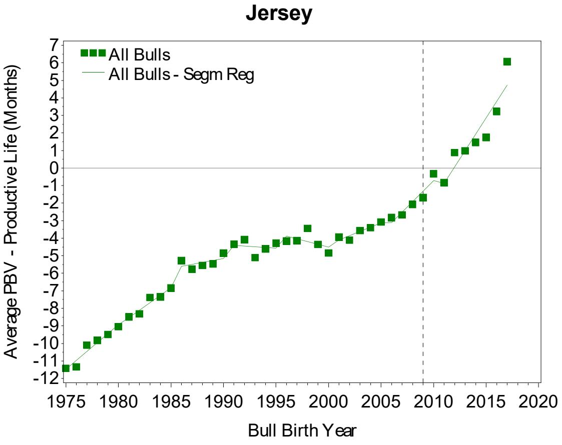
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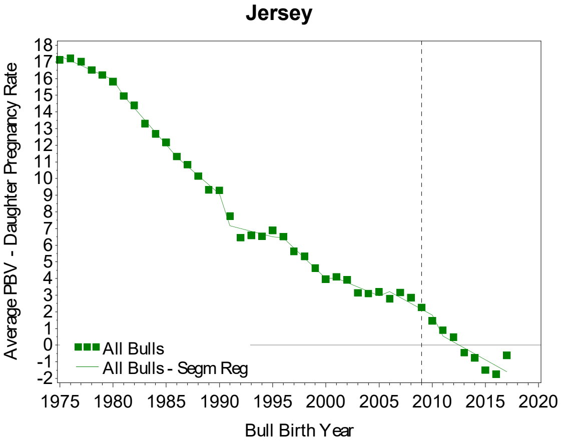
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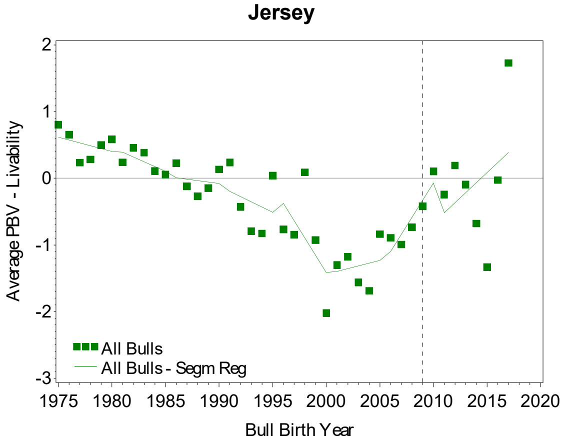
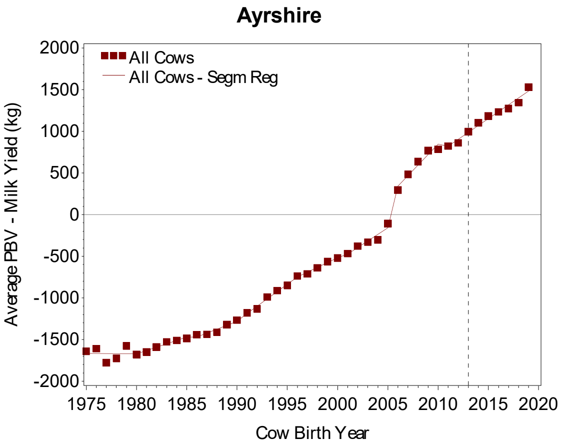


Figure 3.7. Estimates of genetic change per year from segmented regressions of PBV on birth year for JE bulls for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.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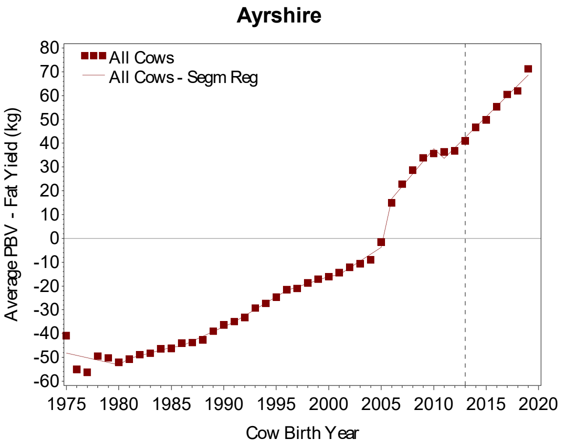
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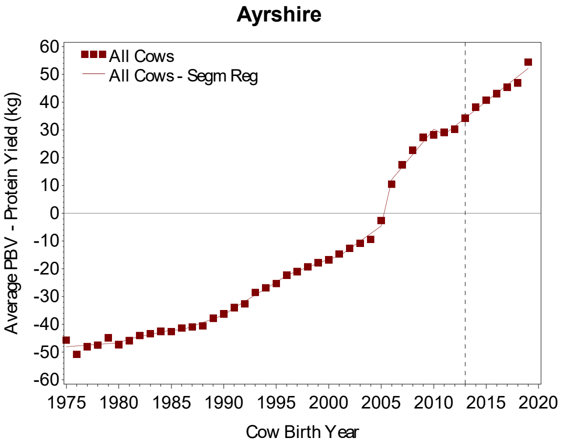
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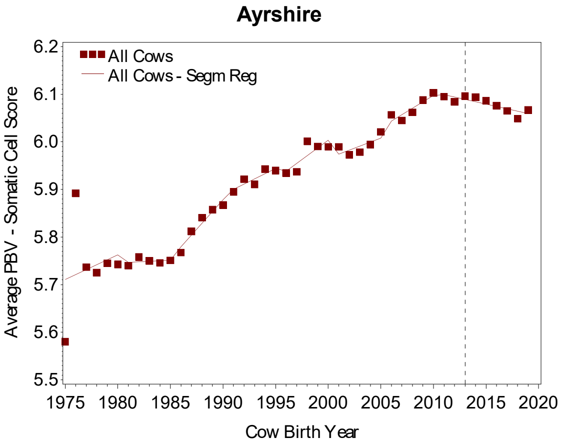
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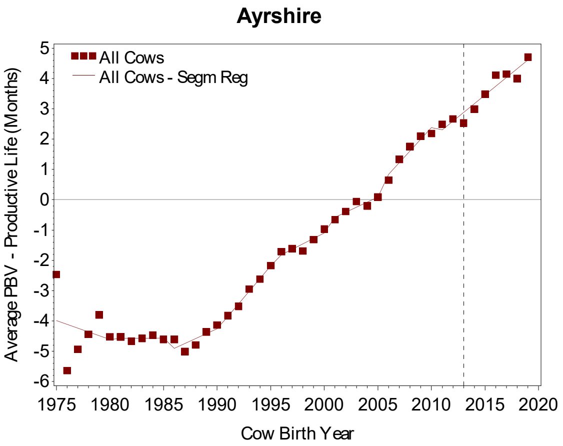
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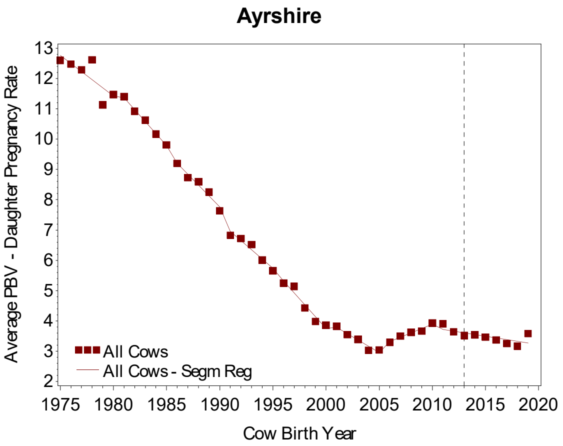
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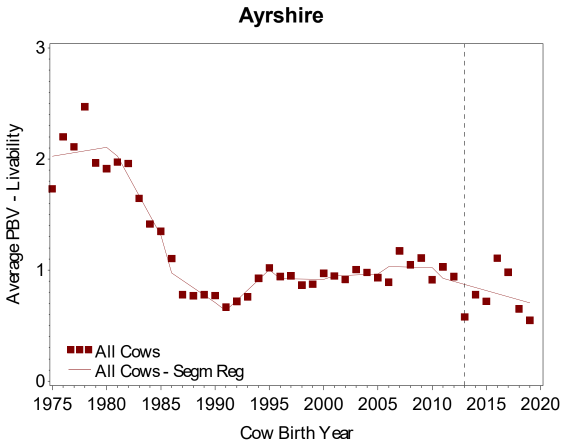
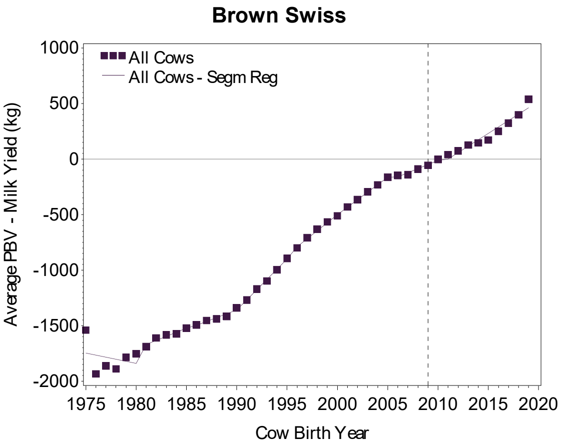
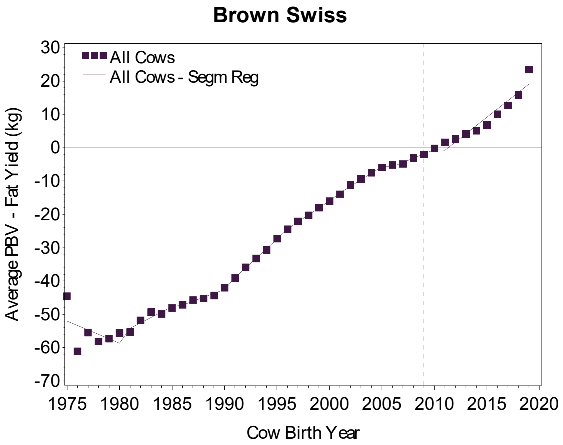
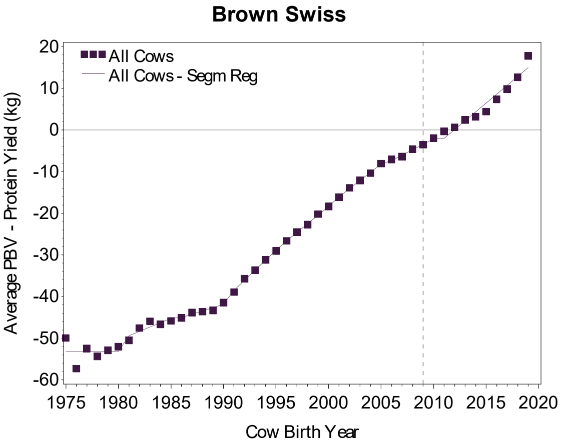


Figure 3.8. Estimates of genetic change per year from segmented regressions of PBV on birth year for AY cows for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.


Brown Swiss


Brown Swiss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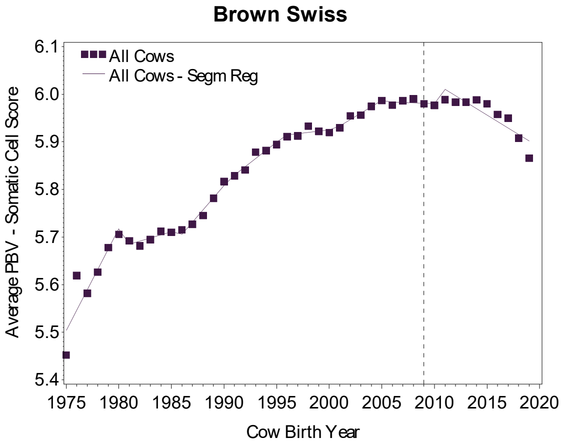
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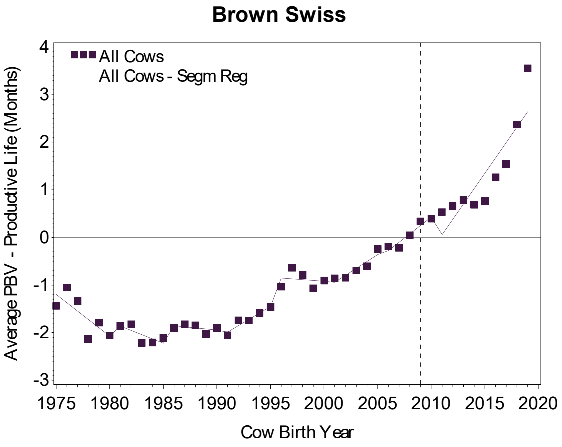
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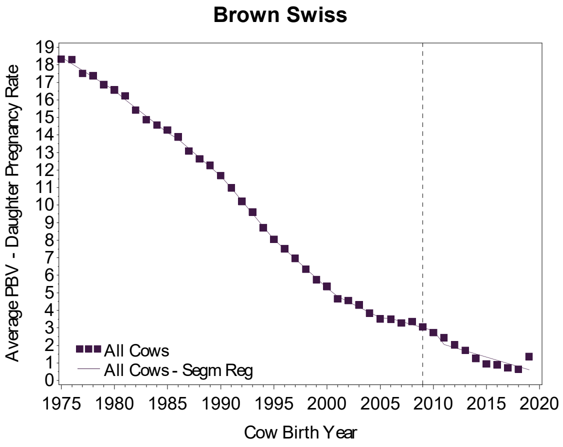

Brown Swiss

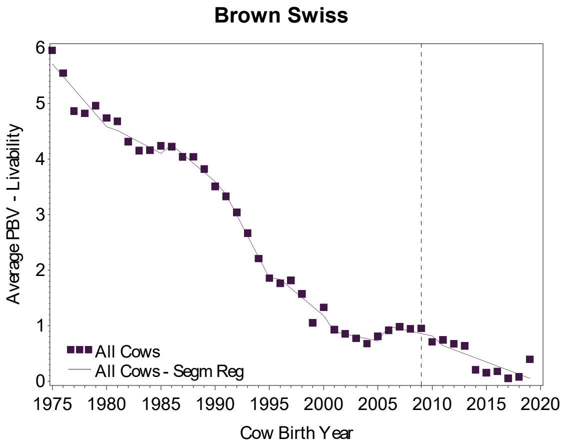
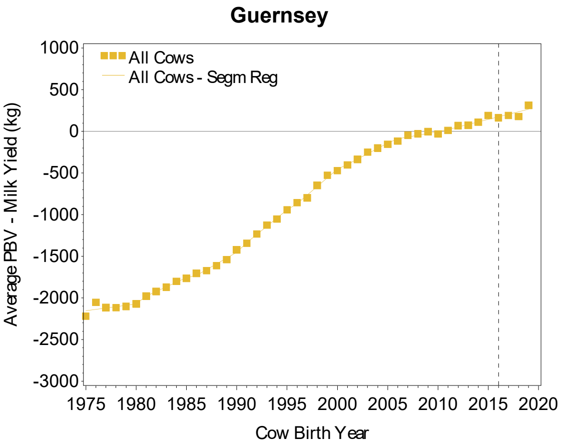
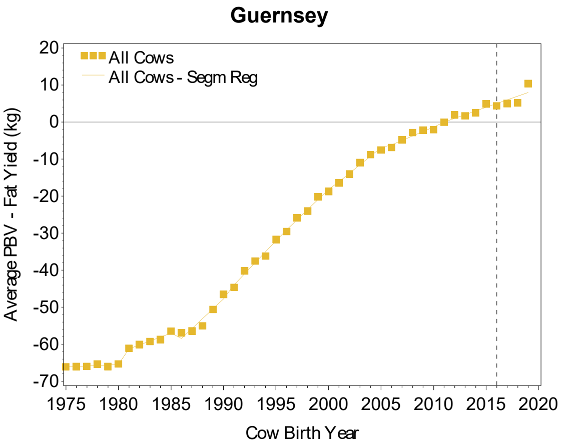


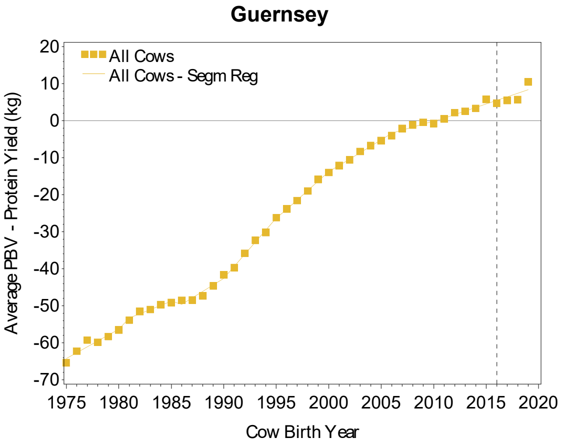
Figure 3.9. Estimates of genetic change per year from segmented regressions of PBV on birth year for BS cows for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.



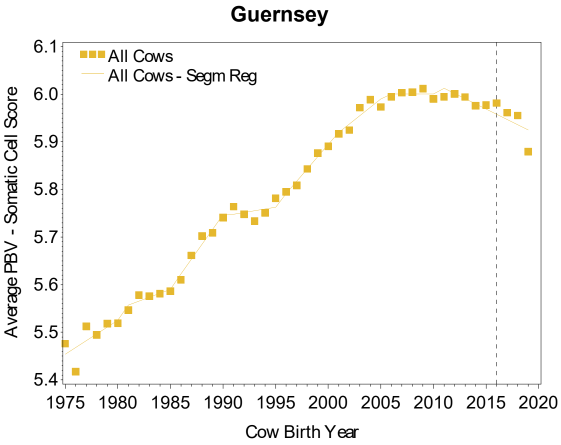
Guernsey



Guernsey



Guernsey



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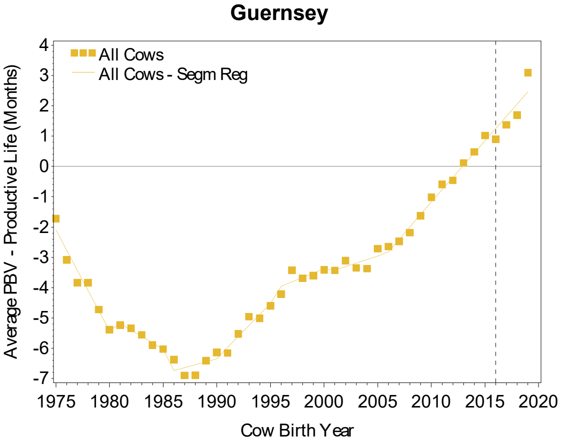
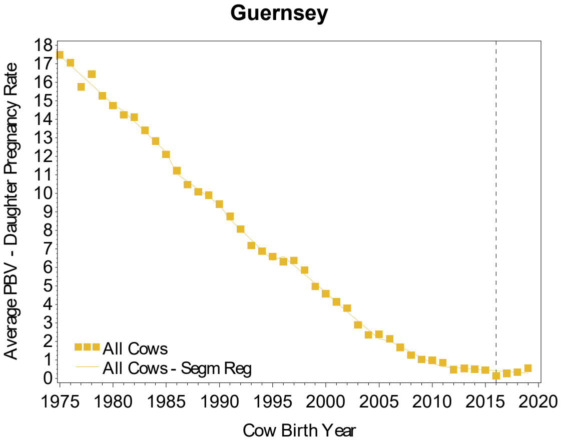


Guernsey



Guernsey

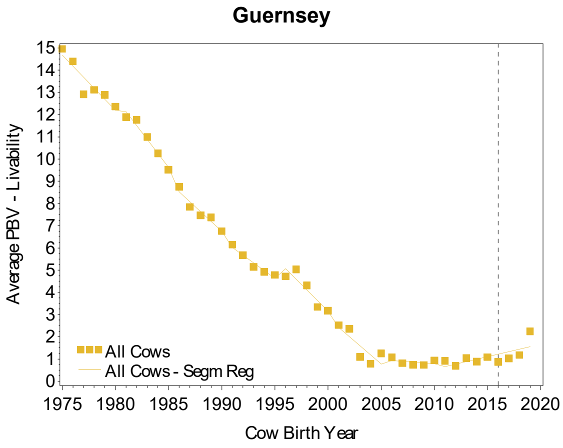
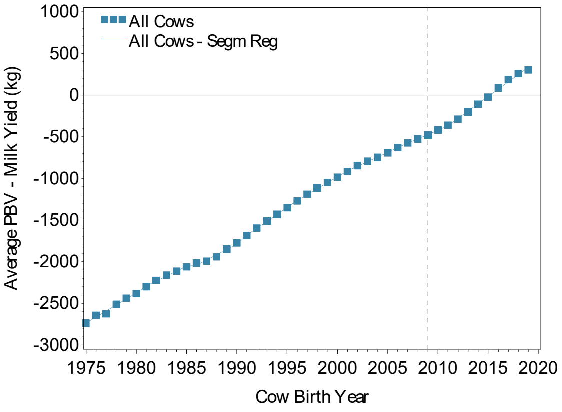
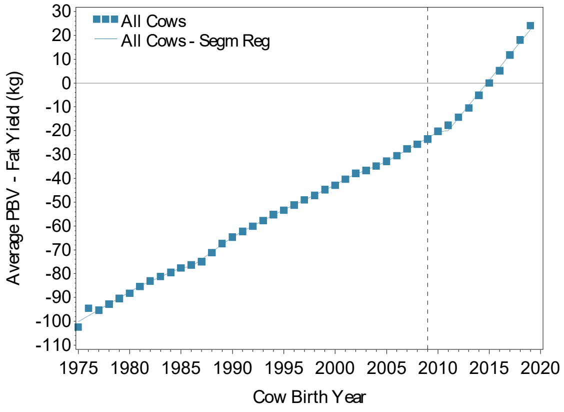


Figure 3.10. Estimates of genetic change per year from segmented regressions of PBV on birth year for GU cows for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.

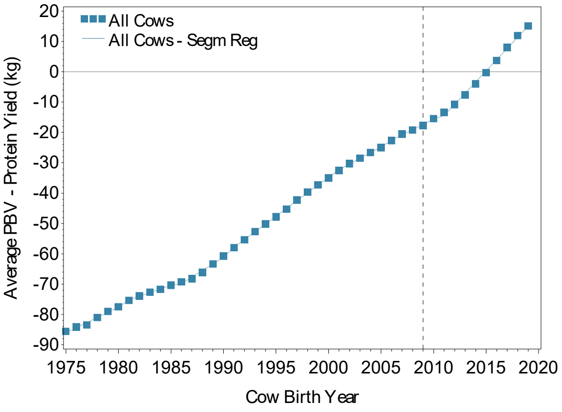
Holstein



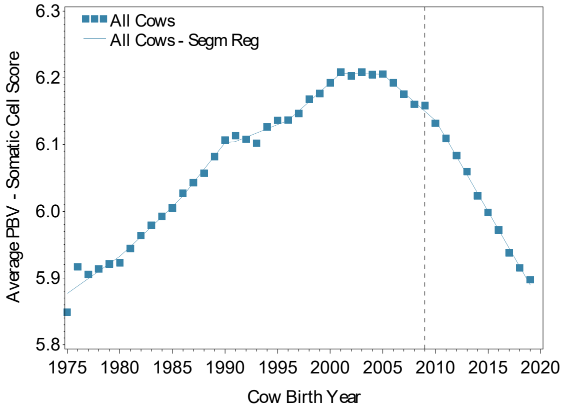
Holstein



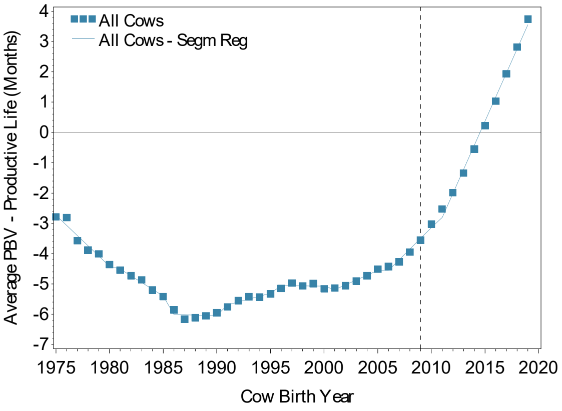
Holstein



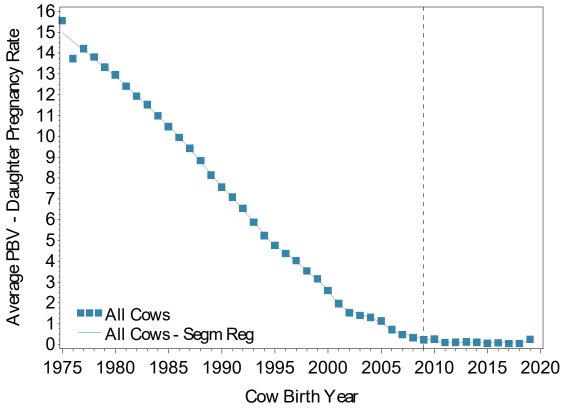
Holstein



Holstein



Holstein



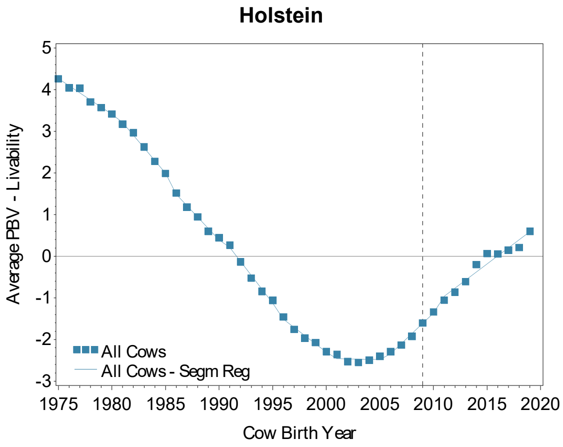
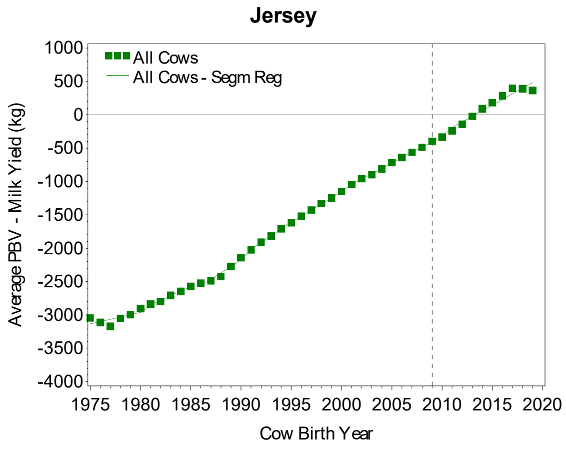
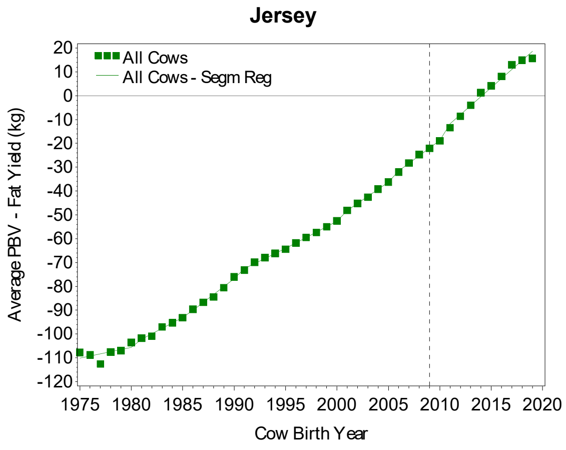
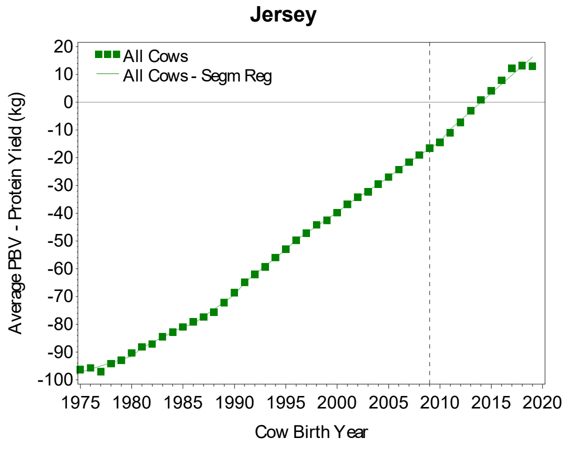
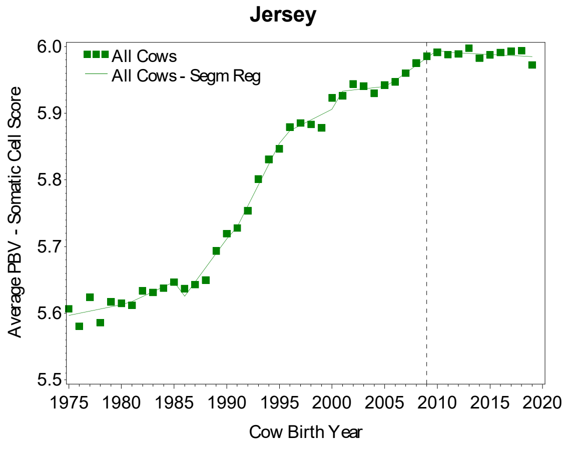


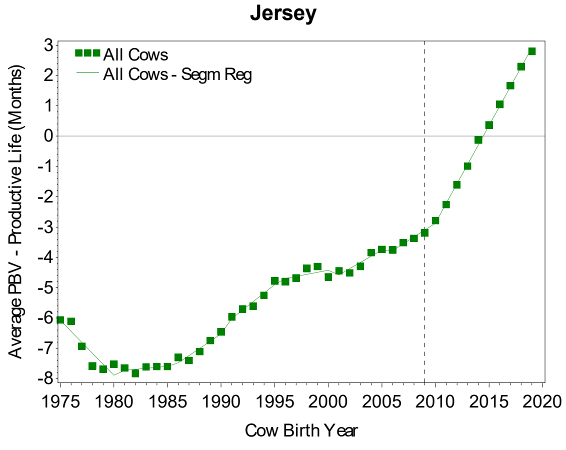
Figure 3.11. Estimates of genetic change per year from segmented regressions of PBV on birth year for HO cows for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.

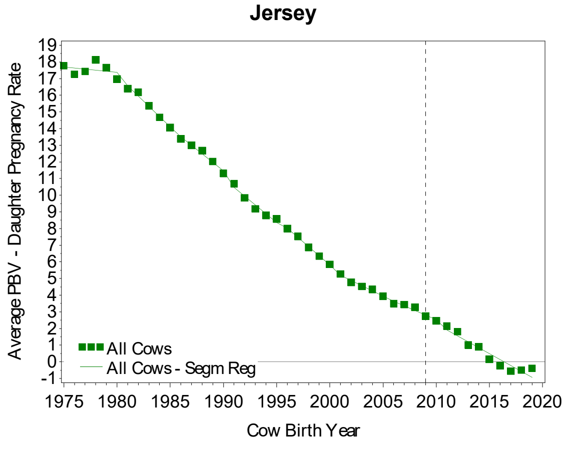

Jersey
All Cows
All Cows - Segm Reg
Average PBV - Milk Yield (kg)
1000
500
0
-500
-1000
-1500
-2000
-2500
-3000
-3500
-4000
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Cow Birth Year


Jersey
All Cows
All Cows - Segm Reg
Average PBV - Fat Yield (kg)
20
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
-110
-120
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Cow Birth Year


Jersey
All Cows
All Cows - Segm Reg
Average PBV - Protein Yield (kg)
20
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Cow Birth Year


Jersey
All Cows
All Cows - Segm Reg
Average PBV - Somatic Cell Score
6.0
5.9
5.8
5.7
5.6
5.5
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Cow Birth Year


Jersey
All Cows
All Cows - Segm Reg
Average PBV - Productive Life (Months)
3
2
1
0
-1
-2
-3
-4
-5
-6
-7
-8
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Cow Birth Year


Jersey
All Cows
All Cows - Segm Reg
Average PBV - Daughter Pregnancy Rate
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
-1
1975 1980 1985 1990 1995 2000 2005 2010 2015 2020
Cow Birth Year

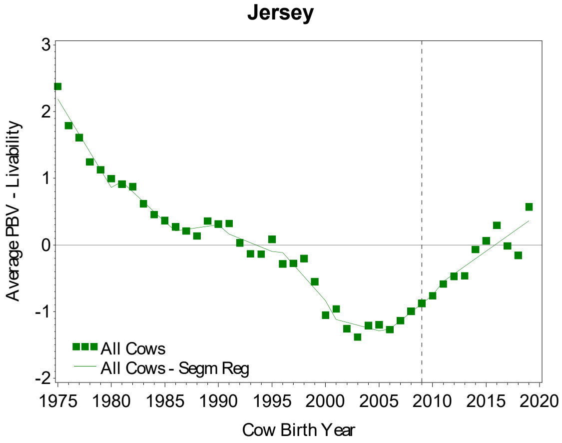
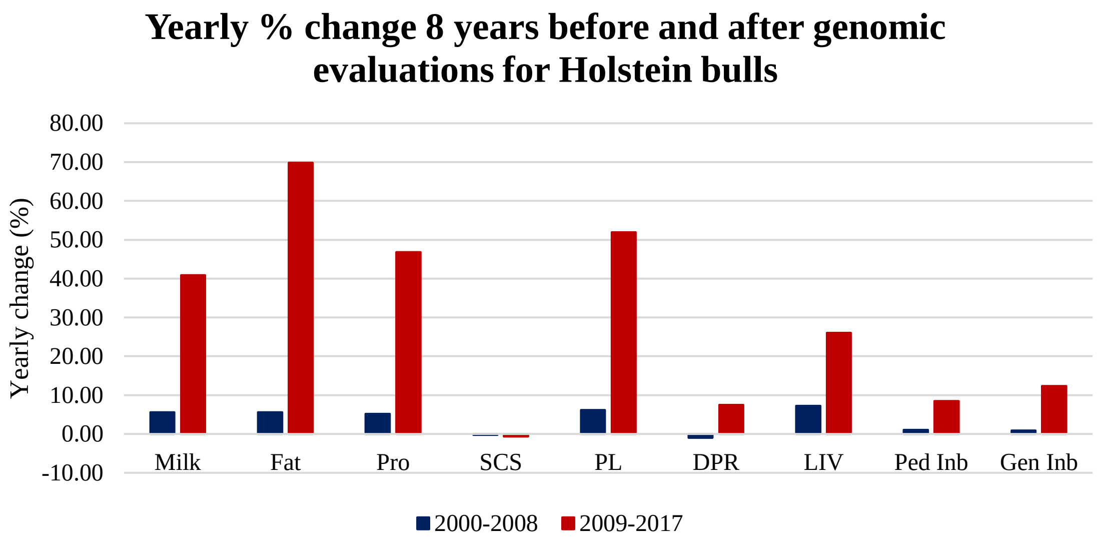
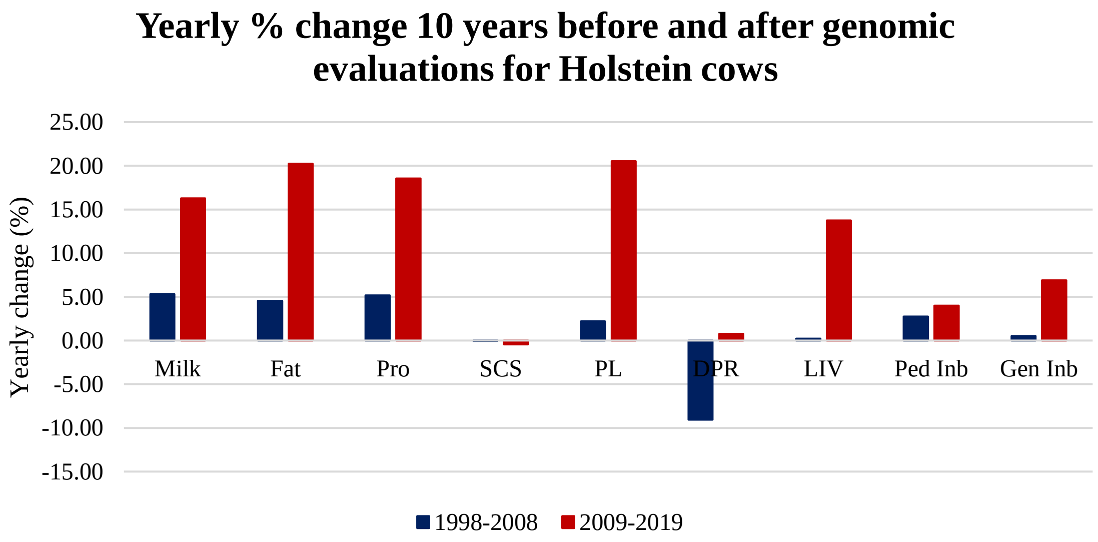
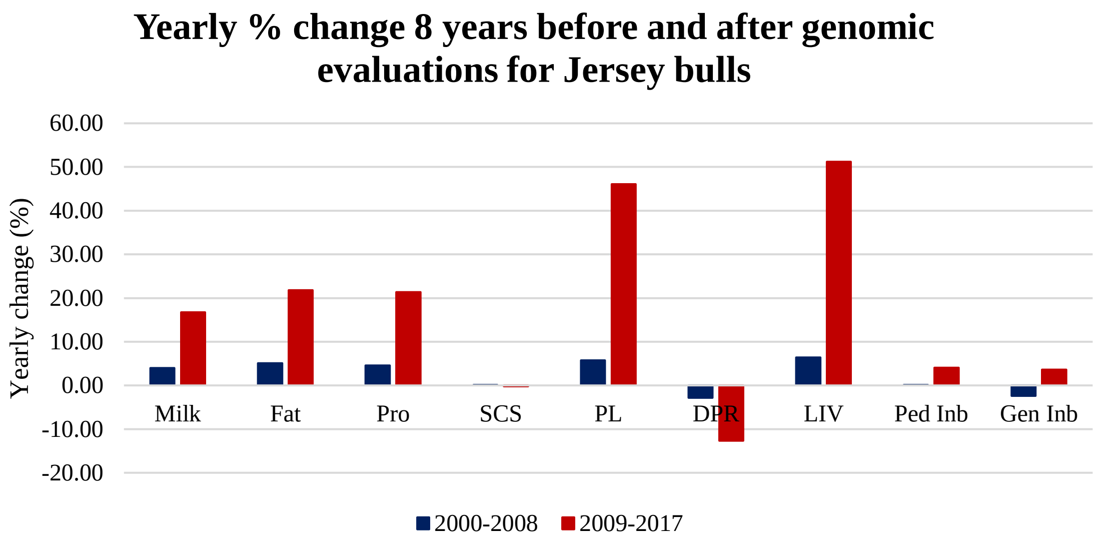


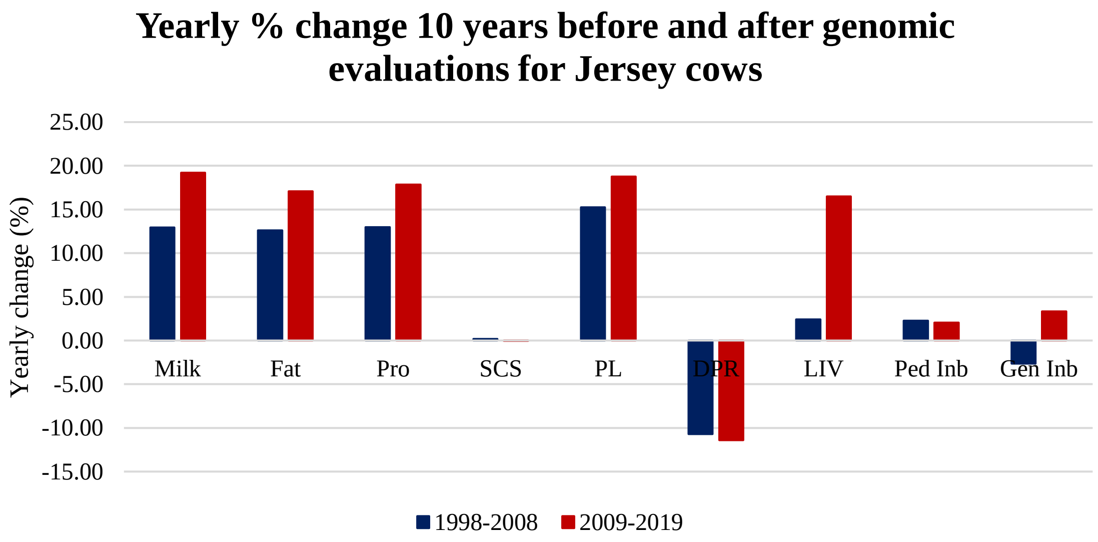
Figure 3.12. Estimates of genetic change per year from segmented regressions of PBV on birth year for JE cows for seven traits: milk, fat, and protein yields; SCS; PL; DPR, and LIV.


Yearly % change 8 years before and after genomic evaluations for Holstein bulls


Yearly % change 10 years before and after genomic evaluations for Holstein cows



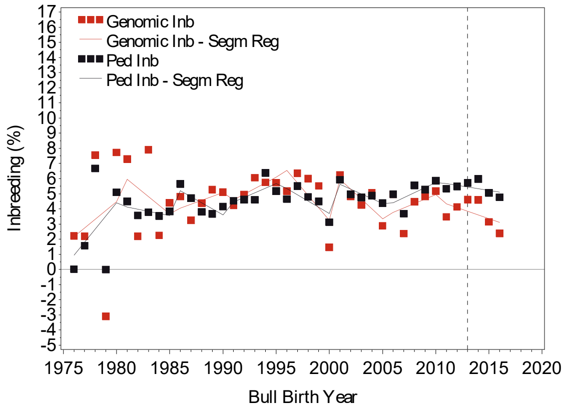
Yearly % change 8 years before and after genomic evaluations for Jersey bulls



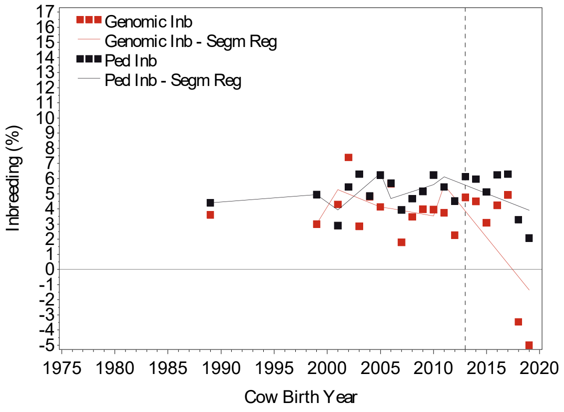
Yearly % change 10 years before and after genomic evaluations for Jersey cows

Figure 3.13. Yearly percentage change before and after genomic evaluations for HO and JE bulls and cows.

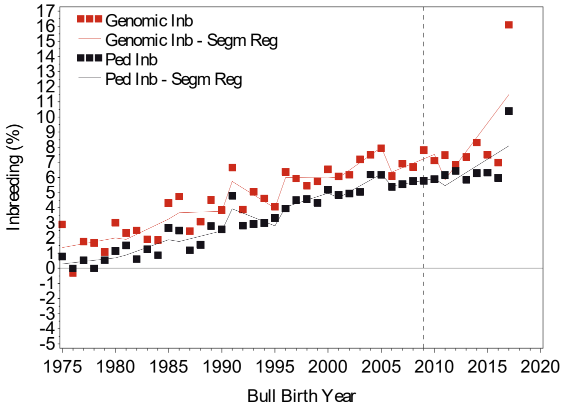
Ayrshire Bulls



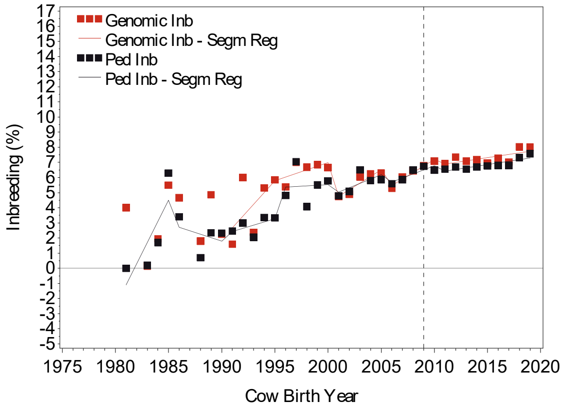
Ayrshire Cows



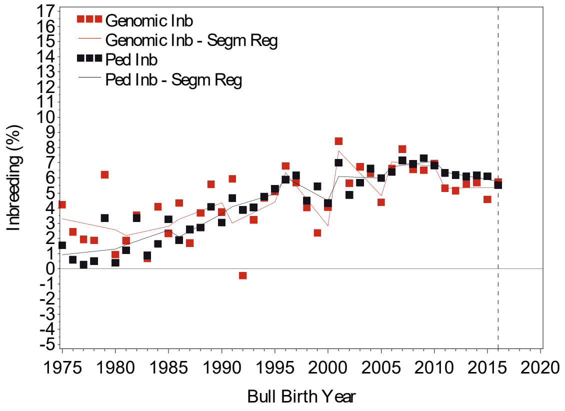
Brown Swiss Bulls



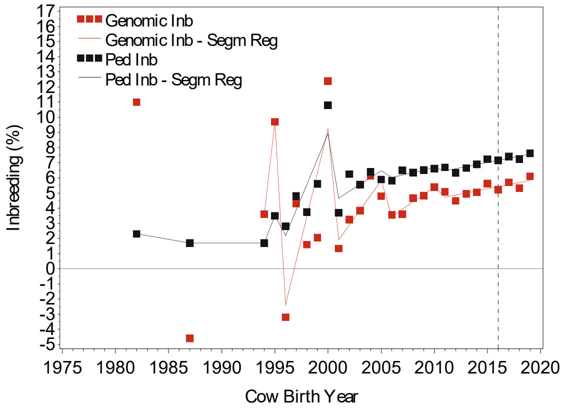
Brown Swiss Cows



Guernsey Bulls



Guernsey Cows



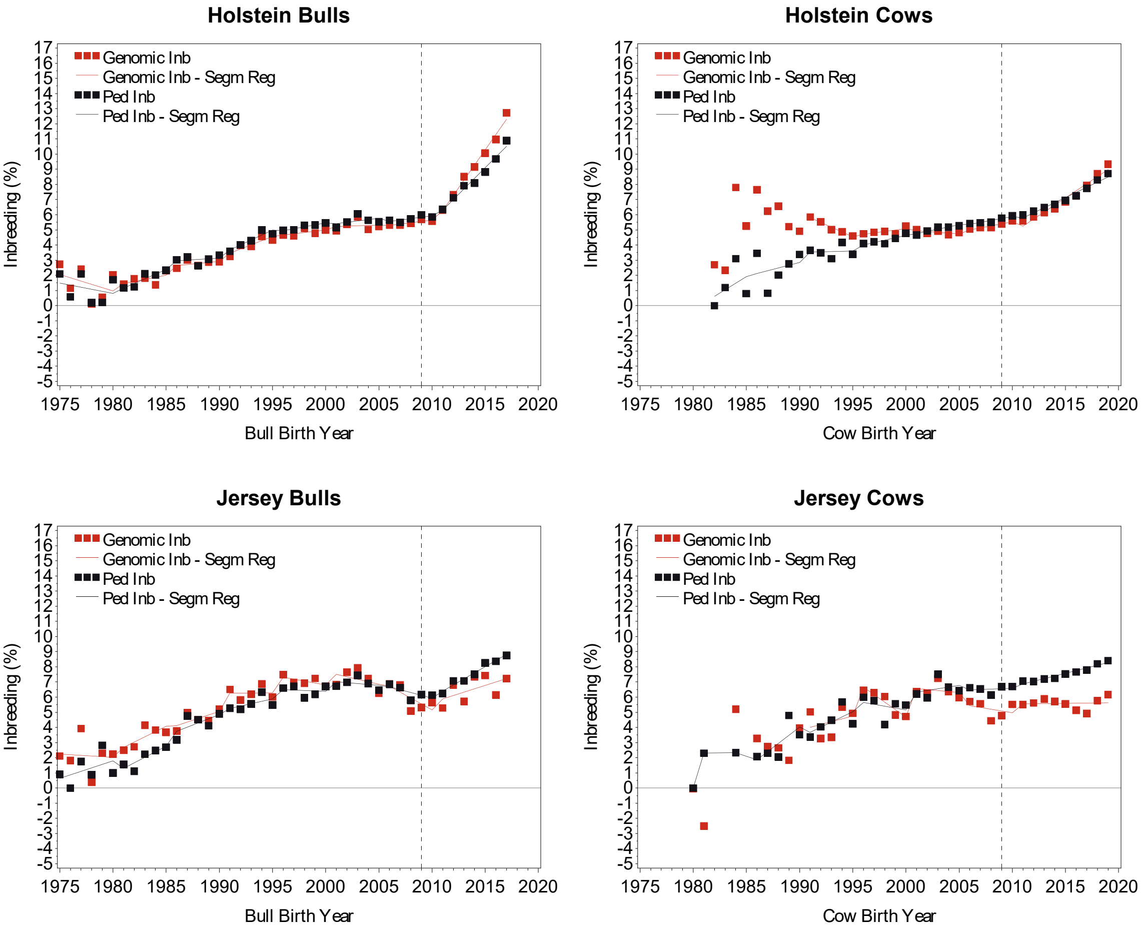
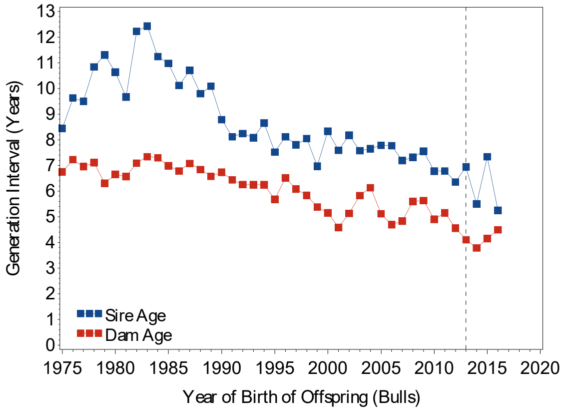
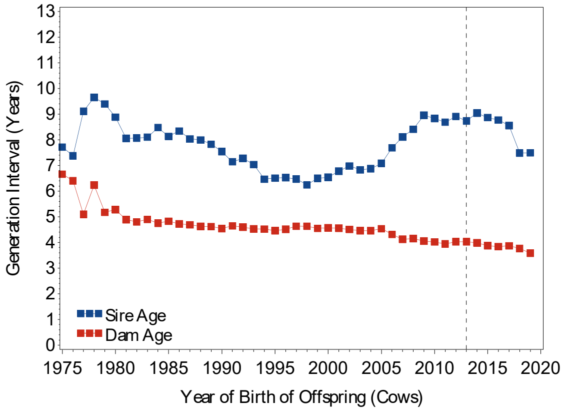


Figure 3.14. Pedigree and genomic inbreeding levels for all breeds by birth year since 1975.

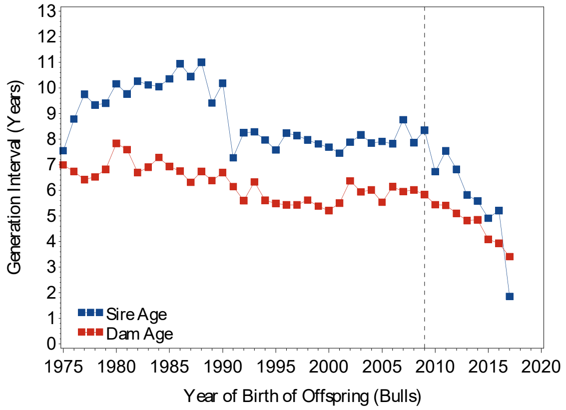
Ayrshire Bulls



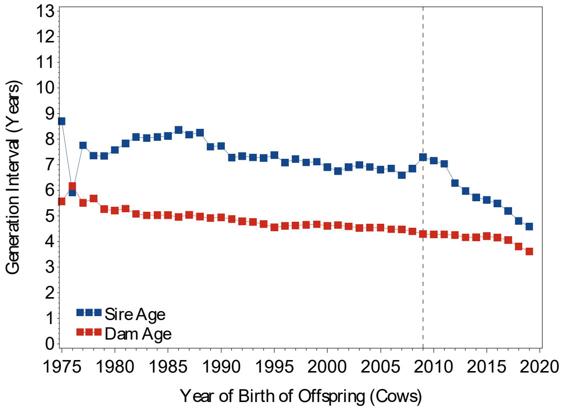
Ayrshire Cows



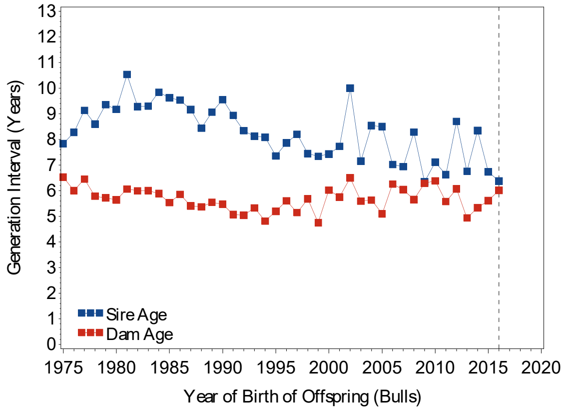
Brown Swiss Bulls



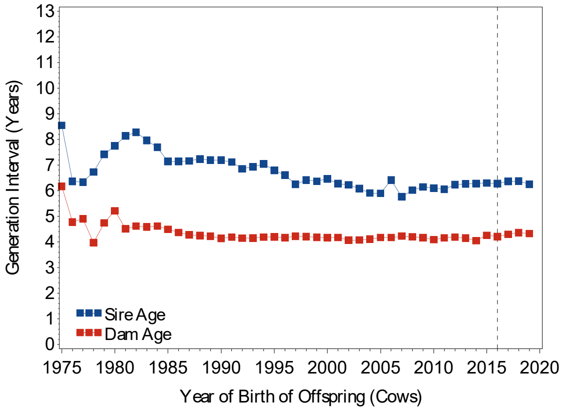
Brown Swiss Cows



Guernsey Bulls



Guernsey Cows



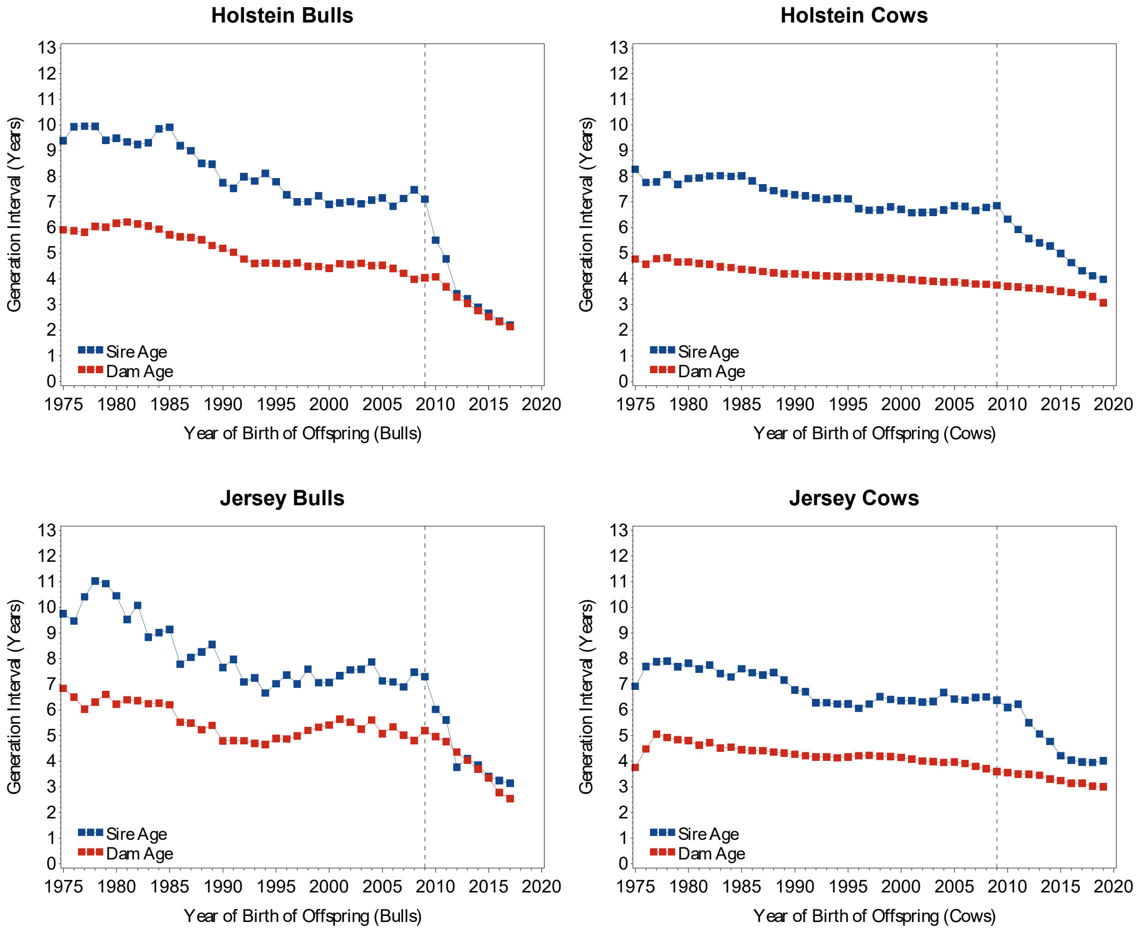


Figure 3.15. Generation Intervals for sires and dams of all breeds by birth year since 1975.

CHAPTER 4

HERD STATISTICS FOR DAIRY CATTLE IN THE U.S.[2]

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[2] Fiona Louise Guinan, George Wiggans, Duane Norman, João Dürr, John B. Cole, Taylor M. McWhorter, and Daniela Lourenco. To be submitted to Journal of Dairy Science.

ABSTRACT

The Dairy Herd Improvement (DHI) milk recording program provides participating dairy producers with up-to-date information on milk production and composition, reproductive efficiency, and herd health on an individual cow and herd basis. The information provided is utilized in herd management decisions. Herds enrolled in the DHI program generally outproduce herds that are not enrolled. A decision support tool was developed by summarizing the contents of the National Cooperator Database maintained by the Council on Dairy Cattle Breeding (CDCB, Bowie, MD). Descriptive statistics were calculated and aggregated into a user interface. Test-day records and 305-day standardized milk yields calculated for genetic evaluations were included. This multipurpose tool is designed to be useful for a broad audience including stakeholders, producers, researchers, and students. Participation in DHI milk recording, standardized lactations averages, herd averages, test-day somatic cell counts, termination codes, reproductive status, and breed composition statistics were defined, calculated, and displayed in this user interface. Herd participation has decreased by 53.9% since 2000, while the percentage of cows participating has increased by 17.7%. Geographically, the number of cows in states such as Idaho has increased 163% due to lower land costs, fewer water restrictions, and less urbanization. Test-day milk yield has increased 4.9 kg over the last 20 years and somatic cell count has decreased 149,000 cells in the same period. Since 2003, calving interval has decreased by 15 days across all breeds. Overall, these phenotypic trends indicate that selection indices are working efficiently and provide a useful tool for producers regarding selection decisions. Moving forward, additional value will be extracted from these data and provided back directly to the producer.

INTRODUCTION

Improvements in genetic gain are attributed mainly to the use of genomics and extension resources to disseminate knowledge and facilitate the application of new technologies (Newton et al., 2021). The collection of phenotypic data for genetic evaluations in the US is predominantly executed by the National Dairy Herd Information Association (NDHIA, Fitchburg, WI). There are approximately 160 million phenotypic records in the National Cooperator Database (Wiggans, 2021). This producer-owned data is shared with the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) and used in genetic evaluations.

National milk recording systems are the foundation of genetic improvement programs (Cole et al., 2021). Milk recording refers to an agricultural technology, which provides individual cow information to farmers regularly in order to support herd monitoring and decision making. The use of milk recording information can improve herd productivity and health as well as reduce the environmental impact of milk production (Läpple et al., 2017). Historically, phenotypic data were predominantly collected for herd management decisions and to contribute to the genetic evaluations. Currently, CDCB is investigating alternative methods to extract value from the National Cooperator Database for dairy producers. This information is crucial for benchmarking production records across the nation and displaying the improvements that have been made over time from genetic evaluations.

Newton et al. (2021) reported that results from a 15-month producer survey indicated that incorporating herd testing into businesses was seen as a risk reduction tool and resulted in more confident decision making. As well as helping justify the investment in new infrastructure, herd testing was also a condition for satisfying bank loan criteria (Newton et al., 2020). Balaine et al., (2020) found that milk recording enhances farm economic and social sustainability through a 4%

net increase in dairy gross margin, a 7% improvement in milk yield, and a 25% reduction in bulk tank somatic cell count (BTSCC). Milk recording is one tool that can help farmers identify cows with low risks of infection at dry-off (through individual SCC readings).

The International Committee on Animal Recording (ICAR; Rome, Italy) recently released an interface for benchmarking dairy production data from countries collected by ICAR (https://my.icar.org/stats/list). Without a recorded pedigree, many cows do not receive a genetic evaluation. To capture value from these animals, they can be included in the calculation of benchmarking statistics. The main benefit of DHI data recording is the ICAR verified method of calculating somatic cell count. New technologies currently lack standardization and validation to provide these records for genetic evaluations (Cole et al., 2021).

Herd managers cull cows to maintain optimal milk production and herd profitability. For this reason, it is essential to continually assess cows to make timely and appropriate culling decisions (Græsbøll et al., 2017). Efficient management systems utilize technology economically, which is usually associated with high productive performance (Oleggini et al., 2001). Until recently, the data were solely stored in reports located on the https://queries.uscdcb.com/publish/dhi.cfm webpage. The purpose of this work was to provide a cow census by summarizing performance data created in a user interface and decision support tool.

This multipurpose tool is designed to be useful for a broad audience including stakeholders, producers, researchers, and students. Participation in DHI milk recording, standardized lactations averages, herd averages, test-day somatic cell counts, termination codes, reproductive status, and breed composition statistics were defined, calculated, and displayed in this user interface. Options were also made available to download the data directly for use in scientific papers, benchmarking, and determining the genetic improvement through phenotypic trends of the national dairy herd.

MATERIALS AND METHODS

Animal Care and Use Committee approval was not needed as data were obtained from preexisting databases.

Data

Data were extracted from the National Cooperator Database maintained by the CDCB in Bowie, Maryland. To benchmark the changes in herd and cow production records over time, rules for extracting the data were organized into a source table. There are seven options in the user interface to view summarized statistics for dairy cattle on DHI milk recording. These include participation, standardized lactation averages, herd averages, somatic cell count, reasons cows left the herd, reproductive status, and breed composition. Participation and herd average reports come from data that include herd test day and yearly average records. The remaining reports are based on individual cow records – pedigree, production, and reproduction data. Breed code is determined by the animals' recorded breed code and herd breed code is defined as at least 75% purebred of a single breed else, herd breed is defined as a mixed breed herd. Statistics can be visualized and determined in numerous ways. For example, statistics can be stratified by state, breed, year or year range, DHI plan tag, herd size, milking frequency, and parity when available.

Phenotypic Definitions & Calculations

Participation is defined as the number of cows on test and is recorded on a herd basis, therefore individual cow data is not included in these calculations. Year is determined by the last sample date, and at least one sample date in a year is required. Herd breed is defined as at least 75% one breed, else herd breed equals crossbred (mixed).

Standardized lactation averages are calculated as the 305-day mature equivalent milk production for individual cows receiving genetic evaluations. Valid sire identification is required, lactations included from cows with >40 days in milk (DIM) and for cows that left the herd >15 DIM is required. Records in progress and other records short of 305 days were projected to 305 days. Only information for a cow's first 5 lactations was included, but first-lactation data were required for any other information to be included. Cows eligible to contribute to genetic evaluations were documented by state and breed (Powell, 1996).

Herd averages are calculated by weighting average herd milk yield by the number of cows on test for each test day record. Production levels outside of three standard deviations from the mean were excluded, except when the production code was recorded as 1 to 7. Production codes indicate that quality control was carried out for production records that appear unusual. Production codes 1-7 indicate that checking has been completed and the record is accurate. Cow years is defined as the average number of cows in a herd on a 365-day rolling average. Herds with less than 5 cow-years were excluded. Cow-years per herd were calculated by dividing the total cow-years by the number of herds.

Somatic cell score (SCS) of milk is reported to CDCB as part of an individual cow's test-day yield information. The test-day data used by the CDCB were provided by the dairy records processing centers (DRPC’s). The SCS for individual cows was converted back to a milk somatic cell count (SCC) in cells per milliliter [$SCC = 2^{(SCS - 3)} \times 100{,}000$] for calculating herd and state averages. The SCC for each cow was weighted by milk yield and used to compute herd mean on test day. Data for this calculation are extracted from the test day segment. The mean for each state was derived by weighting herd test-day SCC by herd test-day milk yield (Norman et al., 2000). Production metrics in this table are also weighted by the number of cows.

Reasons cows left the herd are presented as the percentage of lactations in a year by termination code. Year equaled to calving date plus days in milk to ensure the termination codes were summarized accurately for a given year. The following 12 termination codes were recorded in DHI farms: 1: sold for locomotion problems, 2: sold for dairy purposes, 3: sold for poor production, 4: sold for reproductive problems, 5: sold for other reasons, 6: died, 7: sold for mastitis or high SCC, 8: lactation ended with abortion, 9: sold for udder problems, 0: still in the herd, A: sold for undesirable conformation, B: sold for aggressiveness.

Reproduction status statistics include calving interval, conception rate, days from calving to first breeding, days from calving to last breeding, days from first to last breeding, and the average number of artificial inseminations per conception. Records included belong to cows at least 22 months of age and have calving records in 2003 or later. All statistics include the first five parities and cows bred using artificial insemination (AI) breeding with traditional and gender-selected semen; natural services and embryo-transfer cows are excluded. Reproduction status statistics have metric-specific quality control applied to each to ensure the most accurate reproductive status of US dairy cows is represented.

Calving interval is the number of days a subsequent calving occurs after the prior. This is limited to a range of 270 days to 650 days range as used in Hare et al. (2006). Conception rate is reported as a herd-year statistic and defined as the total number of confirmed pregnant cows in a herd-year out of the total number of inseminations in a herd-year. This value is multiplied by 100 to be a percentage. Cows are confirmed pregnant by a reported pregnancy check or if a subsequent calving date occurs within 266 and 294 days of the last AI date. A maximum of 7 AI are considered for each cow. To be included in the conception rate statistic, the herd-year must have at least 50% of milking cow with at least one insemination. Additionally, the reported herd-year conception rate must be greater than 10% and less than 90%. Days from calving to first breeding must be greater than 30, but less than 366 days to be included. From the records that meet these criteria, days from calving to last breeding, and days from first to last breeding are calculated. The average number of artificial inseminations per conception is calculated for each confirmed pregnancy with up to 7 AI.

Breed composition can be broken down by herd breed composition and cow breed composition. Breed code is defined as the cows' recorded breed code (Guinan et al., 2019). Year is based on calving year and only includes cows with days in milk greater than or equal to 1 in a given year. Herd breed thresholds are defined as at least a certain percentage of the herd is one breed. This is determined by the user on a threshold bar. The number of cows per breed and the percentage of cows per breed can be displayed. Similar statistics are available for herd breed composition. Herd breed composition is determined by individual cow breed codes categorized by herd code. Breed is designated on individual cow records, and cow breed is used to determine herd counts. For example, a Holstein herd with a few Jersey cows would be included in the herd count for both Holsteins and Jerseys.

RESULTS AND DISCUSSION

DHI Participation (2000-2020)

In 2020, there are 19 different plan tag options for milk sampling (Table 4.1). These plans are based on how many milkings are weighed and sampled, who collects the weights and samples, and where the information goes besides back to the farm (National Dairy Herd Information Association, 2010). 44.9% of herds and 47.5% of cow's milk record through the DHI-AP recording program. The DHI-AP recording program is defined as ‘less than all milkings weighed and sampled on a test day' and is supervised. The second most frequently used DHI recording program is DHI-OS-AP. 20.7% of herds and 5.2% of cows are under this method, defined as the unsupervised version of DHI-AP. The number of herds participating in milk recording through the NDHIA has been decreasing over time, whilst the number of cows has been increasing (Figure 4.1). In 2000, 27,630 herds were participating in milk recording, in 2020 it was 12,734 (53.9% decrease). The number of herds milking cows three times a day (3X) has increased from 1,737 to 2,072 in 2020. The percentage of cows 3X milking has increased by 9.8% in the same period.

The number of cows participating in milk recording in California has increased from 693,435 in 2000 to 925,105 in 2020. In the past, the majority of dairy cows were located in Wisconsin, Pennsylvania, and California. As drought has taken hold, California is slowly becoming a more arid, brown state, where constraints on water availability threaten a large and growing population (Mann et al., 2015). In Texas, the number of cows has over doubled (115,631–244,105). Due to a lack of resources (water, land), there is a trend appearing of dairy herds moving to states like Texas and Idaho, and the test day performance metrics support this theory. The number of cows participating in Wisconsin increased from 580,656 to 682,102. Idaho has become a dairy hub, attracting dairy farmers to move with favorable conditions such as lower land costs and less urbanization. From 2000 to 2020 the number of herds in Idaho has more than halved (56.8% reduction), while the number of cows has increased a massive 163% (90,643 to 238,768). Conversely, in states in the southeast region, the number of cows on milk recording has been declining. In Georgia, this figure decreased from 56,179 in 2000 to 19,555 in 2020. A similar reduction is visible in Florida in the same period (73,234 to 30,891).

Using the newly developed tool, herd size thresholds can be determined by the user for participation statistics. The minimum herd size is set to 5. The number of herds with at least 1,000 cows has increased from 433 in 2000 to 926 in 2020 (Figure 4.2), while the number of herds with up to 50 cows has decreased significantly, from 8,429 in 2000 to 2,354 in 2020. The number of herds with at least 5,000 cows has increased from 4 in 2000 to 89 in 2020. Sixty-four of these 87 herds in 2020 were milking three times per day.

Standardized lactation averages (2000-2019)

As seen in figure 4.3, for AY, the mean 305-day milk yield has increased by 1,031 kg in 19 years. Standardized fat yield has increased by 50 kg and protein by 35 kg in the same period. BS cows have produced 1,069 kg more milk, 52 kg fat, and 43 kg of protein in the same 19-year period. GU produced 661 kg more milk in 2019 than 2000, 36 kg of fat, and 25 kg of protein. HO cows increased milk yield by 1,484 kg, fat by 87 kg, and protein by 62 kg. For JE, the increase was 1,674 kg of milk, 102 kg of fat, and 72 kg of protein. MS cows increased standardized milk yield by 1,303 kg, fat 67 kg, and protein 45 kg. Fat and protein percentage increased for all breeds between 2000 and 2019. The number of records has decreased for AY, BS, GU, and MS while the number of records for HO, and JE has increased substantially over the same period.

Figure 4.4 shows the yearly percentage increase for standardized milk, fat, and protein yield 10 years pre and post-genomic evaluation in 2009. The largest increases were fat (1.6% per year for HO, and 1.8% per year for JE) since 2009. This is partially due to the increased weight on fat in the Lifetime Net Merit index (VanRaden et al., 2021). Another explanation is the weight DGAT1 which is a polymorphism that affects milk-fat composition (Schennink et al., 2007) receives in the genomic evaluation. Milk did not increase as much as fat and protein after 2009, due to the reduced emphasis it received in the index.

Herd Averages (2000 – 2020)

Oleggini et al., (2001) found that rolling herd averages for milk, fat, and protein were significantly different among the south, mid-south, and northern regions in the US. They compared milk production per cow for each state with Georgia herds. They found Louisiana was the lowest (233 kg/cow less than Georgia) and Virginia was the highest (779 kg/cow higher than Georgia). Also, as herd size increased, so did milk, fat, and protein yield. For this data, herd breed is defined as 75% of one breed, else it is a mixed herd.

Rolling herd averages for milk yield weighted by the number of cows on test in 2020 were 6,730 kg for AY, 8,963 kg for BS, 6,935 kg for GU, 11,826 kg for HO, 8,279 kg for JE, 6,416 kg for MS, and 9,847 kg for XX-XD. The number of XX-XD herds has increased from 2000 to 2020, for all other breeds this metric has decreased. For herds milking 3X per day, milk yield was 12,255 kg, fat yield 474 kg, and protein yield 386 kg.

Selection decisions and breeding programs differ based on herd size, hence why herd size is an option to view summary statistics in the developed tool. Previous studies (Oleggini et al., 2001) found that herd size impacts rolling herd averages for milk, fat, and protein production. For example, for herds with at least 450 cows, milk, fat, and protein rolling averages were higher. Rolling herd averages are indicators of dairy management efficiency. In 2020, herds with at least 450 cows produced 11,325 kg of milk vs 8,242 kg for herds with less than 450 cows. Herds with less than or equal to 100 cows produced a rolling herd average of 7,865 kg of milk, 326 kg of fat, and 254 kg of protein for all breeds. Cow-years (average number of cows in the herd over 365 period) for all breeds increased from 128 in 2000 to 289 in 2020.

Somatic Cell Count (2000 – 2020)

Somatic cell count is an indicator of infection status in dairy cattle and is routinely used for culling decisions by producers. Thus, SCC can be used to reliably detect mastitis incidence, even when clinical symptoms are not yet observable, and react accordingly (Sharma et al., 2011).

The average test day milk yield across all breeds has increased by 4.9 kg from 2000 to 2020. Fat percentage increased 0.3% and protein percentage increased 0.1%. Test day information does not include fat and protein production records, it only includes percentages. Average SCC (cells/ml, 1000's) has decreased significantly from 326,000 cells/ml to 177,000 cells/ml over the same period (Table 4.2).

In the US, the legal maximum BTSCC for "Grade A" milk shipments is 750,000 cells/ml. (USDA, 2010). Previous studies (Norman et al., 2000) have shown that herd test day means for SCC were lowest in the west and highest in the southeast in 1996 and 1997. In 2000, there were 11 states with SCC between 400,000 and 499,000 cells/ml, and the majority of these states are located in the southeast (Florida, Georgia, Alabama, Mississippi, Louisiana, Oklahoma, Arkansas, Tennessee, Kansas, Minnesota, and South Dakota. This highlights the incorporation of SCS in the Lifetime Net Merit index in 1994 has been extremely successful. Selection against high somatic cell scores should decrease the incidence of clinical mastitis and provide direct economic benefits through higher milk quality premiums (Schutz, 1994). Payment on SCC was included in milk pricing in most federal milk orders, which also contributed to this improvement. This is also reflected in genetic trends for breeds with sufficient observations. Figure 4.5 determines SCC is affected by parity. In cows with greater than 6 parities, SCC was the highest. In contrast, the group of cows with the lowest SCC throughout the year were parity 1. Monthly trends did not differ greatly among parities.

The states with the lowest SCC in 2020 are: Michigan (143,000 cells/ml), Washington (149,000 cells/ml), Idaho (149,000 cells/ml) and Vermont (150,000 cells/ml) (Figure 4.6). When stratifying the data based on parity, in 2020 cows in parity 1 averaged 125,000 cells/ml, parity 2 147,000 cells/ml, parity 3 202,000 cells/ml, parity 4 259,000 cells/ml, parity 5 312,000 cells/ml and parities 6 and over averaged 384,000 cells/ml across all breeds.

Between 2000 and 2009, HO test day milk yield increased by 1.6 kg. Since 2009 when genomic evaluations were released, HO test day milk yield has increased by 4.2 kg. This is a substantial improvement and the phenotypic trends reflect the genetic trends. Similarly, for JE in this period test milk yield increased 1.7 kg and 2.9 kg respectively. Almost double the increase before genomic evaluations. BS also received genomic evaluations in 2009. Since 2000, TD milk yield for BS has increased 1.5 kg and since 2009 we see a 202 kg increase (Table 4.3). The lower improvements in AY, BS, and GU cows can be attributed to the smaller reference population and therefore lower accuracies in genomic predictions (Cesarani et al., 2021).

Sampling month is known to affect sample day Somatic Cell Score (SCS). Kennedy et al. (1982) reported the lowest sample day SCS during May and the highest SCS during December for cows in Quebec, Canada. This is not reflected in test-day somatic cell counts in the US. In 2020, for all breeds, SCC was lowest in December (162 cells/ml) and highest in August (196 cells/ml). The highest quality milk was produced in November and December (Table 4.4). Seasonal factors influence SCC, it is well documented that SCC increases during summer months in the US due to increasing temperature and humidity along with the associated heat stress (Olde Riekerink et al., 2007).

Reasons Cows Leave the Herd (2000 – 2020)

Frequencies of DHI cows' termination codes were also summarized. A prior study (Norman et al., 2012) showed that the highest frequency geographically for DHI-recorded abortions was in the Southeast region (1.6%) and the lowest was in the Northwest region (0.7%). The number of records for termination codes has increased from 2,396,966 in 2000 to 3,774,209 in 2020. The percentage of lactations ending normally in the US for all breeds has decreased from 69.8% in 2000 to 63.9% in 2020. Lactations ending in abortion decreased 1% in the same period for all breeds. The most frequent termination code in 2020 is 0 or lactation ended normally at 63.9%, while 9.2% of cows left the herd due to unspecified reasons (Table 4.5). These reasons may include misrecorded, unspecified health reasons. Locomotion problems accounted for 0.1% of all recorded termination codes in 2020 and 5% of the cows died. About 5% of cows were sold for dairy purposes, 4.5% left the herd due to reproduction problems, and 7.1% due to low production. Nearly 3.9% of cows left the herd due to mastitis or high SCC and lactations ending with abortion represented 0.1%. There were less than 2,500 records for udder problems, undesirable conformation, and bad behavior in 2020, therefore they represent less than 1%.

The percentage of cows sold for dairy purposes has increased since 2016 from 3.7% to 5.0% in 2020 across all breeds. About 9.5% of JE cows were sold for dairy purposes in 2020; this figure was 9.8% for GU. MS left the herd in 2020 predominantly due to lactation ending normally (41.6%) and being sold for dairy purposes (35.1%). In 2020, 8.1% of cows left the herd due to reproductive problems; this metric was 9.1% in Georgia and Louisiana. In 2020, the percentage of HO leaving the herd due to locomotion problems was 1.5%; this was 0.3% for JE and 1.0% for XX-XD. For termination code 7 (mastitis or high SCC), HO represented 4.0%, JE 3.3% and XX-XD were 3.5%. Interestingly, between 2000 and 2020, termination code 7 (mastitis or high SCC) increased in New York (1.5%), Wisconsin (0.4%), and California (1.0%). Contrarily, during this time, the frequency decreased in states such as Florida (-1.9%), Georgia (-0.9%), and Texas (-0.8%).

Reproductive Status (2003-2019)

More selection emphasis has been placed on fertility in recent years following considerable decline in a few of the important reproductive traits (Norman et al., 2019), dairy farmers need practical information for their decisions regarding reproduction. Poor fertility in cows leads to economic impacts such as longer calving intervals, reduced milk yield, higher culling rates, and a higher number of inseminations (Inchaisri et al., 2010). Despite this, the frequency of termination code 4 (reproduction problems) has only decreased 0.1% from 2000 to 2020 across all breeds.

Milk recording information can help farmers identify the most profitable animals for breeding dairy replacements and make informed culling decisions, leading to increased milk quality and herd production performance (Läpple et al., 2017). The phenotypic averages provided reflect both genetic and environmental changes. Barriers to genetic improvement include low heritability, and insufficient selection intensity on fertility as a consequence of economic drivers of milk production versus fertility (Pryce et al., 2014).

Calving interval has decreased since 2003 across all breeds by 15 days. When stratified by breed, AY, BS, GU, HO, JE, MS, XX-XD have decreased calving intervals by 2, 2, 0, 14, 8, and 9 days, respectively (Figure 4.7). A large population size for HO cows has led to the greatest improvement in reproductive traits. Again, the colored breeds could improve reproductive performance by collecting more phenotypes. Holmann et al. (1984) found that there was a positive value per day open ($.21 to $.40) for all milk-producing abilities when calving interval was increased from 12 to 13 mo. and a consistently negative value per day open (−\$.04 to −\$.23) when it was increased from 13 to 15 mo.

Breed Composition (2000-2020)

Cow breed composition can be stratified by state. In California, the number of JE cows has increased from 38,393 in 2000 to 169,740 in 2020; HO have increased 150,510 and XX-XD cows increased 18,135 (Table 4.6). For Wisconsin and New York, a similar trend to California was visible for HO, increasing 208,208 and 123,827, respectively. However, the same increase in JE and XX-XD cows was not shown. The number of JE cows in Texas has increased from 6,981 to 106,223 in the same period. For XX-XD, Texas has increased from 268 in 2000 to 64,109 in 2020 while the number of HO cows increased by 19,073. Herd breed has changed substantially over time by state; the number of purebred herds has decreased significantly since 2000, while the number of crossbred herds has increased.

CONCLUSIONS

Dairy producers are relocating around the US. Improvements are evident in production yields, somatic cell counts, and reproductive status for some breeds. For the JE breed, more work is needed on shifting the trend in reproduction traits despite the additive genetic component limitation. More phenotypic records and genotypes are needed for the colored breeds like AY, BS, GU, and MS to identify the phenotypic progress before and after implementing genomic selection. Crossbred animals have made excellent progress since 2010 for most traits. Moving forward, more traits will be included in this newly developed tool to increase capabilities, and additional value will be captured from the national cooperator database to provide back directly to the producers. This decision support tool will aid in management decisions, setting goals for improvement, and achieving selection objectives. The success of both traditional and genomic selection relies on the collection of accurate phenotypes to provide reliable estimates of genetic merit and gain.

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TABLES

Table 4.1. Participation in 2020 by plan tag. These plans are based on how many milkings are weighed and sampled, who collects the weights and samples and where the information goes besides back to the farm.

Plan Tag	Herds	Herds (%)	Herds (3X Milking)	Cows	Cows (%)	Cows (3X Milking)
DHI	305	2.2	48	123612	3.2	15.3
DHI-APCS	810	5.8	507	935846	24	58.3
DHIR	245	1.7	48	44536	1.1	16.7
DHIR-APCS	217	1.5	122	121059	3.1	52.5
DHIR-AP	1760	12.5	222	299830	7.7	12.8
DHI-AP	6444	45.9	1009	1856060	47.6	15.4
DHI-MO	14	0.1	8	17857	0.5	55.6
DHI-MO-AP	14	0.1	2	5678	0.1	14.3
DHI-OS	435	3.1	16	35457	0.9	2.9
DHI-OS-AP	2877	20.5	79	202011	5.2	3.1
DHI-OS-APCS	237	1.7	45	38366	1	18.4
DHI-OS-MO	29	0.2	11	16469	0.4	23.4
DHI-OS-MO-AP	11	0.1	3	3012	0.1	27.3
DHI-OS-AC	7	0	3	3173	0.1	26.4
DHI-SS	15	0.1	6	7762	0.2	33.3
DHI-SS-AP	560	4	82	143860	3.7	14.9
DHI-SS-APCS	57	0.4	27	36423	0.9	49.1
DHI-SS-MO	7	0	1	4356	0.1	14.3
DHI-SS-MO-AP	8	0.1	3	3351	0.1	37.5
Total	14052	100	2242	3898718	100	25.9

Table 4.2. Test day milk, fat, protein, and SCC from 2000 – 2020 for all breeds.

Year	Total Cows	Cows per herd	Milk (kg)	Fat (%)	Protein (%)	SCC (cells/ml, 1000's)
2000	3,006,279	64	31.2	3.7	3.13	326
2001	3,054,951	69.7	31.3	3.68	3.06	329
2002	3,347,552	77.3	31.7	3.7	3.06	321
2003	3,523,266	86.4	31.5	3.69	3.06	324
2004	3,388,073	90.7	31.3	3.7	3.08	297
2005	3,648,111	97.3	32.3	3.69	3.07	300
2006	4,071,989	113.4	32.3	3.7	3.07	293
2007	4,234,899	122.6	32.3	3.69	3.08	277
2008	4,347,421	128.6	32.4	3.7	3.09	260
2009	4,406,608	134.9	32.7	3.69	3.08	233
2010	4,456,497	143.4	33	3.67	3.09	228
2011	4,527,957	153.7	33.2	3.72	3.1	216
2012	4,630,150	160.9	33.7	3.74	3.11	200
2013	4,617,886	167.3	34.1	3.79	3.12	199
2014	4,674,250	176.9	34.6	3.77	3.13	199
2015	4,722,438	184.9	35	3.77	3.12	203
2016	4,730,157	194.6	35.4	3.81	3.13	201
2017	4,715,740	205.7	35.5	3.86	3.15	195
2018	4,684,392	221.1	35.3	3.91	3.17	190
2019	4,553,937	242	35.5	3.95	3.19	186
2020	4,427,338	250.2	36.1	3.98	3.19	177

Table 4.3. Test day milk yield (kg) for AY, BS, GU, HO, JE, MS, XX-XD cows from 2000 to 2020.

Year	Ayrshire	Brown Swiss	Guernsey	Holstein	Jersey	Milking Shorthorn	Crossbred
2000	22.9	25.6	21.2	31.9	22.5	22.5	26.7
2001	23.1	25.7	21.4	32	22.6	22.8	26.5
2002	23.7	26.1	22.2	32.4	23	23.2	27.1
2003	23.4	26	22.6	32.3	23.3	23.7	26.9
2004	23.1	25.7	21.9	32.1	23.1	23.8	27
2005	23.9	26.5	22.3	33.1	23.8	24.2	27.9
2006	23.9	26.6	22.5	33	23.8	24.4	27.4
2007	23.6	26.6	22.5	33.1	23.9	24.2	27.4
2008	23.7	26.7	22.3	33.2	24	23.7	27.7
2009	23.9	27.1	22.5	33.5	24.2	23.9	28.1
2010	23.9	27.6	22.9	33.9	24.6	23.9	28.7
2011	23.8	27.4	22.8	34.1	24.8	23.5	29.1
2012	24	28	23.2	34.7	25.4	23.7	29.6
2013	24	27.9	23.1	35.2	25.8	23.4	30.1
2014	24.5	28.1	23.1	35.7	26.4	24	31
2015	24.8	28.6	23.8	36.2	26.7	24.3	31.4
2016	25.3	28.8	23.7	36.7	27.1	24.3	31.7
2017	25.6	28.8	23.9	36.8	27.1	24	32
2018	25.6	28.6	23	36.8	26.8	24.1	31.8
2019	25.9	28.5	22.8	37.2	26.9	25.5	31.8
2020	26.9	29.3	23.1	37.7	27.1	28.7	32.4

Table 4.4. Test day milk yield, fat and protein percentage, SCC per month for all breeds in 2020.

Month	Milk (kg)	Fat (%)	Protein (%)	SCC (cells/ml, 1000's)
January	35.8	4.04	3.24	174
February	35.9	4.04	3.23	175
March	36.3	3.99	3.19	174
April	36.4	3.97	3.17	172
May	36.2	3.95	3.16	171
June	36.5	3.83	3.08	183
July	36.2	3.8	3.06	191
August	35.9	3.87	3.11	196
September	35.9	3.9	3.16	191
October	35.8	4.03	3.24	174
November	35.9	4.11	3.28	166
December	36.0	4.16	3.3	162
Yearly	36.1	3.98	3.19	177

Table 4.5. Summary of termination codes in 2020 for all breeds.

Termination Code	**AY %**	**BS %**	**GU %**	**HO %**	**JE %**	**MS %**	**XX-XD %**	**All %**
Lactation Ended Normally (0)	65.7	63.7	59.7	64.1	62	41.6	65.6	63.9
Lactation Ended with Abortion (8)	0.2	0.2	0.1	0.1	0.1	0.1	0.2	0.1
Sold for Dairy Purpose (2)	5.8	5.1	9.8	4	9.5	35.1	7.8	5
Locomotion Problems (1)	1.1	1.9	1.2	1.5	0.3	0.7	1	1.3
Low Production (3)	5.7	4.6	3.4	7	8	5.9	6.8	7.1
Reproduction Problems (4)	5.3	7.3	7.3	4.7	3.2	3.5	3.3	4.5
Unspecified Reasons (5)	8.9	8.8	7.8	9.4	8.6	8.6	7.7	9.2
Mastitis or High SCS (7)	2.5	3	2.2	4	3.3	1.8	3.5	3.9
Udder Problems (9)	0.1	0.1	0.1	0	0	0.1	0.1	0
Undesirable Conformation (A)	0	0	0	0	0	0	0	0
Bad Behavior (B)	0	0	0	0	0	0	0	0
Died (6)	4.8	5.1	8.3	5.1	4.9	2.6	4.2	5

Table 4.6 Breed composition by state from 2000 to 2020 for HO, JE, and XX-XD.

State	**Holstein**		**Jersey**		**Crossbred**	
	2000	2020	2000	2020	2000	2020
California	501,712	652,222	38,393	169,740	841	18,976
New York	191,192	315,019	7,203	11,282	53	6,460
Pennsylvania	215,117	225,425	8,836	12,170	677	9,824
Wisconsin	326,958	535,166	8,117	25,091	524	17,182
Texas	43,525	62,598	6,981	106,223	268	64,109

FIGURES

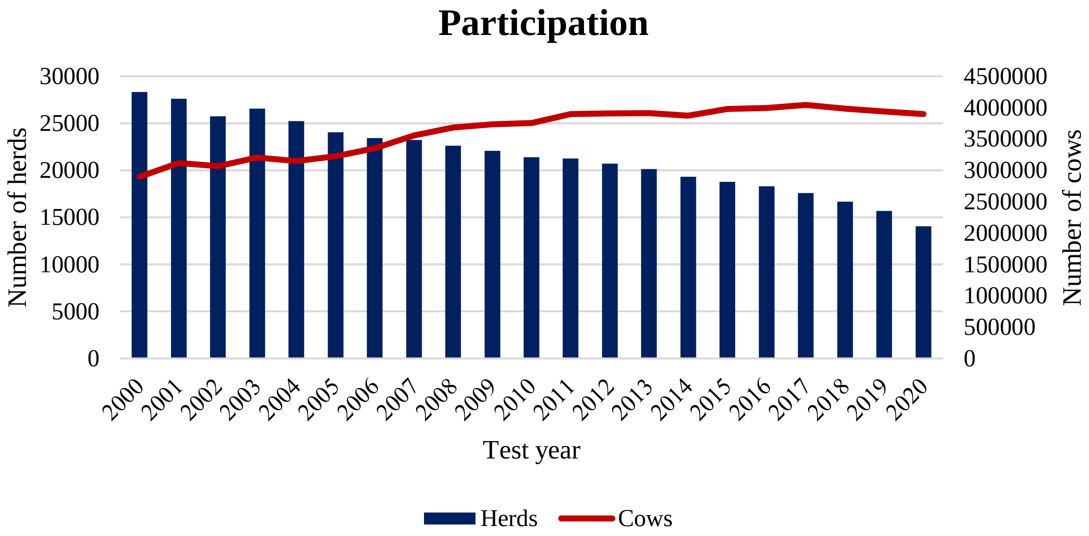

Figure 4.1. Participation by herds and cows in DHI recording since 2000.

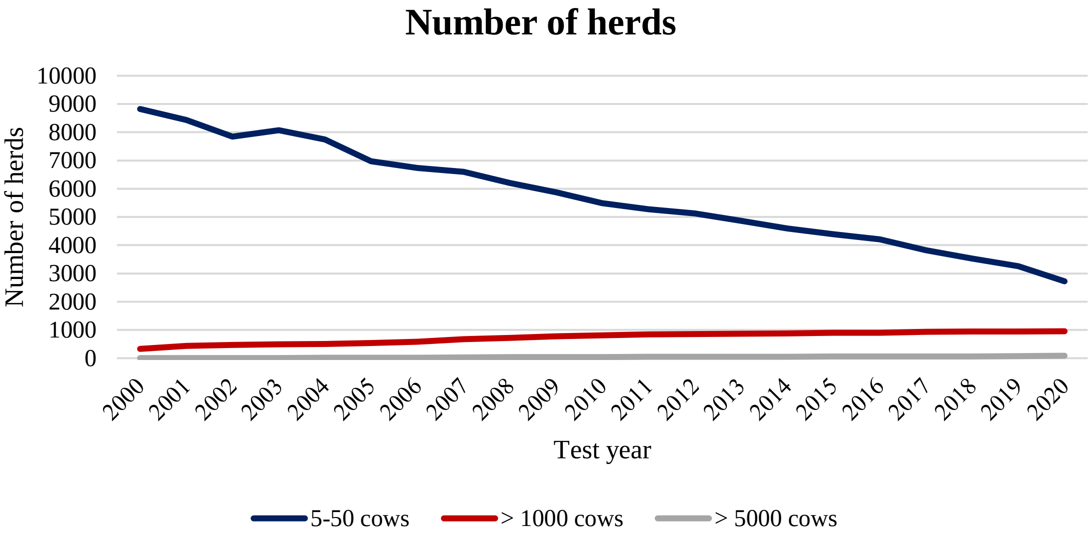

Figure 4.2. Number of herds from 2000 – 2020 by herd size.

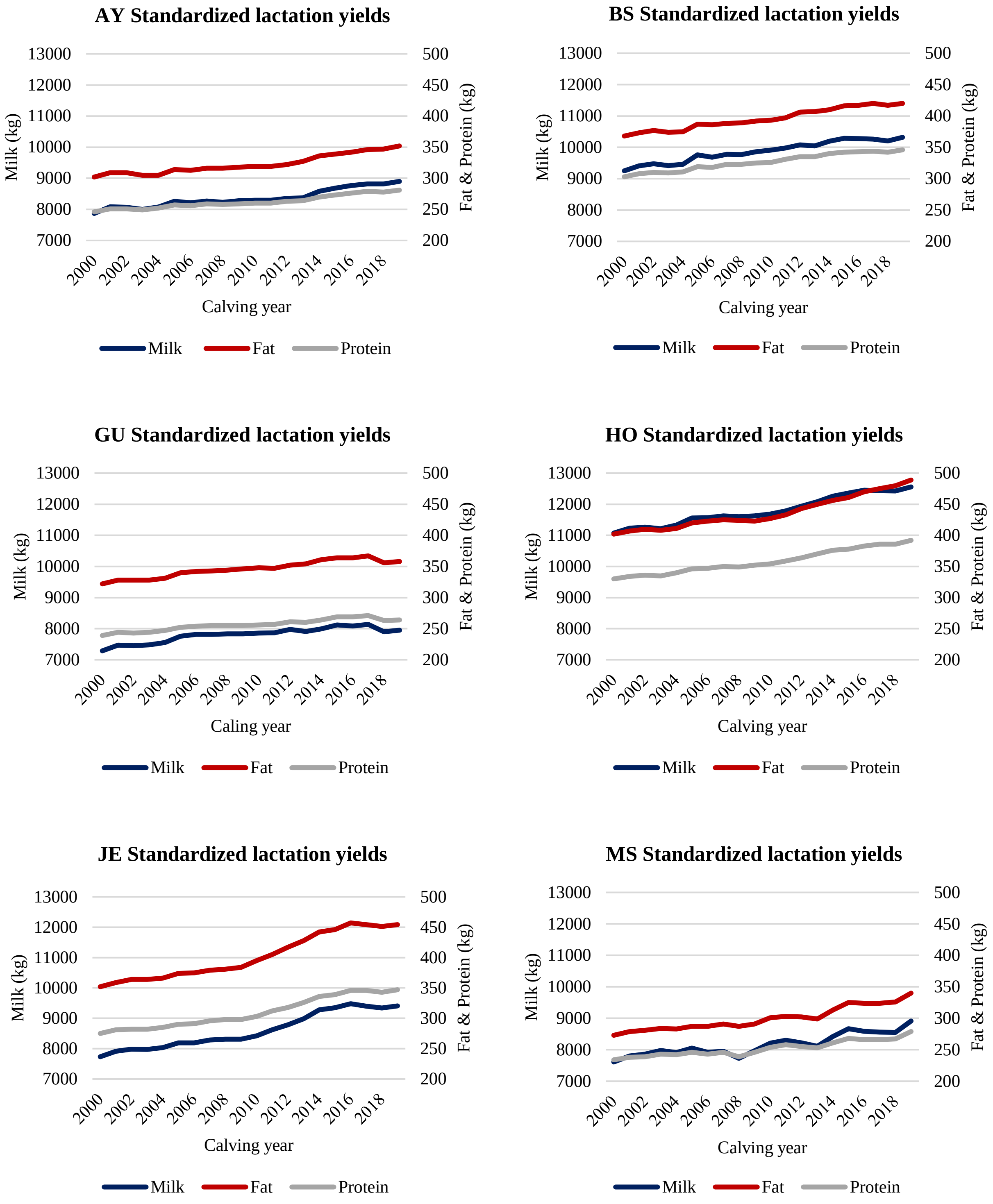

Figure 4.3. Standardized milk, fat, and protein yields 2000 – 2019.

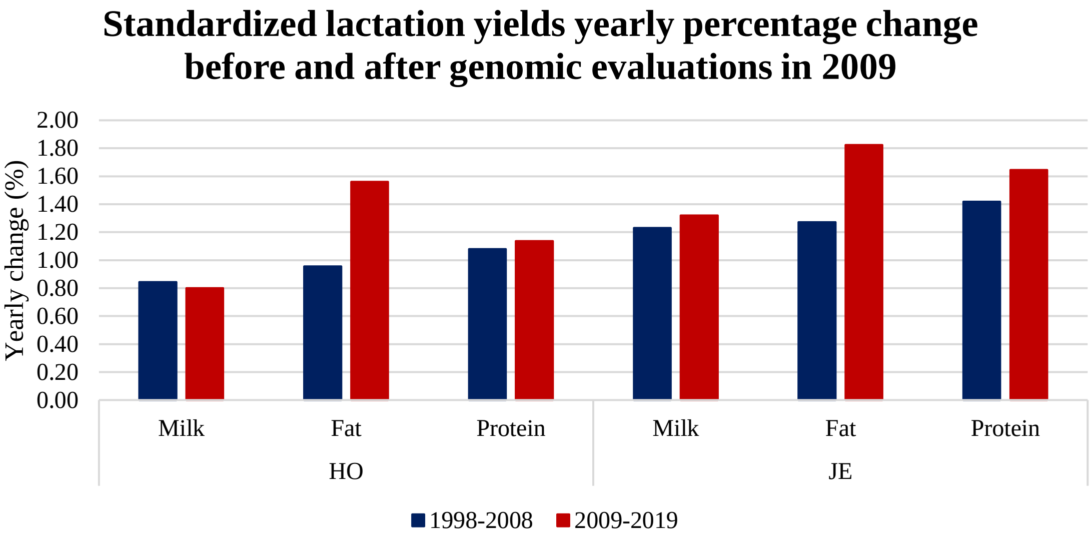

Figure 4.4. Standardized lactation yields yearly percentage change before and after genomic evaluations in 2009 for HO and JE.

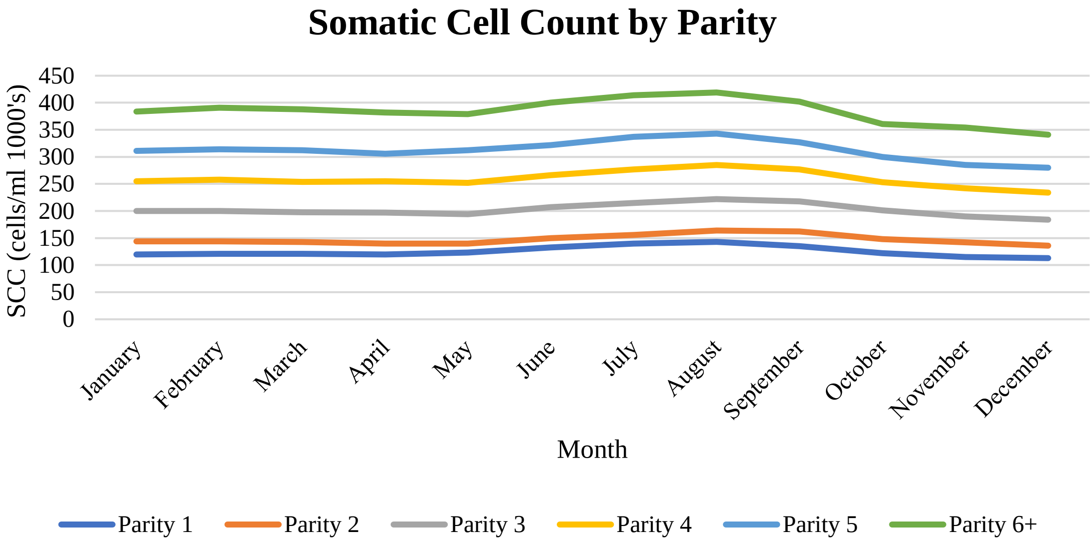

Figure 4.5. SCC per month by parity in 2020.

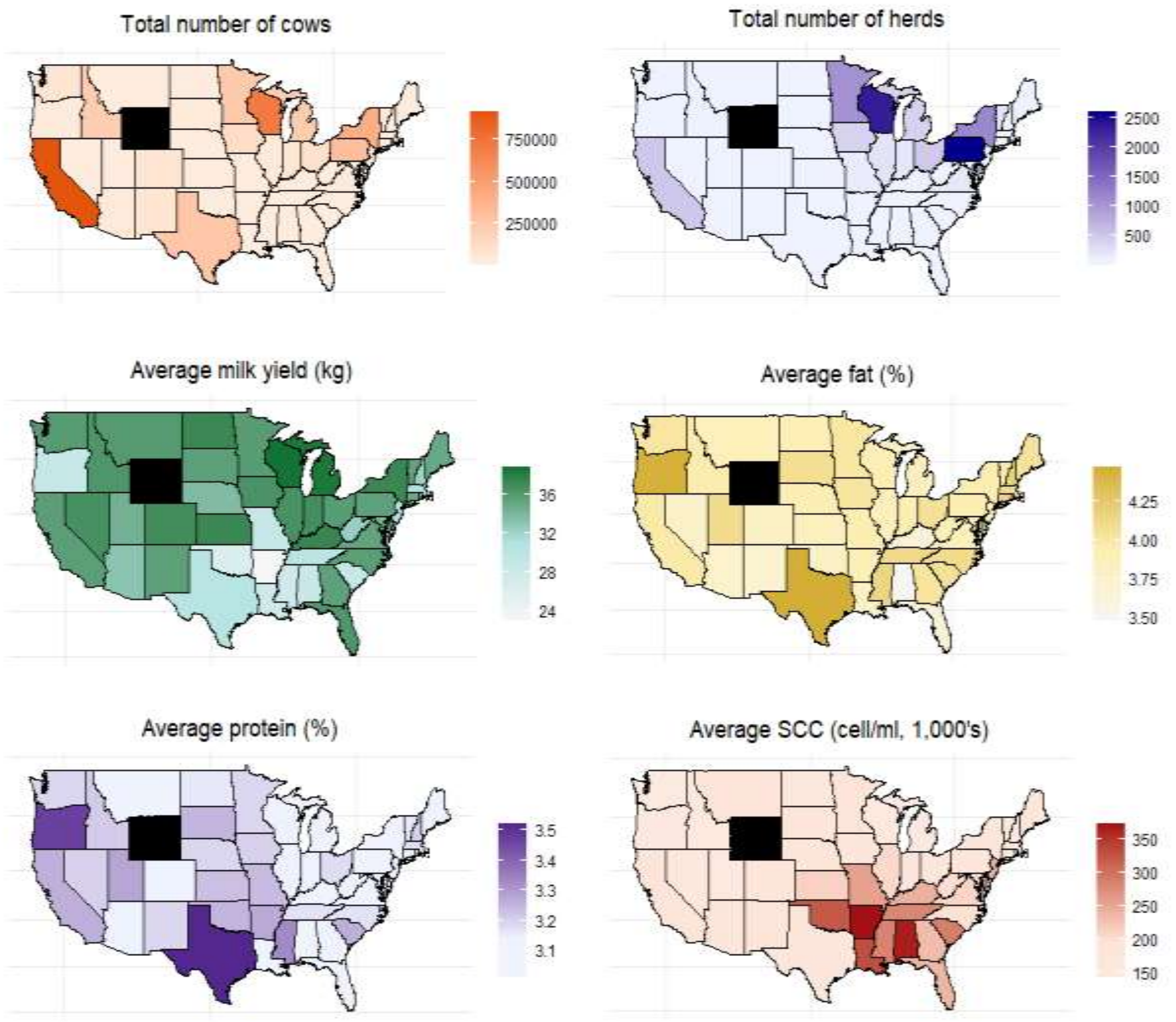

Figure 4.6. Characteristics of test-day milk yield, somatic cell count (SCC), fat and protein percentages from Dairy Herd Improvement herds by state during 2020. There are no cows on DHI milk recording in Wyoming in 2020.

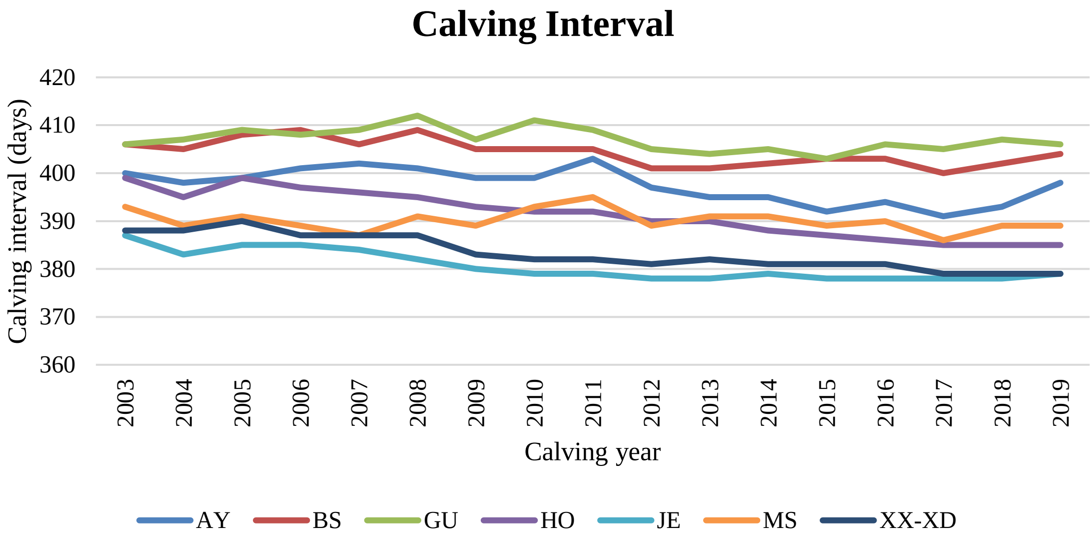

Figure 4.7. Calving interval (days) for all breeds from 2003 – 2019.

CHAPTER 5

CONCLUSIONS

Genetic trends show the genetic improvement that has occurred in the US since the implementation of genomic evaluations. Fat yield has increased almost 6-fold for Holstein bulls while Livability has increased over 4-fold for JE bulls. These trends also indicate areas, such as Daughter Pregnancy Rate for the majority of breeds that need more attention and focus in the selection indexes used to achieve breeding goals. Generation intervals, the main driver of response to selection have decreased for the majority of breeds since the implementation of genomic evaluations. This study should be updated in another five years to give breeds that received genomic evaluations later than 2009 further opportunity to develop. Phenotypic trends show the improvement achieved that includes the environment portion and the genetics. The phenotypic trends reflect the genetic trends closely. Colored breeds could benefit greatly from increased phenotyping and genotyping. Milk recording is paramount to data collection in the dairy sector, and further work has to be done to build on the 100 plus years of milk recording completed in the US. The dairy cow population is changing, yields are increasing steadily while reproductive traits have made some progress for Holsteins. To increase the value the producer receives from the data supplied to CDCB for national genetic evaluations, further studies will be required and more decision support tools will need to be developed.