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GENETIC EVALUATION OF BROWN SWISS CATTLE IN THE UNITED STATES

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by
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ABSTRACT

Genetic parameters were estimated for Brown Swiss dairy cattle using a population from the United States born in 2000 and later. The data set consisted of 108,633 first through fifth lactation records from 45,464 cows for yield, somatic cell score, days open, and productive life. Approximately half of the records also had observations for 18 linear type traits and 41,074 had observations for milking speed. Heritabilities and correlations amongst yield, fitness, and type traits were evaluated with 3-trait models in ASREML with fixed effects for lactation, age, and herd-calving cluster, and random effects for animal, permanent environment, and residual. The heritabilities of milk, fat, and protein yield were 0.30, 0.20, and 0.20, respectively. The heritabilities of productive life, days open, SCS, and milking speed were 0.11, 0.03, 0.12, and 0.26, respectively. Milk, fat, and protein yield had strong positive correlations with productive life (0.67 to 0.71), days open and SCS had strong negative correlations with productive life (-0.69 and -0.60, respectively), and milking speed had a positive correlation with productive life (0.26). All three yield traits were slightly unfavorably correlated with days open, but there was little relationship found between yield traits and SCS or milking speed. Correlations of body traits with yield and fitness traits tended to be small, though dairy form was positively correlated with yield (0.31 to 0.40) and negatively correlated with days open (0.36 to 0.67). Of the feet and leg traits, mobility was most favorably correlated with yield (0.26 to 0.27) and productive life (0.50). For udder traits, yield traits were positively correlated with rear udder height and rear udder width, ranging from 0.19 to 0.48, and negatively correlated with udder depth and fore udder attachment, ranging from -0.04 to -0.40. However, udder depth and fore udder attachment were more favorably correlated with SCS (-0.26 and -0.14, respectively) than rear udder height and rear udder width (-0.02 and 0.18, respectively). Productive life was most strongly correlated with fore udder attachment, rear udder width, udder depth, and rear udder height (0.44, 0.40, 0.35, and

0.33, respectively). Due to the importance of the relationship between udder traits with yield and fitness traits, an additional analysis was performed using the same data set to create an “udder efficiency” trait for Brown Swiss cows using Data Envelopment Analysis (DEA). The DEA assigned units, individual cows in this case, with an efficiency measure ranging from 0 to 1 based on their ability to minimize inputs and maximize outputs relative to other cows in the same herd. The sole input was the inverse of milking speed and the outputs were defined as milk, fat, and protein yield, and the inverse of somatic cell score. The most efficient cows would be those that milked quickly and produced large volumes of milk, fat, and protein with a low somatic cell score. The 40,960 udder efficiency records were derived and evaluated using 3-trait ASREML models as previously described. The heritability of udder efficiency was estimated to be 0.23 ± 0.0133 . Genetic correlations with udder efficiency were positive and moderate for yield traits (0.40 to 0.42), favorable with SCS (-0.21), and strongly positive for milking speed (0.86). Udder efficiency was also strongly correlated with productive life (0.69). Of the udder traits, rear udder height (0.30), teat length (-0.28), fore udder attachment (0.25), and rear udder attachment (0.21) were most favorably correlated to udder efficiency. The correlation of udder depth with udder efficiency was 0.16. Based on these findings, DEA could be a useful and novel method for evaluating udder efficiency, helping to identify traits that enable selection for mastitis resistance without compromising yield. Results from the estimation of genetic parameters for U.S. Brown Swiss will allow for improved genetic selection for the breed.

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Chapter 1

Review of the Literature

Genetic Selection

Livestock populations have been subjected to selective breeding by humans for centuries, extending back to Robert Bakewell's work in the mid 1700's (<http://www.ars.usda.gov/Research/docs.htm?docid=4700>). The idea behind genetic selection is to define a breeding goal to enhance traits that are identified as economically important. This selection alters the allele frequencies that exist in the animal population, and the response depends on the heritability of a given trait multiplied by the selection differential (Falconer and Mackay, 1996).

There is variation observed in all quantitative traits, and whether or not that variation is due to differences in genes determines if that trait is heritable. Heritability explains the relationship between an animal's phenotype and their breeding value, and can be calculated by determining the ratio between additive genetic variance and total phenotypic variance for a given trait. Selection differential measures how superior the parent population is compared to the total population (Falconer and Mackay, 1996). Selection intensity measures what proportion of the total population are selected as parents for the next generation (Bourdon, 1997) and can be found by dividing the selection differential by the genetic standard deviation.

In dairy cattle, tremendous progress has been realized through the implementation of sophisticated genetic selection programs and statistical models. Use of the animal model allows for the derivation of an animal's predicted transmitting ability (PTA), which is a measure of that animal's merit as a parent. The PTA combines information from an animal's performance, as well as a weighted average of the performance of its relatives and progeny. The amount of this

information is characterized by reliability, which is the squared correlation between the PTA and the unknown true transmitting ability (VanRaden and Wiggans, 1991).

Estimates of heritability, repeatability, as well as genetic, phenotypic, and environmental correlations among important traits have been well established over the past 50 years. In addition to the establishment of these genetic parameters, sire and dam evaluations have allowed for widespread use and availability of genetically superior breeding stock (White et al., 1981). In more recent years, adoption of modern reproductive technologies such as embryo transfer and in vitro fertilization has further accelerated genetic progress due to the reduction of generation intervals (Togashi et al., 2004).

Multiple Trait Selection

Dairy cattle have become more economical producers of milk through genetic selection, with many traits influencing a cow's overall profitability. This progress has been facilitated by genetic evaluation techniques which allow dairy producers to select for the improvement of several traits at once. In the United States, these genetic evaluations have changed greatly over time. The United States Department of Agriculture (USDA) introduced their first economic selection index called "Predicted Difference Dollars" in 1971. The index included milk and fat yield, and estimated gross income for a cow's lactation. Over the years, protein yield was added, as well as traits influencing health, fitness, and conformation, and the name of the index was changed to "Net Merit Dollars". Price estimates for the different inputs and outputs of traits included in the index change over time, therefore estimates are updated as needed to predict future markets (VanRaden, 2004).

While Net Merit Dollars is an index that can be used for all breeds of dairy cattle, many breed associations have developed specific indices for use in their respective breeds. For Brown Swiss cattle, the Brown Swiss Association uses what they call the "Progressive Performance

Ranking” (PPR). It is a ranking system for sire and cow genetic evaluations, and includes varying weights on protein and fat yield, somatic cell score, productive life, udder composite, mobility score, and daughter pregnancy rate. In the most recent edit to the PPR formula, the Brown Swiss Association reduced the weight of somatic cell score and productive life, and raised the weight of daughter pregnancy rate in order to further breed progress in the area of reproduction (<http://www.brownswissusa.com/Breed/LatestNews/tabid/199/articleType/ArticleView/articleId/93/Udder-Composite-and-PPR-Formulae-Revised-for-December-Evaluations.aspx>).

Another method for evaluating multiple criteria simultaneously is data envelopment analysis (DEA). A DEA is a statistical technique which measures the efficiency of a system, termed a decision making unit (DMU), as a whole based on its use of different inputs to produce outputs. Therefore, it can be a tool to measure and analyze performance as well as to provide benchmarks. A DEA scores DMUs on a scale of zero to one (with one indicating there are no input or output inefficiencies), and compares a given DMU relative to other DMUs in the data set. This identifies those DMUs that are producing most efficiently relative to the group (Stokes et al., 2007). In dairy cattle research, DEA has been applied to identify efficient producers based on production costs and generated income (Stokes et al., 2007; Heinrichs et al., 2013).

The Brown Swiss Breed

It is speculated that Brown Swiss have one of the largest global populations of any dairy breed with approximately 7 million animals worldwide (<http://www.brownswissusa.com/Breed/BrownSwissBreed/tabid/173/Default.aspx>). While they are the third most popular breed in the United States, they only represent less than one percent of the country’s dairy herd. In 2013, there were 17,997 Brown Swiss cows in herds in the U.S. that were enrolled in Dairy Herd Improvement (DHI) compared to 2,175,009 Holsteins and 253,850 Jerseys. These large-framed animals originated in Switzerland, and are comparable in size to the modern Holstein, allowing

them to fit comfortably in facilities designed for Holsteins. Though, on average, their fluid milk production is less than that of a Holstein, they offer an attractive characteristic in that the composition of their milk makes it well suited for cheese production. In a changing dairy market where cheese production is increasing, this is an economically appealing characteristic. In the past 25 years, cheese production in the United States has doubled (Johnson and Lucy, 2006) with approximately half of the nation's milk supply being used to make cheese (<http://www.ers.usda.gov/topics/animal-products/dairy/background.aspx>).

When compared to milk from Holstein-Friesian cows, milk from Brown Swiss cows in Italy was significantly higher for percentage of fat, percentage of protein, and percentage of casein (a major component of cheese). This allowed Brown Swiss cows to yield an average of 15% more cheese per kilogram of milk produced. On a per day basis, Brown Swiss cows produced 5% more cheese despite yielding 9% less milk than Holstein-Friesians. In addition, milk from Brown Swiss cows coagulated more quickly with a firmer curd, both advantages from a cheese processing standpoint. Lastly, Brown Swiss cows produced milk that was higher in concentration of several monounsaturated fatty acids and polyunsaturated fatty acids that are favorable for human health (De Marchi et al., 2008).

Brown Swiss cattle also offer advantages for some longevity traits, especially when breeds are compared across different geographical regions. When compared to Jerseys and Holsteins, Brown Swiss had a higher probability of surviving to five years of age in the Northeast, North Central, Northwest, South Central, and Southeast regions of the United States. Brown Swiss lived significantly longer than both Holsteins and Jerseys in the Northeast, significantly longer than Jerseys in the North Central, and significantly longer than Holsteins in the Northwest, Southeast, and South Central. In an additional analysis, the risk was determined for each breed's failure to continue to accumulate days in milk (due to culling or death). Brown

Swiss were at a lower risk than Holsteins in the Northeast, Northwest, South Central, and Southeast (Garcia-Peniche et al., 2005).

Yield Traits

A majority of the income on a dairy farm (approximately 85 percent) is generated through sale of milk and milk solids, making milk production of primary economic concern. Therefore, dairy cattle have been genetically selected to produce large volumes of milk. The average mature Holstein cow born in 1970 produced 15,438 pounds of milk, 564 pounds of fat, and 500 pounds of protein, compared to the average cow born in 2012 making 27,639 pounds of milk, 1034 pounds of fat, and 852 pounds of protein (<https://www.cdcb.us/eval/summary/trend.cfm>). This marked increase has been made possible by a combination of improvements in management and increases in genetic potential.

Traits for yield (milk, fat, and protein) are moderately heritable in dairy cattle, allowing for progress to be made more quickly than traits with low heritabilities. Heritability of milk yield in Holsteins has been reported as low as 0.16 (Schutz et al., 1990) up to 0.44 (Misztal et al., 1992); a more moderate estimate of 0.25 to 0.32 (Dechow et al., 2004 and Jamrozik and Schaeffer, 1997) is more frequently reported. Currently, a heritability of 0.20 is assumed for national genetic evaluations (VanRaden and Cole, 2014). Heritability estimates for fat and protein yield also range from 0.16 and 0.13, respectively (Schutz et al., 1990) up to 0.42 and 0.40 (Misztal et al., 1992). As with milk yield, 0.20 is the heritability assumed for fat and protein yield in national genetic evaluations (VanRaden and Cole, 2014). Genetic correlations between yield traits are positive and moderate to strong. The strongest relationship is seen between milk and protein yield, and has been reported as 0.82 (deJager and Kennedy, 1987) and 0.88 (Dematawewa and Berger, 1998). The aforementioned work estimated genetic correlations for fat and protein yield ranging from 0.66 to 0.77, and 0.57 to 0.61 for milk and fat yield. Genetic correlations

assumed for national genetic evaluation in the United States for yields of protein and milk, protein and fat, and fat and milk are 0.83, 0.59, and 0.43, respectively.

In Brown Swiss dairy cattle, heritability estimates for yield traits have been reported to be slightly higher than estimates for Holsteins. In two separate evaluations of Brown Swiss in Italy, heritabilities of milk, fat and protein yield were estimated to be 0.22, 0.19, and 0.18 (Samoré et al., 2010) and 0.28, 0.30, and 0.26, respectively (Santus et al., 1993). In addition, in a 1960 study of Brown Swiss in the United States, Johnson and Fourt reported the heritability of fat production to range from 0.23 to 0.28. This is reflected in national genetic evaluation, which assumes 0.23 as the heritability for milk, fat, and protein yield for Brown Swiss compared to 0.20 used for Holsteins. Correlations between yield traits were also slightly higher, being reported in the two aforementioned studies as 0.90, 0.87, and 0.79 and 0.93, 0.89, and 0.85 for milk and protein, fat and protein, and milk and fat, respectively.

Type Traits

Selection for conformation of dairy cattle has also been practiced for many years. Selecting for type traits which are correlated with increased production and herd-life provides the opportunity for an economic benefit. In Holsteins, scoring for linear type traits, called classification, began in 1929, and continues today. The heritabilities and correlations of these type traits has been well documented in the literature (Foster et al., 1989; Misztal et al., 1992; Short and Lawlor, 1992; VanRaden et al., 1990). Generally, the most highly heritable of the linear type traits refer to the body size and frame structure of the cow (stature, strength, body depth, dairy form/angularity, rump angle, and thurl width). Of these traits, stature is most highly heritable, ranging from 0.34 to 0.42. Estimates of heritability for the other body traits range from 0.22 for strength to 0.35 for body depth based on the above referenced studies. Estimates for udder traits (fore udder attachment, rear udder height, rear udder width, udder cleft, and teat placement) tend

to be more variable with slightly lower heritabilities. Of these traits, udder depth has the highest estimate across studies, ranging from 0.24 to 0.26, with other traits ranging from 0.10 for udder cleft to 0.25 for teat placement. Feet and leg traits (rear leg side view, rear leg rear view, and foot angle) are also scored, and tend to have the lowest heritabilities, ranging from 0.08 for foot angle to 0.17 for rear leg side view

Genetic correlations between these traits are typically positive or near-zero. Highest genetic correlations (0.64 to 0.93) are seen between the body size traits (Misztal et al., 1992; Short and Lawlor, 1992; VanRaden et al., 1990) with cows that are taller also tending to be stronger with deeper bodies and more width between the thurls. Larger cows also tended to have higher scores for all linear udder traits. Larger cows also tended to have higher pins (-0.17 between strength and rump angle; Short and Lawlor, 1992) and straighter rear legs (-0.20 between strength and rear leg set; Misztal et al., 1992). Rump angle tends to be negatively correlated with udder traits, indicating that cows with more sloped rumps tend to have less desirable mammary systems that are deeper with looser attachments. The largest observed correlation was -0.34 between rump angle and rear udder height (Short and Lawlor, 1992). This is similar for rear leg set, with the genetic correlation with udder cleft being -0.20 (Misztal et al., 1992). Cows with more sloped rumps and more sickled legs tended to have a lower foot angle, with the most unfavorable genetic correlation being reported by Misztal et al. (1992) between rear leg set and foot angle as -0.40. The combination of sloped rumps, sickled legs, and a low foot angle could be of concern for the locomotion of the cow. Foot angle was favorably correlated with udder traits amongst studies. In Misztal et al. (1992), Short and Lawlor (1992), and VanRaden et al. (1990), genetic correlations between all udder conformation traits are near-zero or positive. However, when teat length was evaluated, genetic correlations were negative with all other udder traits, ranging from -0.03 with median suspensory ligament (udder cleft) to -0.20 with teat placement. This indicates that shallower udders with stronger, more desirable attachments are related to a

shorter teat (Boettcher et al., 1998). This could be of concern in extreme cases, as milking units are more likely to fall off of shorter teats.

Misztal et al. (1992) and Short and Lawlor (1992) also reported genetic correlations between linear type traits and milk, fat, and protein yield, and milk yield, respectively. Dairy form was most highly related to yield in both studies ranging from 0.52 with milk (Short and Lawlor, 1992) to 0.68 with fat (Misztal et al.). Relationships between body size and feet and leg traits and milk yield were inconsistent, ranging from near-zero (Short and Lawlor, 1992) to slightly positive. The highest genetic correlations were observed between yield and body depth, being 0.15, 0.26, and 0.23 for milk, fat, and protein, respectively, and foot angle, being 0.10, 0.13, and 0.17 for milk, fat, and protein, respectively (Misztal et al., 1992). For udder traits, the most unfavorably correlated to yield in both studies was udder depth, which is to be expected that shallower udders yield a lower volume of milk, fat, and protein. Estimates ranged from -0.29 with fat yield to -0.44 with milk yield (Misztal et al., 1992) with other values falling between. In addition, both studies found an unfavorable correlation between fore udder attachment and yield, ranging from -0.12 with fat yield to -0.31 with milk yield (Misztal et al., 1992). The other udder traits had near-zero to moderately positive genetic correlations with yield. Rear udder width was the most related trait to yield, ranging from 0.16 with milk yield (Short and Lawlor, 1992) to 0.40 with protein yield (Misztal et al., 1992). When final classification score was evaluated, genetic correlations with yield were inconsistent, ranging from 0.16, 0.33, and 0.27 with milk, fat, and protein yield, respectively (Misztal et al., 1992) to 0.06 with milk yield (Short and Lawlor, 1992).

In Brown Swiss cattle, heritabilities of type traits were fairly consistent with Holstein estimates, particularly in Italian Brown Swiss as evaluated by Samoré et al. (2010). However, using older data and methods of linear scoring, Johnson and Fourt (1960) and Van Vleck et al. (1980) reported higher estimates. Using categorical traits (general appearance, dairy character, body capacity, rump, feet and legs, mammary system, fore udder, and rear udder) that combine

individual linear traits, heritability estimates were much higher for Brown Swiss than Holsteins for rump (0.36 to 0.44) and feet and legs (0.19 to 0.20). This was inconsistent with Samoré et al. (2010) which found feet and leg trait estimates to be much closer to those reported for Holsteins ranging from 0.06 for heel depth (similar to foot angle) to 0.12 for rear leg set.

In the two older studies, genetic correlations between trait categories were all positive. In Johnson and Fourt (1960), all trait categories were highly related, particularly mammary system, in which correlations ranged from 0.83 with feet and legs to 0.99 with dairy character. In Van Vleck et al. (1980), genetic correlations amongst trait categories were smaller but still large to moderate. General appearance was most highly related to other trait categories, ranging from 0.68 with dairy character to 0.88 with rump. In Italian Brown Swiss, similar relationships to what was seen in Holsteins were observed between rump angle and udder traits, with more sloping rumps being genetically related to less desirable udder traits, particularly lower and narrower rear udders (-0.24 and -0.26, respectively). Higher scores for udder traits were genetically correlated to shorter teat length, with the largest relationships observed with teat placement (-0.56) and fore udder attachment (-0.30). Other correlations between udder traits were all positive and similar in magnitude for reported values in Holsteins, with the exception of rear udder width and udder depth (-0.20) suggesting that wider rear udders were also deeper (Samoré et al., 2010).

Johnson and Fourt (1960) estimated genetic correlations between fat yield and the type categories, and found favorable relationships between all of them, ranging from 0.21 for rump to 0.48 for rear udder. Van Vleck et al. (1980) also found favorable relationship between all type categories and milk yield. In this study, a lower score for the type category corresponded to more desirable type, therefore negative genetic correlations represented higher milk yield. The correlations ranged from near-zero with feet and legs (-0.03) to moderate for mammary system and fore udder (both -0.23) Results from Samoré et al. (2010) were similar to observed genetic correlated from Misztal et al. (1992) for Holsteins. Body size traits were slightly to moderately

correlated with yield, with the most significant trait being body depth (0.22, 0.26, and 0.23 with milk, fat, and protein yield, respectively). Feet and leg traits were generally genetically unrelated to yield traits. As seen in Holsteins, the most unfavorable udder trait with yield was udder depth, with genetic correlations for milk, fat, and protein yield of -0.37, -0.28, and -0.29, respectively. Rear udder height and width were moderately favorable with yield, ranging from 0.20 between rear udder height and protein yield and 0.39 between rear udder width and milk yield. The most favorable trait with yield was fore udder attachment, with observed genetic correlations of 0.45, 0.44, and 0.44 with milk, fat and protein yield, respectively. The relationship between fore udder/fore udder attachment and yield was the most striking difference when comparing Brown Swiss to Holsteins, due to the favorable genetic correlation observed in all three studies between stronger fore udder attachments and more yield (Johnson and Fourt, 1960; Samoré et al., 2010; Van Vleck et al., 1980).

Udder Health

As noted, dairy cattle have been intensely selected for milk production in previous years, yet with little pressure placed on selection for fitness traits despite these traits also having a large influence on overall profitability. Unfortunately, yield traits often have unfavorable genetic correlations with health and fitness. In terms of udder health, an increase in genetic susceptibility for mastitis has accompanied the genetic increase in milk yield. Mastitis has been reported to be the most costly disease to the dairy industry (Shook and Schutz, 1994) due to high incidence and its responsibility for lost milk yield, increased culling, higher veterinary costs, and lower milk price due to payment systems regarding milk quality (Rupp and Boichard, 1999). For these reasons, udder health of dairy cattle is of increasing importance and concern.

However, data containing reliable records of clinical mastitis occurrences can be difficult to obtain and evaluate because the trait is subjective and there is no national standardized

recording system for mastitis in the United States. Therefore, somatic cell count (SCC) or its transformed log score, somatic cell score (SCS), is frequently used as an indicator for udder health because of its routine measurement in milk recording programs. Given that the genetic correlation between clinical mastitis and SCC averages 0.70 (Rupp and Boichard, 1999), selection for reduced SCC should be successful in lowering susceptibility to udder infections. Indirect selection for udder health based on SCC offers several advantages. As noted, it is routinely measured and is more objective in nature, allowing for more accurate evaluation. In addition, the heritability of SCC has been reported as approximately 0.15 (Boettcher et al., 1998; Rogers et al., 1991; Rupp and Boichard, 1999; Samoré and Groen, 2006) which is higher than that of clinical mastitis (generally <0.10 , Emanuelson et al., 1988; Lund et al., 1996). The higher heritability of SCC allows for higher reliabilities in genetic evaluations and faster genetic improvement.

Genetic relationships between SCC/SCS and milk yield have been reported in numerous studies. In a population of first lactation Holstein cows in France, genetic correlations of kilograms of milk, fat, and protein produced with SCS averaged across the lactation were 0.15, 0.11, and 0.27, indicating that selection for increased yield would result in higher SCS (Rupp and Boichard, 1999). This is supported by an evaluation of Italian Brown Swiss in which genetic correlations between milk, fat, and protein yield with SCS were 0.18, 0.03, and 0.07 (Samoré et al. 2010).

Selection for udder conformation has also been a consideration in most dairy cattle breeding programs, and has the potential to reduce SCC and positively influence udder health. Many of the genetic correlations between udder traits and SCC are favorable. Several studies have examined this relationship in Holsteins using different populations. In Canadian Holsteins, correlations between three scorecard composite traits and six linear udder traits with lactation average SCC were estimated using two different REML methods. The three scorecard composites

were scored from one (poor) to six (excellent) and were mammary system, fore udder, and rear udder. Genetic correlations with SCC ranged from -0.16 to -0.22 using one REML method, and from 0.01 to -0.14 using the other, suggesting that cows with more desirable udders would have a reduced SCC. The correlations between SCC and the six linear traits were mostly small and inconsistent. Linear traits were scored on scale from one to three, with one being desirable and three being undesirable, therefore positive correlations indicated a favorable relationship with SCC. Correlations were favorable using both REML methods for rear attachment (0.14 to 0.15), fore teat placement (0.03 to 0.30), and rear teat placement (0.01 to 0.28). Due to the large ranges of estimates for fore teat placement and rear teat placement, these numbers should be interpreted with caution, but it appears that tighter rear udder attachments, and closer front and rear teats have a favorable effect on SCC (Monardes et al., 1990).

Similar relationships were examined in Canadian Holsteins by Boettcher et al. (1998). Estimates were derived for correlations between lactation average SCS and nine objectively measured linear traits and three subjective scorecard traits (mammary system, fore udder, and rear udder) that were composites of the other nine traits. The scorecard traits were scored on an eighteen point scale, with a higher number being more desirable. Genetic correlations were approximately -0.20 for all three traits, suggesting that a balanced, shapely udder with a high, wide rear attachment, strong fore udder attachment, and close teat placement is less susceptible to mammary infection. Similar to the previous study (Monardes et al., 1990), genetic correlations with linear traits were generally small. The two traits most strongly correlated with SCS were udder depth (-0.26) and fore udder attachment (-0.24), favoring a shallow udder with the fore udder strongly attached.

Relationships between udder health and linear type traits have also been estimated in European Holstein/Holstein-Friesian populations. In a French population of first lactation Holstein cows, data was available for SCS, nine linear udder type traits, and also clinical mastitis

occurrence. This allowed for the comparison of correlations between type traits and an indirect measure of udder health (SCS) and a direct measure (clinical mastitis). The linear traits were scored from one to nine, and correlations for udder depth and fore udder attachment with lactation average SCS were consistent with previously reported estimates (-0.40 and -0.32 respectively). Shallow udders with strong fore udders were also favorably correlated with clinical mastitis, with estimates of -0.46 for udder depth and -0.36 for fore udder attachment. A trait that was also related to both SCS and clinical mastitis that was not available in other studies was udder balance. A score of 1 corresponded to an udder with much lower rear quarters than fore quarters and a score of 9 with an udder having much higher rear quarters than fore quarters. The genetic correlation was -0.29 between SCS and udder balance and -0.32 between clinical mastitis and udder balance, favoring an udder with higher rear quarters. Also moderately correlated with both SCS and clinical mastitis were front teat distance (0.16 and 0.20) and side teat distance (0.26 and 0.20), with wider teats being related to a higher SCS (Rupp and Boichard, 1999). In first lactation Holstein Friesians in Italy, correlations between linear type traits and SCS were mostly consistent with previously discussed results. However, the genetic correlation between rear udder width and lactation average SCS was 0.28 compared to previous estimates that were near-zero or negative. This result suggests that cows with wider rear udders were more susceptible to mastitis (Samoré and Groen, 2006).

Such relationships have also been examined for Holsteins in the United States. Genetic correlations were estimated between body, feet and leg, and udder linear type traits and SCC measured in first lactation cows, and between type traits measured in first lactation and SCC measured in second and third lactation using several data sets. Results for the body and feet and leg traits were small and inconsistent amongst the different data sets, suggesting there is little genetic association with SCC. Results for udder traits with SCC were also variable between data sets, but were mostly consistent with other Holstein populations. The traits most related to SCC

were fore udder attachment, udder depth, and teat placement. General correlations with SCC averaged amongst data sets and weighted by the inverse of their standard errors were -0.32, -0.35, and -0.22 respectively. It was also reported that teat length was unfavorably correlated with SCC (0.16 to 0.20), perhaps due to longer teats being more susceptible to injury. Once again, shallow, well-attached mammary systems with closer teat placement are favorable for mastitis resistance. It was concluded that selection for these traits should reduce or slow the increase in SCC from selection for increased milk production (Rogers et al., 1991).

While the relationship between SCC/SCS and udder traits has been well examined in Holsteins using several populations, this is not the case for Brown Swiss. However, genetic parameters relating to longevity have been estimated for primiparous Brown Swiss cows in Italy. Monthly SCC data was converted to SCS and averaged across the lactation, and linear type traits were measured on a scale of one to fifty. Heritability estimates for SCS were consistent with those that have been observed in Holsteins at 0.14 with a standard error of 0.02. As seen in Holsteins, body and feet and leg traits generally had low correlations with SCS, however in this Brown Swiss population, genetic correlation between pasterns and SCS was -0.23. This suggests that cows with shorter, stronger pasterns were less susceptible to having a high SCS. Observed genetic correlations between udder traits and SCS were slightly different from relationships seen in Holsteins. Udder depth was the most highly related trait, with a genetic correlation of -0.46, however fore udder was much less related with a genetic correlation of 0.07. The next two traits that had the highest correlations were teat length and rear udder width (0.22 and 0.20, respectively). Based on this data, Brown Swiss cows with shallower udders, shorter teats, and narrower rear attachments were less susceptible to udder infections (Samoré et al., 2010).

Milking Speed

Another trait of interest to udder health is milking speed, also termed milking ease and milkability. This is of interest due to slower-milking cows impeding the efficiency of milking the herd, and the high proportion of labor in the cost of producing milk. Decreased time for milking each cow also reduces the wear on milking equipment, and utility costs for operating the parlor. While this is desirable, faster-milking cows may be more susceptible to udder infection if the reason they milk out more quickly is because of reduced tension in the teat sphincter (Boettcher et al., 1998). This could allow pathogens to enter the udder via the teat end more easily. If the milking speed is too rapid, the cow might be more susceptible to milk leakage prior to milking (Wiggans et al., 2007). Milking speed can also be difficult to interpret because of the subjectivity of its recording. The most common method of recording milking speed are farmer-rated scores on a scale of one to five or one to eight, with a higher number indicating a faster milking cow. While the correlation between these subjective scores with total milking time measured objectively have been reported to be as high as 0.92 (McClelland, 1983), there is still opportunity for error or bias.

Using Canadian Holsteins where milking speed was subjectively recorded on a scale of one to five, estimated heritability was 0.15 (Boettcher et al., 1998). This was comparable to the estimate of 0.17 for subjective milking ease of French Holsteins (Rupp and Boichard, 1999) and electronically recorded milking duration for Holsteins in the United States (Zwald et al., 2005). This is lower than the heritability of 0.21 reported by Meyer and Burnside in 1987. It was suggested that the lower heritability could be because producers were not evaluating the trait as conscientiously as when it was new and experimental (Boettcher et al., 1998). In the Canadian study 83% of the cows were indicated by the producer as being “average” or “fast” milkers relative to the herd, while only approximately 15% were indicated as being “very slow” or “slow” (Boettcher et al., 1998). In French Holsteins, the average milking ease score was 3.3 on a one to

five scale (Rupp and Boichard, 1999) and in U.S. Holsteins, the average milking duration was 4.5 minutes with a range of one to thirteen (Zwald et al., 2005). This indicates that in general, the average Holstein cow is already skewed towards faster milking.

In Canadian Holsteins, the genetic correlation between one measurement of milking speed during the first two months after calving and lactation average SCS for primiparous cows was 0.41. That correlation was smaller (~ 0.25) for lactation average SCS during the second and third lactation. That could be due to milking speed only being measured during the first lactation, or that udder confirmation traits have a greater effect on mastitis resistance in later lactations (Boettcher et al., 1998). Using French Holstein data, correlations were estimated between milking ease and lactation average SCS and incidence of clinical mastitis. Correlation between milking ease and SCS was consistent observations for Canadian Holsteins, with an estimate of 0.44. However, there was minimal genetic relationship identified between milking ease and clinical mastitis (0.06). Faster milking cows had a higher SCS but were not found to be more susceptible to clinical mastitis cases (Rupp and Boichard, 1999). For first lactation Italian Holstein cows, correlations between SCS and milking speed EBVs of their sires were estimated. Bulls that sired the highest proportion of slow-milking daughters, also sired daughters with the lowest SCS, and bulls that sired the highest proportion of fast-milking daughters, also sired daughters with the highest SCS. However, the relationship was not linear across classes of milking speed EBV therefore the results were difficult to interpret (Samoré and Groen, 2006). An unfavorable genetic relationship between bull PTAs for milking duration and somatic cell score was also seen in U.S. Holsteins (Zwald et al., 2005). The genetic correlation was -0.15, which suggested that as milking duration decreased, somatic cell score increased.

As with SCC/SCS, udder confirmation traits also have an effect on milking speed. For Canadian Holsteins, the biggest genetic relationships between milking speed and udder traits were observed for rear udder width, udder texture, teat length, and udder depth, with correlations

of -0.24, 0.18, -0.18, and 0.18, respectively (Boettcher et al., 1998). Cows that milked out more quickly tended to have narrower rear udders, with softer, more pliable udder texture, shorter teats, and a shallower udder overall. In an analysis of correlations between PTAs for milking duration and udder type traits in U.S. Holsteins, front teat length was most highly related (0.20) also indicating the relationship between faster milking and shorter teats. PTAs between milking duration and rear udder width and udder depth however were small and not significantly different than zero. The only other udder trait that was significantly related to milking duration was front teat placement, with a correlation between PTAs of -0.14, meaning that bulls that sire faster milking daughters also tend to sire daughters with closer teat placement (Zwald et al., 2005).

Evaluation of milking speed in Brown Swiss cattle in the United States yielded slightly different results in comparison to Holsteins. Wiggans et al. (2006) estimated genetic parameters for Brown Swiss using owner reported milking speed scores on a scale of one (slow) to eight (fast). Similar to Holsteins, it seems the distribution of milk speed scores is skewed towards faster milking cows, with 60% of cows in the study being assigned a score of six, seven, or eight. The heritability of milking speed in Brown Swiss was slightly higher than was had previously been reported with an estimate of 0.22 and a repeatability of 0.42. Correlations between evaluations of milking speed, SCS, productive life, and type traits were also estimated for a base group of 121 bulls born 1994 to 1999 with ten or more daughters. There was a favorable positive correlation with productive life of 0.56, and a correlation with SCS of -0.40 suggesting that bulls that sired faster milking cows also sired daughters with a lower SCS. This result was unexpected, and the correlation was reduced to -0.14 when estimated using only 60 of the original 121 bulls that had a sire with five or more sons. The authors hypothesized that the opposite direction of this relationship could be due to slower milking cows not getting milked out fully, resulting in a higher SCS, or could be a breed difference since other studies had examined Holstein data. Correlations between milking speed and type were negative for teat length (-0.35) and strength (-

0.31) favoring a less strong cow with a shorter teat. The strongest positive correlation was 0.22 for both dairy form and fore udder attachment, favoring a more angular cow with a stronger fore udder. Previous work had stated the unfavorable relationship between milking speed and teat length (Boettcher et al., 1998; Zwald et al., 2005), but found little relationship with fore udder attachment, and did not examine relationship with body traits.

A measure of milking speed was also included in the genetic evaluation of first lactation Brown Swiss in Italy (Samoré et al., 2010). They used the objective measure of average milk flow using a flowmeter device measured in kilograms of milk produced per minute. Heritability of the trait was estimated as 0.33. It was hypothesized that the heritability could be higher than what is typically observed due to it being an objective measure as opposed to producer recorded scores. Genetic correlations between yield traits were 0.16, 0.24, and 0.30 for protein, fat, and milk yield, respectively indicating that cows with higher yields tended to be faster milking. However, contradictory to what was observed in U.S. Brown Swiss, the genetic correlation between average milk flow and SCS was 0.46. Genetic correlations with linear type traits were fairly consistent with previous studies, but the most highly related trait was rear udder width (0.53), favoring wider rear udders. This was followed by hock quality, rump angle, heel depth, leg set, and udder depth with correlations of 0.40, 0.32, -0.28, 0.28, and -0.25, respectively. Cows with faster average milk flow were therefore genetically associated with having flatter, more flexible hocks, lower pins, lower heel depth, more sickled rear legs, and deeper udders. While measures of milking speed and udder depth have been reported as favorable (Boettcher et al., 1998; Wiggans et al., 2007), this suggests that may be due to shallower udders holding less milk rather than having higher flow rates.

Mobility

Another functional trait of economic importance in dairy cattle breeding programs is locomotion. Lameness is one of the top reasons for involuntary culling in dairy herds, and problems associated with a cow's mobility are a source of economic loss for the dairy producer through direct and indirect costs. Examples of direct costs are increased labor costs for hoof trimming and setting up foot baths, cost of treatments (antibiotics and/or chemicals for foot baths), and veterinary costs. Indirectly, lameness causes lower milk production, reduced reproductive success and productive life, a higher incidence of involuntary culling, and a decreased carcass weight for those culled animals (Politiek et al., 1986). In addition, lameness is a concern from an animal welfare standpoint. A cow's ability to move comfortably on her feet and legs is necessary in intensively managed herds where cows are often standing or walking on wet concrete, and in grazing herds where cows must travel long distances.

While a large proportion of variability in cow locomotion is due to environmental effects, genetic variation exists as well indicating an opportunity to reduce lameness through selection based on lameness or mobility scores, or linear type traits. However, previous work has shown heritabilities of lameness and mobility scores to be low in Holsteins. For Holsteins on Wisconsin, Minnesota, and Virginia farms, heritability estimates for clinical lameness ranged from 0.09 to 0.22 depending on if a linear or threshold model was used (Boettcher et al., 1998). The cows were scored for clinical lameness on a scale of zero (no lameness) to three (severe lameness). It was also observed that lameness decreased with increasing stage of lactation, but increased with parity. However, this study used a small sample size (1,624 records from 1,342 cows). For Canadian Holsteins, estimates for heritability of locomotion score were also small at 0.05 to 0.07. Cows were scored in a similar manner with one indicating the cow walked effortlessly to five for cows that were severely lame. An unfavorable genetic correlation was also reported between

locomotion score and body condition (-0.27) and 150-day milk (-0.28). Cows with higher locomotion scores (lame cows) were more susceptible to being thinner and having lower milk production. This study also used a relatively small sample size of 5,774 records from 3,298 cows (Van Dorp et al., 2004). Heritability estimates for locomotion for Danish Holsteins were consistent with previously reported values. Using a scale from 1 (lame) to 9 (no abduction with a long, even step), heritability was 0.09 (Laursen et al., 2009).

Genetic correlations between conformation traits and measures of mobility in Holsteins were also reported (Boettcher et al., 1998; Van Dorp et al., 2004). As expected, the greatest genetic correlations were found to be between locomotion scores and feet and leg traits. In both studies, foot angle was most related, ranging from -0.64 to -0.84, with a lower foot angle making the cow more susceptible to becoming lame. In Canadian Holsteins, a large genetic correlation was also observed between locomotion score and rear leg set (0.81), faulting more curved rear legs (Boettcher et al., 1998), while in U.S. Holsteins, a low correlation with rear leg side view (0.07-0.13) was observed (Van Dorp et al., 2004). In Boettcher et al. (1998), the next highest correlation was observed with rear leg rear view, ranging from -0.64 to -0.68, suggesting that cows with straighter rear legs when view from the rear would have less susceptibility to lameness. The moderate correlations between rump width (0.62 to 0.63), dairy form (0.31 to 0.60), and body depth (0.42 to 0.43) also suggest that wider, sharper, deeper-bodied cows are more susceptible to locomotion problems. Of the body traits, the only one that was significant with locomotion score in Van Dorp et al. 2004 was rump (-0.25) with higher pins leading to increasing lameness. For Holsteins in the U.S., moderate genetic correlations were reported between clinical lameness and several udder traits, with the largest correlations being with udder cleft (-0.42 to -0.46), udder depth (-0.35 to -0.44), and rear udder width (0.35 to 0.40). There was a genetic relationship between lame cows and those with deeper udders, weaker clefts, and wider rear attachments (Boettcher et al., 1998). In the Canadian data set, udder depth was also significantly

correlated with locomotion score, but to a lesser degree (-0.22), with other significant traits being udder texture (-0.31), front udder attachment (-0.30), and rear udder height (-0.27) (Van Dorp et al., 2004). As previously noted, due to the small sample sizes of these two studies, these genetic correlations should be interpreted with caution.

In Brown Swiss cattle, scoring for the rear leg rear view trait began in 2004, supported by findings that it was highly correlated with decreased lameness in Holsteins (Boettcher et al., 1998). The Brown Swiss Cattle Breeders' Association of the USA began scoring this trait to detect bulls that would be more likely to sire daughters with poor mobility, and therefore decreased herd life and fertility. Using data from 2004 to 2006, heritability was estimated to be 0.10. A large positive correlation was observed between rear leg rear view and rear udder width (0.71) and moderate positive correlations were observed with strength (0.49), thurl width (0.47), dairy form (0.44), and body depth (0.40). The largest negative correlation was with rump angle (-0.19) suggesting a relationship between a more sloped rump and rear legs that "hock in" (Wiggans et al., 2006). Next, in 2007, The Brown Swiss Cattle Breeders' Association of the USA began scoring for a mobility trait to measure the cow's overall ability to move in addition to foot, pastern, and leg structure. The mobility trait replaced the previously used feet and legs composite trait. The trait is score from 50 (poor) to 99 (ideal), and makes up 20% of a cow's final score. The heritability of mobility was estimated to be 0.21, which was higher than that of rear leg side view, foot angle, and rear leg rear view (0.14, 0.09, and 0.06, respectively). Traits with the highest genetic correlations with mobility were final score (0.78), rear leg rear view (0.72), rear udder width (0.51), and foot angle (0.47). Correlations between PTAs for Brown Swiss bulls for mobility and yield and fitness traits were also estimated. Mobility had a favorable correlation with milk, fat, and protein yield (0.41, 0.36, and 0.40, respectively) and also with net merit (0.39) and productive life (0.31). The correlation between PTA for mobility and PTA for daughter pregnancy rate was -0.27, suggesting a relationship between higher mobility score and reduced

fertility. That result was not expected, because studies for Holsteins suggested that reproductive success improves with unimpaired mobility. However, because of its higher heritability (0.21 vs. 0.15) and higher correlation with productive life (0.31 vs. 0.19) mobility was implemented into the Brown Swiss Progressive Performance Ranking in place of the feet and legs composite (Wright et al., 2013).

Fertility

As noted with udder health, genetic relationships between yield traits and fertility in dairy cattle are antagonistic, and emphasis on yield has resulted in a deterioration of reproductive performance. As a result, poor reproduction has become a worldwide economic burden on dairy producers (Zink et al., 2011). Infertility accounts for a substantial proportion of cows that are culled for involuntary reasons (reasons other than poor milk production); and therefore, it is unfavorably associated with herd-life. The genetic correlation between survival and days open across parities for Holsteins was estimated to be -0.13, indicating a relationship between increased days open and mortality (Dematawewa and Berger, 1998). Observed relationships for Holsteins between days open and 305 day milk, fat and protein yield averaged 0.63, 0.42, and 0.42, respectively across parities, and when evaluated per parity were higher for third and later lactation cows than for younger animals (Dematawewa and Berger, 1998). These values were higher than the estimated genetic correlation between mature equivalent milk and days open for Holsteins of 0.38 (Dechow et al., 2004). For Brown Swiss cows, this unfavorable relationship was characterized using Italian data. The genetic correlations between number of services to conception and peak milk and lactation milk yield were 0.24 and 0.34, respectively (Tiezzi et al., 2011).

Most reproductive measures also have low heritabilities. In Dematawewa and Berger (1998) reported the heritability of days open as 0.04, which is equal to the estimate from Dechow

et al. (2004). Using data from Czech Holsteins, heritability of days open for first parity cows was also 0.04, but was reduced to 0.02 for second parity (Zink et al., 2011). For Italian Brown Swiss, slightly higher estimates were obtained (0.06) for the interval from parturition to conception (Tiezzi et al., 2011). These low heritabilities hinder the speed of genetic progress from selection for reproductive traits such as daughter pregnancy rate (DPR; calculated from days open) and result in thousands of daughters needed to achieve high reliabilities for bull PTAs. However, considerable genetic variation for fertility measures exists and substantiates the opportunity for genetic selection to improve cow fertility (Philippson, 1981). In addition, use of genomic technology has allowed for accurate evaluations of DPR for bulls without daughters (VanRaden et al., 2009).

Genetic correlations between select linear type traits and days open in Czech Holstein cattle were reported for first lactation and second lactation animals (Zink et al., 2011). For first lactation cows, the largest relationships were observed between days open and body condition score, angularity, and rear leg set (-0.46, 0.33, and 0.27). This suggests that less fertile cows tended to have lower body condition score, and be more angular with more sickled rear legs. For second lactation cows, correlations with days open and the three body size traits (stature, chest width, and body depth) were moderately unfavorable (0.25, 0.21, and 0.37) despite being largely unrelated for first lactation animals. These results favor a smaller framed animal for improved fertility. Results for body condition score and rear leg set were comparable for second and first lactation cows, but foot angle was more related for second lactation cows than for first lactation cows (0.22 versus 0.06). The results for genetic correlation between days open and body condition score and dairy form (similar to angularity) were confirmed by Dechow et al. in 2004, which estimated values as -0.30 and 0.48, respectively.

Longevity

Involuntary culling of dairy cows for reasons such as poor health and infertility affects the profitability of the farm. Culling cows before they reach their peak production potential in their third-fourth lactation represents a lost opportunity of high yielding animals, and also results in higher replacement costs. Correlations between milk yield and length of herd life can be deceiving depending on if the culling being measured is voluntary (due to low milk production) or involuntary (indicative of poor fitness). Positive correlations are observed between yield and herd life when the measure of herd life evaluates voluntary culling, as cows that produce more milk are favored by producers (Rogers et al., 1989). However, a negative correlation is often observed between yield traits and herd life when involuntary culling is evaluated. This suggests that cows that produce more milk are more likely to experience poor health and/or infertility (Bertrand et al., 1985). Selection for linear type traits correlated with herd life could potentially be a method of controlling an increase in involuntary culling (Rogers et al., 1989), especially due to the low heritability of most measure of productive life (0.01 to 0.10; Short and Lawlor, 1992.)

Holstein data has estimated correlations between milk yield and with measures of longevity estimated for both registered and grade cows (Short and Lawlor, 1992). Measures of longevity were presence or absence at second calving, 54, and 84 months of age, true herd life (months from first calving to date of last DHI test), and functional herd life (true herd life adjusted for first lactation milk yield). True herd life is supposed to measure effects of both voluntary and involuntary culling, while the adjusted functional herd life removes the effect of voluntary culling for low milk yield. In a combined analysis of both grade and registered cows, milk yield was moderately correlated with longevity (0.28 to 0.51) for all measures except functional herd life (0.08). This is different than correlations reported by Dematawewa and Berger (1998), where there was an adverse relationship between survival (whether a cow was

alive or dead at the end of a 305 day lactation) and adjusted 305 day milk, fat, and protein yield. When evaluated across parities, correlations with survival were -0.14, -0.32, and -0.20 for milk, fat, and protein yield respectively.

Estimated genetic correlations were reported between linear type traits and several measures of longevity, including survival to 48, 54, and 84 months of age as well as age at last record for U.S. Holsteins (Rogers et al., 1989). Body traits relative to the size of cows (stature, strength, body depth, and rump width) were all negatively correlated to survival, with body depth being most unfavorable (-0.15 to -0.36). Genetic correlations between feet and legs traits were either slightly positive or inconsistent across measures of survival, and correlations for most udder traits were also low. Udder support and teats rear view had highest correlations with survival to 48 months (0.21 and 0.20 respectively) and udder depth had the highest correlation with survival to 84 months (0.14). When adjusted for milk yield, body traits were still negatively correlated with survival, but to a lesser extent. Body depth remained the most unfavorable trait (-0.08 to -0.23). Rear leg side view remained largely unrelated, but the correlation between foot angle and survival became stronger later in the cow's life (0.22 for survival to 84 months). Genetic correlations between all measures of survival and udder traits also were stronger when adjusted for yield, with udder support and teats rear view remaining highest with survival to 48 months (0.28 and 0.29 respectively) and udder depth becoming more important with increasing age (0.27 with survival to 84 months). When correlations were measured with survival adjusted for both yield and culling in the first lactation, the unfavorable relationship with body size and survival was largely reduced. The most genetically related traits to survival to 84 months of age were udder depth (0.24), foot angle (0.20), teats rear view (0.19), and rump angle (-0.17) favoring cows with shallower udders, steeper foot angles, closer rear teats, and pins higher than hips. Despite the hypothesis, it was concluded that most type traits have little value in reducing involuntary culling rates (Rogers et al., 1989).

As evaluated by Short and Lawlor (1992), most of the type traits had positive correlations with all measures of longevity. Some of the body traits (stature, strength, and body depth) had slight negative correlations with longevity, though less negative than previously reported (Rogers et al., 1989). Udder traits were more favorably correlated to longevity than reported (Rogers et al., 1989) with the strongest correlation being between functional herd life and udder depth (0.44). In general, the two traits most highly related to all measures of longevity were dairy form (0.23 to 0.46) and final classification score (0.30 to 0.41). When correlations were estimated separately for grade cows and registered cows, the values were slightly different. For registered cows, body size traits were less unfavorably correlated to survival, and some positive with some measures (0.25 between stature and survival to second lactation) while for grade cows, the traits were moderately negative with survival. In addition, dairy form was more highly correlated with survival in registered (0.27 to 0.45) versus grade cows (0.06 to 0.37) as was final classification score (0.38 to 0.54 for registered versus 0.07 to 0.19 for grade cows). Correlations between survival and udder traits were also generally lower for grade cows. These differences suggest that the driving factors for culling decisions vary between registered and grade herds.

As with Holsteins, the relationship between yield and longevity also varies in Brown Swiss dairy cows. In an evaluation of Brown Swiss using data from Switzerland (Vukašinović et al., 1995), measures of longevity were similar to those used for Holsteins (Short and Lawlor, 1992), where true productive life was number of months a cow remained in the herd from first calving to last milk test, and functional productive life was true productive life adjusted for the effect of first lactation milk yield. Each were evaluated at 48, 66, and 84 months of age and were all highly genetically correlated to one another (0.72 to 0.99). Lower heritabilities were estimated for functional productive life (0.03 to 0.05) than for true productive life (0.12 to 0.14). Genetic correlations of true productive life with milk (0.81 to 0.86), fat (0.70 to 0.72), and protein yield (0.73 to 0.75) were positive and high, but were reduced by more than half between yield and

functional productive life. Longevity adjusted for milk yield was also used in an evaluation of Brown Swiss cattle in Italy, termed functional longevity, with a heritability of 0.06. Contrary to the study of cows in Switzerland however, yield was unfavorably correlated (-0.09 to -0.13) with functional longevity in Italian Brown Swiss (Samoré et al., 2010).

In the Swiss evaluation, genetic correlations between type traits and measures of longevity were almost all positive, besides muscularity which was slightly to moderately negative amongst all six measures (-0.02 to -0.20). Body measurement traits (wither height and heart girth) were slightly positive or near-zero with true productive life, and slightly negative or near-zero with functional productive life. Feet and legs were slightly to moderately correlated with both true and functional productive life (0.10 to 0.43) but less so than udders (0.40 to 0.66). Teat traits were more highly correlated with functional productive life (0.56 to 0.72) than with true productive life (0.29 to 0.56) (Vukašinović et al., 1995). Genetic correlations between functional longevity and type traits using Italian data were much more variable. The most related traits were rear leg set, udder depth, and stature with correlations of -0.56, 0.42, and -0.22, respectively. Cows that had less sickled rear legs, shallower udders, and shorter stature were genetically less susceptible to involuntary culling. The other body size traits (strength and body depth) as well as angularity were slightly to moderately unfavorable with longevity. The relationship between the other udder traits and functional longevity were near-zero (Samoré et al., 2010).

Summary/ Logic for Research

Genetic parameters have been often evaluated for Holstein dairy cattle in the United States. However, this is not the case for Brown Swiss, where most of the data is either from several decades ago or from populations in Italy or Switzerland. The objective of the following research was to update genetic parameters for U.S. Brown Swiss, and evaluate the heritabilities and correlations amongst yield, fitness, and type traits. In addition to this main genetic evaluation,

the potential to use data envelopment analysis (DEA) was also investigated in order to characterize the efficiency of the udders of Brown Swiss cows. While DEA has been used to measure efficiency of whole farm systems, it has not previously been used in genetic evaluation.

Chapter 2

Relationships between yield, fitness, and type traits in U.S. Brown Swiss cattle

Abstract

Genetic parameters have been well estimated for the U.S. Holstein population; however, this is not the case for Brown Swiss. The objective of this research was to evaluate heritabilities and correlations among yield, fitness, and type traits for Brown Swiss cattle born in 2000 and later. The data set used consisted of 108,633 first through fifth lactation records from 45,464 cows for yield, somatic cell score (SCS), days open, and productive life. Approximately half of the records had observations for 17 type traits and 41,074 had observations for milking speed. These data were analyzed using a series of three trait models in ASREML with fixed effects for lactation, age, and herd-calving cluster, and random effects for animal, permanent environment, and residual. The heritabilities of milk, fat, and protein were 0.30, 0.20, and 0.20, respectively. The heritabilities of productive life, days open, SCS, and milking speed were 0.11, 0.03, 0.12, and 0.26, respectively. Milk, fat, and protein yield had strong positive correlations with productive life (0.67 to 0.71), days open and SCS had strong negative correlations with productive life (-0.69 and -0.60, respectively), and milking speed had a moderate positive correlation with productive life (0.26). All three yield traits were slightly unfavorably correlated with days open, but there was no relationship found between yield traits and SCS or milking speed. For udder traits, yield traits were positively correlated with rear udder height and rear udder width, ranging from 0.19 to 0.48, and negatively correlated with udder depth and fore udder attachment, ranging from -0.04 to -0.40. However, udder depth and fore udder attachment were more favorably correlated with SCS (-0.26 and -0.14, respectively) than rear udder height and rear udder width (-0.02 and 0.18,

respectively). Productive life was most strongly correlated with fore udder attachment, rear udder width, udder depth, and rear udder height (0.44, 0.40, 0.35, and 0.33, respectively). These updated genetic parameters will allow for improved genetic selection in the Brown Swiss breed.

Introduction

In dairy cattle breeding, high yields of milk have been of primary concern for selection because the sale of milk and milk solids account for approximately 85 percent of the income on a dairy farm. In addition to being selected for milk production, physical confirmation of cows has also been a consideration. For Holsteins, the recording of type traits (classification) began in 1929 (Short and Lawlor, 1992) and continues today. One of the rationales for collecting type data is to aid producers in selecting for cows that will remain functional and avoid early culling (Misztal et al., 1992). In more recent years, traits affecting the fitness of dairy cows have also been established as economically important (Boettcher et al., 1998). In 1994, productive life and somatic cell score traits were added to USDA's net merit index in order to improve longevity and mastitis resistance, and in 2003 daughter pregnancy rate was added to improve fertility (VanRaden, 2004).

Unfortunately, most of the fitness traits in dairy cattle are unfavorably correlated with yield; therefore the heavy emphasis on production traits has led to a decline in fertility and an increase in susceptibility to disease. Mastitis has been reported to be the most costly disease affecting dairy cattle (Shook and Schutz, 1994) and in North Carolina herds, correlated response to increased milk yield resulted in an estimated increase of 1.1 days open per year from 1980 to 1993 (Abdallah and McDaniel, 2000). In addition, higher yields of milk, fat, and protein result in more involuntary culling due to compromised health and fertility (Bertrand et al., 1985). In order to best select for profitable animals, it is important to understand the genetic parameters and relationships between yield traits, fitness traits, and type traits of dairy cattle.

While these parameters and relationships have been well documented for Holstein cattle in the United States, such is not the case for Brown Swiss cattle. Holsteins make up approximately 85% of the U.S. dairy herd while Brown Swiss represent less than one percent. However, Brown Swiss cattle offer benefits from a cheese-making standpoint, and were reported to yield 5% more cheese despite producing 9% less milk on a per day basis (De Marchi et al., 2008). This is an attractive characteristics in a changing dairy market, where in the United States cheese production has doubled over the past 25 years (Johnson and Lucy, 2006). Additionally, Brown Swiss offer some advantages for longevity in certain regions of the U.S. as compared to Holsteins and Jerseys (Garcia-Peniche et al., 2006). The objectives of this study were to estimate heritabilities and correlations amongst yield, fitness, and type traits using a population of Brown Swiss cows in the United States in order to update genetic parameters and facilitate progress for the breed.

Materials and Methods

Data

Data were from first through fifth lactation Brown Swiss cows in the United States born in 2000 or later from herds involved in Dairy Herd Information testing. There were 108,633 records from 45,464 cows in 386 herds and 8,420 herd calving clusters. Herd calving clusters were comprised of cows that calved in the same herd in the same time period and were generated with the FASTCLUS procedure of SAS (v9.4 Cary, NC). Records were only kept from cows having a record for first lactation to avoid selection bias. In total, 105,991 of the records had values for milk, fat, and protein yield which were adjusted to 305-day mature equivalents, and 104,909 records had a lactation average somatic cell score value. There were 83,343 records that had a value for days open. The 2,642 records missing yield data were from cows that calved but

that died or were culled early in lactation and before they had a 305-d yield. These records were still considered for productive life evaluations. Days open less than 25 were recoded as missing and days open greater than 250 were set to 250 consistent with national genetic evaluations (VanRaden et al., 2002). Productive life was available for 31,489 cows and was expressed as months in milk with the diminishing credits procedure as described by VanRaden et al. (2006). Data for these traits was provided by the Council on Dairy Cattle Breeding. In addition, producer assigned milking speed scores and classification scores were provided by the Brown Swiss Cattle Breeders' Association of the USA. There were 41,074 milking speed records on a scale of 1 (slow milking) to 8 (fast milking) and approximately 52,250 records for 16 linear type traits scored on a scale of 1 to 50, and final classification score on a scale of 60 to 94. There were also 35,442 mobility records scored on a scale of 50 to 99. Number of records, means, and standard deviations for each trait are summarized in Table 2-1. The final data set included 45,464 first lactation, 29,998 second lactation, 18,327 third lactation, 10,111 fourth lactation, and 4,733 fifth lactation records. The pedigree file included 127,401 animals including 5,728 bulls with daughters that had records.

Statistical Model

These data were analyzed using a series of three trait models in ASREML (Gilmour et al., 2006). The model for the analyses was:

$$y_i = \mu + L_j + Age_k + HCC_l + A_m + PE_n + \varepsilon_{ijklmn}$$

where y_i = the record for trait i , fixed effects where lactation (L ; $j=1$ to 5), age (Age , $k= 1$ to 94), and herd calving cluster (HCC ; $l=1$ to 8,420). Random effects were animal (A ; $m= 127,401$), permanent environment (PE ; $n= 45,464$), and residual (ε). PE was not included for productive life.

Following these initial evaluations, genetic correlations among some traits (dairy form and days open) varied significantly (0.36-0.67) depending on the third trait in the model. Therefore, an 11-trait model (milk yield, fat yield, protein yield, somatic cell score, stature, udder depth, dairy form, days open, milking speed, mobility, and productive life) was evaluated using DMU (Madsen and Jensen, 2013) using the same effects as described above. The purpose of this 11-trait model was to estimate genetic correlations amongst key traits simultaneously and clarify ambiguous results from the 3-trait analyses. Every 33rd sample was kept from 40,000 rounds following a 1,625 round burn-in period.

Results

Heritabilities of yield traits (milk yield, fat yield, and protein yield) and fitness traits (somatic cell score, milking speed, days open, and productive life) and correlations amongst them are shown in Table 2-2 from the 3-trait models. When multiple estimates of the same heritability or correlation were generated, the estimates were averaged across analyses. The heritability estimates of milk, fat, and protein yield were 0.30, 0.20, and 0.20, respectively. Heritability estimates of somatic cell score, milking speed, days open, and productive life were 0.12, 0.26, 0.03, and 0.11, respectively. Genetic correlations between yield traits were strong and positive, ranging from 0.75 between milk and fat yield to 0.90 between milk and protein yield. Genetic correlations between fitness traits were small for somatic cell score and milking speed (-0.10), somatic cell score and days open (0.13), and milking speed and days open (0.19). Milking speed was moderately related to productive life (0.26), indicating a relationship between faster milking cows and those that stayed in the herd longer. Genetic correlations between productive life and days open and somatic cell score were strong and negative (-0.60 and -0.69, respectively) favoring cows with fewer days open and lower somatic cell score. Genetic correlations between yield traits and somatic cell score and milking speed were near-zero. They were slightly positive

with days open (0.15, 0.18, and 0.11 with milk, fat, and protein yield, respectively) suggesting that higher yield resulted in more days open. Relationships between yield and productive life were positive and strong, ranging from 0.63 with fat yield and 0.71 with protein yield.

Parameters for yield traits and linear body traits (stature, strength, body depth, rump angle, rump width, and dairy form) are shown in Table 2-3. Heritabilities of linear traits were small to moderate, ranging from 0.15 for both strength and rump width to 0.42 for stature. Genetic correlations between traits referring to frame size (stature, strength, body depth, rump width) were positive and moderate to strong, ranging from 0.31 between stature and strength to 0.69 between strength and body depth. Dairy form was positively related to stature and body depth (0.45 and 0.31) with taller, deeper cows being more angular, but negatively related to strength (-0.30), and unrelated to rump angle and rump width. Correlations between yield traits and dairy form were moderately positive (0.40, 0.35, and 0.31 for milk, fat, and protein yield, respectively). Correlations between yield and body depth and stature were slightly positive ranging from 0.11 between milk yield and stature to 0.26 between fat yield and body depth. Strength, rump angle, and rump width were mostly unrelated to yield, with genetic correlations ranging from -0.04 between fat yield and rump angle to 0.14 between fat yield and rump width.

Table 2-4 summarizes relationships between yield traits and linear feet and leg traits (foot angle, rear leg side view (RLS), rear leg rear view (RLR), and mobility). Heritability estimates for feet and leg traits were small, ranging from 0.04 for RLR to 0.14 for RLS. Genetic correlations of RLS with RLR and foot angle were negative (-0.25 and -0.48, respectively) indicating that cows with more sickled hocks also had less straight rear legs when viewed from the rear and lower foot angles. Genetic correlation between RLS and mobility was near-zero. There was a moderate genetic correlation between foot angle and RLR of 0.51. Foot angle and RLR were much more related to mobility than was RLS with genetic correlations of 0.44 and 0.69. Foot angle and RLS were largely unrelated to milk, fat, and protein yield. Genetic

correlations between yield traits and RLR and mobility were slightly positive, ranging from 0.17 between fat yield and RLR to 0.28 between protein yield and RLR, favoring those cows with straighter legs when viewed from the rear and higher mobility scores.

Heritabilities and correlations for yield traits with linear udder traits (udder depth, fore udder attachment, rear udder height, rear udder width, udder cleft, teat placement, and teat length) are shown in Table 2-5. Heritability estimates for udder traits were larger than observed for feet and leg traits, and ranged from 0.15 for rear udder width to 0.35 for teat length. Nearly all genetic correlations amongst udder traits were positive, ranging from 0.11 between rear udder height and teat placement to 0.76 between udder depth and fore udder attachment. In addition, correlations between teat length and the six other udder traits were all negative, ranging from near-zero (-0.02 between teat length and rear udder height) to moderate (-0.40 between teat length and teat placement). This indicates that as other udder traits became more desirable, teats became shorter.

The udder trait most unfavorably correlated to yield was udder depth, with correlations with milk, fat, and protein yield being -0.40, -0.24, and -0.37, respectively. In addition, fore udder attachment was negatively correlated, though to a lesser extent than udder depth, with estimates ranging from -0.04 with fat yield to -0.21 with milk yield. These relationships indicate that shallower, more tightly-attached udders held less milk. Rear udder height and rear udder width had moderately positive correlations with yield, ranging from 0.19 between protein yield and rear udder height to 0.48 between milk yield and rear udder width.

Next, relationships between fitness traits (somatic cell score, milking speed, days open, and productive life) and each category of linear traits (body, feet and legs, and udder) were examined. Table 2-6 shows parameters for fitness traits with linear body traits. Genetic correlations between somatic cell score and stature, strength, and rump angle were near-zero. Correlations were small between somatic cell score and rump width (0.11), body depth (0.13) and dairy form (0.17). Relationships between milking speed and linear body traits were near-zero to

small, ranging from -0.09 with rump angle to 0.10 with dairy form. Days open was more genetically related to body traits, particularly rump width (0.18), stature (0.27), and body depth (0.43). Dairy form was also unfavorably correlated to days open, with estimates ranging from 0.36 to 0.67 (depending on what third trait was included in the model) indicating that more angular cows were genetically susceptible to poor fertility. Correlations with productive life were near-zero for stature, strength, rump angle, and rump width, and were small for body depth (-0.11) and dairy form (0.12).

Table 2-7 summarizes the relationships between fitness traits and linear feet and leg traits. Days open was not correlated with RLS, but was unfavorably correlated with foot angle (0.10), mobility (0.24), and RLR (0.29). Genetic correlations of productive life with foot angle, RLR, and mobility were positive (0.11, 0.31, 0.50, respectively) and the genetic correlation between productive life and RLS was slightly negative (-0.14).

Table 2-8 contains genetic correlations amongst fitness traits and linear udder traits. Relationships between somatic cell score and rear udder height and teat length were near-zero, but favorable for teat placement, fore udder attachment, udder cleft, and udder depth (-0.11, -0.14, -0.25, and -0.26, respectively). Rear udder width was unfavorably correlated with somatic cell score (0.18). Genetic correlations between milking speed and udder traits ranged from -0.35 with teat length to 0.37 with udder depth, and were positive for the other five traits. Therefore, udders with shorter teats and more desirable attachments generally milked out more quickly. Correlations of days open with fore udder attachment, teat placement, and teat length were near-zero. Udder depth had a slightly favorable relationship with days open (-0.19) with cows having shallower udders also having fewer days open. Genetic correlations between days open and the remaining udder traits were unfavorable, and ranged from 0.20 with udder cleft to 0.55 with rear udder width. With the exception of teat length, the other six udder traits were significantly related

the productive life. Fore udder attachment had the strongest genetic correlation with productive life of 0.44, followed by rear udder width (0.40), udder depth (0.35), and rear udder height (0.33). Genetic correlations between productive life and udder cleft and between productive life and teat placement were 0.31 and 0.22, respectively. All of these relationships were favorable, with a more desirable linear score for a more strongly attached, capacious udder corresponding to a longer productive life.

Relationships between linear traits in each of the categories were also estimated. In Table 2-9, correlations are shown between linear body traits and linear feet and leg traits. Foot angle was correlated with stature (0.31), strength (0.24), and rump width (0.28) with taller, stronger, wider-rumped cows having a steeper foot angle. Genetic correlation between foot angle and dairy form was negative, though small (-0.15). For RLS, genetic correlations were near-zero for stature, body depth, rump angle, and rump width, positive for dairy form (0.25), and negative with strength (-0.13). Cows with more sickled rear legs therefore tended to be more angular and narrower. For RLR, correlations were favorable with strength (0.22), rump width (0.20) and stature (0.11). Of the feet and leg traits, mobility was most correlated with body traits, particularly dairy form (0.38), stature (0.34), rump width (0.26), and body depth (0.20), with more angular, taller, wider, and deeper cows having higher mobility scores.

In Table 2-10, correlations are shown between linear udder traits and linear body traits. Genetic correlations between stature and udder traits were marginally favorable, with the strongest relationships being with rear udder height, udder depth, and rear udder width (0.21, 0.18, and 0.14, respectively). Strength was most related to fore udder attachment (0.33), rear udder width (0.30), teat placement (0.17), and udder cleft (0.15). Body depth was unfavorable correlated with udder depth (-0.29) with deeper bodied cows also having deeper udders. However, genetic correlations between body depth and rear udder width and udder cleft were positive (0.35 and 0.17). Genetic correlations between rump angle and udder traits were all near-

zero or unfavorable. The largest correlations were with fore udder attachment (-0.26) and udder depth (-0.18), with cows having more sloped rumps having deeper, more loosely attached udders. Rump width was favorably correlated with udder traits, with the largest genetic correlations being observed with rear udder width (0.35), udder cleft (0.23), and fore udder attachment (0.21). Relationships amongst dairy form and udder traits were variable. The largest negative correlations were with udder depth and fore udder attachment (-0.28 and -0.19) and the largest positive correlations were with rear udder height and rear udder width (0.42 and 0.37). More angular cows tended to have more capacious rear udders; however, their mammary systems were deeper and more loosely attached.

In Table 2-11, correlations are shown between linear udder traits and linear feet and leg traits. Generally, genetic correlations were near-zero or small. Foot angle was favorably correlated with udder depth and fore udder attachment (0.35 and 0.30). Genetic correlations between udder traits and RLS were mostly negative and unfavorable with the strongest correlations seen with udder depth (-0.16) and fore udder attachment (-0.19). RLR was favorably correlated with udder traits, ranging from 0.13 with teat placement to 0.29 with rear udder width, with the exception of teat length which was near-zero. Of the feet and leg traits, mobility was most highly correlated with udder traits. Genetic correlations between mobility and rear udder height and rear udder width were moderate (0.57 and 0.47). The other udder traits (with the exception of teat length) were also favorably correlated, with genetic correlations between mobility and udder cleft, fore udder attachment, teat placement, and udder depth being 0.34, 0.33, 0.32 and 0.26, respectively.

Table 2-12 reports heritability, genetic, and phenotypic correlations from the 11-trait model. Heritability estimates for most traits were very similar to previously reported values using 3-trait models. However, estimates for fat yield and protein yield were slightly higher (0.26 and 0.29). Somatic cell score also had a slightly higher heritability estimate of 0.16. The most striking

difference was for productive life, in which the heritability estimate was 0.39, which was drastically different than the estimate of 0.11 (Table 2-2).

Most of the genetic correlations amongst these 11 traits were also consistent with previous values. One notable difference was between yield and somatic cell score, which was previously near-zero. Using the 11-trait model, genetic correlations between somatic cell score and milk, fat, and protein yields were -0.28, -0.33, and -0.32, respectively, suggesting lower somatic cell score with increased yield. Genetic correlations were also negative between milk, fat, and protein yield and days open (-0.09, -0.05, -0.14, respectively). Other observed differences were an increased favorable relationship between mobility and somatic cell score (-0.30) and a near-zero correlation between mobility and days open. Udder depth was also less related to productive life (0.23). The genetic correlation between days open and dairy form fell within the previously reported range at 0.43.

Genetic and phenotypic correlations were also estimated amongst final classification score and yield traits, fitness traits and select linear type traits, and are shown in Table 2-13. Heritability of final score was estimated to be 0.27. Genetic correlations with yield were favorable, ranging from 0.16 to 0.39. Final score and somatic cell score were genetically unrelated, and the correlation with milking speed was favorable (0.39). The genetic correlation between final score and days open was moderate and unfavorable (0.45) but correlation with productive life was moderate and favorable (0.57). Select type traits analyzed with final score were stature, dairy form, rear udder height, rear udder width, and mobility. Genetic correlations were estimated to be 0.48, 0.42, 0.67, 0.62, and 0.81, respectively.

Discussion

Heritabilities

Heritability estimates for yield traits in Brown Swiss were slightly higher than what is sometimes reported for Holsteins (Schutz et al., 1990), as reflected in national genetic evaluations where milk, fat, and protein yield heritabilities are estimated to be 0.23 for Brown Swiss versus 0.20 for Holsteins (<http://aipl.arsusda.gov/reference/nmcalc-2014.htm>). The heritability estimate for milk yield in the current study was consistent with the estimate reported by Santus et al. (1993) for Brown Swiss cows in Italy. Heritabilities for fat yield and protein yield using the ASREML three trait models were not as high as reported by Santus et al. (1993) and were more similar to those reported by Samoré et al. (2010). However, fat and protein yield heritability estimates were higher in the 11-trait model, consistent with Santus et al. (1993).

Of the fitness traits, somatic cell score had an estimated heritability that was comparable to 0.15 as typically reported for Holsteins (Boettcher et al., 1998; Rogers et al., 1991; Rupp and Boichard, 1999; Samoré and Groen, 2006) and 0.14 as reported for Italian Brown Swiss (Samoré et al., 2010). The estimated heritability for producer assigned milking speed in the current study of 0.26 was very similar to the estimate of 0.22 reported by Wiggans et al. (2006) using the same scale for U.S. Brown Swiss, though not as high as for average milk flow in Italian Brown Swiss (0.33). Results from the current study confirm that milking speed seems to be slightly more heritable in Brown Swiss as compared to Holsteins, where milking speed measures have ranged in heritability from 0.15 (Boettcher et al., 1998) to 0.21 (Meyer and Burnside, 1987). The heritability of days open was low, which was consistent with estimates <0.05 in Holsteins (Dechow et al., 2004; Dematawewa and Berger, 1998) and 0.06 in Italian Brown Swiss (Tiezzi et al., 2011), suggesting that fertility is no more heritable in Brown Swiss than in Holsteins. Heritability estimate for productive life in the current study was also low (0.11) and similar to

previous literature using the diminishing credit measure of productive life (VanRaden et al., 2006) and unadjusted measures of herd life in Holsteins in the United States (Short and Lawlor, 1990), and unadjusted herd life in Brown Swiss in Switzerland (Vukašinović et al., 1995).

For linear type traits, heritability estimates in the current study tended to be slightly lower than previously reported estimates for Holsteins (Misztal et al., 1992; Short and Lawlor, 1992; VanRaden et al., 1990) and Brown Swiss (Samoré et al., 2010) with the exception of stature, in which the estimate was consistent with previous reports and was the most heritable type trait across all studies. Dairy form was the trait with the next highest heritability in the current study, which was generally the trend in previous work (Foster et al., 1989; Misztal et al., 1992; Short and Lawlor, 1992; VanRaden et al., 1990). Body depth tended to be relatively heritable in comparison to other body traits in previous studies with estimates ranging from 0.25 (Samoré et al., 2010) to 0.35 (Misztal et al., 1992), however the heritability was smaller in the current study. Strength, rump angle, and rump width tended to be the least heritable body traits in current and previous work, and current heritability estimates were consistent with findings from Samoré et al. (2010).

Heritability estimates for feet and leg traits were small overall. For the older Holstein data (Misztal et al., 1992; Short and Lawlor, 1992; VanRaden et al., 1990) estimates were not available for RLR or mobility, but foot angle and RLS heritability estimates were comparable to the current study. This was also the case for Italian Brown Swiss (Samoré et al., 2010). For U.S. Brown Swiss, heritability estimates for foot angle and RLS from work by Wiggans et al. (2006) were consistent with the current study, but estimate for RLR was higher than the current estimate of 0.04. Heritability estimates for all feet and leg traits in the current study were also evaluated by Wright et al. (2013) for U.S. Brown Swiss. Foot angle, RLS, and RLR estimates were nearly identical, however mobility estimate in the current study was much lower than reported by Wright et al. (2013).

For linear udder traits, heritability estimates in the current study were consistent with estimates for Holsteins (Boettcher et al., 1998; Misztal et al., 1992; Rupp and Boichard, 1999; Short and Lawlor; 1992; VanRaden et al., 1990) and Brown Swiss (Samoré et al., 2010). Estimates across Holsteins and Brown Swiss studies are similar suggesting there are not differences between the two breeds.

Correlations

Genetic correlations amongst yield traits in the current study were slightly higher than what has been reported for Holsteins (deJager and Kennedy, 1987; Dematawewa and Berger, 1998) and consistent with those reported for Italian Brown Swiss by Samoré et al. (2010). For correlations amongst fitness traits, the relationship between somatic cell score and milking speed in the current study was notably different from most previous literature (Boettcher et al., 1998; Rupp and Boichard; 1999; Samoré et al., 2010; Zwald et al., 2009) which found an unfavorable relationship between milking speed and somatic cell score in Holsteins and in Italian Brown Swiss. However, Wiggans et al. (2006) also found a favorable correlation between milking speed and somatic cell score in U.S. Brown Swiss. Possible explanations are that slower milking cows were not milked out completely, thus raising somatic cell score, or that a breed difference exists between Holsteins and Brown Swiss. Correlation between somatic cell score and days open was unfavorable, indicating that cows with compromised udder health were open for longer periods of time, as seen in Holsteins (Miller et al., 2001). Additionally, the strong negative correlation between somatic cell score and productive life suggests that cows with lower resistance to mastitis leave the herd more quickly. The favorable correlation between milking speed and productive life indicates that faster milking cows are either able to more easily avoid involuntary culling or are favored by producers. Lastly, the strong negative correlation between days open and productive life also suggests that less fertile cows leave the herd more quickly.

Genetic correlations between yield traits and somatic cell score were different in the current study than some other literature, which reported that increased yield results in an elevated somatic cell score (Rupp and Boichard, 1999; Samoré et al., 2010). This relationship was even more different when evaluated with the 11-trait model, where correlations between milk, fat, and protein yield and somatic cell score were near -0.30. The near-zero correlations between yield traits and milking speed were consistent with those reported in Zwald et al. (2005). The unfavorable relationship between yield and fertility was less antagonistic in the current study than reported for Holsteins (Dechow et al., 2004; Dematawewa and Berger, 1998) and Italian Brown Swiss (Tiezzi et al., 2011). Once again, the difference was even more notable when evaluating results from the 11-trait model, where the relationship between yield and fertility was shown to be near-zero for milk and fat yield, and slightly favorable for protein yield. Because of the magnitude of this difference from other published data, the relationship should be interpreted with caution. Genetic correlations between yield and productive life were consistent with findings for Brown Swiss in Switzerland (Vukašinović et al., 1995) when herd life was unadjusted for yield, indicating that cows with higher yield were able to avoid voluntary culling.

The genetic correlations between yield traits and linear body traits were positive but generally small and consistent with previous findings (Misztal et al., 1992; Samoré et al., 2010; Short and Lawlor, 1992). Of traits describing body size (stature, strength, body depth, and rump width), body depth was most related to yield. Dairy form was moderately correlated to yield in all studies, with more angular cows yielding more milk, fat, and protein. Relationships between body traits and somatic cell score in the current study were very similar to those reported in Samoré et al. (2010) for Italian Brown Swiss. Genetic correlations were near-zero between somatic cell score and stature, strength, and rump angle and were small with rump width and body depth. The most related trait to somatic cell score was dairy form, suggesting that sharper cows were more likely to have compromised udder health. In the current study, milking speed was generally

unrelated to linear body traits, with all genetic correlations being less than 0.10, despite correlations between PTAs for milking speed and type traits ranging from 0.21 with rump width to -0.31 with strength for U.S. Brown Swiss in Wiggans et al. (2007). Of the fitness traits, days open was the most related to body traits, with most correlations being unfavorable. The antagonistic relationship between dairy form and fertility has been well documented, and was found to be most unfavorable with days open in current and previous work (Dechow et al., 2004; Zink et al., 2011) with more angular cows being less fertile. In addition, in the current study and in Zink et al. (2011), larger-framed cows were also found to have increased days open. In the current study, genetic correlations between productive life and body traits were generally near-zero, with the exception of dairy form which was slightly positive, likely due to its positive relationship with yield. This was in agreement with genetic correlations reported by Short and Lawlor (1992) for Holsteins. Relationships between body traits and longevity have been variable in other previous literature, depending on the measure of longevity used, though it generally seems that linear body traits have little effect on productive life.

Linear feet and leg traits tend to be mostly unrelated to yield traits, particularly foot angle and RLS. In the current study, genetic correlations were near-zero between milk, fat, and protein yield and foot angle and RLS consistent with Samoré et al. (2010) and Short and Lawlor (1992). RLR was not evaluated in the aforementioned studies, though it was favorable with yield in the current study. Mobility was also favorable with milk, fat, and protein yield, though to a lesser degree than correlations between mobility and yield PTAs as estimated by Wright et al. (2013). Somatic cell score was unrelated to RLS and RLR, but slightly favorable with foot angle, confirmed by Samoré et al. (2010). Genetic correlation was also favorable between somatic cell score and mobility, in agreement with Wright et al. (2013). Cows with steeper foot angles and higher mobility scores were likely more comfortable on their feet and legs and healthier overall, allowing them to maintain healthier udders. In the current study, genetic correlations were

favorable and stronger between milking speed and foot angle and RLR than suggested by correlations between PTAs in Wiggans et al. (2007) for U.S. Brown Swiss. Results were inconsistent with Samoré et al. (2010) for Italian Brown Swiss, in which RLS was favorable with average milk flow and heel depth (similar to foot angle) was unfavorable. The unfavorable genetic correlation between mobility and days open is in agreement with results for U.S. Brown Swiss in Wright et al. (2013), where there was a negative genetic correlations between PTA for mobility score and PTA for daughter pregnancy rate (transformed from days open so that higher number is more desirable). Despite its unfavorable relationship with fertility, mobility was positively associated with productive life in the current study and in Wright et al. (2013), suggesting that cows with improved locomotion avoided voluntary culling.

Of the linear type traits, udder traits were most related to yield traits. In the current study and in previous literature for Holsteins (Misztal et al., 1992; Short and Lawlor, 1992) and Brown Swiss (Samoré et al., 2010), udder depth was most unfavorably correlated with yield. Udders that are shallower have less capacity for milk, fat, and protein. Previous literature using Holstein data also found an unfavorable correlation between yield and fore udder attachment, faulting stronger attachments, which is consistent with findings from the current study. This was contrary to results from other studies using Brown Swiss data (Johnson and Fourt, 1960; Samoré et al., 2010; Van Vleck et al., 1980) which found a favorable correlation between stronger fore udder attachments and higher yield. In previous studies for Holsteins and Brown Swiss (Misztal et al., 1992; Samoré et al., 2010; Short and Lawlor, 1992) and in the current study, rear udder height and rear udder width were most favorably related to yield, with higher, wider rear udder attachments corresponding to more capacious udders that held more milk. Udder cleft had small positive correlations with yield (particularly fat and protein yield) in previous work in Holsteins (Misztal et al., 1992) and in Brown Swiss. Teat placement also was previously found to be favorable with

yield in Brown Swiss (Samoré et al., 2010), however, in the current study, both traits had near-zero correlations with yield, as did teat length.

Of linear type traits, udder traits were also most related to fitness traits. Udder depth was most favorably correlated with somatic cell score in previous work in Holsteins (Boettcher et al., 1998; Rogers et al., 1991; Rupp and Boichard, 1999; Samoré and Groen, 2006) and Brown Swiss (Samoré et al., 2010) and in the current study. In the current study, udder cleft was the second most favorably correlated trait, which was confirmed in Italian Brown Swiss by Samoré et al. (2010), though correlations with udder cleft and somatic cell score were near-zero for Holsteins for Boettcher et al. (1998) and unclear in Rogers et al. (1991). Fore udder attachment and teat placement were also favorable with somatic cell score in the current study, though to a lesser extent than in Rogers et al. (1991). Shallower udders with stronger fore udder attachments, stronger clefts, and closer teat placement are kept closer to the body therefore less prone to injury and udder infection. Rear udder width in the current study had a small positive correlation with somatic cell score, consistent with results from Italian Holsteins (Samoré and Groen, 2006) and Italian Brown Swiss (Samoré et al., 2010), suggesting that cows with wider rear udders tend to have an elevated somatic cell score and udders that are less healthy. Rear udder height and teat length had near-zero correlations, despite teat length being unfavorable in previous studies (Rogers et al., 1991; Samoré et al., 2010) due to longer teats being more susceptible to injury.

For milking speed, the most favorable trait was udder depth, contrary to previous findings (Samoré et al., 2010; Wiggans et al., 2007; Zwald et al., 2005). In Samoré et al. (2010), udder depth was unfavorably correlated with average milk flow, with shallower udders milking out more slowly. Therefore, in the current study, the favorable correlation may be due to shallower udders holding less volume rather than actually milking out more quickly. Other genetic correlations in the current study were in the same direction and of similar magnitude to estimates

of correlations amongst PTAs from Wiggans et al. (2007), though teat placement was more related and rear udder width less related.

For days open, rear udder height and rear udder width were moderately unfavorably correlated, indicating that cows with higher, wider rear udders would be more likely to have more days open. This association could be due to the positive correlation between rear udder traits and yield, despite the fact that yield and days open were less antagonistic in this study than expected. The unfavorable correlation between rear udder width and somatic cell score (which was unfavorable with days open) could also be a contributing factor. Udder cleft was unfavorable with fertility, which was unexpected due to the near-zero correlations with yield and favorable correlation with somatic cell score. While fore udder attachment, teat placement, and teat length were largely unrelated, udder depth was the only udder trait favorably correlated with days open, potentially due to shallower udders yielding less milk, fat, and protein.

With the exception of teat length which had a near-zero correlations with productive life, all other linear udder traits were favorable in the current study. This was in agreement with an evaluation of Brown Swiss in Switzerland (Vukašinović et al., 1995) which found fore udders and rear udders to be highly correlated with unadjusted herd life. Due to genetic correlations amongst fore udders and somatic cell score and rear udders with yield, it is logical that these traits would promote extended herd life. Genetic correlations amongst linear udder traits and longevity were small and more variable in Rogers et al. (1989) and Samoré et al. (2010) potentially due to measures of longevity being adjusted for milk yield.

Results from Misztal et al. (1992), Samoré et al. (2010), and Short and Lawlor (1992), were mostly in agreement with the current study regarding correlations between yield, fitness, and select type traits with final classification score. For U.S. Brown Swiss in the current study, U.S. Holsteins (Misztal et al., 1992) and Italian Brown Swiss (Samoré et al., 2010), final score was favorably correlated with milk, fat, and protein yield. In Short and Lawlor (1992), final score

was also favorable with herd life, consistent with the current study. Across all studies, genetic correlations between final score and stature, dairy form, rear udder height, and rear udder width were strong and positive. This could help explain the positive unfavorable correlation between final score and days open in the current study, as the previous four linear traits were also unfavorable with days open.

Conclusions

Genetic parameters were estimated using a population of Brown Swiss in the United States calving in the year 2000 and later. Yield was found to be moderately heritable and less antagonistic with somatic cell score and fertility compared to previous results for Holsteins. Of linear type traits, rear udder width and rear udder height were most strongly correlated with yield, while most body and feet and leg traits had small or near-zero correlations with yield. Cows with high yield, low somatic cell score, fast milking speed, and few days open were favored and remained in the herd longer. Larger, deeper, more angular cows tended to have compromised fertility, as did cows with higher mobility scores. However, mobility was favorably correlated with productive life. Cows having shallower udders with stronger fore udder attachments and udder clefts were more resistant to mastitis. Likely due to their positive correlations with yield, rear udder height and rear udder width had moderate correlations with productive life. Fore udder attachment and udder depth were also identified as important traits due to their favorable correlations with somatic cell score. The correlations amongst productive life and udder traits provide an analysis of what udder traits promote longevity in the Brown Swiss breed, and were used by the Brown Swiss Cattle Breeders' Association of the USA to develop a new udder composite formula.

Table 2-1. Descriptive statistics of yield, fitness, and type traits¹

	n	Mean	S.D.
MY	105,991	21,780 lbs.	469.9
FY	105,991	879 lbs.	204.9
PY	105,991	724 lbs.	153.7
SCS	104,909	2.76	1.3
MS	41,074	5.8	1.5
DO	83,343	149.9	68.5
PL	31,489	25.7	17.8
STAT	52,263	29.2	7.8
STR	52,262	26.0	7.6
BD	52,262	27.4	7.7
RA	52,259	24.3	7.2
RW	52,248	26.6	7.2
DF	52,257	27.9	8.1
FA	52,249	28.5	7.9
RLS	52,259	24.0	6.4
RLR	44,198	30.2	7.3
MO	35,442	84.1	4.3
UD	52,258	29.3	7.4
FU	52,251	27.5	8.1
RUH	52,246	28.2	7.3
RUW	52,240	28.8	7.7
UC	52,238	26.0	8.2
TP	52,254	25.8	7.5
TL	52,255	24.3	8.3
FS	52,262	84.2	3.3

¹MY= milk yield; FY= fat yield; PY= protein yield; SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life; STAT= stature; STR= strength; BD= body depth; RA= rump angle; RW= rump width; DF= dairy form; FA= foot angle; RLS= rear leg side view; RLR= rear leg rear view; MO= mobility score; UD= udder depth; FU= fore udder attachment; RUH= rear udder height; RUW= rear udder width; UC= udder cleft; TP= teat placement; TL= teat length; FS= final score

Table 2-2. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among yield traits and fitness traits¹

	MY	FY	PY	SCS	MS	DO	PL
MY	0.30	0.75	0.90	0.01	0.04	0.15	0.67
FY	0.75	0.20	0.86	-0.09	0.07	0.18	0.63
PY	0.90	0.84	0.20	-0.02	0.03	0.11	0.71
SCS	-0.21	-0.18	-0.20	0.12	-0.10	0.13	-0.69
MS	0.03	0.03	0.02	-0.05	0.26	0.19	0.26
DO	0.13	0.10	0.12	0.02	0.01	0.03	-0.60
PL	0.25	0.23	0.26	-0.18	0.08	-0.12	0.11

¹ MY= milk yield; FY= fat yield; PY= protein yield; SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life

Standard errors range from 0.0035 to 0.0089 for heritability estimates, range from 0.0111 to 0.0556 for genetic correlations, and range from 0.0013 to 0.0105 for phenotypic correlations.

Table 2-3. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among yield traits and linear body traits¹

	MY	FY	PY	STAT	STR	BD	RA	RW	DF
MY	0.30	0.75	0.90	0.11	0.02	0.17	0.06	0.09	0.40
FY	0.75	0.20	0.86	0.12	0.12	0.26	-0.04	0.14	0.35
PY	0.90	0.84	0.20	0.16	0.11	0.22	0.06	0.13	0.31
STAT	0.06	0.06	0.08	0.42	0.31	0.36	-0.11	0.49	0.45
STR	-0.02	0.02	0.02	0.25	0.15	0.69	-0.12	0.62	-0.30
BD	0.09	0.11	0.11	0.26	0.52	0.19	-0.17	0.46	0.31
RA	0.01	-0.02	0.01	0.09	-0.03	-0.05	0.21	-0.22	-0.05
RW	0.04	0.05	0.05	0.27	0.37	0.32	-0.02	0.15	0.01
DF	0.28	0.22	0.24	0.16	-0.19	0.16	-0.01	0.04	0.19

¹MY= milk yield; FY= fat yield; PY= protein yield; STAT= stature; STR= strength; BD= body depth; RA= rump angle; RW= rump width; DF= dairy form

Standard errors range from 0.0081 to 0.0134 for heritability estimates, range from 0.0351 to 0.0701 for genetic correlations, and range from 0.0050 to 0.0062 for phenotypic correlations

Table 2-4. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among yield traits and linear feet and leg traits¹

	MY	FY	PY	FA	RLS	RLR	MO
MY	0.30	0.75	0.90	-0.01	0.08	0.21	0.27
FY	0.75	0.20	0.86	0.01	0.09	0.17	0.26
PY	0.90	0.84	0.20	0.00	0.02	0.28	0.27
FA	0.00	0.01	0.00	0.09	-0.48	0.51	0.44
RLS	0.00	0.00	-0.02	-0.22	0.14	-0.25	-0.02
RLR	0.05	0.04	0.06	0.12	-0.10	0.04	0.69
MO	0.15	0.13	0.17	0.25	-0.05	0.31	0.11

¹MY= milk yield; FY= fat yield; PY= protein yield; FA= foot angle; RLS= rear leg side view; RLR= rear leg rear view; MO= mobility score

Standard errors range from 0.0081 to 0.0124 for heritability estimates, range from 0.0385 to 0.0809 for genetic correlations, and range from 0.0050 to 0.0088 for phenotypic correlations

Table 2-5. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among yield traits and linear udder traits¹

	MY	FY	PY	UD	FU	RUH	RUW	UC	TP	TL
MY	0.30	0.75	0.90	-0.40	-0.21	0.20	0.48	-0.07	-0.07	0.08
FY	0.75	0.20	0.86	-0.24	-0.04	0.25	0.34	-0.02	0.06	0.00
PY	0.90	0.84	0.20	-0.37	-0.18	0.19	0.37	0.10	-0.03	0.05
UD	-0.18	-0.12	-0.17	0.30	0.76	0.31	-0.16	0.22	0.26	-0.20
FU	-0.03	0.03	-0.01	0.39	0.18	0.45	0.28	0.14	0.38	-0.20
RUH	0.17	0.14	0.16	0.16	0.26	0.20	0.51	0.14	0.11	-0.02
RUW	0.28	0.22	0.26	-0.12	0.00	0.33	0.15	0.27	0.27	-0.03
UC	0.01	0.02	0.03	0.19	0.11	0.13	0.11	0.17	0.30	-0.05
TP	-0.01	0.02	0.00	0.17	0.19	0.06	0.01	0.21	0.23	-0.40
TL	0.04	0.02	0.04	-0.08	-0.04	0.00	0.05	0.03	-0.19	0.35

¹MY= milk yield; FY= fat yield; PY= protein yield; UD= udder depth; FU= fore udder attachment; RUH= rear udder height; RUW= rear udder width; UC= udder cleft; TP= teat placement; TL= teat length

Standard errors range from 0.0081 to 0.0139 for heritability estimates, range from 0.0386 to 0.0593 for genetic correlations, and range from 0.0042 to 0.0062 for phenotypic correlations

Table 2-6. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among fitness traits and linear body traits¹

	SCS	MS	DO	PL	STAT	STR	BD	RA	RW	DF
SCS	0.12	-0.10	0.13	-0.69	0.02	0.06	0.13	0.04	0.11	0.17
MS	-0.05	0.26	0.19	0.26	0.08	-0.01	0.05	-0.09	0.01	0.10
DO	0.02	0.01	0.03	-0.60	0.27	0.03	0.43	-0.11	0.18	0.36 – 0.67
PL	-0.18	0.08	-0.12	0.11	-0.02	-0.01	-0.11	-0.04	0.05	0.12
STAT	0.05	0.02	0.02	-0.02	0.42	0.31	0.36	0.10	0.49	0.45
STR	0.06	-0.04	-0.02	0.01	0.25	0.15	0.69	-0.12	0.62	-0.30
BD	0.05	0.00	0.00	-0.01	0.26	0.52	0.19	-0.17	0.46	0.31
RA	0.02	0.04	-0.01	-0.02	0.09	-0.03	-0.05	0.21	-0.22	-0.05
RW	0.05	0.00	0.01	0.00	0.27	0.37	0.32	-0.02	0.15	0.01
DF	-0.05	0.07	0.08	0.03	0.16	-0.19	0.16	-0.01	0.04	0.19

¹SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life; STAT= stature; STR= strength; BD= body depth; RA= rump angle; RW= rump width; DF= dairy form

Standard errors range from 0.0035 to 0.0134 for heritability estimates, range from 0.0322 to 0.0773 for genetic correlations, and range from 0.0049 to 0.0056 for phenotypic correlations

Table 2-7. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among fitness traits and linear feet and leg traits¹

	SCS	MS	DO	PL	FA	RLS	RLR	MO
SCS	0.12	-0.10	0.13	-0.69	-0.18	0.03	0.05	-0.14
MS	-0.05	0.26	0.19	0.26	0.14	-0.09	0.22	0.31
DO	0.02	0.01	0.03	-0.60	0.10	-0.02	0.29	0.24
PL	-0.18	0.08	-0.12	0.11	0.11	-0.14	0.31	0.50
FA	-0.01	0.01	0.00	0.02	0.09	-0.48	0.51	0.44
RLS	0.00	-0.01	0.00	-0.04	-0.22	0.14	-0.25	-0.02
RLR	0.01	0.05	0.02	0.05	0.12	-0.10	0.04	0.69
MO	-0.01	0.09	0.02	0.14	0.25	-0.05	0.31	0.11

¹SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life; FA= foot angle; RLS= rear leg side view; RLR= rear leg rear view; MO= mobility score

Standard errors range from 0.0035 to 0.0124 for heritability estimates, range from 0.0222 to 0.0809 for genetic correlations, and range from 0.0050 to 0.0088 for phenotypic correlations

Table 2-8. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among fitness traits and linear udder traits¹

	SCS	MS	DO	PL	UD	FU	RUH	RUW	UC	TP	TL
SCS	0.12	-0.10	0.13	-0.69	-0.26	-0.14	-0.02	0.18	-0.25	-0.11	0.09
MS	-0.07	0.26	0.15	0.26	0.37	0.35	0.26	0.09	0.15	0.25	-0.35
DO	0.02	0.01	0.03	-0.61	-0.19	-0.02	0.32	0.55	0.20	0.06	0.09
PL	-0.18	0.08	-0.12	0.11	0.35	0.44	0.33	0.40	0.31	0.22	-0.06
UD	-0.10	0.16	-0.01	0.08	0.30	0.76	0.31	-0.16	0.22	0.26	-0.20
FU	-0.06	0.13	-0.02	0.10	0.39	0.18	0.45	0.28	0.14	0.38	-0.20
RUH	-0.06	0.11	0.02	0.10	0.16	0.26	0.20	0.51	0.14	0.11	-0.02
RUW	0.01	0.03	0.10	0.10	-0.12	0.00	0.33	0.15	0.27	0.27	-0.03
UC	-0.09	0.10	0.18	0.06	0.19	0.11	0.13	0.11	0.17	0.30	-0.05
TP	-0.03	0.10	0.02	0.06	0.17	0.19	0.06	0.01	0.21	0.23	-0.40
TL	0.02	-0.14	0.03	-0.03	-0.08	-0.04	0.00	0.05	0.03	-0.19	0.35

¹SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life; UD= udder depth; FU= fore udder attachment; RUH= rear udder height; RUW= rear udder width; UC= udder cleft; TP= teat placement; TL= teat length

Standard errors range from 0.0035 to 0.0139 for heritability estimates, range from 0.0386 to 0.0593 for genetic correlations, and range from 0.0042 to 0.0062 for phenotypic correlations

Table 2-9. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among linear body traits and linear feet and leg traits¹

	STAT	STR	BD	RA	RW	DF	FA	RLS	RLR	MO
STAT	0.42	0.31	0.36	0.10	0.49	0.45	0.31	0.09	0.11	0.34
STR	0.25	0.15	0.69	-0.12	0.62	-0.30	0.24	-0.13	0.22	0.14
BD	0.26	0.52	0.19	-0.17	0.46	0.31	-0.05	0.07	0.07	0.20
RA	0.09	-0.03	-0.05	0.21	-0.22	-0.05	-0.04	-0.01	-0.07	-0.12
RW	0.27	0.37	0.32	-0.02	0.15	0.01	0.28	0.03	0.20	0.26
DF	0.16	-0.19	0.16	-0.01	0.04	0.19	-0.15	0.25	0.02	0.38
FA	0.13	0.09	0.04	-0.02	0.03	-0.04	0.09	-0.48	0.51	0.44
RLS	-0.02	-0.06	0.00	0.01	0.01	0.11	-0.22	0.14	-0.25	-0.02
RLR	0.03	0.06	0.07	-0.01	0.07	0.03	0.12	-0.10	0.04	0.69
MO	0.14	0.13	0.19	-0.06	0.12	0.13	0.25	-0.05	0.31	0.11

¹STAT= stature; STR= strength; BD= body depth; RA= rump angle; RW= rump width; DF= dairy form; FA= foot angle; RLS= rear leg side view; RLR= rear leg rear view; MO= mobility score

Standard errors range from 0.0092 to 0.0134 for heritability estimates, range from 0.0222 to 0.0809 for genetic correlations, and range from 0.0049 to 0.0088 for phenotypic correlations

Table 2-10. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among linear udder traits and linear body traits¹

	UD	FU	RUH	RUW	UC	TP	TL	STAT	STR	BD	RA	RW	DF
UD	0.30	0.76	0.31	-0.16	0.22	0.26	-0.20	0.18	-0.02	-0.29	-0.18	0.06	-0.28
FU	0.39	0.18	0.45	0.28	0.14	0.38	-0.20	0.09	0.33	-0.01	-0.26	0.21	-0.19
RUH	0.16	0.26	0.20	0.51	0.14	0.11	-0.02	0.21	-0.05	0.02	-0.11	0.14	0.42
RUW	-0.12	0.00	0.33	0.15	0.27	0.27	-0.03	0.14	0.30	0.35	-0.07	0.35	0.37
UC	0.19	0.11	0.13	0.11	0.17	0.30	-0.05	0.06	0.15	0.17	-0.03	0.23	-0.01
TP	0.17	0.19	0.06	0.01	0.21	0.23	-0.40	0.04	0.17	0.13	-0.11	0.09	0.01
TL	-0.08	-0.04	0.00	0.05	0.03	-0.19	0.35	0.13	0.08	0.10	0.02	0.05	0.00
STAT	0.10	0.06	0.08	0.09	0.01	0.00	0.10	0.42	0.31	0.36	0.10	0.49	0.45
STR	-0.05	0.16	-0.01	0.18	0.03	0.04	0.07	0.25	0.15	0.69	-0.12	0.62	-0.30
BD	-0.16	0.09	0.06	0.22	0.05	0.06	0.08	0.26	0.52	0.19	-0.17	0.46	0.31
RA	0.07	-0.11	-0.05	-0.04	-0.04	0.05	0.01	0.09	-0.03	-0.05	0.21	-0.22	-0.05
RW	-0.05	0.08	0.04	0.21	0.03	0.01	0.05	0.27	0.37	0.32	-0.02	0.15	0.01
DF	-0.10	-0.06	0.22	0.19	0.03	0.02	0.03	0.16	-0.19	0.16	-0.01	0.04	0.19

¹UD= udder depth; FU= fore udder attachment; RUH= rear udder height; RUW= rear udder width; UC= udder cleft; TP= teat placement; TL= teat length; STAT= stature; STR= strength; BD= body depth; RA= rump angle; RW= rump width; DF= dairy form

Standard errors range from 0.0110 to 0.0139 for heritability estimates, range from 0.0222 to 0.0809 for genetic correlations, and range from 0.0049 to 0.0088 for phenotypic correlations

Table 2-11. Heritabilities (diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among linear udder traits and linear feet and leg traits¹

	UD	FU	RUH	RUW	UC	TP	TL	FA	RLS	RLR	MO
UD	0.30	0.76	0.31	-0.16	0.22	0.26	-0.20	0.35	-0.16	0.21	0.26
FU	0.39	0.18	0.45	0.28	0.14	0.38	-0.20	0.30	-0.19	0.21	0.33
RUH	0.16	0.26	0.20	0.51	0.14	0.11	-0.02	0.13	-0.10	0.27	0.57
RUW	-0.12	0.00	0.33	0.15	0.27	0.27	-0.03	0.03	0.02	0.29	0.47
UC	0.19	0.11	0.13	0.11	0.17	0.30	-0.05	0.11	-0.03	0.18	0.34
TP	0.17	0.19	0.06	0.01	0.21	0.23	-0.40	0.16	-0.02	0.13	0.32
TL	-0.08	-0.04	0.00	0.05	0.03	-0.19	0.35	-0.18	0.12	-0.06	-0.12
FA	0.13	0.13	0.06	0.04	0.04	0.04	0.01	0.09	-0.48	0.51	0.44
RLS	-0.06	-0.09	-0.06	-0.05	-0.01	0.00	0.01	-0.22	0.14	-0.25	-0.02
RLR	0.00	0.05	0.09	0.11	0.02	0.02	-0.01	0.12	-0.10	0.04	0.69
MO	0.04	0.19	0.21	0.21	0.08	0.08	0.00	0.25	-0.05	0.31	0.11

¹UD= udder depth; FU= fore udder attachment; RUH= rear udder height; RUW= rear udder width; UC= udder cleft; TP= teat placement; TL= teat length; FA= foot angle; RLS= rear leg side view; RLR= rear leg rear view; MO= mobility score

Standard errors range from 0.0092 to 0.0139 for heritability estimates, range from 0.0222 to 0.0809 for genetic correlations, and range from 0.0049 to 0.0088 for phenotypic correlations

Table 2-12. Heritabilities (diagonal) and genetic (above diagonal) correlations among 11 traits¹ using DMU

	MY	FY	PY	SCS	DO	STAT	DF	UD	MS	MO	PL
MY	0.30	0.76	0.90	-0.28	-0.09	0.09	0.41	-0.26	0.12	0.39	0.67
FY		0.26	0.86	-0.33	-0.05	0.10	0.37	-0.14	0.14	0.40	0.64
PY			0.29	-0.32	-0.14	0.13	0.36	-0.22	0.12	0.40	0.73
SCS				0.16	0.37	0.10	0.07	-0.29	-0.18	-0.30	-0.66
DO					0.04	0.19	0.43	-0.23	-0.01	0.02	-0.58
STAT						0.43	0.43	0.20	0.08	0.29	-0.02
DF							0.19	-0.24	0.15	0.37	0.10
UD								0.31	0.39	0.28	0.23
MS									0.27	0.33	0.26
MO										0.11	0.46
PL											0.39

¹MY= milk yield; FY= fat yield; PY= protein yield; SCS= somatic cell score; DO= days open; STAT= stature; DF= dairy form; UD= udder depth; MS= milking speed; MO= mobility score; PL= productive life

Table 2-13. Genetic (top) and phenotypic (bottom) correlations between final classification score, yield traits, fitness traits, and select linear type traits¹

	MY	FY	PY	SCS	MS	DO	PL	STAT	DF	RUH	RUW	MO
FS	0.16	0.22	0.39	-0.08	0.39	0.45	0.57	0.48	0.42	0.67	0.62	0.81
	0.23	0.22	0.26	-0.07	0.21	0.04	0.18	0.27	0.31	0.43	0.40	0.61

¹FS= final classification score; MY= milk yield; FY= fat yield; PY= protein yield; SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life; STAT= stature; DF= dairy form; RUH= rear udder height; RUW= rear udder width; MO= mobility score

Standard errors range from 0.0035 to 0.0139 for heritability estimates, range from 0.0355 to 0.0457 for genetic correlations, and range from 0.0050 to 0.0053 for phenotypic correlations

Chapter 3

Analyzing udder efficiency of Brown Swiss cattle using Data Envelopment Analysis

Abstract

Udder conformation traits such as udder depth are favorably associated with somatic cell score (SCS) and mastitis resistance, but unfavorably associated with yield, resulting in unclear selection aims. Data envelopment analysis (DEA) is an approach to characterize the efficiency of different units based on inputs and outputs. The objective of this research was to use DEA to create an efficiency trait for udders of Brown Swiss cattle, which we termed udder efficiency, and to evaluate the genetic relationship of udder efficiency with yield, fitness, and udder conformation. The lone input was identified as the inverse of milking speed and the outputs were milk, fat, and protein yield, and the inverse of SCS. A SAS® DEA macro was used to determine udder efficiency of each cow relative to her herdmates, with the most desirable cows milking quickly, producing large volumes of milk, fat, and protein with a low SCS. Values for the trait ranged from 0.03 (very inefficient cows) to 1.0 (efficient cows). Records from 45,464 first through fifth lactation cows born 2000 or later were available with 105,991 observations for milk, fat, and protein yield and 104,909 observations for SCS. There were also approximately 52,250 observations for type traits and 41,704 milking speed observations with a higher score corresponding to faster milking speed. From these, 40,960 udder efficiency records were derived. These data were analyzed using a series of three trait models in ASREML that included fixed effects for lactation, age, and herd-calving cluster. Random effects were animal, permanent

environment, and residual. The heritability of udder efficiency was estimated to be 0.23 ± 0.0133 . Genetic correlations with udder efficiency were positive and moderate for yield traits (0.40 to 0.42), favorable with SCS (-0.21), and strongly positive for milking speed (0.86). Udder efficiency was also strongly correlated with productive life (0.69). Of the udder traits, rear udder height (0.30), teat length (-0.28), fore udder attachment (0.25), and rear udder attachment (0.21) were most favorably correlated to udder efficiency. The correlation of udder depth with udder efficiency was 0.16. Based on these findings, DEA could be a useful and novel method for evaluating udder efficiency, helping to identify traits that enable selection for mastitis resistance without compromising yield.

Introduction

In dairy cattle breeding programs, milk yield has been of primary concern due to its economic importance. However, the increased genetic potential for milk production resulted in an increase in the genetic susceptibility to mastitis, which has been reported as the most costly disease affecting dairy cattle (Shook and Shultz, 1994). Rather than clinical mastitis records, somatic cell count (SCC) or its transformed log score, somatic cell score (SCS) is generally used as an indicator of udder health due to its higher heritability and routine measurement in milk recording programs (Rupp and Boichard, 1999). In the United States, SCS has been assessed in national genetic evaluations and included in the net merit index since 1994 (VanRaden, 2004). In addition, selection for linear udder traits that are favorably correlated with udder health has helped to mitigate the correlated response in SCC as a result of increased milk yield (Rogers et al., 1991).

However, while traits such as udder depth and fore udder attachment are favorably correlated with SCC (Boettcher et al., 1998; Rogers et al., 1991; Rupp and Boichard, 1999), they are unfavorably correlated with milk, fat, and protein yield (Misztal et al., 1992). This makes

selection more difficult as cows that have high yield with low SCC are desirable. Additionally, milking speed is another trait of consideration when evaluating dairy cattle due to its importance from a management standpoint. Slow-milking cows can impede the flow of cows through the parlor (Wiggans et al., 2007), decreasing parlor efficiency and resulting in higher labor costs. Fast-milking cows spend less time in the parlor, but may be more susceptible to udder infection if the reason they milk out more quickly is due to reduced tension in the teat sphincter (Boettcher et al., 1998). An elevated SCS with faster milking speed was observed in Canadian Holstein cows (Boettcher et al., 1998) and in an evaluation of PTAs for US Holstein sires (Zwald et al., 2005).

These relationships have been well-documented for Holsteins, but are less consistent in Brown Swiss dairy cows. For example, in Italian Brown Swiss, fore udder attachment was favorable with yield (Samoré et al., 2010) and milking speed was slightly favorable with SCS in U.S. Brown Swiss (Wiggans et al., 2007). Due to these unclear associations, the objective of this study was to create an udder efficiency trait using DEA and to evaluate genetic correlations with other traits to determine those which are favorable for mastitis resistance while maximizing milk, fat, and protein yield in Brown Swiss dairy cattle in the United States.

Materials and Methods

Data

Data were from first through fifth lactation Brown Swiss cows in the United States born in 2000 or later from herds involved in Dairy Herd Information testing. There were 108,633 records from 45,464 cows in 386 herds and 8,420 herd-calving clusters. Herd calving clusters were generated with the FASTCLUS procedure of SAS (v9.4 Cary, NC). Records were only kept from cows having a record for first lactation to avoid selection bias. In total, 105,991 of the records had values for milk, fat, and protein yield which were adjusted to 305-day mature equivalents, and 104,909 records had a lactation average somatic cell score value. 83,343 records had a value for

days open. The 2,642 records missing yield data were from cows that calved but that died or were culled early in lactation and before they had a 305-d yield. These records were still considered for productive life evaluations. Days open less than 25 were recoded as missing and days open greater than 250 were set to 250 consistent with national genetic evaluations (VanRaden et al., 2002). Productive life was available for 31,489 cows and was expressed as months in milk with the diminishing credits procedure as described by VanRaden et al. (2006). Data for these traits was provided by the Council on Dairy Cattle Breeding. In addition, producer assigned milking speed scores and classification scores were provided by the Brown Swiss Cattle Breeders' Association of the USA. There were 41,074 milking speed records on a scale of 1 (slow milking) to 8 (fast milking) and approximately 52,250 records for 16 linear type traits scored on a scale of 1 to 50, and final classification score on a scale of 60 to 94. There were also 35,442 mobility records scored on a scale of 50 to 99. The data set included 45,464 first lactation, 29,998 second lactation, 18,327 third lactation, 10,111 fourth lactation, and 4,733 fifth lactation records. The pedigree file included 127,401 animals including 5,728 bulls with daughters that had records.

Using traits from this data set, an udder efficiency trait was created using a SAS® DEA macro. The lone input for the DEA analysis was defined as the inverse of milking speed. The inverse was used because a higher number corresponded to a faster, more desirable milking speed but DEA methodology favors minimized values for inputs. The outputs were defined as milk, fat, and protein yield, and the inverse of somatic cell score. In this case, the inverse was used because a smaller somatic cell score corresponded to a healthier udder but DEA methodology favors maximized values for outputs. In order to generate a value for udder efficiency, a record needed to have observations for all five traits of interest. 40,960 udder efficiency records were derived.

Statistical Model

These data were analyzed using a series of three trait models in ASREML (Gilmour et al., 2006). The model for the analyses was:

$$y_i = \mu + L_j + Age_k + HCC_l + A_m + PE_n + \varepsilon_{ijklmn}$$

where y_i = the record for trait 1, fixed effects were lactation (L; j=1 to 5), age (Age, k= 1 to 94), and herd calving cluster (HCC; l=1 to 8,420). Random effects were animal (A; m= 127,401), permanent environment (PE; n=45,464), and residual (ε). PE was not included for productive life.

Results

The heritability estimate for the udder efficiency trait was 0.23 with a standard error of 0.0133. Cows were compared to other animals in the same herd, and across the entire data set, the trait values ranged from 0.03, corresponding to the least efficient cows, to 1.0, corresponding to the most efficient cows. The mean was 0.63 with a standard deviation of 0.19. Heritabilities and correlations amongst the five traits included in the DEA as well as their relationships with linear type traits are shown and discussed in Chapter Two.

Genetic and phenotypic correlations of udder efficiency with yield and fitness traits are shown in Table 3-1. Genetic correlations of udder efficiency with yield traits were moderate and positive, ranging from 0.40 to 0.42. With fitness traits, udder efficiency was favorably related to somatic cell score (-0.21) and highly positive with milking speed (0.86). There was a small unfavorable correlation of udder efficiency with days open (0.25) but a strong positive correlation with productive life (0.69).

Genetic and phenotypic correlations amongst udder efficiency and linear type traits are shown in Table 3-2. Genetic correlations of udder efficiency with linear body traits (stature, strength, body depth, rump angle, rump width, and dairy form) were mostly near-zero. Dairy

form was the trait most related to udder efficiency with a genetic correlation of 0.25. For linear feet and leg traits (foot angle, rear leg side view, rear leg rear view, and mobility score), genetic correlations with foot angle and rear leg side view were also near-zero. Rear leg rear view and mobility score were positively correlated with udder efficiency, with estimates of 0.26 and 0.38, respectively.

Of linear type traits, udder traits (udder depth, fore udder attachment, rear udder height, rear udder width, udder cleft, teat placement, and teat length) were most highly correlated with udder efficiency. Teat length was the only trait that had a negative correlation with udder efficiency (-0.28). The genetic correlations of udder efficiency with other udder traits were positive and ranged from 0.12 with udder cleft to 0.30 with rear udder height. Udder efficiency was also positively correlated with final classification score (0.41)

Discussion

The estimated heritability of udder efficiency (0.23) was comparable to the heritability of yield traits and larger than the heritability of most of the fitness traits reported in Chapter Two. Genetic correlations of yield traits with udder efficiency were all moderately positive, suggesting that selection for the udder efficiency trait would result in increased yields. In addition, the relationship with somatic cell score was favorable, suggesting that selection for udder efficiency would result in improved udder health. The genetic correlation between udder efficiency and milking speed is very strong, perhaps because milking speed was the only input included in the DEA. These results indicate that selection for the udder efficiency trait would simultaneously result in increased yield, reduced somatic cell score, and faster milking speed. As noted in Chapter Two and in agreement with other U.S. Brown Swiss data (Wiggans et al., 2007), the unfavorable relationship between milking speed and somatic cell score seen in Holsteins (Boettcher et al., 1998; Zwald et al., 2005) was not observed. While udder efficiency had a small

unfavorable genetic correlation with days open, it was strongly and positively correlated with productive life, indicating that more efficient cows remained in the herd for longer.

The near-zero correlations of udder efficiency with most linear body traits was expected, due to the small correlations between body traits and the five traits used to create udder efficiency. Dairy form was most favorably associated with udder efficiency likely due to its positive correlation with milk, fat, and protein yield as reported in Chapter Two (0.40, 0.35, and 0.31, respectively). The same is true for linear feet and leg traits, where foot angle and rear leg side view were genetically unrelated to udder efficiency likely due to their near-zero correlations with yield traits and small correlations with somatic cell score and milking speed. The positive correlations of udder efficiency with rear leg rear view and mobility score is likely due to their favorable correlations with yield as reported in Chapter Two, ranging from 0.17 between rear leg rear view and fat yield to 0.28 between rear leg rear view and protein yield. In addition, genetic correlations of milking speed with rear leg rear view and milking speed with mobility score were found to be positive (0.22 and 0.31, respectively). However, this could be an effect of cows with straighter rear legs from the rear (thus higher mobility scores) being easier to attach milking units onto in the parlor, rather than being indicative of a truly faster milking speed.

The genetic correlations of udder efficiency with linear udder traits reflect the relationships between linear udder traits with yield and fitness traits discussed in Chapter Two. Rear udder height was most positively correlated with udder efficiency, likely due to its positive relationship with milk, fat, and protein yield (0.20, 0.25, and 0.19, respectively), near-zero correlation with somatic cell score, and favorable correlation with milking speed (0.26). The relationship observed of teat length with udder efficiency in the current analysis (-0.28) suggests that a shorter teat would correspond to a more efficient udder, and is likely due to the association of a shorter teat with a faster milking speed, reported in Chapter Two (-0.35). Despite its unfavorable relationship with yield (-0.04 with fat yield to -0.40 with milk yield), fore udder

attachment was favorable with udder efficiency due to its relationship with milking speed (0.35) and somatic cell score (-0.14). While rear udder width was most favorable with yield (0.34 with protein yield to 0.48 with milk yield), its near-zero correlation with milking speed and small unfavorable correlation with somatic cell score (0.18) made it less related to udder efficiency than the aforementioned udder traits. Of udder conformation traits, udder depth had the most favorable genetic correlations with milking speed (0.37) and somatic cell score (-0.26), but it was most unfavorable with yield (-0.24 with fat yield to -0.40 with milk yield), making udder depth generally unimportant to udder efficiency in the current analysis.

Conclusions

Data Envelopment Analysis was used as a potential tool for genetic evaluation, assessing the efficiency of udders of Brown Swiss cattle in the United States. An efficient udder was defined to be one that produced large volumes of milk, fat, and protein with a low somatic cell score and fast milking speed. Correlations between the created udder efficiency trait and yield, fitness, and linear type traits were then evaluated. Udder efficiency was positive with milk, fat, and protein yield, favorable with somatic cell score, and positive with milking speed. Despite a small unfavorable correlation with days open, udder efficiency was strongly favorable with productive life, indicating that cows with more efficient mammary systems based on the defined criteria also remained in the herd for longer. The most related type traits to udder efficiency were rear udder height, teat length, and fore udder attachment, favoring an udder with a higher rear attachment, shorter teat length, and stronger fore udder attachment. While udder depth is highly related to somatic cell score and milking speed, its unfavorable relationship with yield made it less associated with overall udder efficiency in the current study. Based on its heritability (0.23) and favorable genetic relationships with yield and fitness traits, the udder efficiency trait indicates that DEA is a potentially novel tool for characterizing efficiency in genetic analysis.

Table 3-1. Genetic correlations (top) and phenotypic correlations (bottom) amongst udder efficiency and yield and fitness traits¹

	MY	FY	PY	SCS	MS	DO	PL
UDEFF	0.40	0.40	0.42	-0.21	0.86	0.25	0.69
	0.46	0.43	0.45	-0.25	0.88	0.06	0.16

¹UDEFF= udder efficiency; MY= milk yield; FY= fat yield; PY= protein yield; SCS= somatic cell score; MS= milking speed; DO= days open; PL= productive life

Standard errors range from 0.0035 to 0.0089 for heritability estimates, range from 0.0338 to 0.0527 for genetic correlations, and range from 0.0049 to 0.0065 for genetic correlations

Table 3-2. Genetic (top) and phenotypic (bottom) correlations amongst udder efficiency and linear type traits¹

	STAT	STR	BD	RA	RW	DF	FA	RLS	RLR	MO	UD	FU	RUH	RUW	UC	TP	TL	FS
UDEFF	0.11	0.00	0.11	-0.07	0.03	0.25	0.09	-0.05	0.26	0.38	0.16	0.25	0.30	0.21	0.12	0.17	-0.28	0.41
	0.04	-0.03	0.04	-0.04	0.02	0.18	0.00	-0.01	0.06	0.14	0.07	0.11	0.17	0.14	0.09	0.08	-0.08	0.28

¹UDEFF= udder efficiency; STAT= stature; STR= strength; BD= body depth; RA= rump angle; RW= rump width; DF= dairy form; FA= foot angle; RLS= rear leg side view; RLR= rear leg rear view; MO= mobility score; UD= udder depth; FU= fore udder attachment; RUH= rear udder height; RUW= rear udder width; UC= udder cleft; TP= teat placement; TL= teat length; FS= final classification score

Standard errors range from 0.0092 to 0.0139 for heritability estimates, range from 0.0312 to 0.0786 for genetic correlations, and range from 0.0048 to 0.0065 for phenotypic correlations

Chapter 4

Summary and Conclusion

In the analysis of yield, fitness, and type traits in Brown Swiss cattle it was observed that milk, fat, and protein yield were moderately heritable and less antagonistic with somatic cell score and fertility than sometimes observed. Milk, fat, and protein yield, and milking speed were positively correlated with productive life and somatic cell score and days open were negatively correlated with productive life. Therefore, cows with higher yield, faster milking speed, lower somatic cell score, and fewer days open were favored and remained in the herd for longer. Larger-framed, more angular cows tended to have compromised fertility, as did cows with higher mobility scores. However, mobility was positively correlated with productive life. Of udder traits, rear udder height and rear udder width had the strongest positive correlations with yield traits and fore udder attachment and udder depth had the strongest negative correlations with yield traits. However, fore udder attachment and udder depth were more favorably correlated with somatic cell score than rear udder traits, as was udder cleft. The udder traits with the strongest positive correlations with productive life were fore udder attachment, rear udder width, udder depth, and rear udder height. Based on the parameters of udder traits, particularly their genetic correlations with productive life, the Brown Swiss Cattle Breeders' Association of the USA developed a new udder composite formula.

Due to the important relationships observed between yield and fitness traits with udder traits, the udder efficiency trait was created using Data Envelopment Analysis (DEA), which has not previously been applied to genetic evaluation. A cow's efficiency was measured relative to

her herdmates, with the most efficient animals being those that milked quickly, produced large volumes of milk, fat, and protein, and had a low somatic cell score. Based on their relationships with yield, somatic cell score, and milking speed, the most highly correlated udder traits with udder efficiency were rear udder height, teat length, and fore udder attachment. Due to the moderate heritability of udder efficiency and its favorable genetic correlations with yield, somatic cell score, milking speed, and productive life, DEA could be a novel tool for characterizing efficiency in genetic analysis.

For future research, more traits could be included in a DEA to develop an overall efficiency trait. For such an analysis, additional inputs of interest could be age at calving and days open (values to be minimized) and additional outputs could be some measure of body size and/or body condition (values to be maximized) to reflect potential salvage value. For an across-lactation measure of efficiency, whether or not a live calf was produced or information regarding pregnancy could also be used as an output. The udder efficiency trait as well as this overall efficiency trait could then be compared to a trait such as Net Merit through correlations of sire PTAs to measure its economic relevance, and determine if efficiency based on the DEA measure corresponded to what would be most profitable at the producer level.

References:

- Abdallah, J. M., and B. T. McDaniel. 2000. Genetic parameters and trends of milk, fat, days open, and body weight after calving in North Carolina experimental herds. *J. Dairy Sci.* 83:1364-1370.
- Bertrand, J. A., P. J. Berger, A. E. Freeman, and D. H. Kelley. 1985. Profitability in Daughters of High Versus Average Holstein Sires Selected for Milk Yield of Daughters. *J. Dairy Sci.* 68:2287-2294.
- Boettcher, P. J., J. C. Dekkers, and B. W. Kolstad. 1998. Development of an udder health index for sire selection based on somatic cell score, udder conformation, and milking speed. *J. Dairy Sci.* 81:1157-1168.
- Boettcher, P. J., J. C. Dekkers, L. D. Warnick, and S. J. Wells. 1998. Genetic analysis of clinical lameness in dairy cattle. *J. Dairy Sci.* 81:1148-1156.
- De Jager, D., and B. W. Kennedy. 1987. Genetic parameters of milk yield and composition and their relationships with alternative breeding goals. *J. Dairy Sci.* 70:1258-1266.
- De Marchi, M., G. Bittante, R. Dal Zotto, C. Dalvit, and M. Cassandro. 2008. Effect of Holstein Friesian and Brown Swiss breeds on quality of milk and cheese. *J. Dairy Sci.* 91:4092-4102.
- Dechow, C. D., G. W. Rogers, L. Klei, T. J. Lawlor, and P. M. VanRaden. 2004. Body condition scores and dairy form evaluations as indicators of days open in US Holsteins. *J. Dairy Sci.* 87:3534-3541.
- Dematawewa, C. M., and P. J. Berger. 1998. Genetic and phenotypic parameters for 305-day yield, fertility, and survival in Holsteins. *J. Dairy Sci.* 81:2700-2709.
- Foster, W. W., A. E. Freeman, P. J. Berger, and A. Kuck. 1989. Association of Type Traits Scored Linearly with Production and Herdlife of Holsteins. *J. Dairy Sci.* 72:2651-2664.
- Garcia-Peniche, T. B., B. G. Cassell, and I. Misztal. 2006. Effects of breed and region on longevity traits through five years of age in Brown Swiss, Holstein, and Jersey cows in the United States. *J. Dairy Sci.* 89:3672-3680.
- Heinrichs, A. J., C. M. Jones, S. M. Gray, A. P. Heinrichs, S. A. Cornelisse, and R. C. Goodling. 2013. Identifying efficient dairy heifer producers using production costs and data envelopment analysis. *J. Dairy Sci.* 96:7355-7362.
- Jamrozik, J., and L. R. Schaeffer. 1997. Estimates of genetic parameters for a test day model with random regressions for yield traits of first lactation Holsteins. *J. Dairy Sci.* 80:762-770.
- Johnson, K. R., and D. L. Fourn. 1960. Heritability, Genetic and Phenotypic Correlations of Type, Certain Components of Type, and Production of Brown Swiss Cattle. *J. Dairy Sci.* 43:975-981.
- Laursen, M. V., D. Boelling, and T. Mark. 2009. Genetic parameters for claw and leg health, foot and leg conformation, and locomotion in Danish Holsteins. *J. Dairy Sci.* 92:1770-1777.

- Madsen, P., and J. Jensen. 2013. DMU. dmu.agrsci.dk/DMU/Doc/Current/dmuv6_guide.5.2.pdf
- McClelland, L. A. 1983. A comparison of objective and subject measures of milking speed in Canadian Holstein-Friesians. M. Sc. Thesis, Univ. Guelph, Ont.
- Meyer, K., and E. B. Burnside. 1987. Scope for a Subjective Assessment of Milking Speed. *J. Dairy Sci.* 70:1061–1068.
- Miller, R. H., J. S. Clay, and H. D. Norman. 2001. Relationship of somatic cell score with fertility measures. *J. Dairy Sci.* 84:2543–2548.
- Misztal, I., T. J. Lawlor, T. H. Short, and P. M. VanRaden. 1992. Multiple-Trait Estimation of Variance Components of Yield and Type Traits Using an Animal Model. *J. Dairy Sci.* 75:544–551.
- Monardes, H. G., R. I. Cue, and J. F. Hayes. 1990. Correlations between udder conformation traits and somatic cell count in Canadian Holstein cows. *J. Dairy Sci.* 73:1337–1342.
- Philipsson, J. 1981. Genetic aspects of female fertility in dairy cattle. *Livest. Prod. Sci.* 8:307–319.
- Politeik, R. D., O. Distl, T. Fjeldaas, J. Heeres, B. T. McDaniel, E. Nielson, D. J. Peterse, A. Reurink, and P. Strandberg. 1986. Importance of claw quality in cattle: review and recommendations to achieve genetic improvement. Rep. E.A.A.P. Working Group on “Claw Quality in Cattle”. *Livest. Prod. Sci.* 15:133–152
- Powell, R. L., and H. D. Norman. 2006. Major advances in genetic evaluation techniques. *J. Dairy Sci.* 89:1337–1348.
- Rogers, G. W., G. L. Hargrove, T. J. Lawlor, and J. L. Ebersole. 1991. Correlations among linear type traits and somatic cell counts. *J. Dairy Sci.* 74:1087–1091.
- Rogers, G. W., B. T. McDaniel, M. R. Dentine, and D. A. Funk. 1989. Genetic Correlations Between Survival and Linear Type Traits Measured in First Lactation. *J. Dairy Sci.* 72:523–527.
- Rupp, R., and D. Boichard. 1999. Genetic parameters for clinical mastitis, somatic cell score, production, udder type traits, and milking ease in first lactation Holsteins. *J. Dairy Sci.* 82:2198–2204.
- Samoré, A. B., and A. F. Groen. 2006. Proposal of an udder health genetic index for the Italian Holstein Friesian based on first lactation data. *Ital. J. Anim. Sci.* 5:359–370.
- Samoré, A. B., R. Rizzi, A. Rossoni, and A. Bagnato. 2010. Genetic parameters for functional longevity, type traits, SCS, milk flow and production in the Italian Brown Swiss. *Ital. J. Anim. Sci.* 9:145–152.
- Santus, E. C., R. W. Everett, R. L. Quaas, and D. M. Galton. 1993. Genetic parameters of Italian brown Swiss for levels of herd yield. *J. Dairy Sci.* 76:3594–3600.

- Schutz, M. M., L. B. Hansen, G. R. Steuernagel, J. K. Reneau, and A. L. Kuck. 1990. Genetic Parameters for Somatic Cells, Protein, and Fat in Milk of Holsteins. *J. Dairy Sci.* 73:494–502.
- Shook, G. E., and M. M. Schutz. 1994. Selection on somatic cell score to improve resistance to mastitis in the United States. *J. Dairy Sci.* 77:648–658.
- Short, T. H., and T. J. Lawlor. 1992. Genetic parameters of conformation traits, milk yield, and herd life in Holsteins. *J. Dairy Sci.* 75:1987–1998.
- Stokes, J. R., P. R. Tozer, and J. Hyde. 2007. Identifying efficient dairy producers using data envelopment analysis. *J. Dairy Sci.* 90:2555–2562.
- Tiezzi, F., C. Maltecca, M. Penasa, A. Cecchinato, Y. M. Change, and G. Bittante. 2011. Genetic analysis of fertility in the Italian Brown Swiss population using different models and trait definitions. *J. Dairy Sci.* 94:6162–1672.
- Togashi, K., C. Y. Lin, and K. Yokouchi. 2004. Overview of genetic evaluation in dairy cattle. *Anim. Sci. J.* 75:275–284.
- Van Dorp, T. E., P. Boettcher, and L. R. Schaeffer. 2004. Genetics of locomotion. *Livest. Prod. Sci.* 90:247–253.
- Van Vleck, L. D., P. J. Karner, and G. R. Wiggans. 1980. Relationships among Type Traits and Milk Yield of Brown Swiss Cattle. *J. Dairy Sci.* 63:120–132.
- VanRaden, P. M. 2004. Invited review: selection on net merit to improve lifetime profit. *J. Dairy Sci.* 87:3125–3131.
- VanRaden, P. M., and J. B. Cole. 2014. Net merit as a measure of lifetime profit: 2014 revision. *AIPL Res. Rep. NM\$5 (10-14)*. Online Available: <http://aipl.arsusda.gov/reference/nmcalc-2014.htm>. Accessed June 1, 2015.
- VanRaden, P. M., E. L. Jensen, T. J. Lawlor, and D. A. Funk. 1990. Prediction of transmitting abilities for Holstein type traits. *J. Dairy Sci.* 73:191–197.
- VanRaden, P. M., A. Sanders, M. Tooker, B. Miller, and D. Norman. 2002. Daughter pregnancy rate evaluation of cow fertility. *AIPL Research Report: DPR(11-02)*. Available at https://aipl.arsusda.gov/reference/fertility/DPR_rpt.htm. Accessed June 1, 2015.
- VanRaden, P. M., and G. R. Wiggans. 1991. Derivation, calculation, and use of national animal model information. *J. Dairy Sci.* 74:2737–2746.
- VanRaden, P. M., C. P. Van Tassell, G. R. Wiggans, T. S. Sonstegard, R. D. Schnabel, J. F. Taylor, and F. S. Schenkel. 2009. Invited review: reliability of genomic predictions for North American Holstein bulls. *J. Dairy Sci.* 92:16–24.
- Vukašinović, N., J. Moll, and N. Künzi. 1995. Genetic relationships among longevity, milk production, and type traits in Swiss Brown cattle. *Livest. Prod. Sci.* 41:11–18.

White, J. M., W. E. Vinson, and R. E. Pearson. 1981. Dairy Cattle Improvement and Genetics. *J. Dairy Sci.* 64:1305–1317.

Wiggans, G. R., L. L. M. Thornton, R. R. Neitzel, and N. Gengler. 2006. Genetic parameters and evaluation of rear legs (rear view) for Brown Swiss and Guernseys. *J. Dairy Sci.* 89:4895–4900.

Wiggans, G. R., L. L. M. Thornton, R. R. Neitzel, and N. Gengler. 2007. Short communication: Genetic evaluation of milking speed for Brown Swiss dairy cattle in the United States. *J. Dairy Sci.* 90:1021–1023.

Wright, J. R., G. R. Wiggans, C. J. Muenzenberger, and R. R. Neitzel. 2013. Short communication: genetic evaluation of mobility for Brown Swiss dairy cattle. *J. Dairy Sci.* 96:2657–2660.

Zink, V., M. Štípková, and J. Lassen. 2011. Genetic parameters for female fertility, locomotion body condition score, and linear type traits in Czech Holstein cattle. *J. Dairy Sci.* 94:5176–518

Zwald, N. R., K. A. Weigel, Y. M. Chang, R. D. Welper, and J. S. Clay. 2005. Genetic evaluation of dairy sires for milking duration using electronically recorded milking times of their daughters. *J. Dairy Sci.* 88:1192–1198.