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GENETIC PARAMETERS OF DAIRY CALF AND HEIFER HEALTH

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ABSTRACT

The overall objective of this dissertation was to evaluate genetic parameters of dairy calf and heifer health which are important considerations for animal wellbeing and farm profitability. Despite this, little research has been conducted regarding the genetics of health in dairy youngstock.

In Chapters 1 and 2, we report genetic parameters for serum total protein in calves and explore regions of the genome that may influence serum total protein. In Chapter 1, we explore serum total protein as a novel trait for selection in dairy calves. Serum total protein was measured and recorded by producers on-farm and then extracted from herd management software. Failure of passive transfer of immunity was declared for serum total protein values less than 5.2 g / dL. Stayability until 365 days of age was defined as a binary trait where calves were assigned a value of 2 if they remained in the herd and 1 if they were removed from the herd for any reason. For each trait, two datasets were analyzed: one that included all Holstein sired calves (n = 16,725) and a more restrictive dataset that required Holstein sired calves to have a recorded Holstein maternal grandsire (n = 7,518). Heritability estimates for serum total protein ranged from 0.06 to 0.08, and heritability estimates for failure of passive transfer of immunity ranged from 0.04 to 0.06. Stayability heritability estimates ranged from 0.08 to 0.11. The genetic correlation estimate between serum total protein and failure of passive transfer of immunity was near 1 while the genetic correlation estimates between serum total protein and stayability ranged from 0.19 to 0.25. Approximate genetic correlations were estimated between serum total protein and predicted transmitting abilities for health, fertility, and production

traits evaluated by the Council on Dairy Cattle Breeding. Serum total protein exhibited positive approximate genetic correlations with cow livability, productive life, net merit dollars, and milk yield, and favorable correlations were also found with calving traits. Our results suggest that serum total protein is heritable and favorably correlated with measures of cow health and production.

After showing that serum total protein is heritable, in Chapter 2, we explore regions of the genome that may influence serum total protein using the Holstein sired dataset. We identified 9 SNP across the genome that were significantly associated with serum total protein in calves. These SNP were located on BTA 1, 5, 6, 7, 11, 12, 15, and 20, with 2 SNP located on BTA 20. Further, a peak on BTA 11 located around 79 Mbp was identified that explained a substantial portion of additive variance. These result help show that serum total protein is a polygenic trait and likely influenced by regions across the genome.

The objectives of Chapter 4 were to estimate genetic parameters of calf health in organic US Holstein calves for three calf health traits: calf respiratory disease until 365 days of age, calf scours until 60 days of age, and heifer stayability until 365 days of age. Heritability estimates were 0.100, 0.075, and 0.085 for respiratory disease, scours, and stayability, respectively. Signs were reversed when presenting correlations such that higher correlations between scours, respiratory disease and stayability were all favored and corresponded with resistance to disease rather than risk. The genetic correlation estimate between respiratory disease resistance and stayability was 0.675. However, genetic correlation estimates between respiratory disease and scours (0.148) and between

scours and stayability (0.165) were low. We also estimated approximate genetic correlations of calf health traits with other traits evaluated nationally by the Council on Dairy Cattle Breeding. These were generally low to moderate in magnitude. The strongest genetic correlation estimates were with longevity, particularly between stayability and heifer livability (0.417) and between stayability and cow livability (0.475); respiratory disease was also favorably correlated with heifer (0.355) and cow (0.296) livability. Because the approximate genetic correlation between stayability and heifer livability was only moderate in magnitude, we evaluated the random interaction of herd by sire which may indicate potential genotype by environment interaction effects; results showed that herd by sire interaction accounted for approximately 2 % of total variance. Overall, results suggest there is significant genetic variation in organic calf health, and there was potential evidence of genotype by environment interaction.

Finally, in Chapter 4, we estimated genetic parameters for direct treatment costs in US organic Holstein nulliparous animals (n = 17,93). Producers provided cost estimates for veterinary treatment, on-farm supplies, and on-farm labor for respiratory disease and scours. Unique events were declared if 4 and 5 days elapsed between events for scours and respiratory disease, respectively, and treatment costs for scours and respiratory disease per animal were calculated as the product of mean treatment cost and number of unique event occurrences. Total treatment cost was calculated as the sum of respiratory disease cost, scours cost, and disposal cost (fixed at $6.00) for animals that were removed from the herd. All treatment costs were summed until 18 months of age. Average treatment costs were $56.37 and $25.21 for respiratory disease and scours,

respectively. The average cost per animal were $10.19, $25.03, and $25.00 for respiratory disease, scours, and total costs, respectively. Heritability estimates ranged from 0.047 for total treatment cost to 0.057 for scours treatment costs. Total treatment cost was genetically correlated with both respiratory disease cost (0.495) and scours cost (0.465). The genetic correlation estimate between respiratory disease cost and scours cost was -0.331. Because total treatment cost was semi-continuous and right-skewed, we investigated various response variables for total treatment cost; these included total treatment cost, log-transformed treatment cost, and 2-trait conditional model with response variables any treatment cost (0 = no treatment costs; 1 = treatment cost greater than $0) and log-transformed total treatment cost conditional on treatment cost being greater than $0. The model with log-transformed total treatment cost as the response variable resulted in the highest heritability and reliability estimates while the response variable in the 2-trait model had the lowest. Predicted transmitting ability correlations with traits evaluated by the Council on Dairy Breeding were low and mostly not significant. This suggests that calf and heifer treatment costs are generally not genetically correlated with current national traits in the United States. While genetic variation for youngstock heath treatment costs was detected, heritability estimates were comparable to estimates for binary disease events despite the continuous nature of treatment costs.

In conclusion, significant additive variance exists for dairy calf and heifer health traits such as serum total protein, youngstock disease, and youngstock disease treatment costs. In addition, disease and disease treatment costs were generally lowly to moderately

correlated with current genetic evaluations in the United States. These results suggest there is potential to improve calf and heifer health through genetic selection.

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Chapter 1

Literature review

CALF HEALTH

Calf morbidity and mortality are extremely important when considering animal welfare and on-farm profitability. The most common calf and heifer diseases in are scours and respiratory disease with scours being most prevalent during the preweaning period and respiratory disease being most prevalent during the postweaning period (USDA, 2018). Recently, it was estimated that scours occurs in 18.9% of preweaned dairy calves while respiratory disease is estimated to occur in 11.3% of preweaned calves (Urie et al., 2018a). The USDA NAHMS also conducts periodic national surveys that evaluate calf health which help to track changes in calfhood disease across time. These estimates have remained relatively stable across time despite small numeric decreases. In 2006, scours was estimated to affect 23.9% of preweaned calves and respiratory disease was estimated to affect 12.4% of preweaned calves (USDA, 2010). In weaned calves, 5.9% and 1.9% of animals are affected by respiratory disease and scours (USDA, 2010). In preweaned calves in 2013, 21.1% had scours and 12.0% had respiratory disease (USDA, 2018). In weaned heifers, 5.1% and 1.0% of animals were affected by respiratory disease and scours, respectively (USDA, 2018). In addition, scours and respiratory disease are the leading causes of preweaned and weaned deaths, respectively, with scours accounting for 56.5% of preweaned deaths and respiratory disease accounting

for 46.5% of weaned deaths (USDA, 2018). National estimates of calf mortality have also remained consistently high across time and above recommended levels (USDA, 2010; Urie et al., 2018b). In 2006, 7.8% of preweaned calves died and 1.8% of weaned calves died (USDA, 2010). In 2013, mortality during preweaning was 6.4% and post-weaning was 1.9% (USDA, 2018).

Both scours and respiratory disease are umbrella terms. Scours can refer to any form of digestive upset during early life regardless of causal agent while respiratory disease encompasses all causal agents affecting the respiratory system (Jones and Heinrichs, 2006). Throughout this dissertation, respiratory disease will be used to describe any type of respiratory system disease regardless of causal agent and scours will be used to describe disease impacting the digestive system.

Economics of calf health and rearing

Raising replacement heifers is consistently one of the largest expenses on-farm. Various estimates are available regarding the cost of raising heifers: Heinrichs et al. (2013) estimated the cost of a single heifer from birth until calving to be $1,808 using herds in Pennsylvania; Karszes and Hill (2020) calculated the cost on a subset of 26 Northeast dairy farms to be $2,355 in 2019. Feed is the largest expense in raising heifers from birth until calving followed by labor; however, even excluding labor which accounted for 11-13% of total rearing costs, the cost of raising heifers from birth until calving is substantial (Heinrichs et al., 2013; Karszes and Hill, 2020). In the two highlighted studies, the preweaning period has the highest daily expense ($2.17 – $3.31)

followed by the breeding to first calving period ($1.89 - $2.20; Heinrichs et al., 2013; Karszes and Hill, 2020). The large daily expense during breeding to first calving helps highlight the important of targeting an age at first calving around 22 to 24 months of age as a month of delayed calving would be worth approximately $57 to $67 per animal during this rearing period. While health costs were relatively small portion of total heifer rearing costs (Heinrichs et al., 2013; Karszes and Hill, 2020), they nonetheless can represent a substantial expense on farm.

Cost of calf disease

Kaneene and Hurd (1990) estimated the cost of common calf disease treatment and prevention from birth until calving with most costly diseases in preweaned calves being gastrointestinal ($33.46 per calf-year) and respiratory disease ($14.71 per calf-year); costs were substantially lower from weaning until calving with the most order of expense being respiratory disease ($1.95 per calf-year) and gastrointestinal ($0.71 per calf-year). It is important to note that these are per calf-year and not per case and as such represent the estimated cost of treatment and prevention for a typical calf on an annual basis and not the typical cost associated with a single case of disease. More recently Dubrovsky et al. (2020) estimated the preweaning cost of respiratory disease on California dairies to be $36.43 for first treatment case.

CONSEQUENCES OF ADVERSE CALF HEALTH

Calf morbidity and survival

Adverse health events during rearing can have negative consequences on later heifer performance and performance as a lactating cow. Waltner-Toews et al. (1986) found that calves treated for respiratory disease during the first 3 months of life were 2.5 times more likely to die during the proceeding heifer period; the authors also found calves treated for scours were more likely to be sold during the same periods. Closs and Dechow (2017) found reduced survival to 24 months of age following respiratory disease treatment or treatment for any health incident during the first 6 months of life. Urie et al. (2018a) found that morbidity during the preweaning period increased the odds of death by 4.7 times when compared to calves that did not experience preweaning disease. Further, a recent meta-analysis concluded that experiencing respiratory disease in calves increased the odds of mortality by 2.85 times and increased the odds of not reaching first lactation by 2.30 times compared to healthy calves (Buczinski et al., 2021).

Further the impact of calf disease on lactating productive life within the lactating herd are reported infrequently particularly beyond early first lactation. Heinrichs and Heinrichs (2011) found that days ill and days treated for scours or respiratory disease had no impact on the length of time an animal remained in the herd. Teixeira et al. (2017) did not find a difference in ability to remain in the herd for the first three months following first calving between calves that experienced lung consolidation and healthy calves. While not directly related to calf disease, other environmental factors surrounding rearing

impact cow health. For instance, Hultgren and Svensson (2009a) found that calves experiencing less moves pre-calving had longer productive lives in the milking herd.

Calf morbidity and age at first calving

Results published regarding the impacts of calf morbidity on age at first calving are varied. Waltner-Toews et al. (1986) found that calves that experienced scours during the first three months of life were more 2.9 times more likely to calve after 900 days than calves that did not experience scours. However, Waltner-Toews et al. (1986) did not report a significant difference in the proportion of animals calving by 900 days of age between calves treated for respiratory disease and healthy cohorts. The 900 days used in Waltner-Toews et al. (1986) corresponds to approximately 30 months of age and therefore corresponds to a substantial increase in rearing costs. However, 900 days or 30 months is much older than current on-farm recommendations for age at first calving which generally are reported between 22-24 months of age (Hoffman and Funk, 1992; Ettema and Santos, 2004; Heinrichs and Jones, 2016). Correa et al. (1988) also found that calves experiencing respiratory disease had higher age at first calving than those animals not experiencing respiratory disease; however, they found the opposite association between calf dullness and age at first calving. Heinrichs et al. (2005) showed that increased days of antibiotic treatment for scours or respiratory disease during first 4 months of age showed a trend (p-value = 0.06) with increased age at first calving. However, they did not find an association between days of illness for scours and respiratory disease and age at first calving which may suggest that severity of disease

may also impact the association between calf illness and age at first calving. More recently, Stanton et al. (2012) found that calves experiencing respiratory disease were less likely to calve by 25 months of age; however, Closs and Dechow (2017) did not find an effect of treatment for respiratory disease during the first six months of life on age at first calving and Dunn et al. (2018) found no impact of lung consolidation on age at first calving. Lung consolidation is measured by accessing abnormal lung tissue in the intercostal spaces of the lung using ultrasonography, and the presence of lung consolidation is associated with respiratory disease (Ollivett and Buczinski, 2016; Dunn et al., 2018).

Calf morbidity and yield traits

Calfhood disease may impact later yield particularly during first lactation. Heinrichs and Heinrichs (2011) showed that increased days of illness with either scours or respiratory disease was associated with reduced milk, fat, and protein mature equivalent yields during first lactation and showed a trend between increased days of illness and actual milk, fat, and protein yields during first lactation. Interestingly, the same study showed a trend (p-value ≤ 0.10) between increased days of antibiotic treatment and first lactation mature-equivalent and actual milk production. However, Closs and Dechow (2017) found no impact on daily milk yield during first lactation. Dunn et al. (2018) found that calves exhibiting lung consolidation produced 525 kg of milk less than calves not exhibiting lung consolidation. Abuelo et al. (2021) found no significant difference in mature-equivalent first lactation production between calves with

and without respiratory disease; however, they did find a calves that experienced scours preweaning produced 325 kg less mature equivalent milk during first lactation. Mahmoud et al. (2017) reported the effects of calfhood respiratory disease, scours, and general health on the first two test-days following 1st parturition and found that the occurrence of calfhood disease decreased yields for 2nd test-days; however, the impact on 1st test-days were generally small and not significant. Buczinski et al. (2021) in a meta-analysis found that calves diagnosed with respiratory disease produced 121 kg less milk during first lactation than healthy calves. However, the study of Buczinski et al. (2021) did not include any studies that reported negative or null results due to differences in trait definitions; hence, while it appears that calf morbidity likely negatively impacts first lactation milk yield, it is not conclusive.

The impacts of calfhood disease on lifetime production are less frequently reported in literature. Heinrichs and Heinrichs (2011) found no differences in lifetime production yields based on days ill or days treated for scours or respiratory disease.

Calf morbidity and other performance measures

Growth and mature size: Place et al. (1994) found no association between respiratory disease treatment days and average daily gain in heifers up to four months of age after accounting for DMI, housing, season, and farm; the authors hypothesized that may be due to an effect of DMI which was a significant predictor of average daily gain.

Closs and Dechow (2017) found that calves experiencing calfhood disease weighed 9 to 12 kilograms less than healthy calves during the first 30 days post first

calving; however, the difference in body weight was not present later in lactation. Heinrichs et al. (2005) found that antibiotic treatment during first 4 months of age increased withers height at calving but was not associated with increased body weight. The authors hypothesized it was mediated by an increased AFC which may have allowed for animals to be closer to maximum structural development but with no impact on body weight (Heinrichs et al., 2005). Stanton et al. (2012) found that calves with respiratory disease weighed 16 kg less at breeding age (382 days on average) than healthy calves.

Reproduction: Others have evaluated the impacts of calf health on reproduction in nulliparous animals. Abuelo et al. (2021) found that calves with bovine respiratory disease were less likely to be inseminated than their healthy contemporaries. However, they did not find any differences in number of inseminations until pregnancy or age at first service (Abuelo et al., 2021). Further, Abuelo et al. (2021) found that scours impacted the number of services until pregnancy but did not change the chances of being inseminated or eventually becoming pregnant. The authors also evaluated the impact of any preweaning disease (respiratory disease or scours) and found that calves experiencing any health event preweaning were less likely to be inseminated and to conceive (Abuelo et al., 2021). Teixeira et al. (2017) found that calvers experience lung consolidation by 60-days of age had impaired reproductive performance, including lower pregnancy risk at first service. Schaffer et al. (2016) looked at the effect of bovine respiratory disease during the first 120-days of life and calving interval during first lactation and found no difference between animals that had been diagnosed with bovine respiratory disease and healthy calves.

Cow health: The impacts of calf health on later health as a lactating animal have been infrequently reported in peer-reviewed literature. Mahmoud et al. (2017) compared the odds of disease during first lactation between animals with and without calfhood disease (scours, respiratory disease, and general disease). The authors found that animals without calf scours were more likely to experience nondescript disease during first lactation and more likely to experience clinical mastitis. However, almost all other odds ratios were not significantly different between healthy and diseased calves. Hultgren and Svensson (2009b) compared odds of clinical mastitis between calves without scours, with mild scours, and severe scours. Interestingly, animals with a history of severe calfhood scours were more likely to experience clinical mastitis compared to calves without calfhood scours but calves with mild calfhood scours were less likely to experience clinical mastitis than calves without a history of scours (Hultgren and Svensson, 2009b). The authors did not find a relationship between calfhood respiratory disease and clinical mastitis as a cow.

PASSIVE TRANSFER OF IMMUNITY

When calves are born they lack a fully functioning innate immune system (Godden, 2008). Therefore, calves rely on adequate passive transfer of immunity through colostrum. Colostrum is rich in immunoglobins. Immunoglobulins in colostrum include immunoglobulin (Ig) G, IgA, and IgM. Immunoglobulin G is found in abundance in cow colostrum, accounting for 85 to 90 % of immunoglobins in colostrum (Godden, 2008).

Successful passive transfer of immunity is based on several factors including the quality of colostrum, quantity of colostrum, and timing of administration.

Colostrum quality is mainly impacted the concentration of immunoglobulins and in particular IgG given its large proportion in colostrum. Quality colostrum is generally defined by a IgG concentration of at least 50 mg/mL, a bacteria count below 100,000 cfu/mL, and a fecal coliforms count less than 10,000 cfu/mL (Jones and Heinrichs, 2006). On farm, IgG concentration is generally the most evaluated and can be easily measured using a colostrometer or hydrometer (Godden, 2008). In order to provide an adequate quantity of immunoglobulins to the newborn calf, it is recommended to feed 10-12 % of the newborns body weight in colostrum (Godden, 2008). A more general recommendation that can be easily implemented on farm is at least 4 quarts or liters of colostrum (Godden, 2008). Finally, to achieve successful passive transfer of immunity, the neonatal calf needs to consume colostrum directly after birth. This is to allow for maximum absorption of immunoglobulins across the gut lining and should occur within 1-2 hours after birth (Jones and Heinrichs, 2006; Godden, 2008).

There are various methods that can be used to assess passive transfer of immunity in the neonatal calf. Serum IgG measured in the neonatal calf is generally considered the most reliable method of determining passive transfer of immunity and can be accomplished through several laboratory tests including radial immunodiffusion (RID) and enzyme-linked immunosorbent assay (ELISA; Godden, 2008). However, these procedures to measure serum IgG are mainly used in research settings as they are time consuming and expensive; therefore, it is much more likely that a refractometer is used to measure serum total protein on farm (Godden, 2008). Additionally, a Brix refractometer

can be used to calculate a Brix score that can be used to measure passive transfer with the advantage of a Brix refractometer being the dual use in determining both colostrum quality and passive transfer (Deelen et al., 2014). There is high agreement between passive transfer of immunity determined using serum IgG or serum total protein. Deelen et al. (2014) estimated the correlation between serum total protein and serum IgG to be 0.93 when measured in calves between 3 and 6 days of age. Similarly, Wilm et al. (2018) found that the correlation between serum IgG measured at 24 hours of age with STP from 2 to 9 days of age was generally above 0.80.

Failure of passive transfer is declared when a calf fails to absorb a sufficient quantity of immunoglobins from colostrum. For serum IgG, 10 mg/mL is generally considered the threshold to declare failure of passive transfer (Godden, 2008). Several studies have estimated cutoff values of serum total protein that correspond with 10 mg/mL of IgG with the value most commonly being between 5.0 to 5.5 g/dL (Tyler et al., 1996; Calloway et al., 2002; Urie et al., 2018b). On farm, it is recommended that at least 90 % of calves have serum total protein values above 5.2 g/dL or 80 % above 5.4 g/dL (USDA, 2016). In the United States, it is estimated that 19.2 % of calves experiences failure of passive transfer when defined as a serum IgG concentration below 10 mg/mL (USDA, 2010). Urie et al. (2018b) estimated failure of passive transfer in the United States based on both IgG (13.0%; serum IgG < 10 mg/mL) and serum total protein (15.6%; serum total protein < 5.1 g/dL). Despite this apparent decrease in failure of passive of transfer, only 43.3% of operations had at least 80% of calves with mean serum total protein concentrations of at least 5.4 g/dL, which the authors used to declare excellent passive transfer of immunity (Urie et al., 2018b).

The number of operations that measure passive transfer of immunity on-farm is increasing. In 2006, 2.1% of all operations evaluated serum total protein on-farm; however, when compared across herd sizes, 14.5% of dairies with 500 or more cows measured serum total protein (USDA, 2010). By 2013, the percentage of operations measuring serum total protein on-farm increased to 6.2 % with 38.3 % of farms with more than 500 cows measuring serum total protein (USDA, 2016). Hence, approximately 35.3 % of heifer calves in the United States are monitored for serum total protein (USDA, 2016).

The effects of passive transfer of immunity are well-documented. Passive transfer of immunity has been shown to be associated with mortality, morbidity, and future performance.

Impact on calf and heifer mortality: Robison et al. (1988) found mortality numerically decreased as immunoglobulin concentration increased in calves from birth until 180 days of age (approximately 6 months of age) with animals in the lowest quintile having a mortality rate of 6.78 % compared to 2.59 % in the highest quintile. Donovan et al. (1998) found that increased serum total protein was associated with reduced mortality risk through the first 6 months of age and that mortality risk was lowest for calves with serum total protein concentrations above 6.5 g/dL; however, there was a quadratic effect of serum total protein when evaluating mortality risk suggesting that extremely high serum total protein concentrations may not be desirable. Urie et al. (2018a) found that increased IgG concentrations were associated with a decrease in mortality during the preweaning period while Henderson et al. (2011a) found similar results when evaluating serum total protein and mortality in animals until one month before first calving.

Impact on calf and heifer health: Burton et al. (1989) found that higher IgG concentrations in the neonatal calf were associated with less occurrence of scours until 7 weeks of age but did not find an effect of IgG concentration on respiratory disease. Donovan et al. (1998) looked at the impacts of serum total protein on morbidity until six months of age and found that opposite of Burton et al. (1989): higher serum total protein was associated with decreased respiratory disease incidence but not associated with scours. Further, Donovan et al. (1998) found that the effect of serum total protein mainly operated during early life and the relationship diminished over time. The authors also evaluated the relationships of serum total protein with septicemia and omphalitis (umbilical cord infection) and found that higher serum total protein was associated with reduced septicemia but not omphalitis (Donovan et al., 1998).

Relationship with calf and heifer performance: Robison et al. (1988) found that higher serum total protein was associated with increased average daily gain from birth until 180 days of age. Shivley et al. (2018) looked at predictors of growth in Holstein calves and while serum IgG did not remain in the final multivariate model following backwards elimination, serum IgG was significantly associated with average daily gain when tested as a single predictor. The authors postulated that it did not remain in the final model due to predictors such as calf morbidity remaining in the final multivariate model (Shivley et al., 2018b).

Relationship with cow performance: DeNise et al. (1989) found that higher serum immunoglobulins at birth were associated with increased mature equivalent milk and showed a trend for increased fat yield during first lactation. The authors also compared first lactation culling rates of calves split into quintiles based on serum

immunoglobulin concentration and found that calves in the lowest quintile (smallest concentration of serum immunoglobulins) were more likely to be culled than those in higher quintiles (DeNise et al., 1989). However, median quintiles had the highest survival when compared to either the highest or lowest quintiles (DeNise et al., 1989). In addition, the calves in both Robison et al. (1988) and DeNise et al. (1989) received colostrum through suckling which is rarely practiced on commercial dairies. Therefore, while the results may represent biological conditions, the conditions of the study may not be representative of modern calves. However, as cow-calf separation becomes more of an animal welfare concern, the ability of calves to adequately consume colostrum and therefore immunoglobulins directly through suckling may be of more importance.

GENETIC SELECTION IN US DAIRY CATTLE

Few species shave undergone intense genetic selection to the degree of dairy cattle. Selection in the US has been accomplished through robust progeny testing that has been aided by artificial insemination, an accurate milk recording system, and a large, accurate pedigree record (Weigel et al., 2017). Historically, this means that selection has occurred for traits that are easy to measure, have large sample sizes, and have high economic impact; examples of such traits would include milk, fat, and protein yields. However, more data is recorded on farm beyond yields and more traits have been added across time. In 1994, the USDA introduced its first health related traits: productive life and somatic cell score (Schutz, 1994; Vanraden and Wiggans, 1995). The first fertility trait evaluated was daughter pregnancy rate in 2003 (VanRaden et al., 2004). Additional

fertility traits, including cow conception rate and heifer conception rate, were released in 2009 and incorporated into net merit in 2014 (VanRaden et al., 2009a; VanRaden and Cole, 2014). Cow livability was introduced in 2016 and subsequently added to net merit in 2017 (Wright and Van Raden, 2016; VanRaden et al., 2018). In 2018, evaluations were introduced which allow producers to directly select for improved resistance to diseases such as mastitis and displaced abomasum (Parker Gaddis et al., 2014; VanRaden et al., 2018). Most recently, heifer livability and cow feed efficiency were introduced (Vanraden et al., 2021). Traits will continue to be added as they become available in the future. Cole and VanRaden (2018) proposed that the desirability of future traits should be considered with relationship to correlation with current traits and the value they provide to producers. Lower correlations, both phenotypic and genetic, are favored because this indicates that new traits are contributing new information to the index compared to existing traits (Cole and VanRaden, 2018).

Impact of genetic selection in dairy cattle

The impacts of genetic selection are well-documented within dairy cattle. Average lactational yields for Holsteins increased from 13,017 pounds (5,917 kg) in 1957 to 28,693 (13,042 kg) in 2019 which is equivalent to 15,676 pounds (7,125 kg), of which 9,734 pounds (4,425 kg) can be attributed to genetic change and 5,942 pounds can be attributed to environmental changes (CDCB, 2021a). Thus, 62 % of the improvement in milk production can be attributed to genetic selection. A similar trend can be observed for other breeds and yield traits (CDCB, 2021a).

When intense selection for one trait results in changes (favorable or unfavorable) in another unselected trait, correlated response to selection occurs (Falconer and Mackay, 1996). The cautionary tale relating to correlated response to selection in US dairy cows relates to milk yield and fertility. As previously highlighted, milk yield was one of the first traits dairy producers were able to select upon due to its high economical value and ease of measurement during routine milk recording. When compared to other traits such as fertility, which also has a high economic value and is routinely recorded on farm, milk yield has a higher heritability (0.20) than fertility traits such as daughter pregnancy rate (0.04; VanRaden et al., 2018). The low heritability estimates for fertility was one of the main reasons national genetic evaluations for fertility were not available in the United States until 2003 (VanRaden et al., 2004). From 1957 to 2003 (when national fertility evaluations became available), while milk yield increased by 13,344 pounds (6,065 kg), daughter pregnancy rate in the United States decreased by 12.6 percent (CDCB, 2021a). However, once evaluations became available for daughter pregnancy rate, producers were able to select for both improved yield and improved fertility and fertility trends began to stabilize (CDCB, 2021a).

Selection goals and indices

To effectively select for the aforementioned large number of traits, selection indices were developed to aggregate economically important traits into a single selection goal based on profitability (Cole and VanRaden, 2018). Today the primary economic selection index is lifetime net merit developed by researchers at the USDA Animal

Improvements Programs Laboratory, now Animal Genomics Improvements Laboratory, which was first published in 1994; net merit was preceded by two economic indices, predicted difference dollars in 1971 and milk-fat-protein dollars in 1976 (Cole et al., 2021).

While Net Merit is perhaps the most commonly referenced economic index, other indexes are commonly used in the United States. For instance, most major dairy breed associations in the United States publish indexes that signal the direction the breed is attempting to take. These indexes include Holstein Association USA's Total Performance Index (Holstein Association USA, 2021) , American Jersey Cattle Association's Jersey Performance Index (Jersey Journal, 2020), and Brown Swiss Society's Progressive Performance Ranking (Brown Swiss Association, 2020). In addition, private companies have begun conducting independent evaluations. For instance, Zoetis was one of the first to directly evaluate health traits in the United States and simultaneously developed their Dairy Wellness Profit index which allowed producers to select animals based on both traditional traits and direct health traits (Zoetis, 2021). Similarly, Genex developed the Ideal Commercial Cow index to incorporate propriety traits that were developed in-house (Genex, 2021). This breadth of indices allows producers to select an index that best suits their operation. However, correlations between indexes are generally high (Cole and VanRaden, 2018). This suggests that animal rank remains relatively stable regardless of which index a producer chooses to use.

Genomic Selection

Genomic selection was first implemented in US dairy cattle in 2009 following the work at USDA (VanRaden et al., 2009b). Genomic selection extends traditional pedigree-based analysis and incorporates an animal's genetic markers to predict genetic merit more accurately. For genomic evaluations in the United States, genomic tested animals have their genotypes imputed to a common 80k single nucleotide polymorphisms (SNP) across the genome which is an increase from the 50k SNP that were used when genomic evaluations were first provided in 2009 (CDCB, 2018a). Reliability of genetic predictions, especially in youngstock and unproven bulls, increases with genomic evaluations. Initial gains in reliability were approximately 23 % in bulls when moving from parent averages to genomic evaluations and have continued to increase as more SNP have been added and the number of genotyped animals has increased; currently reliability for unproven genomic tested bulls approaches 80 % for yield traits (VanRaden et al., 2009b; Wiggans et al., 2016). The gain in reliability from genomic evaluations is partially responsible for the more rapid introduction of traits post-genomic selection when compared to pre-genomic selection. Traits that were potentially hard to evaluate due to limited records and low reliability may now be evaluated with enough confidence for producers to select upon. An example of this is selection for disease traits in the United States; reliabilities increased roughly 9 to 15 % for disease traits when genomic information was included compared to only pedigree information (Parker Gaddis et al., 2014).

Producers can currently genomic test females to predict later performance. At the time of this writing, there have been 5 million dairy cattle genotyped within the United States and over 90 % are female (Carrillo and Tokuhisa, 2021). In 2019, it was estimated that approximately 12 % of all females born in the United States were genomic tested (De Vries et al., 2019). Genomic testing fees generally start around $35 per test and additional fees are incurred as more information is provided (https://www.zoetisus.com/animal-genetics/dairy/clarifide/clarifide.aspx; https://www.neogen.com/igenity-dairy/). In order for producers to recoup the cost of genomic testing, various strategies have been proposed including culling excess heifers based on genomic test results and selectively breeding the best genetic animals from genomic testing to sexed semen while breeding the lowest merit animals to beef semen (De Vries et al., 2019).

One impact of genomic selection has been a decrease in the generation interval particularly for sires of bulls and dams of bulls due to the ability to predict genetic merit of animals younger in life. The generation interval for sires of bulls decreased from 7 years to 2.5 years while the generation interval for dams of bulls decreased from 4 years to 2.5 years (García-Ruiz et al., 2016). There has also been a decrease in generation interval in sires of cows from approximately 7 years to 4 years (Makanjuola et al., 2020). This decrease in generation interval allows for an improved rate of genetic gain per year. However, this also means that inbreeding increases more rapidly. From 1990 to 2018, inbreeding increased 0.75 to 1.16 % per generation while post-genomic selection inbreeding increased 1.19 to 2.06 % per generation in Canadian Holsteins (Makanjuola et al., 2020). In the United States, the average inbreeding percentage of Holsteins increased

by 0.05 % per year from 1990 to 2009 but has increased by 0.29 % per year since 2009 (CDCB, 2021b).

Genetics of morbidity and mortality

Cow: Several researchers have demonstrated the ability to estimate genetic parameters for health events that are recorded by producers for management purposes such as establishing antibiotic withdrawal times and facilitating culling decisions. In the United States, Zwald et al. (2004) was one of the first to estimate genetic parameters for disease traits using data recorded by producers on-farm; they estimated genetic parameters for six common diseases in Holstein cows: displaced abomasum, ketosis, mastitis, lameness, cystic ovaries, and metritis. Heritabilities for these diseases across all lactations ranged from 0.05 for cystic ovaries to 0.15 for displaced abomasum (Zwald et al., 2004); the heritability estimates from first lactation only records were higher than those using all lactation records. Parker Gaddis et al. (2014) also estimated the heritabilities for the same six common diseases in Holstein cows and retained placenta. In first lactation animals, heritabilities ranged from 0.02 for lameness to 0.22 for displaced abomasum (Parker Gaddis et al., 2014). In later parity animals, heritability estimates ranged from 0.02 to 0.17 (Parker Gaddis et al., 2014).

Zoetis developed evaluations for common diseases in US dairy cattle, releasing their first commercial evaluations in March 2016 for US Holstein cows (Vukasinovic et al., 2017). Diseases that genetic parameters were estimated for in Holstein cows initially included mastitis, metritis, retained placenta, displaced abomasum, ketosis, and lameness

(Vukasinovic et al., 2017). Heritability estimates ranged from 0.059 for metritis and ketosis to 0.081 for displaced abomasum (Vukasinovic et al., 2017). Later evaluations for disease resistance were also released for Jersey cattle (Gonzalez-Peña et al., 2020) and expanded to include additional disease traits, including those in calves (Gonzalez-Peña et al., 2019, 2020).

While Zoetis was the first to release commercial evaluations of health traits to producers, official evaluations in the United States come from the Council on Dairy Cattle Breeding. The Council on Dairy Cattle Breeding officially released national evaluations for direct disease resistance in Holsteins for the following six traits in April of 2018 following the work of Parker Gaddis et al. (2014): milk fever, displaced abomasum, ketosis, mastitis, metritis, and retained placenta (CDCB, 2018b). Upon release, heritability estimates for the traits evaluated by the Council on Dairy Cattle Breeding ranged from 0.006 for milk fever to 0.031 for mastitis (CDCB, 2018b). One reason for the lower heritability estimates from official evaluations was the change from threshold sire models to linear animal models which resulted in variance components being estimated on the observed scale (0/1) rather than underlying scale (Parker Gaddis et al., 2014; CDCB, 2018b). This was done to allow for an animal model to be fit as opposed to a sire model and to aid in convergence as threshold models using national data did not converge (Parker Gaddis et al., 2020). While linear models generally result in lower heritability estimates than threshold models, animals generally rank the same across models (Koeck et al., 2010). In April 2020, the Council on Dairy Cattle Breeding also began releasing health evaluations for US Jersey cows (CDCB, 2020a). However,

health evaluations are not yet available for other breeds in the United States due to lack of sufficient data.

Researchers at the University of Minnesota have estimated heritabilities for direct disease costs, taking into account veterinary costs and labor costs (Donnelly et al., 2017). Heritabilities were estimated in first lactation Holsteins for the following direct disease cost categories: mastitis ($h^2 = 0.13$), lameness ($h^2 = 0.10$), reproductive disorders ($h^2 = 0.04$), metabolic disorders ($h^2 = 0.12$), miscellaneous disorders ($h^2 = 0.04$), and total treatment cost ($h^2 = 0.27$; Donnelly et al., 2017). Heritabilities were also estimated for several individual disease costs, including metritis ($h^2 = 0.02$), retained placenta ($h^2 = 0.12$), displaced abomasum ($h^2 = 0.12$), and ketosis ($h^2 = 0.18$; Donnelly et al., 2017). Of particular interest was the relatively high heritability estimate for total treatment costs ($h^2 = 0.27$; Donnelly et al. 2017), compared to heritability estimates from others who used binary response variables for disease events (Zwald et al., 2004; Parker Gaddis et al., 2014; Vukasinovic et al., 2017).

Calf and heifer: Despite the importance of calf health for husbandry and improved performance later in life, calf traits relating to morbidity and mortality have received little attention in genetic research and hence genetic selection. Currently, in national evaluations published by the Council on Dairy Cattle Breeding, producers are only able to select for heifer livability which is a measure of mortality (Neupane et al., 2021). However, Zoetis publishes commercial evaluations for calf respiratory disease, calf scours, and calf mortality for Holsteins and Jerseys (Gonzalez-Peña et al., 2019, 2020).

Like heritability estimates for cow health traits, calf health heritability estimates are generally low. Neupane et al. (2021) estimated the heritability of heifer livability to 0.007. However, most other estimates for calf mortality, while still low, are slightly higher. Gonzalez-Peña et al. (2019) estimated the heritability of calf mortality to be 0.060 in US Holsteins. For US Jerseys, the heritability estimate for calf mortality is 0.103 (Gonzalez-Peña et al., 2020). McCorquodale et al. (2013) estimated the heritability of calf mortality to 0.06; however, their estimate also had a relatively large corresponding standard error. Further, Henderson et al. (2011a) estimated the heritability to 0.036 for Holsteins on a commercial heifer raising in New York. In Danish Holsteins, the heritability estimate for heifer mortality was 0.076 (Fuerst-Waltl and Sørensen, 2010). One reason for the differences in heritability estimates from these studies may have to due with the age of calves studied. For example, Neupane et al. (2021) included animals up to 18 months of age while Gonzalez-Peña et al. 2019) evaluated animals until 12 months of age.

For respiratory disease, Henderson et al. (2011b) estimated the heritability of heifer respiratory disease from birth to calving to be 0.09 in Holsteins raised on New York commercial heifer raising operation. Neibergs et al. (2014) estimated the heritability of respiratory disease to be 0.13 in a case-control study involving calves (male and female) from 20 to 60 days of age. Quick et al. (2020) found a similar heritability estimate of 0.11 in calves until 6 weeks of age; however, the researchers estimated a higher heritability (0.24) when evaluated until 3 weeks of age. Others have estimated slightly lower heritabilities for respiratory disease. Gonzalez-Peña et al. (2019) estimated a heritability of 0.04 in US Holsteins from birth until 365 days of age.

Likewise, McCorquodale et al. (2013) estimated the heritability of respiratory disease in Canadian Holsteins from birth until 3 months of age to 0.04. In US Jerseys, the heritability estimate of respiratory disease is 0.055 from birth until 365 days of age (Gonzalez-Peña et al., 2020). Methodologies varied across these studies. For instance, Henderson et al. (2011b) used linear sire models to estimate genetic parameters while Gonzalez-Peña et al. (2019) used threshold models. Quick et al. (2020) clinically evaluated calves for signs of respiratory disease while Gonzalez-Peña et al. (2019) relied on producer recorded data which is more often used as record of treatments.

Heritability estimates for calf scours are found less frequently in the literature but are similar to those of calf mortality and calf respiratory disease. In US Holsteins, Gonzalez-Peña et al. (2019) estimated the heritability of calf scours until 50 days of age to 0.045; while in US Jerseys, the heritability of calf scours during the same time period is estimated at 0.084 (Gonzalez-Peña et al., 2020). In German Holstein-Friesian calves, Mahmoud et al. (2017) estimated the heritability of scours to 0.06 until 2 months of age.

Genetic correlations between calf and cow health traits: Mahmoud et al. (2017) estimated the genetic correlations between calf health (scours and respiratory disease) and cow health (diarrhea, respiratory disease, mastitis, claw health, fertility disorders, and metabolic disorders) with most genetic correlation estimates being small in magnitude with large standard errors. For calf scours, genetic correlations with cow health traits ranged from -0.21 ± 0.17 for metritis to 0.11 ± 0.10 for claw health; while for calf respiratory disease, genetic correlation with cow health traits ranged from -0.18 ± 0.10 for cow diarrhea to 0.22 ± 0.10 for mastitis (Mahmoud et al., 2017). Likewise, Gonzalez-Peña et al. (2020) found small genetic correlations estimates between calf and cow health

traits in US Jerseys with correlations ranging from -0.118 between calf scours and cow displaced abomasum to 0.14 between calf respiratory disease and cow retained placenta. Calf mortality appears to exhibit low to moderate genetic correlation estimates with measures of cow longevity. Neupane et al. (2021) estimated genetic correlations for heifer livability, where higher livability is favorable, to be 0.44 with productive life in the lactating herd and 0.31 with cow livability. Gonzalez-Peña et al. (2019) estimated the genetic correlations of calf mortality with productive life and cow livability to be -0.277 and -0.275, respectively. However, Henderson et al. (2011a) estimated a lower genetic correlation between heifer survival from weaning until calving with productive life of 0.133. In non-US dairy cattle, Pritchard et al. (2013) estimated a genetic correlation between heifer survival until 750 days of age and days of productive in the milking herd of 0.31 in UK Holstein-Friesians; while in Israeli Holsteins, Weller et al. (2021) estimated a genetic correlation of 0.30 between calf survival and lactating cow herd life.

ORGANIC DAIRY PRODUCTION

In the United States, there are approximately 280,000 cows located on just over 2,500 USDA certified organic operations, and the milk value marketed from these cows (4 billion pounds or 1.8 billion kg) is worth $1.4 billion (USDA, 2017). Animal welfare is consistently listed as a one of the primary concerns of organic dairy consumers (Hughner et al., 2007). Differences exist between organic and conventional production practices as well as producer attitudes. For example, USDA organic regulations prohibit the sale of products from dairy animals that have been treated with antibiotics (Coffey

and Baier, 2012). However, antibiotics are used frequently to treat calf diseases with 93.4 % and 74.5 % of preweaned cases of respiratory disease and scours being treated with antibiotics, respectively (USDA, 2010). This is in contrast to US organic dairy producers who are more likely to use antibiotic alternatives, such as herbal remedies, when treating calf diseases (Habing et al., 2016). It should be noted that organic dairy producers in the United States are still required to administer antibiotics if alternative treatments are unsuccessful and the antibiotic treatment is required for animal health; this requires subsequent removal of the animal or products from that animal from the organic market (Coffey and Baier, 2012).

Pempek et al. (2017) reported that organic and conventional producers differ in calf management practices in a survey of producers from Ohio and Michigan. For instance, when evaluating the primary mode of colostrum delivery to newborn calves, 12.6 % of conventional producers reported their primary delivery method was to allow the calf to suckle from the dam compared to 38.3 % of organic producers (Pempek et al., 2017). In addition, organic producers were less likely to report calfhood vaccinations for respiratory disease (14.4 %) compared to conventional producers (43.6%; Pempek et al., 2017). Stiglbauer et al. (2013) also found lower calfhood vaccination on organic operations (67 %) compared to on conventional operations (98 %) when surveying operations in New York, Wisconsin, and Oregon. Approximately one-third of surveyed organic producers in Ohio list pneumonia and calf scours as concerns (Brock et al., 2021).

Genetic selection goals may differ between organic and conventional dairy producers. In the United States, Grazing Merit was developed to assist producers who

substantially graze cattle, which would include organic producers, in selection decisions (Gay et al., 2014). Grazing Merit places greater emphasis on greater emphasis on fertility and less emphasis on longevity than Net Merit (Vanraden et al., 2021). These differences in emphasis between Grazing Merit and Net Merit represent differences between the needs in grazing versus confinement operations with fertility being of greater concern in grazing operations due to increased seasonal calving and longevity being of less concern due to advantages in herd longevity on organic operations (Gay et al., 2014). In a survey of Swedish producers, regardless of production type (organic vs conventional) producers ranked longevity as their highest priority; however, organic producers placed greater importance on disease resistance while conventional producers placed more importance on milk production (Ahlman et al., 2014). In a study of Danish dairy farms, researchers placed producers into 1 of 4 groups based upon selection priorities (health and fertility, production and udder health, survival, and fertility and production; Slagboom et al., 2016); they found that the higher proportion of organic producers were in the production group. The authors also found that organic producers tended to rank milk production and calf mortality higher than conventional producers. This may be because milk production was lower and calf mortality was higher on organic dairies than conventional dairies while cow longevity was higher and cow disease rates lower on organic dairies (Slagboom et al., 2016).

There is also evidence for potential genotype by environment interactions between organic and conventional operations. In Dutch Holsteins, Nauta et al. (2006) estimated the genetic correlations between organic production and conventional production to be 0.80, 0.88, and 0.71 for milk, fat, and protein yields, respectively, which

suggests the presence of genotype by environment interactions; however, the authors did not find evidence of genotype by environment interaction effects for component percentages or somatic cell scores. Shabalina et al. (2021) also found evidence for genotype by environment interactions in German Holsteins when evaluating the genetic correlations between organic and conventional systems; when using single-step methodology, in which the relationship matrix incorporates both genomic and pedigree information, the genetic correlation estimate between organic milk yield and conventional milk yield was 0.75. Shabalina et al. (2021) found stronger evidence of genotype by environment effects in health traits (mastitis, ovarian cycle disorder, and digital dermatitis) with genetic correlation estimates ranging from 0.33 to 0.44 and in productive life with a genetic correlation estimate of 0.66. In US Holsteins, (Hardie et al., 2019) regressed cow phenotypes on sire predicted transmitting abilities for yield and fertility traits; the authors reported regression coefficients differing from expectations for fat yield and fertility traits which may suggest potential genotype by environment interaction effects.

CONCLUSIONS AND OBJECTIVES

Calf health is extremely important when considering animal well-being and future measures of performance. Further, genetic selection has been extremely successful at improving animal performance and national evaluations in the United States are rapidly incorporating new traits, especially related to health and longevity. However, producers currently have few options to genetically improve calf health and survival. Genetic

selection for improved calf health may be of particular importance for organic producers due to regulations which prohibit the sale of products from animals treated with antibiotics and the lower reported use of vaccines. Given these considerations the primary objectives of the research subsequently reported are as follows:

1) Evaluate serum total protein in dairy calves as a novel trait for genetic selection. Results from this objective will be presented in Chapters 2 and 3.

2) Estimate genetic parameters for common diseases in US organic dairy calves and compare with current genetic evaluations derived from conventional cow data. Chapter 4 will report results from this objective.

3) Explore the use of direct treatment costs relating to calf disease as a novel genetic trait. Results are reported in Chapter 5.

Chapter 2

Passive transfer of immunity in dairy calves

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ABSTRACT

Passive transfer of immunity is important for calf health and survival. The objectives of this study were to estimate genetic parameters for calf passive transfer of immunity through producer recorded serum total protein (STP) and to determine associations with other routinely evaluated traits in organic Holstein calves (n = 16,725) that were born between July 2013 to June 2018; a restricted subset (n = 7,518) of calves with known Holstein maternal grandsires was analyzed separately. Producers measured STP on farm, and STP was extracted from farm management software. Failure of passive transfer of immunity (FPT) was declared for calves with STP ≤ 5.2 g/dL. Calves that had the opportunity to reach one year of age were recorded as either staying in the herd or leaving the herd (STAY365). Univariate and threshold models were fit for STP and FPT, respectively, and included the fixed effects of herd-year-month of birth, calf age in days at STP measurement, dam age in years, and random effects of animal and birthdate

within herd. Model effects for STAY365 included the fixed effects of herd-year-month of birth and random effects of animal and birthdate within herd. Multivariate analyses of STP with FPT or STAY365 were conducted to determine the genetic correlation between traits and STP was also regressed on gestation length. Heritability estimates of STP were 0.06 and 0.08 for full and restricted data, respectively. Heritability estimates for FPT were 0.04 and 0.06 for full and restricted data, respectively. The genetic correlation between STP and FPT was near unity. Heritability estimates for STAY365 ranged from 0.08 to 0.11 with genetic correlation estimates between STP and STAY365 ranging from 0.19 and 0.25. Approximate genetic correlations were estimated for sires (n = 302 and n = 256 for full and restricted data, respectively) with at least 10 daughters for STP and predicted transmitting abilities for health, calving traits, and production. Positive approximate genetic correlations were estimated for STP with cow livability, productive life, net merit dollars, and milk yield; favorable approximate genetic correlations were observed for daughter and sire calving ease, and sire stillbirth. Longer gestation length was associated with reduced STP genetically and phenotypically. These results suggest that passive transfer as measured through STP is heritable and favorably correlated with current measures of health, calving, and production.

Key words: serum total protein, heritability, dairy calves

INTRODUCTION

Calf serum immunoglobulin G (IgG) and serum total protein (STP) can be used to gauge passive transfer of immunity in calves. Serum IgG is considered the more accurate

and relevant measure; however, STP is easier and more cost effective to measure on farm using a refractometer (Godden, 2008). There is high agreement between serum IgG and STP during the first days of life. Deelen et al. (2014) estimated the correlation between serum IgG and STP to be 0.93 when taking blood samples from 3 to 6 days of age. Wilm et al. (2018) found the correlations between serum IgG measures at 24-hours of age and STP from 2 to 9 days of age were generally above 0.80. When a calf fails to absorb an adequate level of antibodies from colostrum, failure of passive transfer of immunity (FPT) occurs. In literature, FPT has been defined as a STP value below 5.0 to 5.5 g/dL (Tyler et al., 1996; Calloway et al., 2002).

Multiple studies have demonstrated the importance of successful passive transfer of immunity for calf survival and health. Donovan et al. (1998) showed that calves with higher STP had a lower mortality risk through the first 6 months of life with the lowest mortality in calves with STP $\geq$ 6.5 g/dL. Higher STP was also associated with reduced pneumonia and septicemia, but not diarrhea (Donovan et al., 1998). Henderson et al. (2011a) showed calves with higher STP had a reduced risk of mortality through one month before first calving. Urie et al. (2018a) found that higher serum IgG was associated with reduced risk of mortality and morbidity during the preweaning period. In addition, calf serum IgG is associated with increased first lactation milk production and may impact first lactation culling (DeNise et al., 1989).

Estimates of genetic parameters for passive transfer of immunity in calves are infrequent and inconsistent. Donovan et al. (1986) estimated the heritability of calf STP to be 0.02 with a population of 2,105 calves, whereas Maltecca et al. (2009) estimated the heritability of calf IgG to be 0.18 with a population of 276 calves. Additional studies

have estimated the genetic parameters for blood metabolites in nulliparous heifers and in lactating cows (Jensen and Christensen, 1975; Cecchinato et al., 2018). In non-lactating heifers between 4 and 38 months of age, Jensen and Christensen (1975) estimated the heritability of STP to be 0.09 and of IgG to be 0.12. Cecchinato et al. (2018) estimated a STP heritability of 0.20 in cows.

The percent of US dairy operations measuring calf STP on farm is increasing. From 2007 to 2014, the percentage of operations recording STP on farm increased from 2.1% to 6.2% (USDA, 2010, 2016). However, 38.3% of farms with more than 500 cows recorded STP, and it was estimated that 35.3% of US dairy calves were located on farms that recorded STP (USDA, 2016).

This increase in calf STP recorded on farm represents a potential database of calf health measures that have yet to be exploited for genetic improvement. The success of passive transfer may be of even greater importance to organic dairy operations where regulations limit treatment options for disease. Currently, there are approximately 280,000 organic cows in the United States that produce over 4 billion pounds of milk worth about $1.4 billion (USDA, 2017).

In the present study, our objectives were to estimate genetic parameters for STP for organic calves and to determine if calf STP was genetically correlated with traits routinely evaluated in the United States.

MATERIALS & METHODS

Data

Records were available for 16,725 organic Holstein-sired heifer calves born between July 2013 and June 2018 from multiple herds in the western United States. Calf STP was extracted from herd DairyComp backups (Valley Ag Software, Tulare, CA). Herds in this study routinely collected blood from newborn calves and measured STP using a refractometer. Herds then recorded STP as an event in DairyComp (Valley Ag Software, Tulare, CA). Additional variables extracted from herd management software included ancestry, age of calf when STP was recorded (days: 1, 2, 3), calf birthdate, dam age at parturition (years: 2, 3, 4, 5, >= 6), and gestation length of the dam. We defined FPT as a binary trait where a value of 1 was assigned if STP $\leq$ 5.2 g/dL or a value of 2 was assigned if STP > 5.2 g/dL. This cutoff is supported by Calloway et al. (2002) who suggested a STP value of 5.0 to 5.2 g/dL to declare FPT. Stayability to one year (STAY365) was defined for 14,527 animals that had the opportunity to reach one year of age by the time of the last herd data backup. Therefore, an animal needed to be born at least one year prior to the last herd backup to have a STAY365 phenotype. Further, STAY365 phenotypes were defined only for calves with STP measurements and did not include stillborn calves. On organic dairy operations, animals requiring antibiotic treatment are no longer considered organic but are otherwise healthy to enter a conventional dairy operation. Therefore, stayability was chosen to account for all reasons an animal may leave the herd including mortality, involuntary culling, and the culling of animals that may have required antibiotic treatment. Calves were given a STAY365 value

of 2 if they remained in the herd at one year of age and calves that were no longer present in the herd were given a STAY365 value of 1. Breed status for calves was determined using the calf's recorded breed, sire breed, and maternal grandsire breed. Our primary dataset consisted of calves recorded as Holstein, with a Holstein sire and either Holstein or unknown maternal grandsires. Dams with an unknown sire (unknown calf maternal grandsire) were predominantly Holstein and either purchased or born before the herds began more consistent sire recording. The herds have adopted varying levels of crossbreeding more recently, and it is possible that some dams were not pure Holstein; for that reason, a smaller subset of calves (n = 7,518) with Holstein sires and maternal grandsires was constructed. Of this restricted subset, 6,052 animals had stayability phenotypes. We refer to the Holstein sired data as the "full" data and the maternal grandsire restricted data as the "restricted" data.

Statistical analysis

Variance components for STP, FPT, and STAY365 were estimated using univariate linear and threshold animal models depending on the type of response variable (continuous vs. binary) for both the full and restricted datasets. A linear model was fit for STP using the airemlf90 program (version, 1.139, Misztal et al., 2018). Threshold models were fit for FPT (1 = failure passive transfer; 2 = successful passive transfer) and STAY365 (1 = failed to stay in herd; 2 remained in herd) using the thrgibbs1f90 program (version 2.116, Misztal et al., 2018). For FPT and STAY365 models, 500,000 iterations were used with a 50,000 burn-in and saving every 50 samples. Posterior distributions

were analyzed using postgibbsf90 program (version 3.13, Misztal et al., 2018). Model convergence for FPT and STAY365 were analyzed by inspecting the trace plots.

STP and FPT were evaluated with the following single-trait animal model:

$$y = \mu + HYM_j + age_k + Dage_l + H_m + A_n + e_{jklmn}$$

Where y is the phenotype; μ is the overall mean; *HYM* is the herd-month contemporary group *j* (levels = 98) at birth*; age* is the age in days of STP or FPT measurement (k = 1, 2, or 3); and *Dage* is the age of the dam (*l*=2, 3, 4, 5, ≥6 years); *H* is the random effect for birthdate within herd *m*; *A* is the random effect of animal *n*; *e* is the random residual. In addition to the above model, maternal direct additive and maternal permanent environement effects were fit to a single trait model for STP. However, they were left out of final analyses because variance estimates were not different from zero and their inclusion reduced model fit based on AIC values. We also attempted to fit the fixed effect of maternal-grandsire breed group (Holstein or unknown) for the full data analyses; however, maternal-grandsire breed was not significant and therefore not included in the final analyses. There were 18,566 individuals in the pedigree file for the restricted analyses and 32,910 individuals in the pedigree for the full analyses.

STAY365 was fit using the following model:

$$y = \mu + HYM_j + H_k + A_l + e_{jkl}$$

Where *y* is the phenotype for STAY365; μ is the overall mean; HYM is the herd-year-month contemporary group j (levels = 86); H is the random effect for birthdate within herd *k*; *A* is the random effect of animal *l*; *e* is the random residual. Heritabilities for STP, FPT, and STAY365 were defined as:

$$h^2 = \frac{\sigma_A^2}{\sigma_A^2 + \sigma_H^2 + \sigma_e^2}$$

Where σ_A^2 is additive variance, σ_H^2 is birthdate within herd variance, and σ_e^2 is residual variance.

In addition to univariate models, bivariate models where used to estimate genetic correlations between STP and FPT as well as STP and STAY365. Models used included the same fixed and random effects as previous models and were fit using the airemlf90 program (version, 1.139, Misztal et al., 2018). For the full bivariate analysis of STP and FPT, model convergence was not reached when using airemlf90 (version, 1.139, Misztal et al., 2018). We subsequently attempted to fit a bivariate model of FPT and STP in ASREML (Gilmour et al., 2015). However, convergence was not met due to low genetic variance for FPT coupled with a genetic correlation near unity between FPT and STP. At the time of convergence failure in ASREML, the estimated genetic correlation between the two traits was in excess of 1.0. In addition to the above models, we attempted to estimate (co)variances between STP and FPT or STAY365 in the thrgibbs1f90 program (version 2.116, Misztal et al., 2018) for the purpose of calculating genetic correlations. This allowed us to treat FPT and STAY365 as threshold traits when estimating (co)variances. However, convergence was not met for the bivariate models evaluating STP and FPT. Further, the genetic correlation estimates between STP and STAY365 differed by less than 0.015 regardless of whether STAY365 was treated as a continuous trait or threshold trait.

Standard errors for STP were obtained from airemlf90 output (version, 1.139, Misztal et al., 2018). Reliabilities for STP were calculated using the following equation:

$$rel_i = 1 - \left(\frac{SE_i^2}{(1+f_i)\sigma_{BV}^2}\right)$$

For animal *i,* where $1 + f_i$ is the diagonal of the additive genetic relationship matrix; SE_i is the standard error of the EBV for animal i; and σ_{BV}^2 is the breeding value variance for STP.

EBV for proven sires with at least 10 daughters were used to approximate genetic correlations of STP with other traits commonly evaluated by the Council on Dairy Cattle Breeding (Bowie, MD) using the method of Calo et al. (1973)

$$\hat{r}_{g_{1,2}} = \frac{\sqrt{(\sum_{i=1}^{n} REL_{1i})(\sum_{i=1}^{n} REL_{2i})}}{\sum_{i=1}^{n}(REL_{1i} * REL_{2i})} * r_{1,2}$$

Where $\hat{r}_{g_{1,2}}$ is the approximate genetic correlation between trait 1 and trait 2, REL_{1i} and REL_{2i} are the reliabilities for trait 1 and trait 2 for sire i, and $r_{1,2}$ is the correlation between sire PTA for trait 1 and trait 2.

Standard errors for the approximate genetic correlations were derived as

$$SE = \sqrt{\frac{1 - \hat{r}_{g_{1,2}}}{n-2}}$$

Where $\hat{r}_{g_{1,2}}$ is the approximate genetic correlation and n is the number of sires with at least 10 daughters that have STP phenotypes.

In order to better assess the relationship between STP and STAY365, we regressed STAY365 phenotypes on either STP phenotype or STP EBV in both the full and restricted data using PROC GLM of SAS software (version 9.4, SAS Institute Inc., Cary, NC). Calves were broken into quartiles for either STP phenotype or STP EBV, and

quartile rank was then used as the predictor variable. To account for trends, STP phenotype was broken into quartiles based on HYM of birth.

In addition, we sought to determine the phenotypic relationship between STP and calving related events. Multivariate regression was performed using PROC GLM of SAS software (version 9.4, SAS Institute Inc., Cary, NC). Calf STP was regressed on the fixed effects of dam age, HYM, and gestation length (GL). Dam age and HYM were defined as above. Gestation length was restricted to 250-300 days and split into quartiles for analysis. On-farm measures of calving ease were not available. Likewise, calves born stillborn were not included in the analysis because STP measurements were not available for those calves.

RESULTS AND DISCUSSION

Descriptive statistics

Descriptive statistics are shown in Table 1. Mean STP was 6.37 (±0.01) g/dL for the full calf data and 6.39 (±0.01) g/dL for the restricted calf data. These estimates are higher than estimates from national studies. Urie et al. (2018b) reported a mean STP of 6.0 in a study that involved operations across the US and multiple breed groups. Further, the percent of calves experiencing FPT was 11% for the full data and 10% for the restricted data. These estimates are very close to the recommendation that at least 90% of calves have STP above 5.2 g/dL (USDA, 2016). The FPT rate in our study is less than the 15.6% reported by (Urie et al., 2018b) based on STP. Urie et al. (2018b) defined FPT less

than or equal to 5.0 g/dL which is less stringent than the cutoff used in the present study. The herds in this study have been recording STP for several years and this may have contributed to higher mean STP levels and lower FPT than in other studies. Beam et al. (2009) showed that operations that recorded STP were significantly less likely to experience FPT.

In total, 68% of full data calves had a STAY365 score of 2 meaning that they remained in the herd at one year of age given the opportunity, whereas 69% of calves remained in the herd at one year of age for the restricted data. For animals with a STAY365 score, 9% and 8% of calves were involuntarily removed by 90 days in the full and restricted data, respectively. This is in close agreement with previous estimates of a 8% death loss prior to weaning on primarily conventionally managed western dairy operations (USDA, 2018). From 91 to 365 days, 23% of heifers were involuntarily removed in both the full and restricted data. General management protocols in these herds called for aggressive removal of diseased calves to prevent exposure of other calves as diseased animals have lower survival rates and reduced production (McGuirk, 2008). It is important to note that the herds in this analysis were organic; therefore, any animal with a disease requiring antibiotic treatment must be removed from the herd (Coffey and Baier, 2012).

Heritability

Variance component and heritability estimates for STP, FPT, and STAY365 are reported in Table 2. Heritability estimates of STP were 0.06 in full and 0.08 in restricted

data suggesting that there is opportunity for genetic selection of STP. Very few studies have evaluated the heritability of serum total protein in calves. Donovan et al. (1986) estimated heritability of STP to be 0.02 using paternal half-sib correlation with a population of 2,105 calves that were sired by 81 bulls. However, to the best of our knowledge there are no additional studies looking at the heritability of STP in neonatal dairy calves. While our estimates of STP heritability were higher than that of Donovan et al. (1986), they are similar to estimates in older nulliparous animals. Jensen and Christensen (1975) estimated heritability for STP to be 0.09 in nulliparous Red Danish cattle between 4 and 38 months of age. In lactating animals, heritability is estimated to be around 0.20 which is higher than the estimate of STP that we present (Peterson et al., 1982; Cecchinato et al., 2018).

Additional studies have evaluated the heritability of IgG which is phenotypically closely related to STP (Deelen et al., 2014; Wilm et al., 2018). Maltecca et al. (2009) reported a heritability estimate for IgG of 0.18 in neonatal calves that were ¾ Holstein and ¼ Jersey. Burton et al. (1989) reported a similar estimate for IgG heritability of 0.18 in neonatal Canadian Holstein calves. In older individuals, IgG heritability is more variable. Jensen and Christensen (1975) estimated heritability for IgG to be 0.12 in nulliparous Red Danish cattle between 4 and 38 months of age. Burton et al. (1989) estimated a range for IgG heritability of 0.0 to 0.20 in Canadian Holsteins from 3 to 7 weeks of age. In mature Canadian Holsteins, de Klerk et al. (2018) estimated the heritability of IgG to be 0.27. Results from these studies may indicate that IgG is more heritable than STP. However, given that STP is heritable and more readily recorded on

farm, STP is likely a better candidate for development as a trait for selection to improve calf health.

Because most calf management literature is primarily focused on FPT, we evaluated FPT in a univariate threshold model. Heritability estimates for FPT from univariate threshold models were 0.04 for full data and 0.06 for restricted data. In both cases, standard deviations for the posterior samples were large and suggested that the heritability of FPT was not significantly different from zero.

The heritability estimates of STAY365 were 0.08 in the full data and 0.11 in the restricted data. In organic production in the U.S., any animal treated with antibiotics is no longer considered an organic animal and must be removed from the herd. Thus, we use the term stayability to reflect all reasons that an animal may leave the herd including mortality, involuntary culling, and removal of animals that require antibiotic treatment but would otherwise be healthy to continue in conventional dairy production. We compare our estimates of stayability with estimates of calf mortality which are more commonly available in the literature. Our heritability estimates for STAY365 are similar to the estimate of mortality of Gonzalez-Peña et al. (2019) who estimated the heritability for calf mortality to one year of age to be 0.06 in US Holsteins. On a US commercial heifer operation, the heritability from weaning until exit was estimated lower at 0.036 (Henderson et al., 2011a). In Danish Holstein females, Hansen et al., (2003) estimated mortality from 1 to 180 days of age to be 0.027 which is lower than our estimate and the estimate of Gonzalez-Peña et al. (2019). Further, in a more recent study of Danish Holsteins, estimates of 0.082 from 1 to 30 d of age and 0.076 from birth until first calving were reported (Fuerst-Waltl and Sørensen, 2010).

Our estimates of STP and STAY365 heritabilities are similar or higher than the heritabilities for other traits that have been evaluated in dairy calves. For instance, Gonzalez-Peña et al. (2019) estimated the heritability of respiratory disease to be 0.042 and the heritability of scours to be 0.045; Henderson et al. (2011b) estimated the heritability of respiratory disease to be 0.095 and bloat to be 0.040; and Heringstad et al. (2008) estimated the heritability of calf respiratory disease to be 0.05. This further suggests that STP may be a useful trait to further evaluate relating to calf health.

For both STP and STAY365, requiring two generations of Holstein sires compared to only one generation of Holstein sires resulted in numerically higher heritability estimates. Therefore, the estimates that are provided in this study may be underestimated for animals with more stringent pedigree edits such as three or more generations of known Holstein sires. However, pedigree completeness was scarce in our dataset beyond two generations. Regardless our results suggest that requiring only a known sire is sufficient to detect genetic variance for STP and STAY365.

Correlations

The genetic correlation estimates between STP and FPT in the restricted data was at unity (0.99), and we were not able to reach convergence when attempting to estimate variance components in the bivariate analysis of STP and FPT in the full data because of the high correlation. The purpose of evaluating FPT was that FPT is a common measure considered in calf management recommendations; therefore, our results could be understood relative to those recommendations. However, the high genetic correlation

estimates plus higher heritability estimates for STP suggest that simply evaluating STP as a continuous trait would be most advantageous from a genetic selection standpoint. Further, our estimates of FPT heritability were lower than our STP heritability estimates in both the full and restricted evaluations. Therefore, STP should be the preferred trait when considering the genetics of passive transfer in calves.

The correlation estimates between STP and STAY365 were positive in both calf populations (0.25 in full; 0.19 in restricted). However, the standard deviations around these estimates were large; because of the large SD for the genetic correlation estimates, we split calves into quartiles for STP phenotypes and STP EBV. When establishing STP phenotype quartiles, animals were split into quartiles within HYM to account for trends. We then regressed STAY365 phenotypes on either STP phenotype quartile or STP EBV quartile. Results from these analyses are presented in Table 3. In both full and restricted data, STP EBV quartile was a significant predictor of STAY365. For full data calves, 71% of top STP EBV quartile calves remained in the herd at one year for age compared to 65% of calves in the bottom quartile. For restricted data calves, 73% of calves in the top STP EBV quartile remained in the herd at one year of age compared to 67% of calves in the bottom quartile. Similar to STP EBV quartiles, STP phenotype quartile was a significant predictor of STAY365. In the full dataset, 70% of top STP phenotype quartile calves remained in the herd at one year of age compared to 66% of lowest quartile calves. We found a similar result in our restricted dataset. Additional work is needed to confirm the genetic relationship between STP and stayability. However, our results seem to be in accordance with recent phenotypic data of others whom have shown that as STP

increases the risk of mortality decreases in calves (Henderson et al., 2011a; McCorquodale et al., 2013).

Approximate genetic correlations between STP and common health and fitness traits can be found in Table 4. The results are based on sire EBV derived from correlations with 256 sires within the restricted analysis and 302 sires in the full analysis. Sires in both analyses were included if they had 10 or more daughters with STP measurements; average reliability of STP was 0.45 for full data sires and was 0.36 for restricted data sires. We found a moderate approximate genetic correlation between STP and net merit dollars in the restricted analysis (0.28), suggesting animals genetically inclined for higher STP are also genetically inclined to have higher profit across their lifespans. In the full analysis, the approximate genetic correlation between STP and net merit dollars was positive but numerically lower than the restricted analysis estimate and non-significant. Moderate approximate genetic correlations were also estimated between STP and productive life (0.31 for full; 0.40 for restricted) and between STP and cow livability (0.38 for full; 0.42 for restricted). This seems to be in accordance with DeNise et al. (1989) who found calves with higher IgG at birth had numerically lower levels of culling during first lactation than calves with lower STP at birth.

We found an approximate genetic correlation between STP and milk yield of 0.13 for full data sires and 0.17 for restricted data sires. DeNise et al. (1989) showed a positive phenotypic association between calf IgG levels and subsequent first lactation milk production. Component yields were inconsistent between the two populations. In the full analysis, STP approximate genetic correlations with fat and protein yields were near zero and non-significant. In the restricted analysis, the approximate genetic correlations of

STP with fat and protein yields were positive; however, only the approximate genetic correlation with fat yield was significant. Therefore, it appears that selecting for STP would not negatively impact component yield in later life.

We found low to moderate approximate genetic correlations between STP and calving traits. Related to gestation length (GL), we found the approximate genetic correlations to be -0.18 and -0.30 for full and restricted data, respectively. Further, we found positive approximate genetic correlations between STP and early first calving (0.19 for full; 0.25 for restricted). In particular, STP seems to be correlated with sire calving traits. We found favorable (negative) approximate genetic correlations of STP with calving ease traits and sire stillbirth meaning that STP is genetically correlated with lower calving difficulty and lower rates of stillbirth. For full data sires, the approximate genetic correlations of STP with sire stillbirth and sire calving ease were -0.15 and -0.20, respectively. For restricted sires, the approximate genetic correlations of STP with sire stillbirth and sire calving ease were -0.24 and -0.31, respectively. Further, the approximate genetic correlation between STP and daughter calving ease was -0.24 for restricted sires. In both full and restricted sires, the approximate genetic correlation between STP and daughter stillbirth was near zero. These results suggest that stress around calving may be genetically correlated with lower passive transfer of immunity.

Previous reports were mixed when evaluating phenotypic correlations between FPT and dystocia. Donovan et al., (1986) found an association between higher dystocia and lower passive transfer, while Beam et al., (2009) did not find an association between herd dystocia rates and FPT. It should be noted that Donovan et al., (1986) and Beam et al., (2009) were using the binary FPT while we were using STP. Burton et al., (1989) and

Shivley et al., (2018) found no phenotypic association between calf IgG and dystocia in dairy cattle; however, in beef cattle, there is some evidence that IgG is lower in calves that required an assisted birth (Waldner and Rosengren, 2009).

We also examined the phenotypic relationships of STP with dam age and GL. These results are reported in Table 5. There was a significant and negative association between STP and dam age. Specifically, calves from 2-year-old dams had higher levels of STP in both the full and restricted analyses. This relationship with higher passive transfer in calves born from younger dams has been reported previously when evaluating IgG and lactation number (Shivley et al., 2018a).

Additionally, in both the full and restricted analyses calves in the highest GL quartile had lower STP than calves in the second quartile. This suggests that calves that were the result of average gestations had greater STP levels. The herds in this study did not record calving ease scores; therefore, we did not test direct associations between STP and direct calving ease. It may be that calves who experience abnormal GL also result from more difficult births, which may have a negative impact of STP. Other studies have shown an association between dystocia and GL (Hansen et al., 2004; Vieira-Neto et al., 2017). Generally, these studies have shown an intermediate optimum of GL for calf health.

These results in aggregate suggest that STP is most genetically correlated with longevity and calving traits. The heritability estimates for STP were similar or higher than that observed for most calf health traits; this suggests that STP is a logical candidate for further development in selection programs aimed at improving calf health. Genetic

relationships of STP with specific calf morbidity events are needed to fully access the utility of STP and will be the focus of future evaluations.

CONCLUSIONS

To the best of our knowledge, this the largest genetic study attempting to estimate genetic parameters for calf STP. We estimated the heritability of STP to range from 0.06 and 0.08. Favorable genetic correlations with calving traits and longevity were found. It may be worth incorporating on-farm measurements of passive transfer in evaluations of the genetic merit of calf health given the known impact of STP on calf health and mortality phenotypically. However, future work evaluating the genetic relationships with other measures of calf health is needed.

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Table 2-1: Descriptive statistics for serum total protein (STP), failure of passive transfer of immunity (FPT), and stayability to 365 days (STAY365)

	Restricted dataset			Full dataset[1]		
	STP	FPT	STAY365	STP	FPT	STAY365
n HYM[2]	98	98	86	98	98	86
Calves	7,518	7,518	6,052	16,725	16,725	14,527
Mean (SE) g/dL	6.39 (0.01)	NA	NA	6.37 (0.01)	NA	NA
%	NA	10%	69%	NA	11%	68%

[1]Full dataset permitted the maternal grandsire to be unknown whereas restricted required Holstein maternal grandsires

[2]Herd-year-months of birth

Table 2-2: Estimated variance components, heritabilities, and genetic correlations (SD) for serum total protein (STP), failure of passive transfer of immunity (FPT), and stayability to 365 days (STAY365)

	Restricted Dataset			Full Dataset[1]		
	STP	FPT	STAY365	STP	FPT	STAY365
Birthdate within Herd	0.08 (0.01)	0.24 (0.05)	0.04 (0.02)	0.08 (0.01)	0.18 (0.02)	0.04 (0.01)
Additive	0.05 (0.01)	0.08 (0.07)	0.14 (0.05)	0.04 (0.01)	0.05 (0.04)	0.09 (0.03)
Residual	0.47 (0.01)	*	*	0.48 (0.01)	*	*
Heritability	0.08 (0.02)	0.06 (0.04)	0.11 (0.03)	0.06 (0.01)	0.04 (0.03)	0.08 (0.02)
r_g with STP[2]	NA	0.99 (0.47)	0.19 (0.23)	NA	NA[3]	0.25 (0.17)

[1]Full dataset permitted the maternal grandsire to be unknown whereas restricted required Holstein maternal grandsires

[*]Residual variance was scaled to 1 in threshold models

[2]Genetic correlations with STP

[3]Failed to converge

Table 2-3: LSMEANS for the regressions of stayability to 365 days (STAY365) on serum total protein (STP) phenotype and STP EBV quartiles

	Restricted Dataset		Full Dataset[1]	
	STP Phenotype	STP EBV	STP Phenotype	STP EBV
Quartile 1	0.67[b]	0.67[b]	0.66[b]	0.65[c]
Quartile 2	0.68[b]	0.69[b]	0.68[b]	0.68[b]
Quartile 3	0.71[a]	0.69[b]	0.69[b]	0.69[ab]
Quartile 4	0.71[a]	0.73[a]	0.70[a]	0.71[a]

[1]Full dataset permitted the maternal grandsire to be unknown whereas restricted required Holstein maternal grandsires

[a-c]Different superscripts within a column represent significant differences (p-value < 0.05)

Table 2-4: Approximated genetic correlations (SE) of EBV for serum total protein (STP) with health, fitness, and production traits

Trait[1]	Restricted Dataset	Full Dataset[2]
NM$	0.28 (0.05)*	0.09 (0.05)
PL	0.40 (0.05)*	0.31 (0.05)*
LIV	0.42 (0.05)*	0.38 (0.05)*
SCS	0.01 (0.06)	-0.08 (0.06)
Milk	0.17 (0.06)*	0.13 (0.05)*
Fat	0.16 (0.06)*	-0.04 (0.06)
Protein	0.09 (0.06)	-0.01 (0.06)
DSB	-0.04 (0.06)	0.00 (0.06)
SSB	-0.24 (0.07)*	-0.15 (0.06)*
DCE	-0.24 (0.07)*	-0.11 (0.06)
SCE	-0.31 (0.07)*	-0.20 (0.06)*
GL	-0.30 (0.07)*	-0.18 (0.06)*
EFC	0.25 (0.05)*	0.19 (0.05)*

[1]NM = Net Merit; PL = productive life; LIV = cow livability; SCS = somatic cell score; DSB = daughter stillbirth; SSB = sire stillbirth; DCE = daughter calving ease; SCE = sire calving ease; GL = gestation length; EFC = early first calving

Table 2-5: LSMEANS for the regressions of serum total protein (STP) on gestation length (GL) and age of the dam in years.

	Restricted Dataset	Full Dataset[1]
GL[2]		
1	6.28[ab]	6.33[b]
2	6.33[a]	6.37[a]
3	6.29[ab]	6.31[b]
4	6.26[b]	6.30[b]
Dam Age		
2	6.45[a]	6.47[a]
3	6.29[b]	6.29[b]
4	6.30[b]	6.23[bc]
5	6.31[b]	6.28[bc]
≥6	6.30[b]	6.17[c]

[1]Full dataset permitted the maternal grandsire to be unknown whereas restricted required Holstein maternal grandsires

[2]GL quartile ranges: Restricted: Q1 = 251-273; Q2 = 274-275; Q3 = 276-278; Q4 = 279-298; Full: Q1 = 251-273; Q2 = 274-276; Q3 = 277-279; Q4 = 280-298

[a-c]Different superscripts within a column represent significant differences (p-value < 0.05)

Chapter 3

Genome-wide association study for calf serum total protein in US organic Holstein calves

ABSTRACT

Passive transfer of immunity is important for calf health and survival and can be measured by producers on farm. The objectives of this study were to identify regions of the genome that were associated with calf serum total protein. Serum total protein was measured by producers on farm for 16,725 Holstein sired calves between 1 and 3 days of age. Serum total protein was fitted using a linear model with fixed effects of calf age, dam age, and herd-year-month of birth as well as random effects of birthdate within herd and additive genetics. Genome-wide association was then carried out to determine regions of the genome influencing serum total protein. The mean serum total protein was 6.37 ± 0.01 g/dL and the heritability was 0.061 (SD = 0.012). In total, 9 SNP across the genome were found to be significantly associated with serum total protein. Further, there was a peak on BTA 11, corresponding to around 79 MbP, that appears to explain a substantial portion of additive variation. These results show help illustrate that serum total protein is a polygenic trait and helps to identify potential regions of the genome which may influence passive transfer of immunity.

Key words: serum total protein, GWAS, dairy calves

INTRODUCTION

Calves are born without a fully functioning innate immune system and require colostrum to achieve passive transfer of immunity (Godden, 2008). While serum immunoglobulin G (IgG) is the gold-standard when measuring passive transfer of immunity, it is easier and more economical for serum total protein to be measured on farm using a refractometer (Godden, 2008). Further, levels of serum total protein and IgG have high agreement following birth in newborn calves (Deelen et al., 2014; Wilm et al., 2018). The number of operations within the United States recording serum total protein on farm is growing. In 2006, 2.1 % of operations recorded serum total protein on farm compared to 6.2 % in 2013 (USDA, 2010, 2016). Large herds are more likely to record serum total protein and it is estimated that 35.3 % of all heifer calves in the United States are located on operations that record serum total protein.

Passive transfer of immunity is related to calf health and survival. Donovan et al. (1998) found that increased serum total protein was associated with reduced mortality through 6 months of age while Henderson et al. (2011) found similar results until one month before first calving. Further, Donovan et al. (1998) found that increased serum total protein was associated with reduced respiratory disease through 6 months of age and Urie et al. (2018) found that increased IgG concentrations were associated with reduced morbidity during the preweaning period. In addition, serum IgG may be associated with increased milk yield and increased culling during first lactation (DeNise et al., 1989).

We have previously shown that serum total protein is heritable in US organic Holstein sired calves ($h^2 = 0.06$; Haagen et al., 2021); therefore, the objective of the

current study was to investigate regions of the genome that may influence serum total protein.

MATERIALS & METHODS

Data

For a complete explanation of data available see Haagen et al. (2021). Briefly, records were available for 16,725 Holstein-sired calves born between July 2013 and June 2018 on multiple USDA certified organic operations. Calf STP was recorded on farm by producers and extracted from herd management software (DC305; Valley Ag Software, Tulare, CA). Calves were required to be 3 days of age or younger to be included in our analyses. Calves were assumed to be Holstein if they were recorded in herd management software as Holstein, had a Holstein sire, and either Holstein or unknown sires for additional 3 generations. Calves were genotyped with commercially available chips from either Zoetis (Kalamazoo, MI) or Neogen (Lansing, MI), and genotypes were subsequently imputed to 80k by Council on Dairy Cattle Breeding (CDCB; Bowie, MD). In total, there were 2,347 genotyped Holsteins and 205 animals had both genotype and phenotype records available.

Statistical Analysis

Variance components for STP were estimated using a univariate linear animal model in the airemlf90 program (version, 1.148, Misztal et al., 2018) with the following model:

$$y = \mu + HYM_j + age_k + Dage_l + B_m + A_n + e_{jklmn}$$

Where y is the phenotype; μ is the overall mean; *HYM* is the herd-month contemporary group *j* (levels = 98) at birth*; age* is the age in days of STP (k = 1, 2, or 3); and *Dage* is the age of the dam (*l*=2, 3, 4, 5, ≥6 years); B is the random effect for birthdate within herd *m*; *A* is the random additive genetic effect for animal *n* using relationship matrix H that includes both pedigree and genomic data; *e* is the random residual. Variance components were then used to calculate solutions using blupf90 (version 1.295; Misztal et al., 2018). Heritability was calculated as $h^2 = \frac{\sigma_A^2}{\sigma_A^2+\sigma_{HYM}^2+\sigma_e^2}$.

GWAS and Post-GWAS

Solutions and variances for SNP were estimated using the postGSf90 program (version 1.295; Misztal et al., 2018). Options within postGSf90 included those to calculate p-values and to calculate percent variance explained by 10 SNP moving averages. The closest gene to each SNP was identified within genome build ARS-UCD1.2 (Rosen et al., 2020) using bedtools (version 2.29.2; Quinlan and Hall, 2010). A Bonferroni correction was used to declare SNP significance and was set to a -log10(p-

value) of 6.20. Further, results were compared to quantitative trait loci (QTL) for IgG within the Cattle QTL database (Hu et al., 2019).

RESULTS AND DISCUSSION

Mean STP for calves in this study was 6.37 ± 0.01 g/dL and heritability was estimated at 0.061 (SD = 0.012). Figure 1 shows the Manhattan plot for SNP p-values and the top SNP based on p-values are listed in Table 1. Table 1 also includes the closest gene of the SNP. Nine SNP were significantly associated with STP and were located on BTA 1, 5, 6, 7, 11, 12, 15, and 20 with 2 significant SNP on BTA 20. The top SNP based on significance was located on BTA 5 at bp 54,870,507, and the closest gene was LRIG3 which is a transmembrane protein located 258 kb upstream of the significant SNP. Members of the LRIG gene family are thought to assist in protein recognition (Guo et al., 2004). We also searched for the for the 5 closest genes within 1 mb of significant SNP for potential candidate genes. Of particular interest was RSAD2 on BTA 11 which was 318 kb upstream of the significant SNP on BTA 11 which is involved in innate immunity in mice and humans (Stirnweiss et al., 2010; Jang et al., 2018). This may suggest a potential role of genes related to immune function influencing serum total protein levels in the newborn calf. The gene MYO10 was approximately 838 kb upstream of the SNP located at basepair 57,334,162 on BTA 20 and was identified as a candidate gene related to IgM in Swedish dairy calves (Cordero Solórzano, 2020). Our significant SNP did not overlap with QTL provided in the Cattle QTL database (Hu et al., 2019).

We were particularly interested in the peak on BTA 11 when evaluating percent variance explained (Figure 2). The 10 SNP window corresponding to this peak occurred from 79,203,608 to 79,354,581 bp and accounted for approximately 0.516 % of additive variance. The closest gene to this region was OSR1 which appears to be involved in embryonic development (Howe et al., 2021). We did not find any overlap between significant SNP from Table 1 and peaks from Figure 2 explaining more than 0.2 % of additive variance. Like the significant SNP, this region did not overlap with QTL in the Cattle QTL database (Hu et al., 2019).

CONCLUSIONS

Results suggest that serum total protein is heritable and is a polygenic trait as significant SNP were located across the genome. However, given the small sample size of animals that had both genotypes and phenotypes results should be viewed with caution.

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We are deeply appreciative of the organic dairy producers that supplied the records required for this project. This work was funded by USDA NIFA OREI competitive grant no. 2016 51300 25862. This work was supported by the USDA National Institute of Food and Agriculture and Hatch Appropriations under Project #PEN04691 and Accession #1018545.

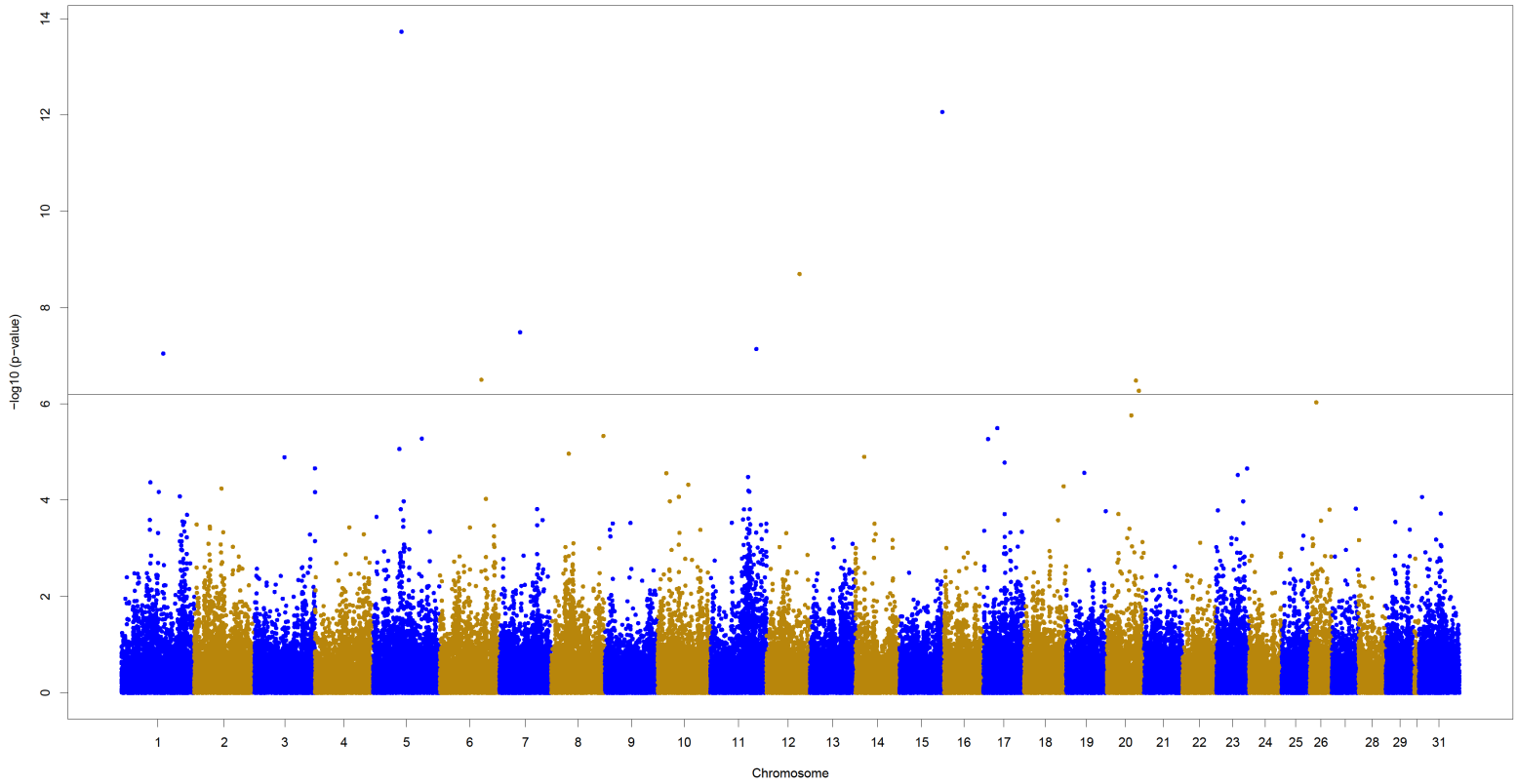

Figure 4-1: Manhattan plot of SNP p-values with horizontal line corresponding to significance threshold

Table 3-1: List of genes closest to significant SNP

Chromosome	Position	SNP	-log10(p-value)	Ensembl Name	Gene	Distance
5	54,870,507	BTA-88188-no-rs	13.73	ENSBTAG00000002227	LRIG3	257,701
15	81,246,518	BovineHD1500024090	12.06	ENSBTAG00000039893	OR9I1	12,333
12	70,124,010	BovineHD1200019369	8.70	ENSBTAG00000047383		
7	37,820,951	ARS-BFGL-NGS-33913	7.49	ENSBTAG00000025345	ARL10	19,092
11	90,374,630	BovineHD1100026142	7.14	ENSBTAG00000051441		31,471
1	96,509,488	BTA-43302-no-rs	7.04	ENSBTAG00000005386	SLC2A2	26,432
6	87,656,822	BovineHD0600024534	6.50	ENSBTAG00000006507	ADAMTS3	
20	57,334,162	BovineHD2000015830	6.48	ENSBTAG00000003219	FBXL7	94,692
20	62,914,219	BovineHD2000017868	6.27	ENSBTAG00000003536	MARCHF6	14,284

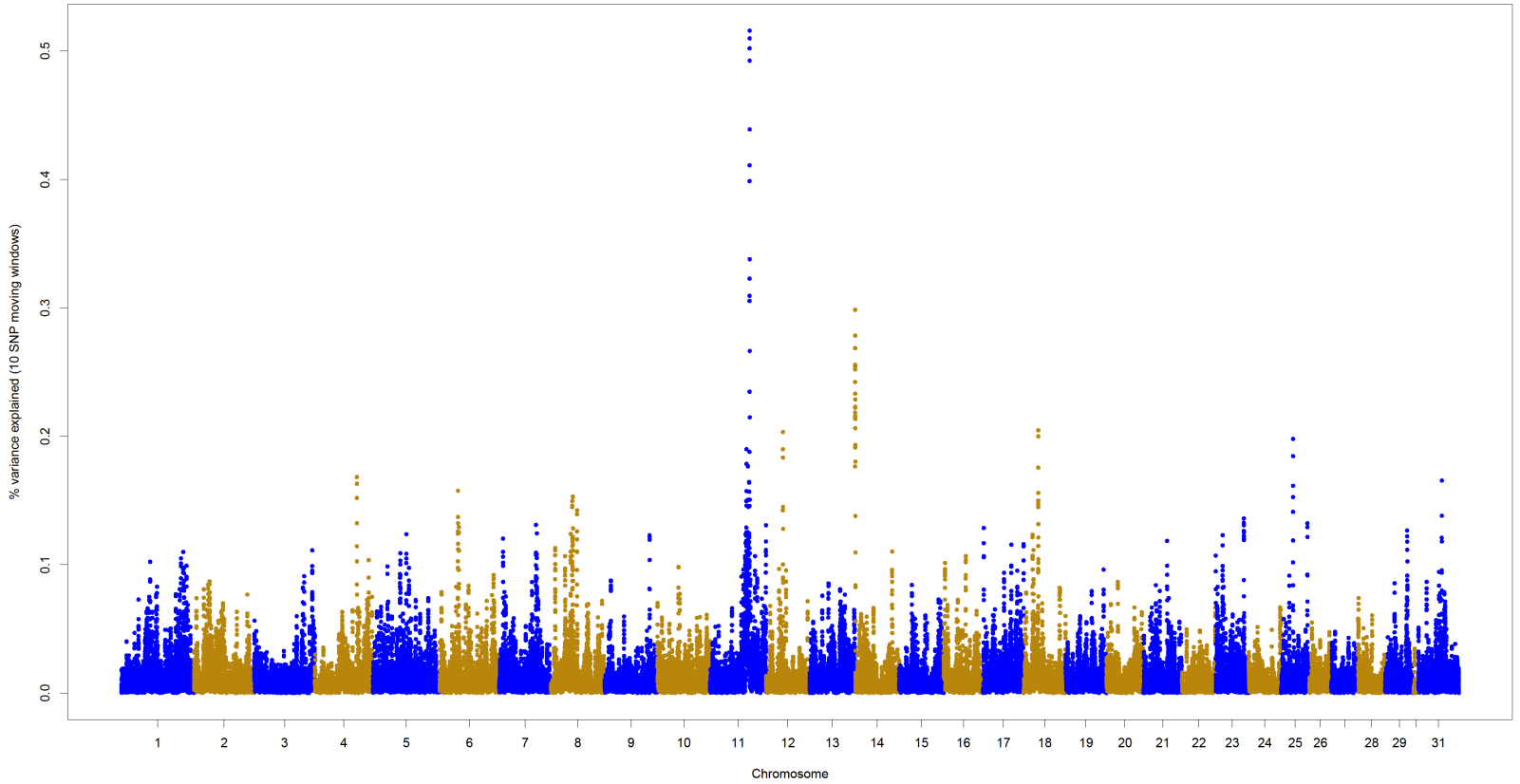

Figure 4-2: Manhattan plot of variance explained by 10-SNP moving windows

Chapter 4

Genetic parameters of calf morbidity and stayability for US organic Holstein calves

This is a modified version of the following manuscript currently under review:
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ABSTRACT

The objectives of this study were to estimate genetic parameters of calf health in organic US Holstein calves. Calves were born on farms across the United States from 2006 to 2019. Three calf health traits were evaluated in the study: calf respiratory disease until 365 days of age, calf scours until 60 days of age, and heifer stayability until 365 days of age. For respiratory disease and scours, animals were assigned a phenotype of 0 if they were healthy and a phenotype of 1 if they were diseased. For stayability, animals were assigned a phenotype of 0 if they were removed from the herd by 365 days of age and 1 if they remained in the herd at 365 days of age. Genetic parameters were estimated from threshold models which included the fixed effects of mean, year-season of birth, and dam age (respiratory disease and scours only) as well as the random effects of herd-year of birth and additive genetic. Heritability estimates were 0.100, 0.075, and 0.085 for respiratory disease, scours, and stayability, respectively. Signs were switched when presenting correlations such that higher correlations between scours, respiratory disease

and stayability were all favored. There was a moderate favorable genetic correlation estimate between respiratory and stayability of 0.675. However, genetic correlation estimates between respiratory disease and scours (0.148) and between scours and stayability (0.165) were low. Approximate genetic correlations with other traits evaluated nationally were generally low to moderate in magnitude. The strongest genetic correlation estimates were with longevity, particularly between stayability and heifer livability (0.417) and between stayability and cow livability (0.475); respiratory disease was also favorably correlated with heifer (0.355) and cow (0.296) livability. Approximate genetic correlations with cow health traits were generally low and unfavorable. Linear models including the random effect of herd-by-sire indicated that herd-by-sire accounted for approximately 2 percent of phenotypic variance for scours and stayability which may indicate a genotype by environment effect for these traits. There is significant genetic variation in organic calf health, and there was evidence of genotype by environment interaction.

INTRODUCTION

Dairy heifer morbidity and mortality are important considerations for animal well-being and farm profitability. Calf mortality is 5.0% on-farms (Urie et al., 2018b) and the two most common diseases in dairy youngstock are scours and respiratory disease. During the preweaning period, 18.9% and 11.3% of calves have been reported to show signs of digestive illness and respiratory disease, respectively (Urie et al., 2018a). During the postweaning period, respiratory disease is the most common illness in dairy cattle

with an overall incidence of 5.1% (USDA, 2018). The incidence of scours and respiratory disease have remained relatively stable across time despite improvements in management. In pre-weaned calves, the incidence of scours was 23.9% while the incidence of respiratory disease was 12.4% for calves born in 2006 (USDA, 2010).

In addition, dairy heifer replacements represent a substantial on-farm expense. Heinrichs et al. (2013) estimated the cost of raising a heifer from birth until calving to be $1,808 from a sampling of Pennsylvanian dairies. Therefore, heifers dying or leaving the operation for involuntary reasons before calving represent a substantial economic loss, especially when additional replacement animals must be purchased to offset losses. Youngstock disease has also been linked to reduced performance later in life, including increased age at first calving (Waltner-Toews et al., 1986; Heinrichs and Heinrichs, 2011); increased risk of being leaving the herd before first calving (Waltner-Toews et al., 1986; Closs and Dechow, 2017); and reduced first lactation yield (Heinrichs and Heinrichs, 2011).

Literature estimating genetic parameters of calf and heifer traits is limited but suggests that genetic selection for calf health and mortality is feasible. Gonzalez-Peña et al. (2019) estimated heritabilities of 0.042 and 0.045 for calf respiratory disease and calf scours, respectively; they also estimated the heritability of calf mortality to be 0.060. Henderson et al. (2011) estimated the heritability of respiratory disease to 0.095 and found heritabilities of 0.040 and 0.139 for bloat and umbilical disease, respectively. In addition, the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) estimates the heritability of heifer livability to be 0.004 and began publishing national evaluations in

the United States for heifer livability in December 2020 (CDCB, 2020b; Neupane et al., 2020).

However, the forementioned studies have largely been for conventional production and may not be relevant to organic dairy calves in the United States. In the United States, there are approximately 280,000 organic cows which are responsible for over 4 billion pounds of milk production and $1.4 billion in milk value (USDA, 2017). Organic dairy consumers consistently place a large emphasis on animal welfare (Hughner et al., 2007). Further, genetic selection for health may be of more importance on organic operations where producers are not able to use antibiotics without then removing the animal from the herd (Coffey and Baier, 2012). Organic producers are less likely to use antibiotics but more likely to use herbal alternatives for the treatment of calf diseases such as scours (Habing et al., 2016). Brock et al. (2021) found that roughly a third of organic producers in a survey of Ohio producers listed calf scours and calf respiratory disease as challenges.

Our primary objective was to estimate genetic parameters of calf health and stayability for US organic dairy calves. Genetic correlations of calf health and stayability were estimated and compared to officially published CDCB evaluations and to determine if genotype by environment interactions influence organic calf health.

MATERIALS AND METHODS

Data

Organic Holstein calves were born between 2006 and 2019 on organic dairy operations across the United States. Calves were required to have a known Holstein sire and maternal grandsire with either Holstein or unknown sires for an additional 2 generations. Producers recorded health events on farm and health event data were extracted from a combination of herd management software and on-farm paper records. Initial event screening restricted event records from birth until one month before calving. Events and remarks were searched for disease trait indicators. Events and remarks that were recorded simultaneously with a vaccination record were excluded. For each trait, only the first observation of the trait of interest was retained for analysis. Only events that were recorded for more than one percent of calves were retained; scours and respiratory disease were present in high enough frequencies to warrant individual investigation. For both diseases, animals recorded as diseased were assigned a phenotype of 1 and healthy animals were coded as 0.

Opportunity periods were established for both scours and respiratory disease which corresponded to when approximately 99 percent of all disease observations had occurred. Animals were required to have reached the opportunity period in age at the time of the last herd backup to be retained. For scours, the opportunity period was 60 days and for respiratory disease the opportunity period was 365 days. Therefore, for an animal to be included in the scours dataset they must have been born at least 60 days

before the last herd backup, and for an animal to be included in the respiratory dataset they must have been born at least 365 days before the last backup.

In addition, stayability to one year of age (0 = did not remain in herd, 1 = remained in herd), was defined for animals having the opportunity to reach one year of age. Therefore, to be included in the STAY365 dataset an animal must have been born at least one year before the last herd backup. As these were organic calves, any animal requiring antibiotic treatment was required to be removed from the herd but may have otherwise been healthy to continue in a conventional herd. Stayability was evaluated to account for all reasons an animal could leave a herd, including mortality, involuntary culling, and the removal of animals requiring antibiotic treatment.

Herd-years were required to have at least one recorded health event and a maximum incidence of 0.95 for respiratory disease and scours. In addition, the maximum incidence edit was applied to herd-weeks to ensure that calves within smaller management groups, for example within a single grouped pen, were treated for clinical disease rather than for prevention. A minimum number of calves to be born within a given herd-year was not imposed beyond requiring both phenotypes (healthy and diseased) be present. A minimum animal edit was not included in data edits because of smaller herds that may or may not have reached a threshold number of Holstein calves born within any given year but were still accurately recording calf disease.

Models

Each calf trait was evaluated with a univariate threshold animal model using the program thrgibbs1f90 (version 2.116, Misztal et al., 2018). For each model, a total of 500,000 iterations was used with a burn-in of 50,000 and saving every 50 samples. Scours and respiratory disease were modeled as:

$$y_{ijkl} = \mu + YS_i + Dage_j + HY_k + A_l + e_{ijkl}$$

Where y is the trait of interest (scours or respiratory disease; 0 = healthy and 1 = diseased), u is the overall mean, YS is the fixed effect of year-season i, D_{age} is the fixed effect of dam age (j = 2, 3, 4+), HY is the random herd-year contemporary birth group k, A is the random additive genetic effect for animal l with relationship matrix H that incorporates both pedigree and genomic information, and e is the residual variance. Stayability was fitted using the same model as scours and respiratory disease except with the omission of D_{age}.

Solutions for EBV and SE were obtained by rerunning the program thrgibbs1f90 (version 2.116, Misztal et al., 2018) with fixed means of variance as estimated from the univariate models and running for 10,000 iterations. Individual EBV for respiratory disease and scours were then transformed by switching signs so that their expression would correspond with disease resistance instead of disease risk. Heritabilities were calculated as:

$$h^2 = \frac{\sigma_A^2}{\sigma_{HY}^2+\sigma_A^2+\sigma_e^2}.$$

Where σ_A^2 is additive genetic variance, σ_{HY}^2 is herd-year variance, and σ_e^2 is residual variance.

Genetic correlations between our three calf health traits were estimated using a 3-trait model in thrgibbs1f90 (version 2.116, Misztal et al., 2018). Model effects remained the same from univariate models. Like the univariate models 500,000 iterations were used with 50,000 burn-in and saving every 50 samples.

Reliabilities for the calculation of approximate genetic correlations with nationally evaluated traits were calculated as follows:

$$REL_i = 1 - \left(\frac{SE_i^2}{(1 + f_i)\sigma_{BV}^2}\right)$$

Where SE is the SE for animal *i*, f is the inbreeding coefficient for animal *i* and σ_{BV}^2 is the breading value variance for the trait.

Approximate genetic correlations between the respiratory disease, scours, or stayability with traits evaluated by CDCB were estimated using the method of Calo et al. (1973):

$$\hat{r}_{g_{1,2}} = \frac{\sqrt{(\sum_{i=1}^{n} REL_{1i})(\sum_{i=1}^{n} REL_{2i})}}{\sum_{i=1}^{n}(REL_{1i} * REL_{2i})} * r_{1,2}$$

Where $\hat{r}_{g_{1,2}}^2$ is the approximate genetic correlation between traits 1 and 2, REL_{1i} and REL_{2i} are the reliabilities for trait 1 and trait 2, respectively, for sire i and $r_{1,2}$ is the Pearson correlation between EBVs for traits 1 and 2. Only sires with at least 75% reliability for lifetime net merit (**NM$)** and 25% reliability for the calf traits of interest where included.

Herd-by-sire interaction

To determine if herd-by-sire interactions existed, we included a random herd-by-sire effect into our models used to calculate variance parameters above. Convergence using a threshold model in thrgibbs1f90 (version 2.116, Misztal et al., 2018) was difficult after 500,000 iterations likely due to low additive variance for scours and stayability; therefore, a linear model was used to estimate variance components using the program airemlf90 (version 1.145, Misztal et al., 2018).

RESULTS AND DISCUSSION

Data

Summary statistics are provided in Table 1. Calves in this study had a respiratory disease incidence of 11.5%. It is important to recognize that the calf sample was from a limited number of organically certified farms. These herds were non-randomly chosen based on recommendations of known disease recording and use of artificial insemination from industry personnel and thus not representative of all organic production. However, the estimates of respiratory disease were similar to published sources. In a national survey, the incidence of respiratory disease was 12.4% in preweaned animals and 5.9% in weaned animals (USDA, 2010). More recently, Urie et al. (2018b) estimated the preweaned incidence of respiratory disease to be 11.3%. Gonzalez-Peña et al. (2019) estimated the incidence of respiratory disease to be 21.0% from birth until 365 days from producer records. Calves in this study had a scours incidence of 44.4%. This estimate was

higher than others; however, the farms in the current study were non-randomly chosen, and therefore, cannot be considered representative of all organic operations. Nationally, the incidence from producer surveys is approximately 23.9% (USDA, 2010). More recently, Urie et al. (2018b) found the incidence of digestive disease to 18.9%. Gonzalez-Peña et al. (2019) estimated the incidence of scours to be 26.1% using producer recorded data.

Stayability to one year of age was 75.0%. Thus, 75.0% of heifers born alive remained in the herd at one year of age and 25.0% of heifers born alive were removed from the herd for any reason. Stayability was chosen as a measure of calf longevity because calves left the herd for various reasons including mortality, involuntary culling, and treatment with antibiotics. Because the study population was US organic calves, an animal receiving antibiotic treatment would no longer be considered organic but may be a viable animal on a conventional operation.

Variance Components

Variance components from univariate models can be found in Table 2. For respiratory disease, the heritability was 0.100. This estimate is similar to that of Henderson et al. (2011), who estimated the heritability for respiratory disease to be 0.09 until calving on a commercial heifer raising operation and Neibergs et al. (2014) who estimated a heritability of 0.13 for calves located in California and New Mexico. Quick et al. (2020) found a similar heritability estimate of 0.11 until 6 weeks of age; however, they estimated a higher heritability of 0.24 when measured until 3 weeks of age. Gonzalez-

Peña et al. (2019) found the heritability to be 0.04 from birth until 365 days of age, which is the same age period that we defined for respiratory disease. McCorquodale et al. (2013) estimated the heritability of calf respiratory disease to be 0.04 when measured from birth until 3 months of age. However, the estimate of McCorquodale et al. (2013) also had a large standard error and was not different from zero.

For scours, the heritability was 0.075. Variance component estimates are less frequent in literature, but the estimate of heritability was similar to those of others. Gonzalez-Peña et al. (2019) estimated the heritability of diarrhea in Holstein calves up to 50 days of age to be 0.045. Mahmoud et al. (2017) found the heritability of calf diarrhea to be 0.06 from birth until 2 months of age in German Holstein-Friesian calves. In US Jerseys, Gonzalez-Peña et al. (2020) estimated a heritability of 0.084. For scours, we found that herd-years accounted for a large proportion of total variance suggesting that herd management and herd management trends may play a large role in phenotypic variation.

For stayability, the heritability was 0.085. Previously, we estimated the heritability for stayability to one year of age to range from 0.08 to 0.11 in a subset of calves that were also used in this present study (Haagen et al., 2021). While most previous literature has focused on mortality and death rates, stayability reflects a broader list of reasons that an animal could leave the herd including death, involuntary culling, and the culling of animals that required antibiotics. The latter is important for organic production as animals requiring antibiotic treatment are no longer viable in organic production but may otherwise be healthy to continue on conventional operations. Regardless, our estimate for the heritability of heifer stayability is similar to the mortality

estimates of others. Gonzalez-Peña et al. (2019) estimated the heritability of calf mortality to be 0.06 when measured until one year of age. McCorquodale et al. (2013) estimated the heritability to 0.06, but with a large corresponding standard error. In Danish Holsteins, Fuerst-Waltl and Sørensen, (2010) estimated the heritability 0.076 from birth until calving. On a New York heifer rearing operation, Henderson et al. (2011a) estimated the heritability of post-weaning heifer survival to be 0.036. The heritability estimate in the present study is higher than that estimated by Neupane et al. (2020), who estimated the heritability of heifer livability to 0.004 from birth until 18 months of age. Differences in heritabilities between stayability and mortality estimates could be due to various reasons, including differences in trait definitions, differences in production systems, and/or differences in producer records.

Genetic Correlations

Estimated genetic correlations among the three calf traits are in Table 3. While phenotypes were coded as 0 = health and 1 = diseased for modeling, signs were reversed for scours and respiratory disease when presenting genetic correlations. Therefore, for results in Table 3, scours and respiratory disease should be considered as disease resistance and positive correlations are favorable. The strongest correlation was between respiratory disease resistance and stayability with a genetic correlation estimate of 0.675. Gonzalez-Peña et al. (2019) estimated a similar genetic correlation between respiratory disease and mortality of 0.70. While definitions of longevity differ between our study and that of Gonzalez-Peña et al. (2019), we used similar calf age restrictions. This suggests a

moderately strong genetic correlation exists between respiratory disease and stayability in calves during the first year of life and that calves with low genetic merit for respiratory disease resistance are less likely to remain in the herd.

The genetic correlations of scours with both respiratory disease (0.148) and stayability (0.165) were low and displayed high standard deviations. The estimates are also lower than the genetic correlation estimates reported in other studies. For scours and respiratory disease, Gonzalez-Peña et al. (2019) estimated a genetic correlation of 0.555 using similar calf age periods as we used; Mahmoud et al. (2017) estimated a genetic correlation of 0.29 between diarrhea and respiratory disease, however calf ages were restricted to two months of age. Gonzalez-Peña et al. (2019) estimated a genetic correlation between scours and mortality of 0.464. Despite the smaller genetic correlation estimates in our study, correlations displayed the same sign directions reported by others. We are unsure of the reason for our low genetic correlation estimates compared to these studies. One potential explanation may be calves in an organic environment are under slightly different genetic control than calves conventionally managed. However, given the low frequency of estimates reported in the literature, it may be simply due to differences in calf populations, sire selection, trait recording on farm, or differences in researcher trait definitions.

Approximate genetic correlations between the three calf traits with traits evaluated by CDCB are in Table 4. In our analyses, respiratory disease and scours are expressed as disease resistance. Therefore, respiratory disease, scours, and stayability are all expressed such that larger EBV are favorable. Most approximate genetic correlations were low in magnitude. For yield traits, scours resistance was positively correlated with

milk (0.132) and protein (0.121). However, approximate genetic correlations with fat yield were unfavorable with scours resistance (-0.118) and stayability (-0.187). The direction of correlation between respiratory disease resistance and yield traits were like those between scours and yield traits but near zero. In German Holsteins, calf diseases exhibited low genetic correlation estimates with yield traits; genetic correlation estimates between calf scours risk and fat yield for the first two test-days during first lactation ranged from -0.14 to -0.15 suggesting increased risk was correlated with reduced fat yield (Mahmoud et al., 2017). Further, Gonzalez-Peña et al. (2019) estimated genetic correlations between scours risk and yield traits that ranged from -0.367 to -0.259 which would indicate increased risk was associated with reduced yield. In the same study, approximate genetic correlations between yield and both respiratory disease and mortality were near zero (Gonzalez-Peña et al., 2019). Henderson et al. (2011b) estimated a genetic correlation between calf respiratory disease resistance and fat yield of -0.17 suggesting that increased resistance was correlated with reduced fat yield. Neupane et al. (2020) estimated correlations between heifer livability and yield traits from 0.34 to 0.36. Therefore, while genetic correlation estimates of calf health and mortality with cow yields are generally small, there are conflicting results surrounding the direction of these correlations. These differences could be due to variety of factors including calf populations and trait definitions; therefore, future research is needed.

Small but positive approximate genetic correlations were found between calf health traits and NM$ that ranged from 0.030 to 0.088. However, because of the sample size and low magnitude these were not significantly different from zero. Fat and protein yields account for 43.7% of the current NM$ formula (VanRaden et al., 2018); given the

small genetic correlation approximations between our calf traits and yield it is not surprising that we did not find a stronger correlation between calf health and NM$. Gonzalez-Peña et al. (2019) estimated favorable genetic correlations between scours risk and NM$ (-0.427) and between mortality risk and NM$ (-0.190) but an unfavorable genetic correlation estimate between respiratory disease risk and NM$ (0.110). Therefore, the relationship between calf health and NM$ between studies appears to have a low to moderate relationship with the current NM$ index. However, the low magnitude highlights the opportunity to improve animal profitability through improved calf health.

Calf health traits generally exhibited the strongest approximate genetic correlations with longevity traits published by CDCB including heifer livability, cow livability, and cow productive life. We were particularly interested in the approximate genetic correlations between heifer livability and our measures of calf health since heifer livability is one of the few calf and heifer traits evaluated nationally by CDCB. The genetic correlation estimate between stayability and heifer livability (0.417) suggests that selection for improved heifer livability should also improve organic calf stayability until one year of age. Additionally, respiratory disease resistance was estimated to be favorably correlated with heifer livability (0.355). However, the approximate genetic correlation between heifer livability and scours resistance was unfavorable albeit low in magnitude (-0.147). This may have been due to differences in our calf population compared to the national population. There are few studies comparing genetic measures of calf health to heifer livability evaluated by CDCB as heifer livability was not publicly available until December 2020 (CDCB, 2020b).

The approximate genetic correlations of respiratory disease resistance with cow livability and productive life were 0.296 and 0.252, respectively; of scours resistance with cow livability and productive life were 0.163 and 0.126, respectively; and of stayability with cow livability and productive life were 0.475 and 0.346, respectively. Our approximate genetic correlation between stayability and productive life is similar to that of Neupane et al. (2020), who estimated a genetic correlation between heifer livability and productive life of 0.44. Gonzalez-Peña et al. (2019) found favorable approximate genetic correlations of calf scours risk with productive life (-0.345) and cow livability (-0.124) as well as between calf mortality risk and both productive life (-0.277) and cow livability (-0.275); however, the same study found unfavorable approximate genetic correlations between calf respiratory disease risk and productive life (0.113) and cow livability (0.132). Our results combined with the results of others, suggest that while calf health appears to be favorably associated with longevity traits, genetic correlations are relatively low and direct selection for calf longevity may be required to facilitate substantial genetic change.

Regarding calving traits, most correlations were low to moderate in magnitude and the majority were not significantly different from zero. Genetic correlation estimates between respiratory disease resistance and sire calving ease (0.167) and sire stillbirth (0.287) suggested that increased respiratory disease resistance was unfavorably correlated with increased calving difficulty and stillbirths. However, respiratory disease resistance was favorably associated with lower daughter stillbirth (-0.138). Scours and stayability were not genetically correlated with calving traits except for an unfavorable genetic correlation approximation between increased stayability and higher sire stillbirth (0.191).

Gonzalez-Peña et al. (2019) also found small approximate genetic correlations between calf health traits and calving traits with approximate genetic correlations between respiratory disease risk and sire calving ease (-0.138) and sire stillbirth (-0.027) which suggest that lower disease risk is unfavorably associated with higher calving difficulty. Gonzalez-Peña et al. (2019) found approximate genetic correlations that were mostly favorable for scours and mortality risks with calving traits except for the relationship between sire calving ease and scours. In literature, phenotypic relationships between calf health and mortality with calving difficulty are mixed. While increased calf mortality and disease were associated with increased calving difficulty in some studies (Lombard et al., 2007; Henderson et al., 2011a), other studies have also found no relationship for calf health and survival with calving difficulty (McCorquodale et al., 2013; Urie et al., 2018a).

Most approximated genetic correlations between calf health traits, particularly respiratory disease resistance and scours resistance, and cow heath traits were low to moderate in magnitude and unfavorable. Approximate genetic correlations between respiratory disease resistance were unfavorable with resistance for milk fever, retained placenta, ketosis, and metritis, ranging from -0.070 to -0.421, but favorable with mastitis resistance (0.167). For scours resistance, approximate genetic correlations were unfavorable with all cow health traits except milk fever and unfavorable correlations ranged from -0.069 to -0.283. However, approximate genetic correlations for stayability were more favorable with cow health being favorably correlated with milk fever resistance (0.139) and mastitis resistance (0.293). All calf traits were unfavorably genetically correlated with ketosis and metritis resistance, and except for ketosis and

metritis, directions for correlations changed from calf trait to calf trait. Gonzalez-Peña et al. (2019) and Mahmoud et al. (2017) also found low to moderate correlations between calf and cow health. Unlike the current study, Gonzalez-Peña et al. (2019) found mostly favorable correlations for calf scours risk and calf mortality risk with cow health. However, Mahmoud et al. (2017) found varying sign directions across genetic correlations. Our results combined with the results of others suggests that improved disease resistance for a single calf trait may not improve disease resistance in cows and vice versa. As such, if producers want to improve calf health through genetic selection, selection pressure should be put onto calf health traits.

The relationships between calf health traits and fertility traits are small. Both scours resistance and stayability do not appear to be associated with fertility as indicated by small approximate genetic correlations. Respiratory disease resistance also exhibited small approximate genetic correlations with fertility traits. Gonzalez-Peña et al. (2019) estimated unfavorable genetic correlations between respiratory disease and fertility but favorable genetic correlations between scours and fertility and between mortality and fertility.

Herd-by-sire interactions

In part due to the lower-than-expected approximate genetic correlation between stayability in the present study and heifer livability evaluated by CDCB, herd-by-sire interactions were determined to indicate genotype by environment interaction (Van Tassell and Berger, 1994). Results from linear models can be found in Table 5. While we

attempted to include a random herd-by-sire interaction in threshold models, we were not able to reach convergence for scours and stayability. Therefore, linear models were used for the three calf traits. Non-convergence was likely due to low additive genetic variance as suggested by our results from linear models in Table 5. Herd-by-sire interactions accounted for approximately 2% of phenotypic variance in both scours and stayability but less than 1% for respiratory disease. While herd-by-sire variance was relatively small, the inclusion of herd-by-sire caused heritability estimates from linear models to be close to zero for scours and respiratory disease and may indicate overestimation of heritability from models not including herd-by-sire effects. The herds in this study were from across the US and have varying management practices. The unadjusted EBV correlation between stayability EBV when estimated from a linear model including herd-by-sire and heifer livability was 0.274 for sires with a reliability for stayability greater than 0.25. Therefore, while we found herd-by-sire accounted for non-trivial amounts of phenotypic variance, stayability remained positively correlated with heifer livability. In the future, additional research is needed to determine how sires rank across organic and conventional environments for calf health traits.

CONCLUSIONS

Results from the present study suggest that calf health traits when evaluated using organically managed calves is heritable. Heritabilities for calf respiratory, calf scours, and calf stayability ranged from 0.075 to 0.100 using threshold animal models. Genetic correlation estimates with other currently evaluated traits were generally low and suggest

that genetic evaluations of calf traits may be needed to increase genetic progress in calf health. However, inclusion of herd-by-sire within linear models suggests phenotypic variance is partially explained by genotype by environment effects.

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Table 4-1: Descriptive statistics for calf respiratory disease until 365 days, calf scours until 60 days, and stayability until 365 days of age.

	Respiratory	Scours	Stayability
Calves (n)	10,527	11,603	13,987
Year-seasons (n)	22	29	49
Herd-years (n)	17	27	51
Pedigree (n)	24,466	28,547	31,919
Genotypes + Phenotypes (n)	253	279	754
Incidence (%)	11.5	44.4	75.0

Table 4-2: Variance components and heritability estimates[1] (SD) for calf health traits

	σ^2_{HY}	σ^2_A	σ^2_e	h^2
Respiratory	0.392 (0.289)	0.153 (0.047)	1.002 (0.020)	0.100 (0.031)
Scours	1.904 (0.777)	0.225 (0.051)	1.002 (0.019)	0.075 (0.021)
Stayability	0.336 (0.097)	0.125 (0.032)	1.003 (0.017)	0.085 (0.020)

[1] σ^2_{HY} = herd-year variance; σ^2_A = additive genetic variance; σ^2_e = residual variance; h^2 = heritability

Table 4-3: Genetic correlation (SD) estimates among calf health traits.

	Scours	Stayability
Respiratory	0.148 (0.195)	0.675 (0.118)
Scours		0.165 (0.153)

Table 4-4: Approximate genetic correlation estimates between calf health and CDCB traits[1] for sires with at least 25% reliability for the calf trait of interest.

	Respiratory	Scours	STAY365
Sires (n)	207	302	275
Milk	0.079	0.132*	0.063
Fat	-0.047	-0.118*	-0.187*
Protein	0.047	0.121*	-0.056
NM$	0.088	0.030	0.033
HLIV	0.355*	-0.147*	0.417*
LIV	0.296*	0.163*	0.475*
PL	0.252*	0.126*	0.346*
DCE	-0.005	-0.012	0.090
DSB	-0.138*	0.009	-0.036
SCE	0.167*	0.066	0.071
SSB	0.287*	0.030	0.191*
EFC	-0.119	-0.114*	0.001
GL	0.030	0.029	0.061
SCS	-0.003	0.193*	-0.080
MAST	0.167*	-0.176*	0.293*
MFEV	-0.193*	0.008	0.139*
DA	-0.070	-0.151*	-0.040
RP	-0.225*	-0.069	0.021
KETO	-0.149*	-0.214*	-0.259*
MET	-0.421*	-0.283*	-0.200*
DPR	-0.104	-0.008	0.048
CCR	-0.064	0.017	0.068
HCR	-0.122	0.035	0.046

[1]NM$ = lifetime net merit dollars; HLIV = heifer livability; LIV = cow livability; PL = productive life; DCE = daughter calving ease; DSB = daughter stillbirth; SCE = sire calving ease; SSB = sire stillbirth; EFC = early first calving; GL = gestation length; SCS = somatic cell score; MAST = mastitis; MFEV = milk fever; DA = displaced abomasum; RP = retained placenta; KETO = ketosis; MET = metritis; DPR = daughter pregnancy rate; CCR = cow conception rate; HCR = heifer conception rate

*p-value < 0.05

Table 4-5: Variance component estimates[1] (SE) from linear models incorporating the random effect of herd-by-sire.

	σ^2_{HY}	σ^2_{HSire}	σ^2_A	σ^2_e
Respiratory	0.0071 (0.0038)	0.0010 (0.0005)	0.0030 (0.0015)	0.0927 (0.0017)
Scours	0.0893 (0.0315)	0.0051 (0.0011)	0.0017 (0.0022)	0.1665 (0.0027)
Stayability	0.0143 (0.0039)	0.0040 (0.0009)	0.0005 (0.0017)	0.1716 (0.0024)

[1] σ^2_{HY} = herd-year variance; σ^2_{HSire} = herd-by-sire variance; σ^2_A = additive genetic variance; σ^2_e= residual variance

Chapter 5

Genetic parameters of direct calf health costs for US organic Holsteins

ABSTRACT

The objective of this study was to estimate genetic parameters for direct treatment costs in US Organic Holstein calves and nulliparous heifers. Treatment costs were derived for 17,936 youngstock located on 16 USDA certified organic operations located throughout the United States. Producers were surveyed for treatment costs related veterinary treatment, on-farm supplies, and on-farm labor for treatment for two calf diseases: respiratory disease and scours. In addition, total treatment cost was calculated as the sum of respiratory disease costs, scours costs, and disposal costs. A minimum of 4 and 5 days were required between scours and respiratory disease events, respectively, to declare a new treatment. All treatment costs were summed until 18 months of age. Genetic parameters for the three calf treatment costs were estimated using a three-trait linear animal model that included the fixed effects of mean, hear-year of birth, dam age, and opportunity age of the calf as well as the random effects of additive genetic and herd-year-season of birth. Because total treatment costs was semi-continuous and right-skewed we also investigated various response variables to assess changes in heritability and reliability estimates; these included a univariate model of total treatment cost, a univariate model of log-transformed treatment cost, and 2-trait conditional model with response variables any treatment cost (0 = no treatment costs; 1 = treatment cost greater

than $0) and log-transformed total treatment cost conditional on any treatment cost. Average treatment costs per case were $56.37 for respiratory disease and $25.21 for scours. The average cost per animal were $10.19 for respiratory disease, $25.03 for scours, and $25.00 for total treatment cost. Heritability estimates were 0.051, 0.057, and 0.047 for respiratory disease, scours, and total treatment costs, respectively. Genetic correlations between total costs and respiratory disease costs and scours costs were 0.495 and 0.645, respectively, while the correlation between respiratory disease costs and scours costs was -0.331. When comparing total treatment cost response variables, the model with log-transformed total treatment cost resulted in the highest heritability and reliability estimates while the 2-trait model had the lowest. Correlations with traits evaluated by the Council on Dairy Breeding based on PTA values were low and mostly not significant suggesting that calf and heifer treatment costs are generally not genetically correlated with current national traits in the United States. Genetic variation for youngstock heath treatment costs was detected; however, heritability estimates were generally low and comparable to estimates for binary disease events despite the continuous nature of treatment costs.

INTRODUCTION

Youngstock represent a substantial expense on dairy operations. Heinrichs et al. (2013) estimated the cost of raising a replacement heifer from birth until calving to be $1,805 on Pennsylvania operations while Karszes and Hill (2020) reported a cost of $2,355 across the Northeast United States. Few estimates are available for health

treatment costs in youngstock in the United States. Recently, Dubrovsky et al. (2019) estimated the cost to treat preweaning respiratory disease to be $36.46 to 36.95 for the first treatment case. Kaneene and Scott Hurd (1990) estimated the preweaning cost of scours and respiratory disease to be $33.46 and $14.71 per calf per year though the costs in weaned heifers was lower at $0.71 to $1.95 per animal per year.

Most reports of heritability estimates for calf and heifer health indicate these traits are lowly heritable. Gonzalez-Peña et al. (2019) reported heritability estimates from producer recorded data for calf scours, calf respiratory disease, and calf mortality with estimates ranging from 0.042 to 0.060. Haagen et al. (*under review*) reported heritability estimates in Organic US Holstein calves for respiratory disease (0.100), scours (0.075), and stayability (0.085). Donnelly et al. (2017) showed that heritability estimates of health costs for individual diseases (h^2 = 0.04 to 0.13) were generally in agreement with their respective binary disease traits; however, they reported a substantially higher heritability estimate for total health costs (h^2 = 0.27) and suggested this might be due to an increase in variation between cows coupled with a continuous measure of health in contrast to a binary disease event. With this in mind, the objective of this study was estimate genetic parameters for calf and heifer disease treatment costs including total treatment cost.

MATERIALS AND METHODS

Data

Youngstock (n=17,396) were located on 16 USDA certified organic dairy operations located across the United States. Health events were extracted from a combination of herd management software (PCDart, DRMS, Raleigh, NC; DC305, Valley Ag Software, Tulare, CA; or DHI-Plus, Amelicor, Provo, UT) and paper records. Calves were all female and required to be listed as Holstein in herd management, have a Holstein sire and maternal grandsire, and have Holstein or unknown sires for additional 2 generations. Events present in greater than 1% of the calf population were considered for further exploration and included respiratory disease and scours.

Producers (n = 10) provided treatment costs associated with respiratory disease and scours which included costs for veterinary treatment, costs for on-farm treatment, and the time associated with on-farm treatment to facilitate the calculation of labor costs. Producers were informed that veterinary treatment referred to costs incurred for disease treatment performed by veterinarians or other off-farm personnel, such as a hoof trimer, and might include stop fees (base fee to visit dairy), off-farm personnel labor charges, and the costs of supplies used for treatment performed by veterinarians or off-farm personnel. On-farm treatment costs refer to total supply costs associated with treatment protocols not involving off-farm personnel. In addition, producers provided the time (minutes) required to perform protocols and the duration of treatment in days associated with protocols. Producers were not asked to describe supplies, such as herbals and other

pharmaceuticals, associated with protocols to ensure privacy. To calculate total labor costs, a fixed hourly labor cost of $18.10 was assumed based upon a standard 40-hour full time equivalent work week and the national average weekly wage for dairy workers of $724 (U.S. Bureau of Labor Statistics, 2020). Animals that died on farm were assigned a direct cost of disposal of $6.00.

Unique event occurrences were established for each disease if the average length of treatment occurred between disease events. Treatment durations averaged 5 days and 4 days for respiratory disease and scours, respectively; therefore, a new event was declared if 5 days had passed between respiratory events or 4 days had passed between scours events. For both respiratory disease and scours, treatment costs per calf were calculated as the product of mean treatment cost and number of event occurrences. In addition, total treatment cost (TOT$) was calculated as the sum of respiratory disease cost (RESP$), scours cost (SCOUR$), and dead calf disposal. All costs were summed until 18 months of age. Our costs correspond to direct treatment costs and do not reflect lost performance in other traits that already receive national genetic evaluations such as age at first calving and milk production.

Models

A three trait model was used to estimate (co)variance components for and between the three calf cost traits in thrgibbs1f90 (version 2.118, Misztal et al., 2018). A total of 200,000 iterations was used with a burn-in of 30,000 and saving every 20 samples. Total treatment cost, respiratory disease cost, and scours costs were modeled as:

$$y_{ijklm} = \mu + YS_i + Dage_j + \beta_1 OppAge + HYS_l + A_m + e_{ijklm}$$

Where YS is year-season of birth i, Dage is dam age in years (j = 2, 3, 4+), OppAge is opportunity age in days until 18 months of age, HYS is the random effect of herd-year-season of birth l, A is random additive genetic effect with relationship matrix H which incorporates both pedigree and genotype information, and e is random residual.

Response variables were semi-continuous with a floor value of $0 and right skewed. Therefore, various trait definitions were compared for total treatment cost and included the following situations 1) untransformed raw total cost (TOT$, 2) natural log-transformed total cost where the response variable was x + 0.01 to facilitate derivation of the transformation for calves with no cost (LOGTOT$), and 3) a 2-trait model which included a binary variable describing whether a calf had any cost (ANY2T; 0 = no treatment costs, 1 = treatment cost greater than $0) and a log-transformed total treatment cost for animals that had costs greater than $0 or missing if they had a cost of $0 (LOGTOT2T$). In situations 1 and 2, univariate linear models were used while in situation 3 a bivariate model was fit. All situations were modeled using the program thrgibbs1f90 (version 2.118, Misztal et al., 2018), and all situations used 200,000 iterations with a burn-in of 30,000 and saving every 20 samples. Predictor variables remained the same as previously described.

Solutions for EBV and SE were obtained by including “option solution mean” within the program thrgibbs1f90 (version 2.118, Misztal et al., 2018). Heritabilities were calculated as:

$$h^2 = \frac{\sigma_A^2}{\sigma_{HYS}^2 + \sigma_A^2 + \sigma_e^2}.$$

Where σ_A^2 is additive genetic variance, σ_{HYS}^2 is herd-year variance, and σ_e^2 is residual variance.

Reliabilities for the were calculated as follows:

$$REL_i = 1 - \left(\frac{SE_i^2}{(1 + f_i)\sigma_{BV}^2}\right)$$

Where SE is the SE for animal *i*, f is the inbreeding coefficient for animal *i* and σ_{BV}^2 is the breading value variance for the trait.

Genetic correlations with other traits

Pearson correlation coefficients between health treatment cost traits and traits routinely evaluated by the Council on Dairy Cattle Breeding (CDCB; Bowie, MD) were calculated using PROC CORR of SAS (version 9.4; Cary, NC). Only sires with at least 75% reliability for lifetime net merit (**NM$)** and at least 20 daughters for the calf traits of interest where included.

RESULTS AND DISCUSSION

Direct disease costs and calf data

Table 1 shows summarized disease costs from producer surveys. The average cost per case among farms for respiratory disease was $56.37 ± 28.87 (range: $7.13 to $252.91). The average cost per case among farms for scours was $25.21 ± 3.98 (range: $3 to $52.61). The median costs per case of respiratory disease and scours were $30.89

and $25.36, respectively. The mean and median costs were very similar for scours; however, there was a $25.48 difference between the mean and median cost for respiratory disease treatment. This was due to one farm reporting a cost for respiratory disease treatment that was very large ($252.91). However, it was assumed that producers were more likely to underreport costs than overreport; therefore, we chose to keep this observation in our calculation for mean costs. For both diseases, on-farm supplies were the largest mean expense and would include all supply costs, such as herbals and pharmaceuticals, administered by on-farm personnel. On-farm supply costs were followed by mean on-farm labor and mean veterinary treatment. Once again, veterinary treatment would include all treatment costs performed by off-farm personnel and could include costs such as stop fees (off-farm personnel fee to visit dairy), supplies (herbals, pharmaceuticals) used by off-farm personnel, and off-farm labor charges. It should be noted that while organic operations in this study were located across the United States, they were non-randomly selected as they were required to use AI and may not be representative of all US organic operations. Very few studies have estimated the cost of calf and heifer disease and to the best of our knowledge this is one of the first reporting youngstock disease costs under organic management. Recently, Dubrovsky et al. (2020) estimated the cost of treating preweaning respiratory disease on Californian dairies to be $36.95 for the first cast of respiratory disease with the cost per case decreasing to approximately $32 in calves requiring subsequent treatment. This estimate is lower than what we report. Dubrovsky et al. (2020) used similar categories to calculate treatment costs including medication and labor costs; however, the aforementioned study also

included a cost associated with lost average daily gain which we did not include in our cost estimates. We estimated higher costs for both on-farm supplies, which roughly correlates with medication costs, and labor (Dubrovsky et al., 2020). We used producer reported average costs per treatment and did not request producer treatment protocols whereas Dubrovsky et al. (2020) calculated average pharmaceutical costs based on producer treatment protocols. We chose not to request treatment protocols to protect producer privacy. Further, our costs represent youngstock both pre- and postweaning whereas Dubrovsky et al. (2020) estimated costs in preweaned calves only. Perhaps the biggest difference between our study and that of Dubrovsky et al. (2020) is that animals in the current study were all raised on USDA certified organic operations which may have resulted in different treatment costs.

A summary of animals used can be found in Table 2 along with the mean cost of treatment per animal until 18 months of age. The average total treatment cost per animal was $25.00, and 53 % of animals had total treatment cost greater than $0.00. Total treatment cost was the sum of respiratory disease cost, scours cost, and disposal cost for dead animals. Therefore, it was possible for an animal to have a total treatment cost that included a disposal fee without a cost for respiratory disease or scours. In addition, the mean natural log transformed total treatment cost was -0.261 for all animals while for animals with a treatment cost greater than zero the mean natural log transformed total treatment cost was 3.589. The mean costs per animal for respiratory disease and scours were $10.19 and $25.03, respectively. Kaneene and Scott Hurd (1990) estimated the cost per calf per year to be $14.71 and $33.46 for respiratory disease and scours, respectively,

in preweaned calves; cost per head per year were $1.95 and $0.71 for respiratory disease and scours, respectively, in weaned animals. Our average costs per animal through 18 months are similar to the estimates of Kaneene and Scott Hurd (1990) through the preweaning period. Kaneene and Scott Hurd (1990) included costs not incorporated in our direct treatment costs such as preventative costs and replacement costs associated with dead calves. Given the gap in publication date, there is also a large difference in assumed labor costs as Kaneene and Scott Hurd (1990) assumed a labor cost of $5.50 / hour while we assume $18.10 / hour. However, Kaneene and Scott Hurd (1990) did not breakdown costs by input (for example supply costs, veterinary costs, labor costs) which would have allowed us to more directly compare cost breakdowns. Finally, our data comes exclusively from organic dairies.

Genetic parameters

Heritability and genetic correlation estimates among the three calf cost traits are presented in Table 3. Heritability estimates were low, ranging from 0.047 for TOT$ to 0.057 for SCOUR$. Respiratory disease cost and scours cost are similar, albeit numerically lower, to the estimates of calf health traits when using binary response variables using a similar dataset (Haagen et al., *under review*); in that study, heritability estimates were 0.100 and 0.075 for respiratory disease and scours, respectively. Our heritability estimates for RESP$ and SCOUR$ were also comparable to other estimates of heritability for binary disease traits in youngstock (Heringstad et al., 2008; Henderson et al., 2011b; Gonzalez-Peña et al., 2019).

Like the present study in calves, Donnelly et al. (2017) reported that heritability estimates between cow disease costs (h^2 = 0.04 to 0.13) and their respective binary disease traits reported in the literature were similar. However, unlike the present study, Donnelly et al. (2017) estimated a substantially higher heritability for total cow health costs (h^2 = 0.27). One reason for this might be that Donnelly et al. (2017) included over 14 cow treatments in their calculation of total health costs which allowed for an increase in variation between animals while we only incorporated 3 treatments (respiratory disease, scours, and disposal) into our total health costs for youngstock. Our heritability estimates suggest that selection for total treatment costs in youngstock may not have an advantage over selection for binary disease traits. However, there may be some advantages in the dissemination of results to industry as it may be easier to translate total treatment dollars from a linear model than calculated probabilities from a binary threshold model.

Total treatment cost was genetically correlated with both RESP$ and SCOUR$ with estimates of 0.495 and 0.645, respectively. This is logical as TOT$ is a function of RESP$ and SCOUR$. Further, it suggests that within our dataset costs associated with treating scours are more strongly genetically correlated with TOT$. However, RESP$ and SCOUR$ exhibited a negative genetic correlation (-0.331; SD = 0.096) suggesting that increased costs for one disease is correlated with decreased cost for another. This relationship was not expected and suggests that treatment for one disease did not dispose calves to treatment for another disease. Using a similar dataset, Haagen et al. (*under review*) previously estimated the genetic correlation between respiratory disease

resistance until 365 days of age and scours resistance until 60 days of age to be 0.148 (SD = 0.195). Using producer recorded data, Gonzalez-Peña et al. (2019) estimated a substantially higher genetic correlation between the binary traits of scours until 50 days of age and respiratory disease until 365 days of age (0.555). Within the current dataset, the phenotypic correlation between RESP$ and SCOUR$ was near zero (0.03) so a moderate genetic correlation is not surprising.

Response variables were semi-continuous with a minimum value of $0 and right skewed. Therefore, we also attempted to fit various response variables to assess changes to heritability estimates and reliability estimates. Three models were evaluated including a univariate model of total treatment cost, a univariate model with log transformed total cost as the response variable and a 2-trait model that included the response variables of whether an animal had any treatment cost (binary) and log-transformed total cost that was conditional on an animal having a treatment cost greater than $0 (continuous). Results from this analysis are reported in Table 4. Heritability estimates were very similar across models with the univariate model of log-transformed total cost having the largest numeric estimate at 0.060. The univariate model with log-transformed total cost as the response variable also had the greatest reliability for sires with at least 20 daughters (rel = 0.528).

Interestingly, the 2-trait model that included the binary response variable of any treatment cost and the conditional log transformed treatment cost resulted in the lowest heritability and reliability. The genetic correlation between natural log transformed treatment cost and the binary trait indicating the presence or absence of treatment was 0.142 (SD = 0.177), which was much lower than anticipated. The low genetic correlation

suggests total treatment cost may be genetically independent of whether an animal was treated.

Correlations with national traits

Pearson correlations between PTA values of treatment costs and genetic traits published by CDCB are reported in Table 5. Correlation estimates were generally low and not significant with total treatment costs except for early first calving (0.179), gestation length (-0.145), and ketosis resistance (0.134). These correlations suggest that increased youngstock treatment costs are associated with an earlier first calving, shorter gestation length, and increased ketosis resistance. Heinrichs et al. (2005) reported from a regression analysis that age at first calving increased (beta estimate = 10 days; p-value = 0.06) as days treated for scours and respiratory disease increased during the first 4 months of age. Heifer livability exhibited a favorable, albeit not significant, correlation (-0.062) with total treatment costs that was in the expected direction. Correlations of natural log transformed total cost and any cost from the 2-trait model were mostly near zero and not significant with the exceptions of early first calving and ketosis which showed similar correlations as total treatment cost. Natural log transformed total cost from the 2-trait model which was conditional on treatment cost being greater than $0 was the only trait to be correlated with yield traits (0.168 to 0.188) and net merit (0.148). This may suggest that for calves treated for calf and heifer disease, increased costs were associated with greater yield and net merit based on PTA correlations.

Respiratory treatment cost exhibited significant correlation estimates with heifer livability (-0.202), mastitis resistance (-0.142) and milk fever resistance (0.113); these correlation estimates suggest that increased respiratory disease treatment costs are correlated with decreased heifer livability heifer livability, decreased resistance to mastitis, and increased resistance to milk fever. Interestingly, scours treatment costs exhibited a correlation of 0.124 with heifer livability which would suggest increased scours costs were associated with increased heifer livability and is opposite of the PTA correlation between respiratory disease costs and heifer livability. In addition, while trivial in magnitude, the correlations of Net Merit with respiratory disease costs (-0.067) and scours costs (0.073) were in opposite directions. This is not entirely surprisingly given the negative genetic correlation estimate between respiratory disease costs and scours costs.

Haagen et al. (*under review*) using a similar dataset also estimated small genetic correlations between the binary traits of respiratory disease resistance and scours resistance with official genetic evaluations in the United States. Taken together, this may suggest that selection of calf health traits (treatment costs or binary resistance) is not strongly genetically correlated with official traits evaluated nationally in the United States. Alternatively, genetic evaluations based on conventional herd data may not translate well to an organic system in regards to calf health. In cows, Hardie et al. (*under review*) evaluated the potential for genotype by environment interactions between organic and conventional animals. Genetic correlations estimates between similar traits less than 0.80 may suggest the presence of genotype by environment interactions (Robertson,

1959). Hardie et al. (*under review*) reported approximate genetic correlations between organic cow health traits and nationally evaluated health traits by CDCB less than 0.80; for example, the approximate genetic correlation between mastitis in US organic cows and mastitis evaluated by CDCB was 0.72 and was the strongest approximate genetic correlation found between health traits estimated in organic cows and CDCB health traits.

CONCLUSIONS

Dairy calf and heifer treatment costs appear to be lowly heritable with heritability estimates ranging from 0.047 for total treatment costs to 0.057 for scours treatment costs. These estimates are similar to other estimates looking at binary disease risk in youngstock. While combining separate health costs into a single measure may simplify estimation of genetic merit for calf health expense, heritability estimates were not improved by considering total treatment costs relative to individual disease costs.

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Table 5-1: Estimates of veterinary treatment, on-farm supplies, on-farm labor, and total costs required to treat respiratory disease and scours

	Veterinary Treatment ($)	On-farm Supplies ($)	On-farm Labor ($)	Total ($)
Respiratory disease				
Mean	10.94 ± 7.26	24.29 ± 17.72	21.14 ± 12.30	56.37 ± 28.87
Median	0.00	6.81	10.86	30.89
Min	0.00	0.00	0.00	7.13
Max	50.00	147.33	105.58	252.91
Scours				
Mean	2.29 ± 2.03	12.24 ± 1.71	10.69 ± 4.23	25.21 ± 3.98
Median	0.00	12.23	8.11	25.36
Min	0.00	3.00	0.00	3.00
Max	20.40	19.00	46.31	52.61

Table 5-2: Descriptive statistics of calves used for estimation of genetic parameters.

	RESP$[1]	SCOUR$	TOT$	LOGTOT$	ANY2T	LOGTOT2T$
Calves (n)	9820	12302	17936	17936	17936	9509
Year-seasons (n)	23	28	54	54	54	54
Herd-year-seasons (n)	32	45	238	238	238	178
Mean	10.193 ± 0.271	25.029 ± 0.226	25.001 ± 0.253	-0.261 ± 0.031	0.530 ± 0.004	3.589 ± 0.008

[1]RESP$ = respiratory disease treatment costs; SCOUR$ = scours treatment costs; TOT$ = total health treatment costs; LOGTOT$ = natural log transformed total treatment cost; ANY2T = binary any treatment cost (0 = no cost; 1 = cost greater than $0) used in 2 trait model; LOGTOT2T$ = natural log transformed total treatment cost for calves with treatment cost greater than $0 used in 2 trait model

Table 5-3: Genetic parameter estimates (SD) from a 3-trait model including RESP$, SCOUR$ and TOT$[1]. Heritability estimates along diagonal; Genetic correlation estimates among calf health traits above diagonal

	σ_A^2	RESP$	SCOUR$	TOT$
RESP$	29.245 (5.299)	0.051 (0.010)	-0.331 (0.096)	0.495 (0.085)
SCOUR$	41.920 (5.392)		0.057 (0.011)	0.645 (0.068)
TOT$	48.949 (7.112)			0.047 (0.007)

[1]RESP$ = respiratory disease treatment costs; SCOUR$ = scours treatment costs; TOT$ = total health treatment costs

Table 5-4: Comparison of h^2 (SD) and reliability for differing definitions of total treatment cost[1]

Response variable	h^2	Reliability*
TOT$	0.047 (0.008)	0.448
LOGTOT$	0.060 (0.009)	0.528
LOGTOT2T$	0.036 (0.010)	0.368

[1]TOT$: untransformed total treatment cost; LOGTOT$: natural log-transformed total treatment cost; LOGTOT2T$: natural log transformed total treatment cost for calves with treatment cost greater than $0 used in 2 trait model

*Average reliability for sires with at least 10 daughters

Table 5-5: PTA correlation estimates between health treatment costs[1] and CDCB traits[2] for sires (n = 320) with at least 25% reliability for the trait of interest

Trait	RESP$	SCOUR$	TOT$	LOGTOT$	ANY2T$	LOGTOT2T$
Milk	-0.041	0.071	0.038	-0.013	-0.036	**0.164***
Fat	-0.057	**0.114***	0.069	0.044	0.034	**0.188***
Protein	-0.016	0.076	0.064	-0.011	-0.034	**0.188***
NM$	-0.067	0.073	0.024	0.017	0.000	**0.148***
HLIV	**-0.202***	**0.124***	-0.062	0.041	0.026	-0.019
LIV	-0.016	-0.086	-0.084	-0.056	-0.074	-0.075
PL	-0.010	0.009	-0.063	0.004	-0.014	0.011
DCE	0.016	0.053	0.056	0.085	0.094	-0.014
DSB	0.099	-0.022	0.051	0.013	-0.000	-0.000
SCE	-0.069	0.013	-0.045	0.014	0.053	**-0.120***
SSB	-0.086	0.046	-0.025	0.002	0.033	**-0.117***
EFC	0.096	0.109	**0.179***	**0.154***	**0.133***	**0.121***
GL	-0.097	-0.075	**-0.145***	-0.046	0.026	**-0.221***
SCS	0.101	-0.038	0.045	-0.030	-0.046	0.057
MAST	**-0.142***	0.062	-0.058	0.074	0.066	-0.096
MFEV	**0.113***	-0.106	-0.006	-0.063	-0.072	**0.138***
DA	0.064	0.002	0.070	0.108	0.076	0.097
RP	0.006	-0.096	-0.086	-0.017	-0.010	-0.042
KETO	0.036	0.089	**0.134***	**0.128***	**0.116***	**0.160***
MET	0.066	0.002	0.065	0.090	0.070	0.099
DPR	0.086	-0.105	-0.021	0.014	0.019	-0.105
CCR	0.027	-0.067	-0.034	0.031	0.038	-0.069
HCR	-0.026	0.023	0.001	0.030	0.060	-0.048

[1]RESP$ = respiratory disease treatment costs; SCOUR$ = scours treatment costs; TOT$ = total health treatment costs; LOGTOT$ = natural log transformed total treatment cost; ANY2T = binary any treatment cost (0 = no cost; 1 = cost greater than $0) used in 2 trait model; LOGTOT2T$ = natural log transformed total treatment cost for calves with treatment cost greater than $0 used in 2 trait model

[2]NM$ = lifetime net merit dollars; HLIV = heifer livability; LIV = cow livability; PL = productive life; DCE = daughter calving ease; DSB = daughter stillbirth; SCE = sire calving ease; SSB = sire stillbirth; EFC = early first calving; GL = gestation length; SCS = somatic cell score; MAST = mastitis; MFEV = milk fever; DA = displaced abomasum; RP = retained placenta; KETO = ketosis; MET = metritis; DPR = daughter pregnancy rate; CCR = cow conception rate; HCR = heifer conception rate

*bolded values: p-value < 0.05

References

Abuelo, A., F. Cullens, and J.L. Brester. 2021. Effect of preweaning disease on the reproductive performance and first-lactation milk production of heifers in a large dairy herd. J. Dairy Sci.. doi:10.3168/jds.2020-19791.

Ahlman, T., M. Ljung, L. Rydhmer, H. Röcklinsberg, E. Strandberg, and A. Wallenbeck. 2014. Differences in preferences for breeding traits between organic and conventional dairy producers in Sweden. Livest. Sci. 162:5–14. doi:10.1016/j.livsci.2013.12.014.

Beam, A.L., J.E. Lombard, C.A. Kopral, L.P. Garber, A.L. Winter, J.A. Hicks, and J.L. Schlater. 2009. Prevalence of failure of passive transfer of immunity in newborn heifer calves and associated management practices on US dairy operations. J. Dairy Sci. 92:3973–80. doi:10.3168/jds.2009-2225.

Brock, C.C., J.A. Pempek, D. Jackson-Smith, K. Weaver, L. da Costa, and G.G. Habing. 2021. Organic dairy producer experiences and decisions related to disease prevention and treatment. J. Dairy Sci. 104:5867–5880. doi:10.3168/jds.2020-19621.

Brown Swiss Association. 2020. Progressive Performance Ranking. Accessed May 16, 2021. https://www.brownswissusa.com/Breed/Genetics/PPRFormula/tabid/312/Default.aspx.

Buczinski, S., D. Achard, and E. Timsit. 2021. Effects of calfhood respiratory disease on

health and performance of dairy cattle: A systematic review and meta-analysis. J. Dairy Res. 104. doi:10.3168/jds.2020-19941.

Burton, J.L., B.W. Kennedy, E.B. Burnside, B.N. Wilkie, and J.H. Burton. 1989. Variation in Serum Concentrations of Immunoglobulins G, A, and M in Canadian Holstein-Friesian Calves. J. Dairy Sci. 72:135–149. doi:10.3168/jds.S0022-0302(89)79089-5.

Calloway, C.D., J.W. Tyler, R.K. Tessman, D. Hostetler, and J. Holle. 2002. Comparison of refractometers and test endpoints in the measurement of serum protein concentration to assess passive transfer status in calves. J. Am. Vet. Med. Assoc. 221:1605–1608.

Calo, L.L., R.E. McDowell, L.D. VanVleck, and P.D. Miller. 1973. Genetic Aspects of Beef Production among Holstein-Friesians Pedigree Selected for Milk Production. J. Anim. Sci. 37:676–682. doi:10.2527/jas1973.373676x.

Carrillo, J., and K. Tokuhisa. 2021. The U.S. Has Recorded 5 Million Genotypes. Accessed May 16, 2021. https://hoards.com/article-29836-the-us-has-recorded-5-million-genotypes.html.

CDCB. 2018a. CDCB Changes to Evaluation System (December 2018) . Accessed June 7, 2021. https://www.uscdcb.com/cdcb-changes-to-evaluation-system-december-2018/.

CDCB. 2018b. New Genetic Evaluations for Health Traits. Accessed May 16, 2021. www.uscdcb.org.

CDCB. 2020a. CDCB Changes to Evaluation System (April 2020) . Accessed May 16,

2021. https://www.uscdcb.com/cdcb-changes-to-evaluation-system-april-2020/.

CDCB. 2020b. Heifer Livability (HLIV). Accessed January 21, 2021. https://www.uscdcb.com/wp-content/uploads/2020/11/CDCB-Reference-Sheet-Heifer-Livability-12_2020.pdf.

CDCB. 2021a. Genetic and Phenotypic Trend. Accessed May 16, 2021. https://queries.uscdcb.com/eval/summary/trend.cfm?R_Menu=HO#StartBody.

CDCB. 2021b. Trend in Inbreeding Coefficients of Cows for Holstein or Red & White. Accessed June 7, 2021. https://queries.uscdcb.com/eval/summary/inbrd.cfm.

Cecchinato, A., T. Bobbo, P.L. Ruegg, L. Gallo, G. Bittante, and S. Pegolo. 2018. Genetic variation in serum protein pattern and blood beta-hydroxybutyrate and their relationships with udder health traits, protein profile, and cheese-making properties in Holstein cows. J. Dairy Sci. 101:11108–11119. doi:10.3168/jds.2018-14907.

Closs, G., and C. Dechow. 2017. The effect of calf-hood pneumonia on heifer survival and subsequent performance. Livest. Sci. 205:5–9. doi:10.1016/j.livsci.2017.09.004.

Coffey, L., and A.H. Baier. 2012. Guide for Organic Livestock Producers. Accessed May 4, 2020. https://www.ams.usda.gov/sites/default/files/media/GuideForOrganicLivestockProducers.pdf.

Cole, J., and P. VanRaden. 2018. Symposium review: Possibilities in an age of genomics: The future of selection indices1. J. Dairy Sci. 3686–3701. doi:10.3168/jds.2017-13335.

Cole, J.B., J.W. Dürr, and E.L. Nicolazzi. 2021. Invited review: The future of selection

decisions and breeding programs: What are we breeding for, and who decides?. J. Dairy Sci. 104:5111–5124. doi:10.3168/jds.2020-19777.

Cordero Solórzano, J. 2020. Genetics of colostrum, milk, and serum antibodies in dairy cattle: Implications for health and production. Doctoral thesis. Swedish University of Agricultural Sciences, Sweden.

Correa, M.T., C.R. Curtis, H.N. Erb, and M.E. White. 1988. Effect of calflhood morbidity on age at first calving in New York Holstein herds. Prev. Vet. Med. 6:253–262. doi:10.1016/0167-5877(88)90037-2.

Deelen, S.M., T.L. Ollivett, D.M. Haines, and K.E. Leslie. 2014. Evaluation of a Brix refractometer to estimate serum immunoglobulin G concentration in neonatal dairy calves. J. Dairy Sci. 97:3838–3844. doi:10.3168/jds.2014-7939.

DeNise, S.K., J.D. Robison, G.H. Stott, and D. V. Armstrong. 1989. Effects of Passive Immunity on Subsequent Production in Dairy Heifers. J. Dairy Sci. 72:552–554. doi:10.3168/jds.S0022-0302(89)79140-2.

Donnelly, M.R., L.B. Hansen, and B.J. Heins. 2017. Genetic control of health treatment costs for Holsteins in 8 high-performance herds. MS Thesis. University of Minnesota, St. Paul, MN.

Donovan, G.A., L. Badinga, R.J. Collier, C.J. Wilcox, and R.K. Braun. 1986. Factors Influencing Passive Transfer in Dairy Calves. J. Dairy Sci. 69:754–759. doi:10.3168/jds.S0022-0302(86)80464-7.

Donovan, G.A., I.R. Dohoo, D.M. Montgomery, and F.L. Bennett. 1998. Associations between passive immunity and morbidity and mortality in dairy heifers in Florida,

USA. Prev. Vet. Med. 34:31–46. doi:10.1016/S0167-5877(97)00060-3.

Dubrovsky, S., A. Van Eenennaam, S. Aly, B. Karle, P. V Rossitto, M. Overton, T. Lehenbauer, and J. Fadel. 2020. Preweaning cost of bovine respiratory disease (BRD) and cost-benefit of implementation of preventative measures in calves on California dairies: The BRD 10K study. J. Dairy Sci. 103:1583–1597. doi:10.3168/jds.2018-15501.

Dubrovsky, S.A., A.L. Van Eenennaam, B.M. Karle, P. V. Rossitto, T.W. Lehenbauer, and S.S. Aly. 2019. Epidemiology of bovine respiratory disease (BRD) in preweaned calves on California dairies: The BRD 10K study. J. Dairy Sci. 102:7306–7319. doi:10.3168/jds.2018-14774.

Dunn, T.R., T.L. Ollivett, D.L. Renaud, K.E. Leslie, S.J. LeBlanc, T.F. Duffield, and D.F. Kelton. 2018. The effect of lung consolidation, as determined by ultrasonography, on first-lactation milk production in Holstein dairy calves.. J. Dairy Sci. 0. doi:10.3168/jds.2017-13870.

Ettema, J.F., and J.E.P. Santos. 2004. Impact of Age at Calving on Lactation, Reproduction, Health, and Income in First-Parity Holsteins on Commercial Farms. J. Dairy Sci. 87:2730–2742. doi:10.3168/jds.S0022-0302(04)73400-1.

Falconer, D., and T. Mackay. 1996. Introduction to Quantitative Genetics. 4th ed. Longman Group Ltd, Harlow, UK.

Fuerst-Waltl, B., and M.K. Sørensen. 2010. Genetic analysis of calf and heifer losses in Danish Holstein. J. Dairy Sci. 93:5436–5442. doi:10.3168/jds.2010-3227.

García-Ruiz, A., J.B. Cole, P.M. VanRaden, G.R. Wiggans, F.J. Ruiz-López, and C.P.

Van Tassell. 2016. Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection. Proc. Natl. Acad. Sci. U. S. A. 113:E3995–E4004. doi:10.1073/pnas.1519061113.

Gay, K.D., N.J.O. Widmar, T.D. Nennich, A.P. Schinckel, J.B. Cole, and M.M. Schutz. 2014. Development of a Lifetime Merit-based selection index for US dairy grazing systems. J. Dairy Sci. 97:4568–4578. doi:10.3168/jds.2013-7474.

Genex. 2021. ICC – GENEX. Accessed May 16, 2021. https://genex.coop/dairy/icc/.

Gilmour, A.R., B.J. Gogel, B.R. Cullis, S.J. Welham, and R. Thompson. 2015. ASReml User Guide Release 4.1. VSN International Ltd, Hemel Hempstead, HP2 4TP UK.

Godden, S. 2008. Colostrum Management for Dairy Calves. Vet. Clin. Food Anim. Pract. 24:19–39. doi:10.1016/j.cvfa.2007.10.005.

Gonzalez-Peña, D., N. Vukasinovic, J.J. Brooker, C.A. Przybyla, A. Baktula, and S.K. DeNise. 2020. Genomic evaluation for wellness traits in US Jersey cattle. J. Dairy Sci. 103:1735–1748. doi:10.3168/jds.2019-16903.

Gonzalez-Peña, D., N. Vukasinovic, J.J. Brooker, C.A. Przybyla, and S.K. DeNise. 2019. Genomic evaluation for calf wellness traits in Holstein cattle. J. Dairy Sci. 102:2319–2329. doi:10.3168/jds.2018-15540.

Haagen, I.W., L.C. Hardie, B.J. Heins, and C.D. Dechow. Under Review. Genetic parameters of calf morbidity and stayability for US organic Holstein calves. J. Dairy Sci.

Haagen, I.W., L.C. Hardie, B.J. Heins, and C.D. Dechow. 2021. Genetic parameters of passive transfer of immunity for US organic Holstein calves. J. Dairy Sci.

104:2018–2026. doi:10.3168/jds.2020-19080.

Habing, G., C. Djordjevic, G.M. Schuenemann, and J. Lakritz. 2016. Understanding antimicrobial stewardship: Disease severity treatment thresholds and antimicrobial alternatives among organic and conventional calf producers. Prev. Vet. Med. 130:77–85. doi:10.1016/j.prevetmed.2016.06.004.

Hansen, M., M.S. Lund, J. Pedersen, and L.G. Christensen. 2004. Gestation length in Danish Holsteins has weak genetic associations with stillbirth, calving difficulty, and calf size. Livest. Prod. Sci. 91:23–33. doi:10.1016/j.livprodsci.2004.06.007.

Hansen, M., P. Madsen, J. Jensen, J. Pedersen, and L.G. Christensen. 2003. Genetic parameters of postnatal mortality in Danish Holstein calves. J. Dairy Sci. 86:1807–1817. doi:10.3168/jds.S0022-0302(03)73766-7.

Hardie, L.C., I.W. Haagen, L. Han, B.J. Heins, D.. Fitzsimmons, and C.D. Dechow. 2019. Relationships between daughter phenotypes and sire PTA for production and fertility traits in US organic Holstein cows. J. Dairy Sci. 101(Suppl.

Hardie, L.C., I.W. Haagen, B.J. Heins, and C.D. Dechow. Under Review. Genetic Parameters for Health Traits in US Organic Holsteinsle. J. Dairy Sci.

Heinrichs, A.J., and B.S. Heinrichs. 2011. A prospective study of calf factors affecting first-lactation and lifetime milk production and age of cows when removed from the herd. J. Dairy Sci. 94:336–341. doi:10.3168/jds.2010-3170.

Heinrichs, A.J., B.S. Heinrichs, O. Harel, G.W. Rogers, and N.T. Place. 2005. A Prospective Study of Calf Factors Affecting Age, Body Size, and Body Condition Score at First Calving of Holstein Dairy Heifers. J. Dairy Sci. 88:2828–2835.

doi:10.3168/jds.S0022-0302(05)72963-5.

Heinrichs, A.J., and C.M. Jones. 2016. Trends in Age at Calving of Heifers in Pennsylvania. Accessed April 27, 2021. https://extension.psu.edu/trends-in-age-at-calving-of-heifers-in-pennsylvania.

Heinrichs, A.J., C.M. Jones, S.M. Gray, P.A. 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. doi:10.3168/jds.2012-6488.

Henderson, L., F. Miglior, A. Sewalem, D. Kelton, A. Robinson, and K.E. Leslie. 2011a. Estimation of genetic parameters for measures of calf survival in a population of Holstein heifer calves from a heifer-raising facility in New York State. J. Dairy Sci. 94:461–470. doi:10.3168/jds.2010-3243.

Henderson, L., F. Miglior, A. Sewalem, J. Wormuth, D. Kelton, A. Robinson, and K.E. Leslie. 2011b. Short communication: Genetic parameters for measures of calf health in a population of Holstein calves in New York State. J. Dairy Sci. 94:6181–6187. doi:10.3168/JDS.2011-4347.

Heringstad, B., Y.M. Chang, D. Gianola, and O. Østerå. 2008. Short Communication: Genetic Analysis of Respiratory Disease in Norwegian Red Calves. J. Dairy Sci. 91:367–370. doi:10.3168/jds.2007-0365.

Hoffman, P.C., and D.A. Funk. 1992. Applied Dynamics of Dairy Replacement Growth and Management. J. Dairy Sci. 75:2504–2516. doi:10.3168/jds.S0022-0302(92)78012-6.

Holstein Association USA, I. 2021. TPI Formula - April 2021. Accessed May 16, 2021. https://www.holsteinusa.com/genetic_evaluations/ss_tpi_formula.html.

Howe, K.L., P. Achuthan, J. Allen, J. Allen, J. Alvarez-Jarreta, M.R. Amode, I.M. Armean, A.G. Azov, R. Bennett, J. Bhai, K. Billis, S. Boddu, M. Charkhchi, C. Cummins, L. Da Rin Fioretto, C. Davidson, K. Dodiya, B. El Houdaigui, R. Fatima, A. Gall, C. Garcia Giron, T. Grego, C. Guijarro-Clarke, L. Haggerty, A. Hemrom, T. Hourlier, O.G. Izuogu, T. Juettemann, V. Kaikala, M. Kay, I. Lavidas, T. Le, D. Lemos, J. Gonzalez Martinez, J.C. Marugán, T. Maurel, A.C. McMahon, S. Mohanan, B. Moore, M. Muffato, D.N. Oheh, D. Paraschas, A. Parker, A. Parton, I. Prosovetskaia, M.P. Sakthivel, A.I.A. Salam, B.M. Schmitt, H. Schuilenburg, D. Sheppard, E. Steed, M. Szpak, M. Szuba, K. Taylor, A. Thormann, G. Threadgold, B. Walts, A. Winterbottom, M. Chakiachvili, A. Chaubal, N. De Silva, B. Flint, A. Frankish, S.E. Hunt, G.R. IIsley, N. Langridge, J.E. Loveland, F.J. Martin, J.M. Mudge, J. Morales, E. Perry, M. Ruffier, J. Tate, D. Thybert, S.J. Trevanion, F. Cunningham, A.D. Yates, D.R. Zerbino, and P. Flicek. 2021. Ensembl 2021. Nucleic Acids Res. 49:D884–D891. doi:10.1093/nar/gkaa942.

Hu, Z.-L., C.A. Park, and J.M. Reecy. 2019. Building a livestock genetic and genomic information knowledgebase through integrative developments of Animal QTLdb and CorrDB. Nucleic Acids Res. 47:D701–D710. doi:10.1093/nar/gky1084.

Hughner, R.S., P. McDonagh, A. Prothero, C.J. Shultz, and J. Stanton. 2007. Who are organic food consumers? A compilation and review of why people purchase organic food. J. Consum. Behav. 6:94–110. doi:10.1002/cb.210.

Hultgren, J., and C. Svensson. 2009a. Heifer rearing conditions affect length of productive life in Swedish dairy cows. Prev. Vet. Med. 89:255–264. doi:10.1016/j.prevetmed.2009.02.012.

Hultgren, J., and C. Svensson. 2009b. Lifetime risk and cost of clinical mastitis in dairy cows in relation to heifer rearing conditions in southwest Sweden. J. Dairy Sci. 92:3274–3280. doi:10.3168/jds.2008-1678.

Jang, J.-S., J.-H. Lee, N.-C. Jung, S.-Y. Choi, S.-Y. Park, J.-Y. Yoo, J.-Y. Song, H.G. Seo, H.S. Lee, and D.-S. Lim. 2018. Rsad2 is necessary for mouse dendritic cell maturation via the IRF7-mediated signaling pathway. Cell Death Dis. 9:823. doi:10.1038/s41419-018-0889-y.

Jensen, P.T., and K. Christensen. 1975. Genetic analysis of the serum level of IgG and total protein in Red Danish cattle. J. Anim. Sci. 40:392–396. doi:10.2527/jas1975.403392x.

Jersey Journal. 2020. Learning More About JPI 2020 . Accessed May 16, 2021. https://usjerseyjournal.com/learning-more-about-jpi-2020/.

Jones, C., and J. Heinrichs. 2006. Calf Care. W.D. Hoard & Sons Company.

Kaneene, J.B., and H. Scott Hurd. 1990. The national animal health monitoring system in Michigan. III. Cost estimates of selected dairy cattle diseases. Prev. Vet. Med. 8:127–140. doi:10.1016/0167-5877(90)90006-4.

Karszes, J., and L. Hill. 2020. Dairy Replacement Program: Cost & Analysis Summer 2019. Accessed May 6, 2021. https://dyson.cornell.edu/wp-content/uploads/sites/5/2020/09/Dairy-Replacement-Costs-Writeup-Final1-VD.pdf.

de Klerk, B., M. Emam, K.A. Thompson-Crispi, M. Sargolzaei, J.J. van der Poel, and B.A. Mallard. 2018. A genome-wide association study for natural antibodies measured in blood of Canadian Holstein cows. BMC Genomics 19:694. doi:10.1186/s12864-018-5062-6.

Koeck, A., C. Egger-Danner, C. Fuerst, W. Obritzhauser, and B. Fuerst-Waltl. 2010. Genetic analysis of reproductive disorders and their relationship to fertility and milk yield in Austrian Fleckvieh dual-purpose cows. J. Dairy Sci. 93:2185–2194. doi:10.3168/jds.2009-2570.

Lombard, J.E., F.B. Garry, S.M. Tomlinson, and L.P. Garber. 2007. Impacts of dystocia on health and survival of dairy calves. J. Dairy Sci. 90:1751–1760. doi:10.3168/jds.2006-295.

Mahmoud, M., T. Yin, K. Brügemann, and S. König. 2017. Phenotypic, genetic, and single nucleotide polymorphism marker associations between calf diseases and subsequent performance and disease occurrences of first-lactation German Holstein cows. J. Dairy Sci 100. doi:10.3168/jds.2016-11767.

Makanjuola, B.O., F. Miglior, E.A. Abdalla, C. Maltecca, F.S. Schenkel, and C.F. Baes. 2020. Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle populations. J. Dairy Sci. 103:5183–5199. doi:10.3168/jds.2019-18013.

Maltecca, C., K.A. Weigel, H. Khatib, M. Cowan, and A. Bagnato. 2009. Whole-genome scan for quantitative trait loci associated with birth weight, gestation length and passive immune transfer in a Holstein x Jersey crossbred population. Anim. Genet.

40:27–34. doi:10.1111/j.1365-2052.2008.01793.x.

McCorquodale, C.E., A. Sewalem, F. Miglior, D. Kelton, A. Robinson, A. Koeck, and K.E. Leslie. 2013. Short communication: Analysis of health and survival in a population of Ontario Holstein heifer calves. J. Dairy Sci. 96:1880–1885. doi:10.3168/jds.2012-5735.

McGuirk, S.M. 2008. Disease Management of Dairy Calves and Heifers. Vet. Clin. North Am. 24:139–153. doi:10.1016/j.cvfa.2007.10.003.

Misztal, I., S. Tsuruta, D. Lourenco, Y. Masuda, I. Aguilar, A. Legarra, and Z. Vitezica. 2018. Manual for BLUPF90 Family of Programs. Accessed January 28, 2020. http://nce.ads.uga.edu/wiki/doku.php?id=documentation.

Nauta, W.J., R.F. Veerkamp, E.W. Brascamp, and H. Bovenhuis. 2006. Genotype by environment interaction for milk production traits between organic and conventional dairy cattle production in The Netherlands. J. Dairy Sci. 89:2729–2737. doi:10.3168/jds.S0022-0302(06)72349-9.

Neibergs, H.L., C.M. Seabury, A.J. Wojtowicz, Z. Wang, E. Scraggs, J.N. Kiser, M. Neupane, J.E. Womack, A. Van Eenennaam, G.R. Hagevoort, T.W. Lehenbauer, S. Aly, J. Davis, and J.F. Taylor. 2014. Susceptibility loci revealed for bovine respiratory disease complex in pre-weaned holstein calves. BMC Genomics 15:1164. doi:10.1186/1471-2164-15-1164.

Neupane, M., J.L. Hutchison, C.P. Van Tassell, and P.M. VanRaden. 2021. Genomic evaluation of dairy heifer livability. J. Dairy Sci.. doi:10.3168/jds.2020-19687.

Neupane, M., C.P. Van Tassell, and P.M. VanRaden. 2020. Genomic evaluation of heifer

livability. J. Dairy Sci. 103(Suppl. 1).

Ollivett, T.L., and S. Buczinski. 2016. On-Farm Use of Ultrasonography for Bovine Respiratory Disease. Vet. Clin. North Am. - Food Anim. Pract. 32:19–35. doi:10.1016/j.cvfa.2015.09.001.

Otani, K., Y. Dong, X. Li, J. Lu, N. Zhang, L. Xu, M.Y.Y. Go, E.K.W. Ng, T. Arakawa, F.K.L. Chan, J.J.Y. Sung, and J. Yu. 2014. Odd-skipped related 1 is a novel tumour suppressor gene and a potential prognostic biomarker in gastric cancer. J. Pathol. 234:302–315. doi:https://doi.org/10.1002/path.4391.

Parker Gaddis, K.L., J.B. Cole, J.S. Clay, and C. Maltecca. 2014. Genomic selection for producer-recorded health event data in US dairy cattle. J. Dairy Sci. 97:3190–3199. doi:10.3168/jds.2013-7543.

Parker Gaddis, K.L., P.M. VanRaden, J.B. Cole, H.D. Norman, E. Nicolazzi, and J.W. Dürr. 2020. Symposium review: Development, implementation, and perspectives of health evaluations in the United States. J. Dairy Sci. 103:5354–5365. doi:10.3168/jds.2019-17687.

Pempek, J.A., G.M. Schuenemann, E. Holder, and G.G. Habing. 2017. Dairy calf management—A comparison of practices and producer attitudes among conventional and organic herds. J. Dairy Sci. 100:8310–8321. doi:10.3168/JDS.2017-12565.

Peterson, R.G., T.E. Nash, and J.A. Shelford. 1982. Heritabilities and Genetic Correlations for Serum and Production Traits of Lactating Holsteins. J. Dairy Sci. 65:1556–1561. doi:10.3168/jds.S0022-0302(82)82381-3.

Place, N.T., A.J. Heinrichs, H.N. Erb, and G.W. Rogers. 1994. The Effects of Disease, Management, and Nutrition on Average Daily Gain of Dairy Heifers from Birth to Four Months.

Pritchard, T., M. Coffey, R. Mrode, and E. Wall. 2013. Understanding the genetics of survival in dairy cows. J. Dairy Sci. 96:3296–3309. doi:10.3168/jds.2012-6219.

Quick, A.E., T.L. Ollivett, B.W. Kirkpatrick, and K.A. Weigel. 2020. Genomic analysis of bovine respiratory disease and lung consolidation in preweaned Holstein calves using clinical scoring and lung ultrasound. J. Dairy Sci. 103:1632–1641. doi:10.3168/jds.2019-16531.

Robertson, A. 1959. The Sampling Variance of the Genetic Correlation Coefficient. Biometrics 15:469–485. doi:10.2307/2527750.

Robison, J.D., G.H. Stott, and S.K. DeNise. 1988. Effects of Passive Immunity on Growth and Survival in the Dairy Heifer. J. Dairy Sci. 71:1283–1287. doi:10.3168/jds.S0022-0302(88)79684-8.

Rosen, B.D., D.M. Bickhart, R.D. Schnabel, S. Koren, C.G. Elsik, E. Tseng, T.N. Rowan, W.Y. Low, A. Zimin, C. Couldrey, R. Hall, W. Li, A. Rhie, J. Ghurye, S.D. McKay, F. Thibaud-Nissen, J. Hoffman, B.M. Murdoch, W.M. Snelling, T.G. McDaneld, J.A. Hammond, J.C. Schwartz, W. Nandolo, D.E. Hagen, C. Dreischer, S.J. Schultheiss, S.G. Schroeder, A.M. Phillippy, J.B. Cole, C.P. Van Tassell, G. Liu, T.P.L. Smith, and J.F. Medrano. 2020. De novo assembly of the cattle reference genome with single-molecule sequencing. Gigascience 9. doi:10.1093/gigascience/giaa021.

Schaffer, A.P., R.L. Larson, N. Cernicchiaro, G.A. Hanzlicek, S.J. Bartle, and D.U. Thomson. 2016. The association between calfhood bovine respiratory disease complex and subsequent departure from the herd, milk production, and reproduction in dairy cattle. J. Am. Vet. Med. Assoc. 248:1157–1164.

Schutz, M.M. 1994. Genetic Evaluation of Somatic Cell Scores for United States Dairy Cattle. J. Dairy Sci. 77:2113–2129. doi:10.3168/jds.S0022-0302(94)77154-X.

Shabalina, T., T. Yin, K. May, and S. König. 2021. Proofs for genotype by environment interactions considering pedigree and genomic data from organic and conventional cow reference populations. J. Dairy Sci. 104:4452–4466. doi:10.3168/jds.2020-19384.

Shivley, C.B., J.E. Lombard, N.J. Urie, D.M. Haines, R. Sargent, C.A. Kopral, T.J. Earleywine, J.D. Olson, and F.B. Garry. 2018a. Preweaned heifer management on US dairy operations: Part II. Factors associated with colostrum quality and passive transfer status of dairy heifer calves. J. Dairy Sci. 101:9185–9198. doi:10.3168/jds.2017-14008.

Shivley, C.B., J.E. Lombard, N.J. Urie, C.A. Kopral, M. Santin, T.J. Earleywine, J.D. Olson, and F.B. Garry. 2018b. Preweaned heifer management on US dairy operations: Part VI. Factors associated with average daily gain in preweaned dairy heifer calves. J. Dairy Sci. 101:9245–9258. doi:10.3168/jds.2017-14022.

Slagboom, M., M. Kargo, D. Edwards, A.C. Sørensen, J.R. Thomasen, and L. Hjortø. 2016. Organic dairy farmers put more emphasis on production traits than conventional farmers. J. Dairy Sci. 99:9845–9856. doi:10.3168/jds.2016-11346.

Stanton, A., D. Kelton, S. LeBlanc, J. Wormuth, and K. Leslie. 2012. The effect of respiratory disease and a preventative antibiotic treatment on growth, survival, age at first calving, and milk production of dairy heifers. J. Dairy Sci. 95:4950–4960. doi:10.3168/jds.2011-5067.

Stiglbauer, K.E., K.M. Cicconi-Hogan, R. Richert, Y.H. Schukken, P.L. Ruegg, and M. Gamroth. 2013. Assessment of herd management on organic and conventional dairy farms in the United States. J. Dairy Sci. 96:1290–1300. doi:10.3168/jds.2012-5845.

Stirnweiss, A., A. Ksienzyk, K. Klages, U. Rand, M. Grashoff, H. Hauser, and A. Kröger. 2010. IFN Regulatory Factor-1 Bypasses IFN-Mediated Antiviral Effects through Viperin Gene Induction. J. Immunol. 184:5179 LP – 5185. doi:10.4049/jimmunol.0902264.

Van Tassell, C.P., and P.J. Berger. 1994. Consideration of Sire Relationships for Estimation of Variance Components with Interaction of Herd and Sire. J. Dairy Sci. 77:313–324. doi:10.3168/jds.S0022-0302(94)76956-3.

Teixeira, A.G.V., J.A.A. McArt, and R.C. Bicalho. 2017. Thoracic ultrasound assessment of lung consolidation at weaning in Holstein dairy heifers: Reproductive performance and survival. J. Dairy Sci. 100:2985–2991. doi:10.3168/jds.2016-12016.

Tyler, J.W., D.D. Hancock, S.M. Parish, D.E. Rea, T.E. Besser, S.G. Sanders, and L.K. Wilson. 1996. Evaluation of 3 Assays for Failure of Passive Transfer in Calves. J. Vet. Intern. Med. 10:304–307. doi:10.1111/j.1939-1676.1996.tb02067.x.

U.S. Bureau of Labor Statistics. 2020. Quarterly Census of Employment and Wages.

Accessed May 31, 2021. https://data.bls.gov/cew/apps/table_maker/v4/table_maker.htm#type=0&year=2019&qtr=A&own=5&ind=11212&supp=0.

Urie, N.J., J.E. Lombard, C.B. Shivley, C.A. Kopral, A.E. Adams, T.J. Earleywine, J.D. Olson, and F.B. Garry. 2018a. Preweaned heifer management on US dairy operations: Part V. Factors associated with morbidity and mortality in preweaned dairy heifer calves. J. Dairy Sci. 101:9229–9244. doi:10.3168/jds.2017-14019.

Urie, N.J., J.E. Lombard, C.B. Shivley, C.A. Kopral, A.E. Adams, T.J. Earleywine, J.D. Olson, and F.B. Garry. 2018b. Preweaned heifer management on US dairy operations: Part I. Descriptive characteristics of preweaned heifer raising practices. J. Dairy Sci. 101:9168–9184. doi:10.3168/jds.2017-14010.

USDA. 2010. Dairy 2007, "Heifer calf health and management practices on U.S. dairy operations, 2007." USDA-APHIS-VS-CEAH, Fort Collins, CO.

USDA. 2016. Dairy 2014, "Dairy Cattle Management Practices in the United States, 2014." USDA–APHIS–VS–CEAH–NAHMS, Fort Collins, CO.

USDA. 2017. Certified Organic Survey: 2016 Summary. Accessed January 27, 2020. https://www.nass.usda.gov/Surveys/Guide_to_NASS_Surveys/Organic_Production/.

USDA. 2018. Dairy 2014, "Health and Management Practices on U.S. Dairy Operations, 2014." USDA-APHIS-VS-CEAH-NAHMS, Fort Collins, CO.

VanRaden, P., G. Wiggans, T. Sonstegard, C. Van Tassell, and L. Walton. 2009a. AIPL Changes to Evaluation System (January 2009). Accessed May 15, 2021. https://aipl.arsusda.gov/reference/changes/eval0901.html.

VanRaden, P.M., and J.B. Cole. 2014. Net Merit as a Measure of Lifetime Profit: 2014 Revision. Accessed May 15, 2021. https://aipl.arsusda.gov/reference/nmcalc-2014.htm.

Vanraden, P.M., J.B. Cole, M. Neupane, S. Toghiani, K.L. Gaddis, and R.J. Tempelman. 2021. Net merit as a measure of lifetime profit: 2021 revision.

VanRaden, P.M., J.B. Cole, and K.L. Parker Gaddis. 2018. Lifetime Net Merit 2018. Accessed November 15, 2020. https://aipl.arsusda.gov/reference/nmcalc-2018.htm.

VanRaden, P.M., A.H. Sanders, M.E. Tooker, R.H. Miller, H.O. Norman, M.T. Kuhn, and G.R. Wiggans. 2004. Development of a national genetic evaluation for cow fertility. J. Dairy Sci. 87:2285–2292. doi:10.3168/jds.S0022-0302(04)70049-1.

VanRaden, P.M., C.P. Van Tassell, G.R. Wiggans, T.S. Sonstegard, R.D. Schnabel, J.F. Taylor, and F.S. Schenkel. 2009b. Invited review: Reliability of genomic predictions for North American Holstein bulls. J. Dairy Sci. 92:16–24. doi:10.3168/jds.2008-1514.

Vanraden, P.M., and G.R. Wiggans. 1995. Productive Life Evaluations: Calculation, Accuracy, and Economic Value. J. Dairy Sci. 78:631–638. doi:10.3168/jds.S0022-0302(95)76674-7.

Vieira-Neto, A., K.N. Galvão, W.W. Thatcher, and J.E.P. Santos. 2017. Association among gestation length and health, production, and reproduction in Holstein cows and implications for their offspring. J. Dairy Sci. 100:3166–3181. doi:10.3168/jds.2016-11867.

De Vries, A., J. Dalton, and D. Moore. 2019. Looking for Greater Economic Value from

Genomic Testing. Accessed June 7, 2021. https://www.progressivedairy.com/topics/a-i-breeding/looking-for-greater-economic-value-from-genomic-testing.

Vukasinovic, N., N. Bacciu, C.A. Przybyla, P. Boddhireddy, and S.K. DeNise. 2017. Development of genetic and genomic evaluation for wellness traits in US Holstein cows. J. Dairy Sci. 100:428–438. doi:10.3168/jds.2016-11520.

Waldner, C.L., and L.B. Rosengren. 2009. Factors associated with serum immunoglobulin levels in beef calves from Alberta and Saskatchewan and association between passive transfer and health outcomes. Can. Vet. J. 50:275–281.

Waltner-Toews, D., S.W. Martin, and A.H. Meek. 1986. The effect of early calfhood health status on survivorship and age at first calving. Can. J. Vet. Res. 50:314–317.

Weigel, K.A., P.M. VanRaden, H.D. Norman, and H. Grosu. 2017. A 100-Year Review: Methods and impact of genetic selection in dairy cattle—From daughter–dam comparisons to deep learning algorithms. J. Dairy Sci. 100:10234–10250. doi:10.3168/jds.2017-12954.

Weller, J.I., M. Gershoni, and E. Ezra. 2021. Genetic and environmental analysis of female calf survival in the Israel Holstein cattle population. J. Dairy Sci. 104:3278–3291. doi:10.3168/jds.2020-19434.

Wiggans, G.R., T.A. Cooper, P.M. VanRaden, C.P. Van Tassell, D.M. Bickhart, and T.S. Sonstegard. 2016. Increasing the number of single nucleotide polymorphisms used in genomic evaluation of dairy cattle.. J. Dairy Sci. 99:4504–11. doi:10.3168/jds.2015-10456.

Wilm, J., J.H.C. Costa, H.W. Neave, D.M. Weary, and M.A.G. von Keyserlingk. 2018. Technical note: Serum total protein and immunoglobulin G concentrations in neonatal dairy calves over the first 10 days of age. J. Dairy Sci. 101:6430–6436. doi:10.3168/jds.2017-13553.

Wright, J.R., and P.M. Van Raden. 2016. Genetic evaluation of dairy cow livability. J. Dairy Sci. 99.

Zoetis. 2021. CLARIFIDE Plus. Accessed May 16, 2021. https://www.zoetisus.com/animal-genetics/dairy/clarifide/clarifide-plus.aspx.

Zwald, N.R., K.A. Weigel, Y.M. Chang, R.D. Welper, and J.S. Clay. 2004. Genetic Selection for Health Traits Using Producer-Recorded Data. I. Incidence Rates, Heritability Estimates, and Sire Breeding Values. J. Dairy Sci. 87:4287–4294. doi:10.3168/JDS.S0022-0302(04)73573-0.

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Haagen, I.W., L.C. Hardie, B.J. Heins, and C.D. Dechow. 2021. Genetic parameters of passive transfer of immunity for US organic Holstein calves. J. Dairy Sci. 104:2018-2026. doi:10.3168/jds.2020-19080.

VanRaden, P.M., M.E. Tooker, T.C.S. Chud, H.D. Norman, J.H. Megonigal, I.W. Haagen, and G.R. Wiggans. 2020. Genomic predictions for crossbred dairy cattle. J. Dairy Sci. 103:1620-1631. doi:10.3168/jds.2019-16634.

MANUSCRIPTS IN PREPARATION

Haagen, I.W., L.C. Hardie, B.J. Heins, and C.D. Dechow. Genetic parameters of calf health on organic dairy farms. J. Dairy Sci. *Submitted.*

Haagen, I.W., L.C. Hardie, B.J. Heins, and C.D. Dechow. Genome-wide association of serum total protein in organic Holstein calves.

Haagen, I.W., L.C. Hardie, B.J. Heins, and C.D. Dechow. Genetic parameters of direct calf health costs for US organic Holsteins.

Haagen, I.W., and C.D. Dechow. Telomere lengths in Holsteins, Montbeliardes, and F1 Montbeliarde x Holsteins.