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

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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 d of age, calf scours until 60 d of age, and heifer stayability until 365 d 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 d of age and 1 if they remained in the herd at 365 d of age. Genetic parameters were estimated from threshold models that 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 genetics. Heritability estimates were 0.100, 0.075, and 0.085 for respiratory disease, scours, and stayability, respectively. Solutions for estimated breeding values for respiratory disease and scours were transformed from disease risk to disease resistance by reversing the signs before calculating genetic correlations such that higher values of scours, respiratory disease, and stayability were favored. There was a moderate favorable genetic correlation estimate between respiratory disease resistance and stayability of 0.675. However, genetic correlation estimates between respiratory disease resistance and scours resistance (0.148) and between scours resistance and stayability (0.165) were low. Estimated breeding value correlations between calf health traits and other traits evaluated nationally were generally low in magnitude. The strongest correlation estimates were with longevity, particularly between stayability and heifer livability (0.217) and between stayability and cow livability (0.288); respiratory disease resistance was also favorably correlated with heifer (0.190) and cow

(0.178) livability. 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% of phenotypic variance for scours and stayability, which may indicate a genotype by environment interaction effect for these traits. In conclusion, there is significant genetic variation in organic calf health, and there was evidence of genotype by environment interaction.

Key words: calf health, organic, genetics

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., 2018a) and the 2 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., 2018b). 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 preweaning calves, the incidence of scours was 23.9% whereas 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;

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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. (2011a) estimated the heritability of respiratory disease to be 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, 2020; Neupane et al., 2020).

However, the aforementioned 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 that 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. In addition, EBV correlations were estimated for calf health and stayability with officially published CDCB evaluations and the influence of genotype by environment interactions on organic calf health was explored.

MATERIALS AND METHODS

Data

Female Holstein calves were born between 2006 and 2019 on 16 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 manage-

ment software and on-farm paper records. Initial event screening restricted event records from birth until 1 mo before calving. Events and remarks were searched for disease trait indicators. Events and remarks that were recorded simultaneously with a vaccination record were excluded as we were not able to determine if the record was associated with disease treatment or prevention. For each trait, only the first observation of the trait of interest was retained for analysis. Only events that were recorded for more than 1% 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. After data edits, the final data sets contained 10,527 and 11,603 calves for respiratory disease and scours, respectively.

Opportunity periods were established for both scours and respiratory disease, which corresponded to when approximately 99% 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 d and for respiratory disease the opportunity period was 365 d. Therefore, for an animal to be included in the scours data set they must have been born at least 60 d before the last herd backup, and for an animal to be included in the respiratory data set they must have been born at least 365 d before the last backup.

In addition, stayability to 1 yr of age (0 = did not remain in herd, 1 = remained in herd) was defined for animals having the opportunity to reach 1 yr of age. Therefore, to be included in the STAY365 data set an animal must have been born at least 1 yr before the last herd backup. Our final stayability data set included 13,987 animals. As these were organic calves, any animal requiring antibiotic treatment was required to be removed from the herd but may have been able 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

$$y_{ijkl} = \mu + YS_i + D_{age,j} + HY_k + A_l + e_{ijkl},$$

where y_{ijkl} is the trait of interest (scours or respiratory disease; 0 = healthy and 1 = diseased), μ is the overall mean, YS_i is the fixed effect of year-season i , $D_{age,j}$ is the fixed effect of dam age ($j = 2, 3, 4+$), HY_k is the random herd-year contemporary birth group k , A_l is the random additive genetic effect for animal l with relationship matrix **H** that incorporates both pedigree and genomic information, and e_{ijkl} 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 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 3 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. As with the univariate models, 500,000 iterations were used with 50,000 burn-in and saving every 50 samples.

Correlations between respiratory disease resistance, scours resistance, or stayability with traits evaluated by CDCB (VanRaden et al., 2021) were estimated as the Pearson correlation coefficient between EBV values using PROC CORR of SAS software (version 9.4,

SAS Institute Inc.). Solutions for calf health traits were obtained from the results of their respective univariate analyses. Only sires with at least 75% reliability for lifetime net merit (NM\$) and 25% reliability for the calf traits of interest were 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, single-trait linear models were used to estimate variance components, with and without the inclusion of a herd-by-sire interaction, 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 nonrandomly chosen based on recommendations of known disease recording and use of AI 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 preweaning animals and 5.9% in weaned animals (USDA, 2010). More recently, Urie et al. (2018b) estimated the preweaning 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 d 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 nonrandomly 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 be 18.9%. Gonzalez-Peña et al. (2019) estimated the incidence of scours to be 26.1% using producer-recorded data.

Stayability to 1 yr of age was 75.0%. Thus, 75.0% of heifers born alive remained in the herd at 1 yr of age and 25.0% of heifers born alive were removed from the herd for any reason. Stayability was chosen as a mea-

Table 1. Descriptive statistics for calf respiratory disease until 365 d, calf scours until 60 d, and stayability until 365 d of age

Item	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 ¹ (n)	253	279	754
Incidence (%)	11.5	44.4	75.0

¹Number of animals that had a phenotypic record and were genotyped.

sure 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 threshold 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. (2011b), who estimated the heritability for respiratory disease to be 0.09 until calving on a New York commercial heifer raising operation and using a linear sire model; Neibergs et al. (2014) estimated a heritability of 0.13 for calves in a case-controlled study located in California and New Mexico. Quick et al. (2020) used a linear model with a binary response variable based on a clinical scoring system for respiratory disease and found a similar heritability estimate of 0.11 until 6 wk of age; however, they estimated a higher heritability of 0.24 when measured until 3 wk of age. Gonzalez-Peña et al. (2019) found the heritability to be 0.04 when using a threshold animal model and producer-recorded data in animals from birth until 365 d of age. McCorquodale et al. (2013) used a linear model and found the heritability of calf respiratory disease to be 0.04 when measured from birth until 3 mo 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 d of age to be 0.045 using a threshold model. Mahmoud et al. (2017) found the heritability of calf diarrhea on the underlying scale to be 0.06 from birth until 2 mo of age in German Holstein-Friesian calves. In US Jerseys, Gonzalez-Peña et al. (2019) 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 1 yr 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 on the underlying scale when measured until 1 yr of age. McCorquodale et al. (2013) estimated the heritability to 0.06, but with a large corresponding standard error using linear models. In Danish Holsteins, Fuerst-Waltl and Sørensen (2010) estimated the heritability 0.076 from birth until calving using a threshold sire model. On a New York heifer rearing operation, Henderson et al. (2011a) estimated the heritability on the observed scale of postweaning 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 mo of age. Differences in heritabilities between stayability and mortality estimates could be due to

Table 2. Variance components and heritability estimates¹ (SD) for calf health traits

Item	σ_{HY}^2	σ_A^2	σ_e^2	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_{HY}^2 = herd-year variance; σ_A^2 = additive genetic variance; σ_e^2 = residual variance; h^2 = heritability.

various reasons, including differences in trait definitions, differences in production systems, or differences in producer records.

Genetic Correlations

Estimated genetic correlations among the 3 calf traits are in Table 3. While phenotypes were coded as 0 = healthy 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 2 mo 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 with these studies. One potential explanation may be that 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 trait definitions.

Estimated breeding value correlations between the 3 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 correlations

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

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

were low in magnitude and not significantly different from zero. The correlation estimate between fat yield and stayability (-0.119) was unfavorable. Correlations between calf health traits and milk yield, while positive, were all less than 0.10 and not significant. 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 2 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 approximate 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 an EBV 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, whereas 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 correlations were found between calf health traits and NM\$ that ranged from 0.020 to 0.055. However, because of the sample size and low magnitude, these were not significantly different from zero. Gonzalez-Peña et al. (2019) estimated favorable approximate genetic correlations between scours risk and NM\$ (-0.427) and between mortality risk and NM\$ (-0.190) but an unfavorable approximate 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.

Calf health traits generally exhibited the strongest correlations with longevity traits published by CDCB including heifer livability, cow livability, and cow productive life. We were particularly interested in the cor-

relations between heifer livability, which is measured until 18 mo of age, and our measures of calf health since heifer livability is one of the few calf and heifer traits evaluated nationally by CDCB. The correlation estimate between stayability and heifer livability (0.217) suggests that selection for improved heifer livability should also improve organic calf stayability until 1 yr of age; however, the relatively low correlation estimate between heifer longevity traits may also indicate a potential genotype by environment interaction. Additionally, respiratory disease resistance was estimated to be favorably correlated with heifer livability (0.190). However, the correlation between heifer livability and scours resistance was numerically unfavorable albeit not significant (−0.081). This may have been due to differences in our calf population compared with the national population. Few studies are available comparing genetic measures of calf health to heifer livability evaluated by CDCB as heifer livability was not publicly available until December 2020 (CDCB, 2020).

Table 4. Estimated breeding value correlation estimates between calf health and Council on Dairy Cattle Breeding traits¹ for sires with at least 25% reliability for the calf trait of interest

Item	Respiratory resistance	Scours resistance	Stayability until 365 d
Sires (n)	207	302	275
Milk	0.050	0.087	0.040
Fat	−0.029	−0.078	−0.119*
Protein	0.029	0.079	−0.035
NM\$	0.055	0.020	0.021
HLIV	0.190**	−0.081	0.217***
LIV	0.178*	0.101	0.288***
PL	0.158*	0.082	0.217***
DCE	−0.003	−0.008	0.056
DSB	−0.085	0.005	−0.023
SCE	0.105	0.043	0.045
SSB	0.177*	0.019	0.118*
EFC	−0.073	−0.072	0.001
GL	0.019	0.019	0.039
SCS	−0.002	0.127*	−0.050
MAST	0.102	−0.110	0.180**
MFEV	−0.105	0.005	0.076
DA	−0.041	−0.089	−0.023
RP	−0.131	−0.041	0.012
KETO	−0.081	−0.125*	−0.148*
MET	−0.246***	−0.170**	−0.117
DPR	−0.065	−0.005	0.030
CCR	−0.040	0.011	0.043
HCR	−0.075	0.022	0.028

¹NM\$ = 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; 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; SCS: lower values favored; MAST, MFEV, DA, RP, KETO, and MET are all expressed such that higher values are favored.

* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

The correlations of respiratory disease resistance with cow livability and productive life were 0.178 and 0.158, respectively, and of stayability with cow livability and productive life were 0.288 and 0.217, respectively. The correlation estimates of scours resistance with cow livability and productive life were 0.101 and 0.082, respectively, and not significantly different from zero. Our correlation estimate between stayability and productive life is lower than that of Neupane et al. (2020), who estimated a 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, EBV 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 in magnitude and the majority were not significantly different from zero. Correlation estimates between respiratory disease resistance and stayability with sire stillbirth were 0.177 or 0.118, respectively, suggesting that increased respiratory disease resistance and stayability were correlated with increased calving difficulty. All other correlation estimates with calving traits were near zero and not significant. 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., 2018b).

Most EBV correlations between calf health traits, particularly respiratory disease resistance and scours

resistance, and health traits evaluated in cows were low to moderate in magnitude and unfavorable. Respiratory disease resistance exhibited an unfavorable correlation with metritis resistance (-0.246), with increased respiratory disease resistance being correlated with decreased resistance to metritis. For scours resistance, correlations were mainly unfavorable with cow health traits; increased scours resistance was correlated with decreased resistance to ketosis (-0.125) and metritis (-0.170). Stayability exhibited a favorable correlation estimate with mastitis resistance (0.180). Ketosis, metritis, and displaced abomasum resistances all exhibited correlation estimates with our calf traits, which were numerically negative; directions for correlations with mastitis, milk fever, and retained placenta resistances 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 approximate genetic 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 correlations. Respiratory disease resistance also exhibited small correlations with fertility traits. Gonzalez-Peña et al. (2019) estimated unfavorable approximate genetic correlations between respiratory disease and fertility but favorable approximate genetic correlations between scours and fertility and between mortality and fertility.

Herd-by-Sire Interactions

In part due to the lower-than-expected 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 with and without the random effect of herd-by-sire interaction can be found in Table 5. Although 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 3 calf traits. Nonconvergence using threshold models was likely due to low ad-

Table 5. Variance component estimates¹ (SE) from linear models with and without the random effect of herd-by-sire interaction

Item	With herd-by-sire interaction			Without herd-by-sire interaction		
	σ_{HY}^2	σ_{HSire}^2	σ_A^2	σ_e^2	σ_{HY}^2	σ_e^2
Respiratory	0.0071 (0.0038)	0.0010 (0.0005)	0.0030 (0.0015)	0.0927 (0.0017)	0.0073 (0.0039)	0.0914 (0.0017)
Scours	0.0893 (0.0315)	0.0051 (0.0011)	0.0017 (0.0022)	0.1665 (0.0027)	0.0877 (0.0310)	0.1581 (0.0030)
Stayability	0.0143 (0.0039)	0.0040 (0.0009)	0.0005 (0.0017)	0.1716 (0.0024)	0.0143 (0.0039)	0.1656 (0.0026)

¹ σ_{HY}^2 = herd-year variance; σ_{HSire}^2 = herd-by-sire variance; σ_A^2 = additive genetic variance; σ_e^2 = residual variance.

ditive genetic variance when including the interaction of herd-by-sire 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. Although 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 due to a reduction in additive genetic variances; heritability estimates for linear models excluding herd-by-sire interaction ranged between 0.05 and 0.06. This may indicate overestimation of heritability from models not including herd-by-sire effects. The herds in this study were from across the United States and had varying management practices. The unadjusted EBV correlation between stayability 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, although we found herd-by-sire accounted for nontrivial 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 are heritable. Heritabilities for calf respiratory, calf scours, and calf stayability ranged from 0.075 to 0.100 using threshold animal models. 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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