Genetic parameters of passive transfer of immunity for US organic Holstein 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 1 yr of age were recorded as either staying in the herd or leaving the herd (STAY365). Univariate and threshold models were fitted 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 transmit-

ting 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 calf

INTRODUCTION

Calf serum 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). During the first days of life, serum IgG and STP have high agreement. Deelen et al. (2014) estimated the correlation between serum IgG and STP to be 0.93 when taking blood samples from 3 to 6 d of age. Wilm et al. (2018) found the correlations between serum IgG measures at 24 h of age and STP from 2 to 9 d 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 mo of life with the lowest mortality in calves with STP ≥ 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 1 mo before first calving. Urie et al.

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(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 affect 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 nonlactating heifers between 4 and 38 mo 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 percentage 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 1.8 billion kilograms 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 AND 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). 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 (**GL**) of the dam. We defined FPT as a binary trait where a value of 1 was assigned if STP ≤ 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 1 yr (**STAY365**) was defined for 14,527 animals that had the opportunity to reach 1 yr of age by the time of the last herd data backup. Therefore, an animal needed to be born at least 1 yr before 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 1 yr 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 data set 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 data sets. A linear model was fitted for STP using the *airemlf90* program (version 1.139, Misztal et al., 2018). Threshold models were fitted 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.

The 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-year-month contemporary group j (levels = 98) at birth; age is the age in days of STP or FPT measurement ($k = 1, 2$, or 3); $Dage$ is the age of the dam ($l = 2, 3, 4, 5, \geq 6$ yr); H is the random effect for birthdate within herd m ; A is the random effect of animal n ; and e is the random residual. In addition to the above model, maternal direct additive and maternal permanent environment effects were fitted 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.

The STAY365 was fitted 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 ; and e is the random residual. Heritabilities (h^2) 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 were 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 fitted 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 2 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 (rel) 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.

The 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):

$$\hat{r}_{g1,2} = \frac{\sqrt{\left(\sum_{i=1}^n REL_{1i}\right)\left(\sum_{i=1}^n REL_{2i}\right)}}{\sum_{i=1}^n (REL_{1i} \times REL_{2i})} \times r_{1,2},$$

where $\hat{r}_{g1,2}$ 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 ; n is the number

Table 1. Descriptive statistics for serum total protein (STP), failure of passive transfer of immunity (FPT), and stayability to 365 d (STAY365)

Item	Restricted data set			Full data set ¹		
	STP	FPT	STAY365	STP	FPT	STAY365
HYM, ² no.	98	98	86	98	98	86
Calves, no.	7,518	7,518	6,052	16,725	16,725	14,527
Mean (SE), g/dL	6.39 (0.01)	NA ³	NA	6.37 (0.01)	NA	NA
%	NA	10	69	NA	11	68

¹Full data set permitted the maternal grandsire to be unknown, whereas the restricted data set required Holstein maternal grandsires.

²Herd-year-months of birth.

³NA = not applicable.

of sires; 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.

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.). Calf STP was regressed on the fixed effects of dam age, HYM, and GL. Dam age and HYM were defined as above. Gestation length was restricted to 250 to 300 d 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 stud-

ies. Urie et al. (2018b) reported a mean STP of 6.0 in a study that involved operations across the United States and multiple breed groups. Further, the percentage 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 1 yr of age given the opportunity, whereas 69% of calves remained in the herd at 1 yr of age for the restricted data. For animals with a STAY365 score, 9% and 8% of calves were involuntarily removed by 90 d in the full and restricted data, respectively. This is in close agreement with previous estimates of a 8% death loss before weaning on primarily conventionally managed western dairy operations (USDA, 2018). From 91 to 365 d, 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 STP 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 no additional studies have looked at the heritability of STP in neonatal dairy calves. Although 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 mo 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 3/4 Holstein and 1/4 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 mo 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 wk 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 United States, 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 1 yr of age to be 0.06 in US Holsteins. On a US commercial heifer operation, the heritability from weaning until exit was estimated to be lower at 0.036 (Henderson et al., 2011a). In Danish Holstein females, Hansen et al. (2003) estimated mortality from 1 to 180 d 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,

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

Item	Restricted data set			Full data set 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)	— ³	—	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 ⁴	0.99 (0.47)	0.19 (0.23)	NA	NC ⁵	0.25 (0.17)

¹Full data set permitted the maternal grandsire to be unknown, whereas the restricted data set required Holstein maternal grandsires.

² r_g = genetic correlation.

³Residual variance was scaled to 1 in threshold models.

⁴NA = not applicable.

⁵NC = not converged.

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 2 generations of Holstein sires compared with 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 3 or more generations of known Holstein sires. However, pedigree completeness was scarce in our data set beyond 2 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 were 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

Table 3. Least squares means for the regressions of stayability to 365 d on serum total protein (STP) phenotype and STP EBV quartiles

Item	Restricted data set		Full data set 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

^{a-c}Different superscripts within a column represent significant differences ($P < 0.05$).

¹Full data set permitted the maternal grandsire to be unknown, whereas the restricted data set required Holstein maternal grandsires.

STP EBV quartile calves remained in the herd at 1 yr of age compared with 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 1 yr of age compared with 67% of calves in the bottom quartile. Similar to STP EBV quartiles, STP phenotype quartile was a significant predictor of STAY365. In the full data set, 70% of top STP phenotype quartile calves remained in the herd at 1 yr of age compared with 66% of the lowest quartile calves. We found a similar result in our restricted data set. 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 who 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 nonsignificant. 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 2 populations. In the full analysis, STP approximate genetic correlations with fat and protein yields were near zero and nonsignificant. 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 affect component yield in later life.

We found low to moderate approximate genetic correlations between STP and calving traits. Related to 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, whereas 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, whereas 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, some evidence indicates 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-yr-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., 2018).

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

Table 4. Approximated genetic correlations (SE in parentheses) of EBV for serum total protein with health, fitness, and production traits

Trait ¹	Restricted data set	Full data set 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)*

¹NM = net merit; PL = productive life; LIV = cow livability; DSB = daughter stillbirth; SSB = sire stillbirth; DCE = daughter calving ease; SCE = sire calving ease; GL = gestation length; EFC = early first calving.

²Full data set permitted the maternal grandsire to be unknown, whereas the restricted data set required Holstein maternal grandsires.

* $P < 0.05$.

Table 5. Least squares means for the regressions of serum total protein on gestation length (GL) and age of the dam

Item	Restricted data set	Full data set 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, yr		
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

^{a-c}Different superscripts within a column represent significant differences ($P < 0.05$).

¹Full data set permitted the maternal grandsire to be unknown, whereas the restricted data set required Holstein maternal grandsires.

²GL quartile (Q) ranges. Restricted: Q1 = 251–273 d, Q2 = 274–275 d, Q3 = 276–278 d, Q4 = 279–298 d. Full: Q1 = 251–273 d, Q2 = 274–276 d, Q3 = 277–279 d, Q4 = 280–298 d.

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 effect on 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 effect 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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REFERENCES

- Beam, A. L., J. E. Lombard, C. A. Koprak, 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.* 92:3973–3980. <https://doi.org/10.3168/jds.2009-2225>.
- 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. [https://doi.org/10.3168/jds.S0022-0302\(89\)79089-5](https://doi.org/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. <https://doi.org/10.2460/javma.2002.221.1605>.
- 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. <https://doi.org/10.2527/jas1973.373676x>.
- 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. <https://doi.org/10.3168/jds.2018-14907>.
- 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>.
- 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. <https://doi.org/10.1186/s12864-018-5062-6>.
- 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. <https://doi.org/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. [https://doi.org/10.3168/jds.S0022-0302\(89\)79140-2](https://doi.org/10.3168/jds.S0022-0302(89)79140-2).
- 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. [https://doi.org/10.3168/jds.S0022-0302\(86\)80464-7](https://doi.org/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. [https://doi.org/10.1016/S0167-5877\(97\)00060-3](https://doi.org/10.1016/S0167-5877(97)00060-3).
- Fuerst-Waltl, B., and M. K. Sørensen. 2010. Genetic analysis of calf and heifer losses in Danish Holstein. *J. Dairy Sci.* 93:5436–5442. <https://doi.org/10.3168/jds.2010-3227>.
- 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, UK.
- Godden, S. 2008. Colostrum management for dairy calves. *Vet. Clin. North Am. Food Anim. Pract.* 24:19–39. <https://doi.org/10.1016/j.cvfa.2007.10.005>.
- 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. <https://doi.org/10.3168/jds.2018-15540>.
- 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. <https://doi.org/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. [https://doi.org/10.3168/jds.S0022-0302\(03\)73766-7](https://doi.org/10.3168/jds.S0022-0302(03)73766-7).
- 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. <https://doi.org/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. <https://doi.org/10.3168/jds.2011-4347>.
- Heringstad, B., Y. M. Chang, D. Gianola, and O. Østerås. 2008. Short communication: Genetic analysis of respiratory disease in Norwegian Red calves. *J. Dairy Sci.* 91:367–370. <https://doi.org/10.3168/jds.2007-0365>.
- 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. <https://doi.org/10.2527/jas1975.403392x>.
- 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. <https://doi.org/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. <https://doi.org/10.3168/jds.2012-5735>.
- McGuirk, S. M. 2008. Disease management of dairy calves and heifers. *Vet. Clin. North Am. Food Anim. Pract.* 24:139–153. <https://doi.org/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 Jan. 28, 2020. <http://nce.ads.uga.edu/wiki/doku.php?id=documentation>.
- 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. [https://doi.org/10.3168/jds.S0022-0302\(82\)82381-3](https://doi.org/10.3168/jds.S0022-0302(82)82381-3).
- 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. 2018. 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. <https://doi.org/10.3168/jds.2017-14008>.
- 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. <https://doi.org/10.1111/j.1939-1676.1996.tb02067.x>.
- 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. <https://doi.org/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. <https://doi.org/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 Jan. 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.
- 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. <https://doi.org/10.3168/jds.2016-11867>.
- 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.
- 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. <https://doi.org/10.3168/jds.2017-13553>.

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