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Short communication: Heritability of twinning rate in Holstein cattle

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ABSTRACT

Multiple births or twinning in cattle is a naturally occurring reproductive phenomenon. For dairy cattle, twinning is considered a detrimental trait as it can be harmful to cow and calf as well as costly to the producer. The objective of this study was to examine recent US calving records for the Holstein breed to determine a current estimate of heritability for twinning rate along with effects of season and parity. Two models were used in this study: a linear sire model and a binary threshold-logit sire model. Both were mixed models considering fixed effects and random effects. Analyses were conducted using a restricted maximum likelihood method. Heritability estimates were 0.0192 ± 0.0009 and 0.1420 ± 0.0069 for the linear and threshold models, respectively. Repeatabilities from the linear and threshold-logit models were 0.0443 ± 0.0012 and 0.2310 ± 0.0072, respectively. The nonzero estimates of heritability indicate the potential to select against this trait for genetic improvement of Holstein cattle.

Key words: twinning, heritability, dairy cattle

Short Communication

Twinning in cattle, especially dairy cattle, is viewed as a negative trait. This is due to the negative ratio of risk to reward in having twin births. There is still a debate about whether there is a benefit of increased milk production from dams that deliver multiple calves in a single calving (Kay, 1978; Kinsel et al., 1998; Hossein-Zadeh, 2010; Sawa et al., 2015) or whether there is a negative effect on milk production (Chapin and Van Vleck, 1980; Nielen et al., 1989; Fricke, 2001). However, even with increased milk production as a possible positive effect, it is associated with multiple negative effects such as abortion, dystocia, stillbirth, retained placenta, metabolic disorders, displaced abomasum, and ketosis (Fricke, 2001; Komisarek and Dorynek, 2002). Additionally, there is the effect on future calving for the dam as twinning increases the calving interval and the time period between calving and conception and reduces mean lifetime production (Andreu-Vázquez et al., 2012). Twinning is neutral with regard to the proportion of fertile replacement female calves to infertile freemartin females from mixed-sex twin births (Komisarek and Dorynek, 2002). The neutrality is from the offset of fertile females from same-sex twin births, though the absolute number would be lessened owing to the lower perinatal survival rate of twins. Even though there is a chance to reduce some of these negatives with adjustments to management (e.g., changes to diet for twin-bearing cows, additional labor), these adjustments would result in increased costs. A range of approximately $50 to $250 loss per twin birth puts a large economic expense on twinning with very minimal, if any, benefits for twins in the dairy industry (Beerepoot et al., 1992; Fricke, 2001). Frequency of twinning in US Holstein cattle has been approximately 5% (Cady and Van Vleck, 1978; Johanson et al., 2001), meaning an annual loss to the industry of $22.5 to $112.5 million assuming a national herd of 9 million cows.

Known contributing factors for twinning need to be accounted for when analyzing heritability. One such factor, as reviewed in Rutledge (1975), is the seasonal effect. This has been expressed as either the month or season of calving or conception, with conception months of September through October and March through April having the highest incidences. Another factor is parity of the dam. As the parity increases so does the chance of twinning, with the largest increase happening between the first and second parities (Rutledge, 1975; Johanson et al., 2001). These effects are presumably effects on ovulation rate, as incidence of monozygotic twinning is low and ovulation rate and twinning rate have a high genetic correlation (Van Vleck et al., 1991; Young and Kirkpatrick, 2016). Additionally, sires can have an influence on twinning rates in their daughters (Rutledge, 1975), suggesting a genetic component to variation. Johanson et al. (2001) grouped Holstein sires based on birth year and demonstrated that the sire group from the most current time points had more

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daughters with higher incidences of twinning. As with heritability, repeatability of twinning tends to be low (Syrstad, 1974; Rutledge, 1975). The objective of the current study was to estimate heritability and repeatability of twinning rate in US Holstein cattle using current calving record information for this population.

Calving records from the years 2010 to 2016 were obtained from AgSource Cooperative Services (Verona, WI). Initially, we obtained more than 2.9 million records from all breeds. Available information included cow, sire and dam identification (**ID**), herd, birthdate, calving date, parity, and multiple birth code. After editing, as described below, only the Holstein breed had sufficient records for estimation of heritability using a sire model. All other breeds had fewer than 20 sires represented in edited data versus more than 2,000 for the Holstein breed (Table 1). Consequently, efforts focused on data from Holsteins and records were removed if they were not Holstein for the cow, sire, and dam. Additionally, records were excluded if the cow, sire, or dam were missing part or all of their ID code or had codes indicating unknown ID. Records were also excluded if a cow had discrepant sire, dam, and birthdate information between records. Duplicate calving entries were eliminated such that there was 1 record per calving. Two sires and corresponding records were removed due to being listed both as a sire and as a cow. Suspected embryo transfer calvings were likewise excluded (indicated by multiple calvings within the same year for a cow). To increase the reliability of the genetic evaluation, only sires with ≥100 daughter records were included in the final data set (n = 2,223; Figure 1). Likewise, only herds with ≥100 records were included (n = 1,748; Figure 1). After editing, 1,440,540 records with 658,436 cows remained for use in the analysis.

Preliminary fixed effects analysis was done using SAS 9.4 (SAS Institute Inc., Cary, NC). Variance components for heritability and repeatability calculations were estimated using ASreml 4.1 (VSN International, Hemel Hempstead, UK). Two models were used in alternative analyses: a linear sire model (**LM**) and a binary threshold-logit sire model (**TLM**). The general form of the model in matrix notation was

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zs} + \mathbf{Ep} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of calving phenotypes (singles or twins) for the LM and a vector of unobserved liabilities for twinning for the TLM; $\mathbf{X}$ is an incidence matrix relating phenotypes to fixed effects of herd, year, season, and parity; $\mathbf{b}$ is a vector of fixed effects; $\mathbf{Z}$ is a matrix relating phenotypes to sire genetic effects; $\mathbf{s}$ is a vector of sire additive genetic effects; $\mathbf{E}$ is a matrix relating phenotypes to permanent environmental effects; $\mathbf{p}$ is a vector of animal environments; and $\mathbf{e}$ is a vector of random residuals. The sire, permanent environment, and residual effects were random effects and herd, year, season, and parity were fixed effects. It was assumed for the LM that the random effects followed normal distributions of $s \sim N\left(0, \mathbf{A}\sigma_s^2\right)$, $p \sim N\left(0, \mathbf{I}\sigma_p^2\right)$, and $e \sim N\left(0, \mathbf{I}\sigma_e^2\right)$, where σ_s^2, σ_p^2, and σ_e^2 represent additive genetic, permanent environment, and residual variances, respectively; $\mathbf{A}$ represents the numerator relationship matrix for sires; and $\mathbf{I}$ is the identity matrix. For the TML, random effects were assumed to have followed normal distributions of $s \sim N\left(0, \mathbf{A}\sigma_{s_T}^2\right)$, $p \sim N\left(0, \mathbf{I}\sigma_{p_T}^2\right)$, and $e \sim N\left(0, \mathbf{I}\frac{\pi^2}{3}\right)$, where $\sigma_{s_T}^2$, $\sigma_{p_T}^2$, and $\frac{\pi^2}{3}$ represent additive genetic, permanent environment, and residual variances, respectively.

Parity for this data was categorized into 4 groups: parity 1 (n = 563,942), parity 2 (n = 415,867), parity 3 (n = 251,010), and parity 4 and above (n = 209,721). Preliminary analysis indicated that means for parities 4 and above were not significantly different ($P < 0.05$), and the number of calving records per parity rapidly diminished with parity 3 and greater (Figure 1). Calving dates were categorized as being in 1 of 4 seasons based on month: season 1 = December through February, season 2 = March through May, season 3 = June

Table 1. Breakdown of records, herds, animals, and sires per breed with corresponding average twinning rates

Breed	Herds (no.)	Animals (no.)	Sires (no.)	Total records (no.)	Average twinning (%)
Holstein	3,074	831,579	20,317	1,806,505	—
Holstein[1]	1,748	658,436	2,223	1,440,540	4.8
Jersey[2]	491	14,938	1,767	29,378	2.7
Brown Swiss[2]	318	5,466	724	11,725	4.6
Guernsey[2]	80	2,846	357	6,062	3.2
Ayrshire [2]	95	983	258	2,151	2.0
Milking Shorthorn[2]	63	563	193	1,359	5.7

[1] Number of records after removal of herds and sires with fewer than 100 records. Data used in the heritability analysis. All other breeds had fewer than 20 sires after similar editing and were not used in heritability estimation.

[2] Number of records before removal of herds and sires with fewer than 100 records.