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Short communication: Genetic evaluation of stillbirth in US Brown Swiss and Jersey cattle

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ABSTRACT

Stillbirth (SB) often results in reduced milk yield, compromised reproductive performance, and decreased dam longevity. Corrective mating can be used as a short-term solution to the problem, but long-term improvement of the population requires the routine calculation of genetic evaluations. Breeding values for SB have been available for Holstein (HO) bulls since 2006, but not for Brown Swiss (BS) or Jersey (JE) bulls. In this study, a multi-breed sire-maternal grandsire threshold model was used to perform genetic evaluations for SB of BS, JE, and HO bulls using more than 14 million purebred and crossbred calving records. Phenotypically, the percentage of SB (%SB) across all lactations were 3.7% in JE, 5.1% in BS, and 6.3% in HO. Direct heritabilities for BS, JE, and HO were 0.008, 0.007, and 0.008, and maternal heritabilities were 0.002, 0.016, and 0.021, respectively. Compared with HO, crossbred calvings from BS and JE bulls bred to HO cows lowered %SB by 1.5 and 1.2%, respectively. In general, %SB increased considerably as calving difficulty increased in all 3 breeds; however, in JE, %SB was constant for dystocia scores of 3 (needed assistance), 4 (considerable force), and 5 (extreme difficulty). Compared with purebred HO calvings, purebred BS and JE calvings had lower phenotypic %SB by up to 5.5 and 7.8%, respectively, and BS × HO and JE × HO crossbred calvings decreased %SB by up to 3.8 and 4.1%, respectively. As expected, SB rates in primiparous cows were higher than those in multiparous cows. Female calves had greater %SB than male calves in all parities for JE and in second-and-later parities for BS. Favorable (decreasing) phenotypic and genetic trends from 1999 to 2009 were observed in all 3 breeds. Heterosis of SB for BS and JE was −0.026 and −0.149, respectively, on the underlying scale, which corresponds to effects on service-sire SB (SSB) and daughter SB (DSB) predicted transmitting ability (PTA) of −0.3 and −0.5% in BS, and −1.5 and −2.7% in JE. Overall, in the current population, BS bulls had the most desirable average SSB PTA of 4.8%, compared with 5.6% for JE and 5.5% for HO. Brown Swiss and JE bulls both had average DSB PTA of 6.5%, lower than that of 7.7% in HO. Average reliabilities of SSB and DSB in 3 breeds ranged from 45 to 50%. The use of a BS-JE-HO multibreed genetic evaluation for SB in the United States is feasible, and the addition of SSB and DSB to the lifetime net merit selection index will help improve the profitability of BS and JE cattle in the United States.

Key words: genetic evaluation, stillbirth, Brown Swiss, Jersey

Short Communication

Stillbirth (**SB**) often results in reduced milk yield, compromised reproductive performance, and decreased longevity of dams (Berry et al., 2007; Bicalho et al., 2007, 2008), and replacing stillborn calves also costs dairy producers substantially each year (Meyer et al., 2001a). Due to the different direct and maternal genetic correlations between SB and calving ease (**CE**) reported, Johanson et al. (2011) recommended evaluating for SB and CE separately. For Holsteins (**HO**) in the United States, genetic evaluations for CE have been available since 1978 (Berger, 1994; Van Tassell et al., 2003), and SB evaluations were first published in 2006 (Cole et al., 2007a). The calving ability index, including economic values of both SB and CE, was added into the 2006 revision of lifetime net merit, the selection index recommended for ranking US dairy cattle, to obtain continuous genetic improvement (Cole et al., 2009). However, SB evaluations have not previously been available for US Brown Swiss (**BS**) and Jersey (**JE**) cattle due to insufficient data (Cole et al., 2007a). The objectives of the current study were (1) to characterize SB data for US BS and JE and (2) to implement a multibreed sire-maternal grandsire (**S-MGS**) threshold model for SB including US BS, JE, and HO.

In the United States, SB is defined to include those calves born dead and those dying within 48 h of birth (Cole et al., 2007a). Stillbirth records (n = 24,311,207) from single births in BS, JE, and HO cattle were

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extracted from the national dairy database (Animal Improvement Programs Laboratory, Agricultural Research Service, US Department of Agriculture, Beltsville, MD), and subjected to a series of data quality edits modeled after Van Tassell et al. (2003). Data included purebred calvings from all 3 breeds, as well as BS × HO and JE × HO first-generation (F_1) crossbred calves, which was similar to the multibreed model used for CE in the United States (Cole et al., 2005). Calf livability was reported on a 3-point scale, where 1, 2, and 3 represented calves born alive, calves born dead, and calves that died within 48 h postpartum, respectively. Records with no livability scores were excluded from the analysis, and scores of 2 and 3 were combined to produce a 2-point scale. To avoid bias from herds that reported only live calves, herds were required to report at least 5 SB to be included in the analysis. At least 1,000 records were required for an individual sire or MGS birth year to be included in the analysis to avoid biased sire birth-year or MGS birth-year group solutions (defined in model 1 below) due to insufficient data. After editing, 14,364,811 SB records were available for analysis. Figure 1 shows distributions of the number of records by dam birth year for BS and JE. The SB data set is a subset of the CE data set, and the complete CE pedigree file (n = 176,683 bulls) was used for the SB analysis.

A multibreed S-MGS threshold model was used to estimate (co)variance components and compute PTA for SB using the THRGIBBS1F90 version 2.56 (Misztal et al., 2002) and CBLUP90IOD version 2.33 (Misztal et al., 2002) packages, respectively:

$$y = HY + YS + PS + Br + Y_s + Y_m + s + m + e, \quad [1]$$

where y is the SB score, $\mathrm{HY} \sim N\left(0, \mathbf{I}\sigma_{HY}^2\right)$ is the random herd-year effect, YS is the fixed year-season effect, PS is the fixed parity-sex combination effect, Br is the fixed breed composition effect, Y_s is the fixed sire birth-year effect, Y_m is the fixed MGS birth-year effect, $\mathrm{s} \sim N\left(0, \mathbf{A}\sigma_s^2\right)$ is the random sire effect, $\mathrm{m} \sim N\left(0, \mathbf{A}\sigma_m^2\right)$ is the random MGS effect, and $\mathrm{e} \sim N\left(0, \mathbf{I}\sigma_e^2\right)$ is the random error, where **A** is a pedigree-based additive relationship matrix, **I** is an identity matrix, and σ_{HY}^2, σ_s^2, σ_m^2, and σ_e^2 are variances of the herd-year, sire additive genetic, MGS additive genetic, and random error effects, respectively.

The levels of fixed effects in the model were defined as follows: year-season groups began in October and May across year boundaries, and parities were first, second, and third or later. Breed composition of calves included HO purebred calvings, BS purebred calvings, BS × HO crossbred calvings, JE purebred calvings, and JE × HO crossbred calvings. Sire birth-year groups were defined as ≤1981, 1982 to 1983, 1984 to 1985, 1986, 1987, . . . , 2007, and ≥2008. Maternal grandsire birth-year groups were different for animals with known and unknown MGS identification (**ID**). For animals with known MGS ID, groups were ≤1981, 1982 to 1983, 1984 to 1985, 1986, 1987, . . . , 2005, and ≥2006; for animals without valid MGS ID, groups were ≤1981, 1982 to 1983, 1984 to 1985, 1986, 1987, . . . , 2007, and ≥2008. These were assigned based on dam birth year, which was approximated as calving year − parity − 1.

Priors were those reported in Cole et al. (2007b): herd-year: 0.08; sire: 0.008; MGS: 0.018; S-MGS: 0.004; and residual: 1.000. These parameters were used in both the multibreed PTA prediction and (co)variance component estimation in each breed of BS, JE, and HO. To estimate genetic (co)variance components, 1 Gibbs chain of 50,000 samples was drawn, the first 10,000 samples were discarded as burn-in, and every fifth sample from the remaining 40,000 samples was included in the summary. No trend was observed in plots of Gibbs samples for each of the random effects; therefore, a longer burn-in period or a longer chain was not necessary. Heritabilities and correlations were

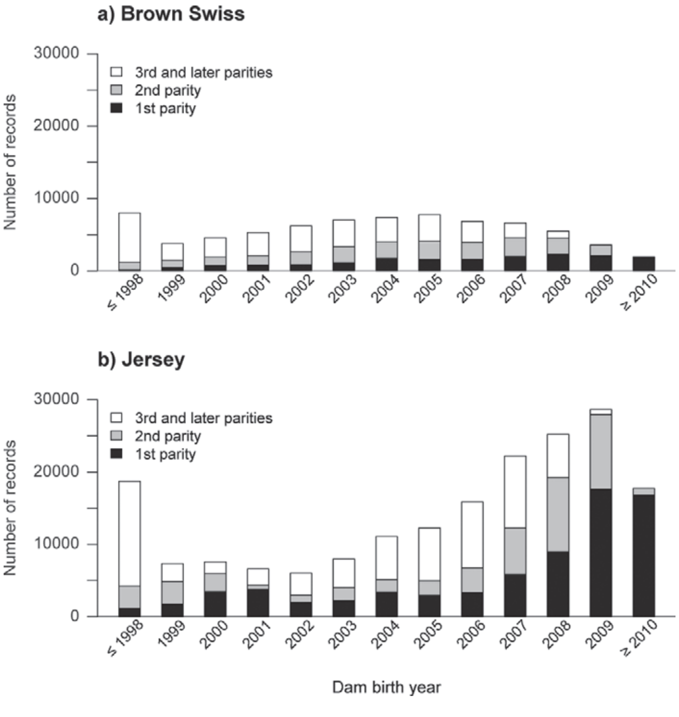

Figure 1. The number of stillbirth records by dam birth year in first (black), second (gray), and third-or-later parities (white) for (a) Brown Swiss purebred and crossbred calvings and (b) Jersey purebred and crossbred calvings.

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