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Genetic analysis of calving traits by the multi-trait individual animal model

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ABSTRACT

Five alternative models were applied for analysis of dystocia and stillbirth in first and second parities. Models 1 and 2 were included only to estimate the parameters required for model 4, and models 3 and 5 are included only as comparisons to the model 4 estimates. Variance components were estimated by multi-trait REML, including cows with valid calving records for both parities. For the effects of sire of calf on first and second parities, variance components were estimated including only calvings with the same sire of calf for both parities. All heritabilities for the cow effect were quite low, but higher for dystocia than for stillbirth and higher in first parity. The sire-of-calf heritabilities were higher than the cow effect heritabilities, except for stillbirth in parity 2. Unlike the effect of cow correlations, all sire of calf correlations were >0.6, and the correlations for the same trait in parities 1 and 2 were >0.9. Thus, a multi-trait analysis should yield a significant gain in accuracy with respect to the sire of calf effects for bulls not mated to virgin heifers. A multi-trait individual animal model algorithm was developed for joint analysis of dystocia and stillbirth in first and second parities. Relationships matrices were included both for the effects of cow and sire of calf. In addition, random herd-year-season and fixed sex of calf effects were included in the model. Records were preadjusted for calving month and age. A total of 899,223 Israeli Holstein cows with first calvings since 1985 were included in the complete analysis. Approximate reliabilities were computed for both sire of cow and sire of calf effects. Correlations between these reliabilities and reliabilities obtained by direct inversion of the coefficient matrix for a sire of cow-sire of calf model were all close to 0.99. Phenotypic trends for cows born from 1983 through 2007 were economically unfavorable for dystocia and favorable for stillbirth in both parities. Genetic trends were economically unfavorable for both dystocia and stillbirth in first parity. First-parity sire of calf trends were unfavorable for dystocia, but favorable for stillbirth. All environmental trends were nearly zero. Regressions of evaluations of the complete analysis on a model including only calvings before 2011 were all >0.8. All evaluations met the Interbull Method 3 criterion for unbiasedness. Model 4, which computed genetic evaluations for all animals for all 4 traits accounting for all known relationships and correlations among the traits, is recommended for routine genetic evaluation of calving traits.

Key words: dairy cattle, multi-trait animal model, dystocia, stillbirth, Israeli Holsteins

INTRODUCTION

Both dystocia or difficult calving (**DC**) and stillbirth (**SB**) affect the profitability of dairy production. The DC reduces the productive life of the cow and decreases the probability of survival of the calf. The DC on first-parity calvings reduced herd-life of Israeli Holsteins by ~180 d (Weller and Ezra, 2015). Despite the economic value of both traits, genetic evaluation is problematic because both traits are categorical, rather than continuous, and both have low heritability. In addition, incidence of both DC and SB are considerably higher for first-parity calvings, and genetic correlations among parities are incomplete (e. g., Liu et al., 2012). Finally, for both traits the phenotype is determined both by the cow calving and the sire of the calf (**SC**). Correlations between these 2 effects are at best minimal, and may even be antagonistic (Weller et al., 1988; Weller and Gianola, 1989). The effect of the cow calving can only be controlled genetically by inclusion of these traits in a selection index, whereas the SC effect can be controlled by a selective mating program. A selective mating plan for virgin heifers to reduce incidence of these traits was introduced in Israel in the 1960s (Bar-Anan et al., 1976). One-year-old sires are mated to first-parity cows; therefore, SC effects of these bulls can only be evaluated based on second-parity calvings. Only sires that have completed a progeny test and returned to general service are mated to virgin heifers. Until the

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year 2000, each bull returned to general service was mated to ~1,000 heifers. Based on the SC evaluations of these bulls for first-parity calving traits, only bulls with economically positive evaluations were selected to mate with the remaining heifers. For the last 15 yr, among the bulls returned to general service, bulls used to mate to virgin heifers were selected based on the SC evaluations of these bulls from the second-parity calvings of the cows mated to these bulls when they were 1 yr old.

Because of the discrete nature of the records, various studies have proposed analysis by threshold models, which assume the existence of an underlying normal variable that is responsible for the observed discrete observations (Djemali et al., 1987; Weller et al., 1988; Berger, 1994). Genetic evaluations for DC were first computed in the United States in 1977 (Van Tassell et al., 2003). A sire-maternal grandsire (**MGS**) threshold model, in which calvings for all parities were considered to be the same trait, was introduced for DC in 2003 (Van Tassell et al., 2003; Wiggans et al., 2003) and for SB in 2006 (Cole et al., 2007a,b). Cue and Hayes (1985) analyzed DC and SB jointly in a 2-trait sire model, but computed separate analyses for first and later parities, and separate analyses for the direct and maternal effects. Wiggans et al. (2008) proposed a multi-trait sire-MGS model in which first and later parities were analyzed as correlated traits; DC and SB were analyzed separately. They assumed that genetic correlations among later parities were equal to unity, although this assumption was not tested. Several studies have shown that DC and SB are correlated both phenotypically and genetically (Cue and Hayes, 1985; Ron et al., 1986; Weller et al., 1988; Weller and Gianola, 1989, Liu et al., 2012); thus, optimally, both traits should be analyzed jointly. Boelling et al. (2007) analyzed calving traits by a multi-trait sire-MGS model including DC, SB, and size of calf in first and later parities, but did not account for relationships.

The individual animal model (Westell and Van Vleck, 1987) came into commercial use during the late 1980s (e. g., Wiggans et al., 1988). The main advantages of the individual animal model are that all known relationships are included in the analysis, the model accounts for genetic merit of mates, and EBV are computed for all animals, not just sires with many progeny. Disadvantages are that computing time is much greater than sire models, reliabilities cannot be directly computed, and the model is generally amenable only to analysis of continuous traits. However, various studies have shown that loss in accuracy is generally minimal if dichotomous traits are analyzed by methods that assume a normal distribution of residuals (e.g., Weller et al., 1988). Jamrozik et al. (2005) analyzed Canadian Holsteins for 8 reproduction traits, including DC and SB by a multi-trait animal model (**MAM**), and estimated variance components by Bayesian methods with Gibbs sampling. However, only 53,158 cows were included in the analysis, and computing time was 1.5 mo. More recently, Van Pelt and De Jung (2011) analyzed SB by a MAM for Dutch Holsteins considering first and later parities as correlated traits. The DC was analyzed by a similar model (https://global.crv4all.com/68143/67761/67689/e14calease). Liu et al. (2012) analyzed DC and SB in first, second, and third parities of German Holsteins as 6 correlated traits by a MAM, with variance components estimated by a sire-MGS model.

In the age of genomics, derivation of EBV for all cows has an extra advantage, as many cow and calves are now routinely genotyped, and this data can be used to derive more accurate genomic EBV. In addition, because DC and SB are genetically correlated for both first and later parities, multi-trait analyses including both traits and first and later parities can use data from later parities to predict SC effects for matings to virgin calves. The objectives of our study were to estimate MAM maternal and SC (co)variance components for DC and SB for first and second parity, to develop a MAM algorithm for routine evaluation of these traits, and to compute phenotypic, genetic, and environmental trends for these traits.

MATERIALS AND METHODS

Data

First- and second-parity calvings of Israeli Holstein cows from January 1985 through May 2015 were analyzed. First-parity records were deleted if (1) SC or sire of cow was unknown, (2) days pregnant was listed as <261 or >292 d, (3) age at first calving was <20 or >30 mo, (4) sex of calf was not listed, or (5) calvings had multiple births. Second-parity records were deleted if no valid first-parity record was present. Both DC and SB were scored dichotomously. With respect to dystocia, farmers scored calvings according to 4 categories: unassisted, assisted but easy, assisted and difficult, or surgical. A calving was considered difficult if either of the last 2 categories was recorded. The SB was defined as birth of a dead calf, or death within 48 h of calving.

Statistical Models

The data were analyzed by 5 statistical models. Models 1 and 2 were used to estimate variance components for the analysis of all records by model 4. Development and testing of model 4 was the main objective of the