A Sire-Dam Threshold Model for U.S. Single-step Calving-Ease Evaluation

S. Savoia*[*1], J. Maskal[1, 2], E. Nicolazzi[1], J. Cole[1], and A. Legarra[1,3]

[1] Council on Dairy Cattle Breeding, Bowie (MD), USA

[2] Department of Animal Sciences, Purdue University, West Lafayette (IN), USA

[3] Department of Animal and Dairy Science, University of Georgia, Athens (GA), USA

Corresponding author: simone.savoia@uscdcb.com

Abstract

The traditional U.S. calving ease (CE) evaluation currently uses a single-trait sire-maternal grandsire (sire-MGS) threshold model implemented in a stand-alone pipeline separate from other trait groups, while the genomic evaluation uses a multi-step approach with de-regressed proofs as input. As the Council on Dairy Cattle Breeding (CDCB) transitions national evaluations toward single-step genomic BLUP (ssGBLUP), a sire-dam threshold model using animal-model pedigree was investigated to better represent maternal information while accommodating incomplete calf identification in U.S. data. CE records from 2002 onward were analyzed using single- and multi-trait threshold models, with first and later calvings modeled either jointly or as correlated traits. Variance components were estimated from an informative subset using Gibbs sampler, and breeding values were subsequently obtained at national scale under both traditional pedigree-based BLUP (pBLUP) and ssGBLUP threshold models using a Newton-Raphson algorithm. Genetic correlations between first and later calvings were high for direct (0.95) and maternal (0.84) effects, supporting adoption of the single-trait model. In the final model, direct and maternal heritabilities were 0.092 and 0.115, respectively, with a genetic correlation of −0.40. Genetic trends from pBLUP and ssGBLUP were very similar, whereas comparisons with the current domestic sire-MGS pBLUP evaluation showed breed- and component-dependent re-ranking, particularly for the maternal effect. The sire-dam threshold model provides a practical framework for integrating CE into the CDCB single-step evaluation system while maintaining continuity with the current U.S. interpretation of the published Sire Calving Ease and Daughter Calving Ease traits.

Key words: Calving Ease; Threshold Model; Sire-Dam; Sire-MGS

Introduction

Genetic evaluations for calving ease (CE) in U.S. Holsteins (HO), date back to 1978 (Berger, 1994). In 2003, the evaluation transitioned to a single-trait sire-maternal grandsire (MGS) threshold model (Van Tassell et al., 2003), incorporating MGS information to partially account for differences in maternal genetic ability and the genetic merit of mates. The evaluation was subsequently extended to consider Brown Swiss (BS) animals in 2005 (Cole et al., 2005) and, in 2020, underwent a broader revision of model effects, data edits, and genetic parameter estimates (Gaddis, 2020). The single-trait sire-MGS structure and its dedicated stand-alone computational pipeline have, however, remained in place and are part of the evaluations currently conducted by the Council on Dairy Cattle Breeding (CDCB; Bowie, Maryland, USA).

For international evaluation, liability-scale solutions are provided to Interbull for MACE evaluation of direct and maternal CE, whereas national evaluations are published as predicted transmitting abilities (PTA) for Sire Calving Ease (SCE) and Daughter Calving Ease (DCE), respectively.

CDCB's transition of the U.S. national genetic evaluation system toward single-step

genomic evaluation provided an opportunity to improve the statistical modeling and reconsider the computational implementation of CE, with the goal of integrating CE into a common evaluation pipeline across trait groups.

The revision process initially considered ICAR guidelines for harmonization of national calving trait evaluations (ICAR, 2026), which favor, in brief, an animal-model formulation accounting for direct and maternal genetic effects and treating first and later parities as distinct but correlated traits.

However, characteristics of the U.S. dairy data precluded direct implementation of the recommended approach. Calf identification is not consistently available in the U.S. National Cooperator Database stewarded by CDCB. Reconstructing dummy calf identities across the entire data set was considered operationally infeasible and would not allow those calves to be linked subsequently to the same animals when they entered the evaluation as calving cows. As an alternative to the current sire-MGS model, a sire-dam formulation was therefore investigated, allowing the dam to contribute directly to the maternal component without requiring identification of the calf as an evaluated animal. Moreover, despite the categorical nature of the CE phenotype, a linear-model approach was initially investigated, prioritizing operational efficiency and facilitating future integration of MACE proofs at national level. Difficulties in transforming and interpreting EBV from the linear scale as expected percentages of difficult calvings redirected the evaluation toward a threshold-model formulation. Maintaining the established definition and interpretation of U.S. CE PTAs was considered an important requirement for the industry; therefore, retaining the threshold model framework allowed continuity in the interpretation and publication of CE evaluations while changing the representation of the maternal component.

The objective of this study was to develop and evaluate a sire-dam threshold model for CE suitable for integration into the CDCB single-step evaluation framework, using the ICAR guidelines as a reference while accommodating the data structure and operational requirements of the U.S. dairy cattle evaluation system.

Materials and Methods

Data

CE records and pedigree information were obtained from the U.S. National Cooperator Database. CE is scored by herd owners on a 5-point scale, where 1 = no problem, 2 = slight problem, 3 = assistance needed, 4 = considerable force, and 5 = extreme difficulty. For genetic evaluation, scores 4 and 5 are combined into a single category. Records were restricted to calvings occurring from 2002 onward to reduce the proportion of observations with missing dam information. To align the CE evaluation with other trait groups, phenotypic records from all dairy breeds and the most common crossbred groups were included, whereas beef-on-dairy crossbreds were excluded. Records were retained for parities 1 through 6 and required known service-sire and dam identification, with dam age at calving falling within predefined parity-specific limits and service-sire required to be older than 12 mo at calving. Observations from multiple birth calvings were excluded, and gestation length was required to fall within predefined limits. Herds were screened based on the distribution of reported CE scores. Contemporary groups were defined as herd-years and were required to contain more than 10 calvings from at least two different service-sires. The resulting dataset used for breeding-value estimation included approximately 23.3 million records, of which about 35% were from first-parity calvings, with a pedigree containing 17.8 million animals. Genotypes were available for approximately 965,000 informative animals, of which 38,968 were included in the APY core (Misztal et al., 2014).

Sire-dam Threshold Models

CE was analyzed using sire-dam threshold models in which service-sires and dams were included in the pedigree as animals together with their ancestors. Missing parent groups were represented by 103 metafounders, defined by sex, breed, and year of birth, and subsequently merged within breed and sex following Legarra and Aguilar (2025). Fixed effects included sex of the calf, dam age within parity, year-season, and covariates accounting for calf heterosis based on ordered sire and dam breed fractions (VanRaden, 1992). Random effects included herd-year contemporary group, correlated genetic effects of the service-sire and dam, and a permanent environmental effect of the dam. Both single-trait and multi-trait formulations were evaluated. In the multi-trait model, first and later calvings were treated as distinct but genetically correlated traits, whereas in the single-trait model were considered expressions of the same trait and analyzed jointly.

Variance components and Breeding Value Estimation

Variance components were estimated from a subset of the data using Gibbs sampling as implemented in GIBBSF90+ v.3.27 (Sorensen et al., 1995; Lourenco et al., 2022), using pedigree information only. For this work and to facilitate biological interpretation, variance and covariance components estimated under the sire-dam parameterization were transformed to the equivalent direct-maternal scale, from which the corresponding genetic parameters were derived. The transformation follows from equating the genetic contributions of the sire-dam and direct-maternal representations of the calving phenotype.

Breeding values were estimated with the sire-dam threshold model at the national scale under both pedigree BLUP (pBLUP) and single-step genomic BLUP (ssGBLUP) using maximum a posteriori estimation with the Newton-Raphson algorithm (Bermann et al., 2026). Estimates on the underlying liability scale from the investigated models were compared with those from the current sire-MGS model, thereby avoiding differences associated with definitions of the phenotypic bases and with transformation to the observed PTA scale. To facilitate comparison of maternal effects, dam-effect solutions (d) from the new model were expressed as $d/2$, placing them on the same scale as the current MGS solutions.

Results & Discussion

Figure 1 shows the phenotypic trends in the incidence of difficult calvings (scores 4 and 5) for first and later parities over the last 20 years. The strong reduction in dystocia likely reflects both genetic selection for improved CE and changes in herd management and reproductive practices, including increased use of sexed semen. This marked phenotypic change, together with the very low incidence of difficult calvings observed in recent years, may have contributed to the poor performance of the linear-model approach, particularly when translating EBV to the observed frequency scale, because the transformation assumes a fixed rate of incidence of dystocia over time.

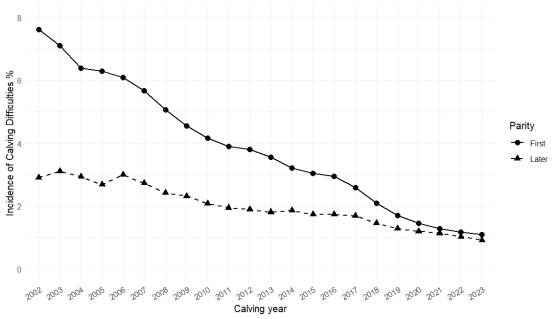


Figure 1. Incidence of difficult calvings (original CE scores 4 and 5, combined as category 4 for evaluation) by calving year in first and later parities.

Table 1 summarizes the genetic parameters obtained from the multi-trait sire-dam threshold model after transformation into the direct-maternal scale to make them comparable to literature. Direct heritability estimates were lower than maternal estimates in both parity groups (first calvings: 0.068 vs. 0.128; later

calvings: 0.048 vs. 0.065). This pattern contrasts with previous studies, in which direct heritability for CE has generally exceeded maternal heritability. For example, Eaglen and colleagues (2012) reported direct and maternal heritabilities of approximately 0.11 and 0.08, respectively, at first parity, compared with 0.03 and 0.02 at later parities.

The direct-effect genetic correlation across parities was close to unity (0.945), whereas the maternal-effect correlation was lower (0.835), but remained indicative of substantial genetic similarity across parity groups. These estimates supported treating first and later calvings as a single trait for subsequent analyses, a choice also consistent with the increasingly similar phenotypic trajectories of the two parity groups in recent years.

Table 1: Direct and maternal genetic parameters for CE from the multi-trait sire-dam threshold model. Heritabilities are shown on the diagonal and genetic correlations below the diagonal

Genetic Effect *	Dir. 1st	Dir. Later	Mat. 1st	Mat. Later
Dir. 1st	0.068			
Dir. Later	0.945	0.048		
Mat. 1st	-0.254	-0.143	0.128	
Mat. Later	-0.208	-0.116	0.835	0.065

* Dir. 1st: direct first calving; Dir. Later: direct later calvings; Mat. 1st: maternal first calving; Mat. Later: maternal later calvings.

Genetic parameters obtained from the single-trait model showed direct and maternal heritabilities of 0.092 and 0.115, respectively, compared with 0.072 and 0.053 under the current single-trait sire-MGS model.

The genetic correlation between direct and maternal effects was -0.403, indicating an antagonistic genetic relationship between the two components. Such negative direct-maternal correlation is consistent with previous CE studies; Eaglen and colleagues (2012) reported estimates of -0.47 and -0.40 for first and later parities, whereas the current U.S. sire-MGS evaluation was originally parameterized with a direct-maternal correlation of approximately -0.12.

The genetic trends from the proposed pBLUP evaluation were broadly consistent with those from the current CDCB evaluation for the direct component, with both showing a gradual decline (reduction of calving difficulties) over time in HO and a similar, although more variable, pattern in BS (Figure 2a). Larger differences were observed for the maternal component. In particular, the new pBLUP model produced a markedly steeper decline in the maternal effect for recent HO birth years than the current sire-MGS evaluation, with a similar but less pronounced divergence in BS (Figure 2b). This is likely to reflect the change in maternal representation from MGS to dam and the resulting increased information and redistribution of genetic signal between direct and maternal components.

Comparisons between pBLUP and ssGBLUP under the new sire-dam threshold model showed very similar genetic trends for proven bulls, as expected, indicating that the main differences relative to the current evaluation were driven primarily by the revised model structure rather than by the incorporation of genomic information.

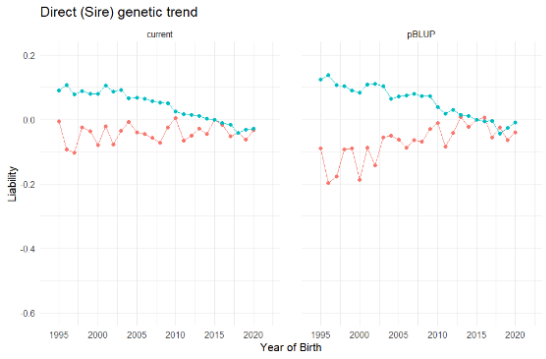


Figure 2a. Genetic trends for CE direct genetic effect under the current CDCB evaluation (left panel) and the proposed sire-dam threshold model (right panel) for HO (cyan) and BS (pink). Solutions were expressed on liability scale relative to a genetic base defined within-breed by bulls born in 2015. All bulls were required to have at least 25 observations distributed across at least two herds.

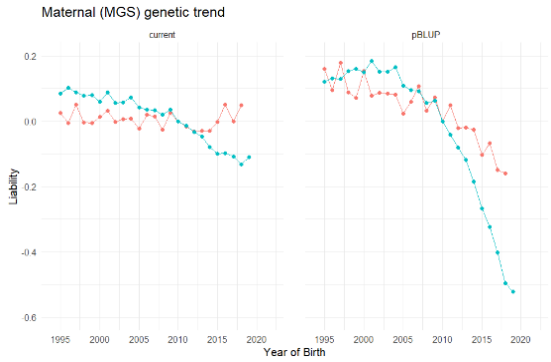


Figure 2b. Genetic trends for CE MGS genetic effect under the current CDCB evaluation (left panel) and the proposed sire-dam threshold model (right panel) for HO (cyan) and BS (pink). Solutions were expressed on liability scale relative to a genetic base defined within-breed by bulls born in 2010. All bulls were required to have at least 25 daughters' observations distributed across at least two herds.

Spearman correlations between solutions from the current CDCB evaluation and the proposed sire-dam pBLUP model indicated re-ranking, with differences across breeds and genetic components. For the direct effect, correlations were 0.79 for BS and 0.84 for HO, whereas for the maternal effect they were 0.72 and 0.87, respectively. The extent of re-ranking may reflect breed-specific differences in data structure, including the amount of information available for individual sires and their use in crossbreeding. These differences may be particularly relevant because the proposed model evaluates a broader population than the current evaluation, which is restricted to HO, BS, and HO × BS crosses. These comparisons were based exclusively on national evaluations; consequently, the magnitude of re-ranking may differ after incorporation of Interbull MACE information, particularly for breeds and bulls with limited domestic information.

Conclusions

The proposed sire-dam threshold model provides a practical framework for integrating CE into the CDCB single-step evaluation system while preserving the established interpretation of SCE and DCE PTAs. High genetic correlations across parities supported a single-trait formulation, and results indicated a stronger maternal contribution than under the current sire-MGS model. Genetic trends from pBLUP and ssGBLUP were very similar, suggesting that differences from the current evaluation were driven mainly by the revised model structure. Overall, the sire-dam threshold model appears suitable for routine national implementation, with future work focused on MACE integration.

Acknowledgments

The authors acknowledge the support of Dairy Herd Improvement (DHI) organizations and Dairy Records Processing Centers (DRPC) for processing and relaying the information to CDCB, as well as purebred breed associations for providing pedigree data.

References

Berger, P.J. 1994. Genetic prediction for calving ease in the United States: Data, models, and use by the dairy industry. *J. Dairy Sci.*, 77, 1146-1153. https://doi.org/10.3168/jds.S0022-0302(94)77051-X

Bermann, M., Legarra, A., Misztal, I., and Lourenco, D. 2026. Methods for joint genetic prediction of multiple ordinal categorical and continuous traits. *Genetics* 233 (1), iyag086. https://doi.org/10.1093/genetics/iyag086

Cole, J.B., Goodling, R.C., Wiggans, G.R., and VanRaden, P.M. 2005. Genetic evaluation of calving ease for Brown Swiss, Jersey, and Holstein bulls from purebred and crossbred calvings. *J. Dairy Sci.*, 88, 1529-1539. https://doi.org/10.3168/jds.S0022-0302(05)72822-8

Eaglen, S.A.E., Coffey, M.P., Woolliams, J.A., and Wall, E. 2012. Evaluating alternate models to estimate genetic parameters of calving traits in United Kingdom Holstein-Friesian dairy cattle. *Genet. Sel. Evol.*,

44:23. https://doi.org/10.1186/1297-9686-44-23

Gaddis, K. P. 2020. Calving Ease, Stillbirth Evaluations Enhanced. Council on Dairy Cattle Breeding, Bowie, MD, USA. https://uscdcb.com/wp-content/uploads/2024/05/CDCB-Parker-Gaddis-Calving-Enhancements-03_2020-1.pdf

ICAR. 2026. Section 09 - Dairy Cattle Genetic Evaluation. ICAR Guidelines. International Committee for Animal Recording. Accessed May 2026. https://wiki.icar.org/index.php/Section_09_%E2%80%93_Dairy_Cattle_Genetic_Evaluation

Legarra, A., and Aguilar, I. 2025. Tools to refine unknown parent group definitions. *J. Dairy Sci.* 108:1747-1756. https://doi.org/10.3168/jds.2024-25408

Lourenco, D., Tsuruta, S., Aguilar, I., Masuda, Y., Bermann, M., Legarra, A. and Misztal, I. 2022. Recent updates in the BLUPF90 software suite. *Proceedings of the 12th World Congress on Genetics Applied to Livestock Production (WCGALP)*, Rotterdam, The Netherlands. 1530-1533.

Misztal, I., Legarra, A., and Aguilar, I. 2014. Using recursion to compute the inverse of the genomic relationship matrix. *J. Dairy Sci.*, 97, 3943-3952. https://doi.org/10.3168/jds.2013-7752

Sorensen, D.A., Andersen, S., Gianola, D., and Korsgaard, I.R. 1995. Bayesian inference in threshold models using Gibbs sampling. *Genet. Sel. Evol.*, 27, 229-249. https://doi.org/10.1051/gse:19950303

VanRaden, P. M. 1992. Accounting for inbreeding and crossbreeding in genetic evaluation of large populations. *J. Dairy Sci.*, 75, 3136-3144. https://doi.org/10.3168/jds.S0022-0302(92)78077-1

Van Tassell, C.P., Wiggans, G.R., and Misztal, I. 2003. Implementation of a sire-maternal grandsire model for evaluation of calving ease in the United States. *J. Dairy Sci.*, 86, 3366-3373. https://doi.org/10.3168/jds.S0022-0302(03)73940-X