# Implementation of a Sire-Maternal Grandsire Model for Evaluation of Calving Ease in the United States

**C. P. Van Tassell,\*,† G. R. Wiggans,\* and I. Misztal‡**
*Animal Improvement Programs Laboratory and
†Bovine Functional Genomics Laboratory,
Agricultural Research Service, USDA, Beltsville, MD 20705-2350
‡Animal and Dairy Science Department, University of Georgia, Athens 30602

## ABSTRACT

The objective of this study was to add a maternal grandsire (MGS) effect to the existing sire model for national calving ease genetic evaluations. The Animal Improvement Programs Laboratory (AIPL) of USDA assumed responsibility for conducting the national genetic evaluation for calving ease and maintaining the associated database in 1999. Existing evaluations used a sire threshold model. Adding an MGS effect to the model was expected to improve accuracy by partially accounting for merit of mates and differences in maternal ability of the dams. Dystocia data were migrated to a relational database integrated with the AIPL production database. This database design allowed more rigorous data edits by comparison with the production data and improved MGS identification (ID) rate by utilizing pedigrees from the production records. Integration of dystocia data with production data increased MGS ID rate from 58 to 73%. In addition, nearly 200,000 duplicate records were identified using the new edit system. Sire and sire-MGS models were compared using over 10 million observations available for the August 2002 national genetic evaluation. The sire model included herd-year, season, sex of calf, parity of dam, birth year group of sire, and sire. For the sire-MGS model, MGS and birth year group of MGS were added, year-seasons rather than seasons were used, and sex of calf and parity of dam were combined into a single interaction effect. Herd-year, sire, and MGS were random effects. Variance components used for the sire model were those previously used in the national evaluation and for the sire-MGS model were estimated in a separate study. Correlations between predicted genetic merits for service sire calving ease from the two models was 85%, indicating general agreement, but with some significant differences in evaluations. A sire-MGS model was implemented in August 2002 for the national calving ease genetic evaluation system.
(**Key words:** calving ease, dystocia, threshold model, genetic evaluation)

**Abbreviation key: AIPL** = Animal Improvement Programs Laboratory, **CE** = calving ease, **%DBH** = PTA for percentage of births that are difficult for first-calf heifers, **ID** = identification, **MGS** = maternal grandsire, **S-MGS** = sire-maternal grandsire.

## INTRODUCTION

With support from the National Association of Animal Breeders, the Animal Improvement Programs Laboratory (**AIPL**) of USDA assumed responsibility for calculating national genetic evaluations for calving ease (**CE**) and maintaining the associated database in 1999.

Calving ease is scored on a scale of 1 (no problem or unobserved) to 5 (extreme difficulty). Each unit increase in score does not represent the same increase in difficulty, so a threshold model based on these ordered categorical data is appropriate. A threshold sire model (Djemali et al., 1987) was introduced for the US genetic evaluation in 1988 (Berger, 1994). Concern about the antagonism between direct and maternal genetic effects on dystocia (Burfening et al., 1981; Thompson et al., 1981; Manfredi et al., 1991) led to interest in adding maternal effects to the evaluation model. Development of an evaluation based on a sire-maternal grandsire (**S-MGS**) model was desirable to increase the accuracy of service sire evaluations by partially accounting for differences in the merit of mates and to provide a calving ease evaluation that included maternal effects. This model improvement also provides a way for dairy producers and breeding companies to include maternal calving performance in breeding programs. The main objective of this research was to implement a S-MGS threshold model for the dystocia genetic evaluation and to assess the impact on evaluations of the change from a sire only model. Because only approximately half of the CE records submitted to AIPL include maternal grandsire (**MGS**) identification (**ID**), an additional chal-
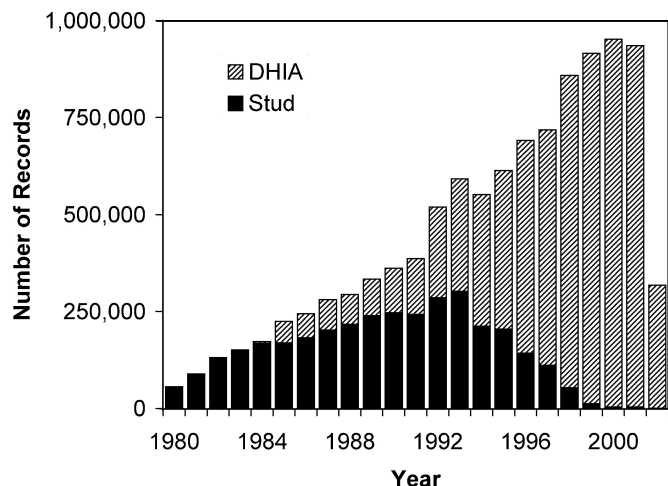
**Figure 1.** Source of data contributing to national calving ease database.

lenge was to integrate the dystocia data with the production database to make the more complete production pedigree and calving records available for cross-referencing. The use of relational databases allowed for more stringent data editing and improved data access, and in some cases, the CE records provided new information for the production database.

Relationships are described relative to the calf born. Specifically, the dam is the cow observed for dystocia, the sire is the service sire for this calving, and the MGS is the sire of the dam. However, the recorded observation is described as the calving of the dam rather than as the birth of the calf.

## MATERIALS AND METHODS

### Data

Dairy Records Management System (Raleigh, NC) provided the historical data, assembles and preedits CE records, and provides biannual updates to AIPL. Data originate both from traditional DHIA data collection pathways as well as from AI organizations through collection by their cooperators. In the first years that CE data were collected, nearly all data came through AI organizations, but over time the portion of data collected through DHIA has increased so that nearly all recent data were collected via DHIA and processed through dairy records processing centers (Figure 1).

### Database Design

Storage of CE records in relational database tables linked to the production database minimized storage requirements by avoiding storage of redundant pedigree information while retaining usable pedigree data that did not qualify for inclusion in the production database. This system allows more stringent editing of pedigree and calving information and better identification of duplicate records.

Two primary tables were created for storage of dystocia data. The primary CE table contains CE data for individual calving records (herd, sire, dam, CE score, parity, calving date, multiple birth code, and data source). Sire and dam ID in this table are stored as animal keys. A unique numeric animal key is assigned to every animal in the production database, allowing multiple ID (e.g., American ID and eartag) to be easily cross-referenced. A second table retains pedigree (i.e., MGS) information for records with dam ID that are not compatible with the production database. An example of an incompatible ID would be a cow name, such as "Suzie," rather than a registration or eartag number. Fields in this table include dam and MGS ID, herd where the observation was recorded, and dam birth date.

### Data Processing

The CE records with a dam ID that is in the production database are stored with the associated animal key (thus linking them to the production pedigree table). If a dam ID is present but not found in the production pedigree table, then a pedigree input record is generated and submitted to the production edit system to add the animal ID and pedigree information. If that pedigree record is accepted, animal keys are assigned for the dam and possibly for the MGS. The MGS ID and birth date are updated if not present in the production pedigree, but existing data in the production database are not modified.

Records that fail production edits or do not include valid dam ID may not be unique. In this case, unique keys are assigned, and pedigree information is loaded into the CE pedigree table. These keys, which will be referred to as CE keys, are negative so that they are easily distinguishable from those in the production data. Thus, records in the primary CE data table contain either a production (positive) key, linking them to the production database, or a CE (negative) key, linking them to the supplemental CE pedigree table. This scheme was designed to facilitate storage of pedigree information for the implementation of an S-MGS model by allowing storage of MGS ID even if dam ID is missing or ambiguous. Each record with unknown dam is assigned a unique CE key. For ID that are not already present in the production database, additional pedigree information is specifically requested from Holstein As-

sociation USA (Bratteboro, VT) and Canadian Dairy Network (Guelph, ON).

A number of data integrity edits are also imposed. An appropriate value for CE is required. Some additional fields are also required. Records included are for calvings since 1980.

## Detection of Duplicate Records

The data undergo preliminary editing to remove duplicates. Based on suggestions from the National Association of Animal Breeders, records were considered duplicates if they contained the same herd, sire, calving date, parity of dam, and sex of calf. For records that originated from a single data source, matching dam was also required. For records with production dam keys, a new and more rigorous definition was applied: records with the same dam and calving dates within 6 mo were considered duplicates. An additional class of duplicates was defined for records with CE keys. Records with dam ID are considered duplicates if they have the same herd, the same (nonzero) dam key, and calving dates within 6 mo. In all duplicate edits, if CE scores disagree, then both records are discarded.

The impact of the edits was evaluated by comparing data extracted for the August 2002 evaluation with the data for the same evaluation prepared using the sire model series of programs.

## Genetic Evaluation Models

*Sire model.* The sire threshold model previously used for the national genetic evaluation was:

$$y_{ijklmno} = hy_i + Season_j + Sex_k + P_l + Y_m + s_{mn} + e_{ijklmno},$$

where $y_{ijklmno}$ = CE score, $hy_i$ = random effect of herd-year i, $Season_j$ = fixed effect of season j, $Sex_k$ = fixed effect of sex k, $P_l$ = fixed effect of parity l, $Y_m$ = fixed effect of sire birth-year m, $s_{mn}$ = random effect of sire n in sire birth year group m, and $e_{ijklmno}$ = random residual effect. The two seasons begin in May and October. Parity effects were assigned for parities 1 and ≥2. Fixed birth year groups were ≤1982, 1983 to 1984, 1985 to 1986, 1987, 1988, ..., 1997, 1998 to 2001, and a group for bulls with unknown birth year. Inverse of the relationships matrix was calculated using only sire and MGS information for bulls represented in the data (Henderson, 1975). The pedigree information was based on the genetic evaluation distribution file for production data from AIPL. Based on research by Djemali et al. (1987), variance components used were 0.1601, 0.0381, and 1.0000 for herd-year, sire, and residual, respectively. These correspond to heritabilities of 0.13 or 0.15

if the herd-year variance is included or excluded, respectively, from the total variance.

Dam and sire breeds were required to be either Holstein or Red and White for records included in the sire model evaluation.

*Sire-MGS model.* The S-MGS threshold model developed in this project and used in national genetic evaluations beginning in August 2002 was:

$$y_{ijklmnop} = hy_i + YS_j + PS_k + BS_l + BM_m + s_{ln} + m_{mo} + e_{ijklmnop},$$

where $y_{ijklmnop}$ = CE score, $hy_i$ = random effect of herd-year i, $YS_j$ = fixed effect of year-season j, $PS_k$ = fixed effect of parity-sex k, $BS_l$ = fixed effect of sire birth year l, $BM_m$ = fixed effect of MGS birth year m, $s_{ln}$ = random effect of sire n in sire birth year group l, $m_{mo}$ = random effect of MGS m in MGS birth year group o, and $e_{ijklmnop}$ = random residual effect. The year-season groups begin in May and October. Parity effects were assigned for parities 1, 2, and ≥3. Birth year groups for sires were <1982, 1982 to 1983, 1984 to 1985, 1986, 1987, ..., 1996, and >1996. Birth year groups for identified MGS were <1982, 1982 to 1983, 1984 to 1985, 1986, 1987, ...,1994, and >1994. The birth year groups will be updated annually. For records without valid MGS ID, separate MGS birth year groups were assigned based on dam birth year. When dam birth years were not recorded, then dam birth year was approximated by calving year – parity – 1. Then birth year groups for MGS were <1982, 1982 to 1983, 1984 to 1985, 1986, 1987, ..., 1997, and >1997. Fixed birth year groups were used to allow for different group specifications for bulls as sires and MGS. The birth year groups for MGS with and without valid ID were separated to allow for different rates of genetic trend and because the grouping assignments based on MGS and dam birth years are not directly comparable. The (co)variance components used were those estimated by Wiggans et al. (2003): herd-year, 0.434; sire, 0.022; S-MGS, 0.009; MGS, 0.016; and residual, 1.000. These components correspond to direct heritabilities of 0.059 or 0.084 and maternal heritabilities of 0.034 or 0.048 if the herd-year variance is included or excluded, respectively, from the total variance. The estimated genetic correlation of direct and maternal components was –0.12. The estimated correlation of sire and MGS effects was 0.48. This positive association includes the genetic antagonism between direct and maternal effects but also the greater positive correlation (0.59) associated with the shared direct components (a portion of the direct or service sire effect of the MGS is included in the MGS effect).

For both models, the first threshold was constrained to be zero. This is done to ensure identifiability, because

**Table 1.** Distributions of calving ease (CE) scores in data for sire and sire-maternal grandsire (S-MGS) models.

| CE Score | Sire model | | S-MGS model | |
| --- | --- | --- | --- | --- |
| | Frequency | % | Frequency | % |
| 1 – No Problem | 8,002,656 | 76.3 | 7,780,662 | 76.3 |
| 2 – Slight Problem | 1,103,097 | 10.5 | 1,069,217 | 10.5 |
| 3 – Needed Assistance | 929,816 | 8.9 | 899,450 | 8.8 |
| 4 – Considerable Force | 300,840 | 2.9 | 292,065 | 2.9 |
| 5 – Extreme Difficulty | 158,188 | 1.5 | 153,703 | 1.5 |
| Total | 10,494,597 | | 10,195,097 | |

the underlying CE scale is arbitrary (Gianola and Foulley, 1983; Harville and Mee, 1984). Models parameterized with residual variance of one and first threshold of zero are often referred to as standardized threshold models.

Herd-years are considered random to avoid the extreme category problems caused when all values for a fixed effect subclass fall in the same category (Harville and Mee, 1984; Misztal et al., 1989). Of the 61,784 herd-years represented in the data, 5582 (9%) included only one calving difficulty score, and 5480 (>98%) of these included only scores of 1. This is not surprising because 76% of records included a CE score of 1, and many herd-year groups are small. The most common herd-year size (17,945 cases) was a single calving, whereas the herd-year size with the most records (45) included 83,925 (0.79%) cases. Over half of the observations occurred in herd-year of <100 records. Tables 1 and 2 provide overall distribution of CE scores and distribution of scores by parity.

There are a number of areas in which the S-MGS model could be further enhanced. Cows averaged 1.5 calvings in data used in the S-MGS model. Because no dam effect was included, some possible covariance is being ignored. Adding a dam effect within MGS would more completely model that covariance (Ducrocq, 2000). In addition, consideration of first- and later-parity records as different traits may be more logical. This extension has been adopted by a number of countries (Pasman et al., 2003).

An additional data restriction imposed for the S-MGS model was the exclusion of records for which the sire was over 15 yr old when the calf was born. This edit was added to exclude data from analysis in cases where the sire was likely incorrect because of typographical mistakes.

**Reporting of Genetic Values**

Genetic merit for CE is reported as PTA for percentage of births that are difficult for first-calf heifers (**%DBH**), where difficult births are those scored ≥4. In both the sire and S-MGS models, a fixed genetic base was implemented as a means to stabilize PTA over time.

For the sire model analysis, bulls born before 1977 were set as the base and forced to average zero on the underlying scale. The sire solution was then calculated as the sum of the solutions for the first parity and sire, with the mean of the solutions for sex of calf and season effects, all on the underlying scale. This sire solution was then converted to %DBH by calculating the probability that a random normal variable with this value as a mean and unit variance exceeds the threshold between categories of CE score 3 and 4 (Berger, 1994; Berger, 2002, personal communication).

For the S-MGS model analysis, both a sire effect (service sire CE) and a MGS effect (daughter CE) are calculated. The MGS effect is reported as a combination of direct and maternal contributions (¼ direct effect and ½ maternal effect), because it is expressed only in that

**Table 2.** Distributions of calving ease (CE) scores in data for sire-maternal grandsire model by parity.

| CE Score[1] | First parity | | Second parity | | Third and later parities | |
| --- | --- | --- | --- | --- | --- | --- |
| | Frequency | % | Frequency | % | Frequency | % |
| 1 | 1,645,428 | 63.0 | 2,400,086 | 80.2 | 3,735,148 | 81.4 |
| 2 | 378,022 | 14.5 | 282,878 | 9.5 | 408,317 | 8.9 |
| 3 | 377,988 | 14.5 | 213,954 | 7.2 | 307,508 | 6.7 |
| 4 | 137,918 | 5.3 | 63,051 | 2.1 | 91,096 | 2.0 |
| 5 | 72,932 | 2.8 | 33,204 | 1.1 | 47,567 | 1.0 |
| Total | 2,612,288 | 25.6 | 2,993,173 | 29.4 | 4,589,636 | 45.0 |

[1]See Table 1 for definition of CE scores.

ratio in daughters and future offspring. For this S-MGS analysis, the fixed base was defined on the observed scale. Currently, the base is defined by bulls born in 1995 for sire effects and bulls born in 1990 for MGS effects. Both sire and MGS solutions are adjusted on the underlying scale so that the mean of those bulls on the observed scale is approximately equal to the mean observed %DBH in the appropriate offspring. Therefore, the mean service sire %DBH for bulls born in 1995 is approximately equal to the observed frequency of difficult births from first-parity cows in calves sired by those same bulls, and the mean daughter %DBH for bulls born in 1990 is approximately equal to the observed frequency of difficult births from first-parity cows that are daughters of those bulls. Because these observed frequencies are quite volatile from year to year, using a multiple-year smoothed mean (rather than a single birth year) may be preferable in the future for defining the base.

Specifically, let $T_3$ be the threshold separating difficulty scores 3 and 4 on the observed scale, $\varepsilon$ be the solution on the underlying scale with fixed sire birth year group added to the sire solution. Then

$$p(\varepsilon > T_3) = \%DBH.$$

Setting the base for the animals represented in the appropriate group (indictated by *),

$$\overline{p(\varepsilon^* > T_3)} = \%DBH^*.$$

Then,

$$\overline{p(\varepsilon^* > T_3)} = \overline{p(Z > T_3 - \varepsilon^*)}$$
$$= 1 - F(T_3 - \varepsilon^*),$$

where F = standard normal cumulative distribution function and Z = standard normal deviate. Next, a constant (c) is added to the underlying scale to achieve the desired base:

$$\overline{1 - F(T_3 - \varepsilon^* + c)} = \%DBH^*.$$

Then,

$$1 - \%DBH^* = \overline{F(T_3 - \varepsilon^* + c)}, \text{ which}$$
$$\Rightarrow F^{-1}(1 - \%DBH^*) \approx T_3 - \overline{\varepsilon^*} + c \text{ and}$$
$$\Rightarrow T_3 + c \approx F^{-1}(1 - \%DBH^*) + \overline{\varepsilon^*}.$$

Finally, substituting to obtain the final equation used to compute %DBH,

$$\%DBH = 1 - [-\varepsilon + F^{-1}(1 - \%DBH^*) + \overline{\varepsilon^*}].$$

This prediction equation, unlike most, is not a direct function of the thresholds or any fixed effect solutions. Those effects, rather, are inferred by the selection of the population used to determine the value of %DBH*.

Reliabilities were calculated using only diagonal information. This simplification results in overestimated reliabilities because it effectively assumes a reliability of one for parents. Specifically,

$$rel_{i,t} = 1 - \frac{diag_{i,t}}{\sigma_t},$$

where, $rel_{i,t}$ is the reliability for bull i and trait t (i.e., sire or MGS effect), $diag_{i,t}$ is the diagonal element from the threshold model equations, and $\sigma_t$ is the genetic standard deviation. This simplification ignores sire relationships and the influence of the distribution of sires within fixed and random effects. The simplification is expected to be a reasonable approximation of the true reliabilities because of the low heritabilities and the use of an S-MGS, not animal model. Improvements in this approximation are an area of current investigation.

The data editing systems and evaluations associated with the S-MGS model were compared with those for the previously used sire model.

## RESULTS AND DISCUSSION

### Data Editing

Of the 11 million records processed, over 95% were accepted by the CE and S-MGS edit systems. The new edits identified 200,000 additional duplicate records and 20,000 records containing other problems. For both the sire and S-MGS models, records were removed for non-Holstein or non-Red and White breed of dam or sire, multiple births, or data recorded before 1980. The improvement in early editing reduced by nearly 100,000 the number of records removed by basic data integrity edits common to the sire and S-MGS models, which indicated an overall improvement in processing efficiency. An additional 75,000 records were excluded from evaluation with the S-MGS model because the sire was over 15 yr old when the calf was born.

### MGS ID

A major effort was made to improve MGS ID rate. By integrating the CE data with the production pedigree information, 1,030,408 additional MGS were identified, increasing the rate of MGS ID from 57.6 to 73.1%. Conservation of available CE data was also a consideration in database design. The creation of the CE pedigree table to store pedigree records incompatible with the production data edits (e.g., dam ID of zero or a name)

preserved 2,532,527 additional pedigree records. Only 10.7% of those records contained MGS ID. Of the nearly 72% of the records with production dam keys, nearly 98% had MGS ID recorded, slightly higher than the 95.3% of production pedigrees from a comparable time period that contain sire identity. Because only 72% of the records had production dam keys, nearly 30% of the dams that were being observed for dystocia were not uniquely identified over time. However, the percentage of dams without unique ID has decreased to around 20 in recent years.

### Data Characteristics

Percentage of male calves was 51.5 in records for both the sire and S-MGS models. Distributions of records across parities were also very similar for the two datasets, with 25.9 (25.6), 29.3 (29.4), and 44.8% (45.0%) first, second and third or later parities for sire model (S-MGS model) data.

Distributions of dystocia scores are shown in Table 1. Changes in data processing did not appreciably alter the distribution of scores in the total dataset. Van Tassell and Sattler (2000) demonstrated considerable variation in these distributions between herds or when evaluated on a herd-year basis. That study identified herds in which the distribution of CE scores differed substantially from the distribution of scores in the population at large. Based on these findings, the data extraction system was designed to include a within-herd CE score distribution criteria, enabling the rejection of herds with an excessive frequency of extreme scores. At this time, however, data for all herds are included. The impact of restricting data based on herd distribution is an area for additional study. Additionally, a minimum herd size could be imposed, and MGS ID could be required.

As has been observed in previous studies (e.g., Berger, 1994), more difficult calving is observed for first parity than for later parities. Distribution of dystocia scores by parity for the S-MGS model data is shown in Table 2. Strong evidence exists for differences in calving ease between first and later parities, whereas the difference between second and later parities is relatively small.

### Genetic Evaluations

Distributions of service sire %DBH are shown in Figure 2 for the sire and S-MGS models. Differences in the distribution of the predicted genetic merit for this trait were relatively minor. Correlation between evaluations for the 33,626 bulls included in both evaluations was correspondingly high: 0.85 for the underlying evalua-
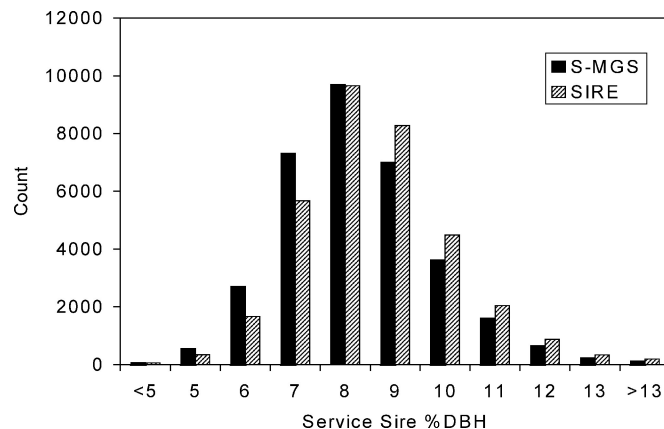


**Figure 2.** Distribution of service sire PTA for percentage of the births that are difficult heifers (%DBH) for bulls represented in sire for first-class and sire-maternal grandsire (S-MGS) analyses.

tions and 0.82 for %DBH. Although these correlations indicate that the service sire evaluations are similar, significant changes are to be expected with correlations substantially less than one. Reliabilities from the sire and S-MGS models were quite similar as well, with a correlation of 0.81. The small difference in the mean %DBH for the two evaluations (8.58 for the sire model and 8.27 for the S-MGS model) is likely attributable to differences in the definition of the base. The distribution of difference in service sire %DBH for bulls analyzed with both models is shown in Figure 3. Reassuringly, almost no directional bias exists, as the changes are nearly symmetrically distributed around the mean difference. Although attributing the differences between the two evaluation systems specifically to differences in data or model is impossible, a reasonable expectation that the largest changes resulted from model differ-
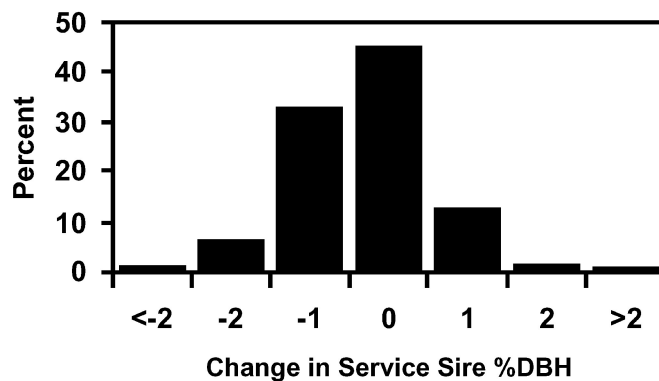


**Figure 3.** Distribution of differences in service sire PTA for percentage of births that are difficult for first-class heifers (%DBH) between the sire and sire-maternal grandsire models.
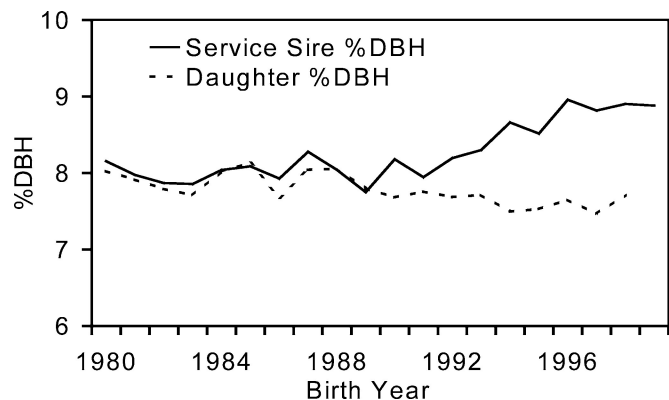
**Table 3.** Numbers of levels, ranges, and SD of solutions from sire-maternal grandsire (MGS) threshold model equations.

| Effect | Levels | Range | SD |
|---|---|---|---|
| Herd-year | 210,944 | 5.72 | 0.55 |
| Year-season | 46 | 0.29 | 0.09 |
| Parity-gender | 6 | 1.02 | 0.40 |
| Sire birth year | 15 | 0.11 | 0.02 |
| MGS birth year | 29 | 0.06 | 0.02 |
| Sire | 122,487 | 1.79 | 0.07 |
| MGS | 122,487 | 0.82 | 0.06 |



**Figure 5.** Distributions of all service sire and daughter PTA for percentage of births that are difficult for first-calf heifer (%DBH) from the sire-maternal grandsire model.
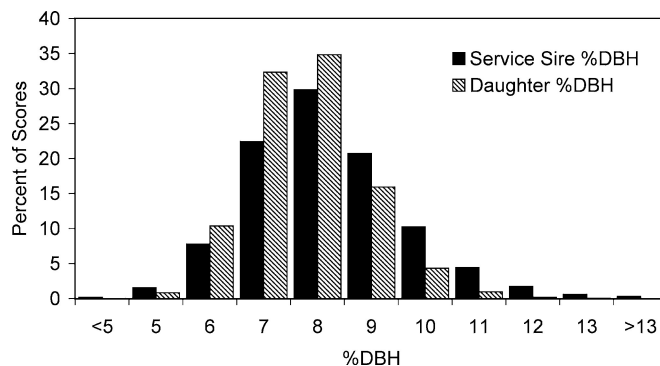
ences, because the vast majority of the data is common for the two systems.

Characteristics of solutions to the S-MGS model are presented in Table 3. Herd-year effects are clearly an important consideration in fitting these models. Even though solutions are regressed to zero because herd-year is fit as a random effect, the range and standard deviation are substantially greater than for all other effects. The impact of birth year for both sire and MGS was very small. This result is a bit surprising given the genetic trend for service sire %DBH shown in Figure 4. A significant increase in dystocia has occurred in the last 10 yr. Considering the correlation of service sire and daughter %DBH (0.53), the lack of trend in daughter %DBH is also somewhat surprising.

The trend in service sire %DBH may be the result of the heavy use of a few bulls that were high for %DBH as sire of sons. Means calculated for %DBH of bulls with sons born in each year, weighted by the number of sons, jumped to over 9.5 in 1994. Means for all other years were between 7.5 and 8.5. In 1994, three of the four most heavily used bulls had service sire %DBH of ≥11, and seven of the top 10 widely used bulls had service sire %DBH of ≥9. The wide use of these bulls in the cow population likely influenced the genetic trend

in %DBH through bull dams in years since 1994, and in 1995 and later, the weighted mean of MGS service sire %DBH has increased. The mean daughter %DBH calculated the same way shows a flat to even slightly decreasing trend over the same period.

The comparison of distributions of service sire %DBH and daughter %DBH is shown in Figure 5. For both traits, a %DBH of 8 is the most common. However, the distribution of daughter %DBH is more compact than the distribution of service sire %DBH, which is expected because of its smaller genetic variance. The correlation between solutions on the underlying scale for service sire and daughter effects was 56%, slightly higher than the genetic correlation of 48% used in the evaluation system. On the %DBH scale, the correlation dropped slightly to 53%. This drop could be due to the nonlinearity of the transformation from the underlying scale to the observed scale or to the granularity of the observed scale, as only whole percentages are reported for %DBH.

Distributions of reliabilities for service sire and daughter %DBH are shown in Figure 6. An upward bias is created by the simplification used in calculating the reliability. This effect is apparent from the large fraction of evaluations, 25 and 35% for service sire and daughter %DBH, respectively, at lower reliabilities (46 to 50%). In general, the reliabilities for service sire %DBH are higher than those for daughter %DBH, and the correlation between the two reliabilities was relatively high (0.76). As with service sire and daughter %DBH, the reliabilities for a bull will be positively correlated in part because of the part-whole relationship of the two evaluations.



**Figure 4.** Mean service sire and daughter PTA for percentage of births that are difficult for first-calf heifers (%DBH) by birth year of bull.

## CONCLUSIONS

An S-MGS model evaluation system was implemented in August 2002. By integrating records with
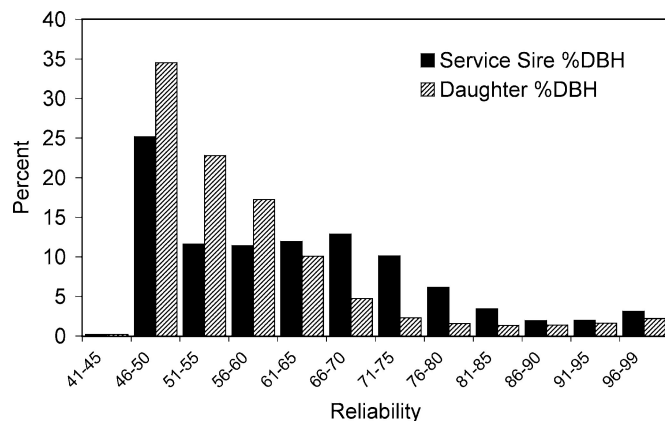
**Figure 6.** Distributions of reliabilities (%) for service sire and daughter PTA for percentage of births that are difficult for first-calf heifer (%DBH).

pedigree information from production data, more than 70% of the dam ID could be linked to the production pedigree table. The rate of MGS ID was increased from 57.6 to 73.1%, an improvement that will increase the accuracy of genetic evaluations. Correlation of service sire %DBH from the sire and S-MGS evaluations was relatively high at 85% but low enough to allow for substantial reranking of bulls for this trait. Daughter %DBH evaluations were introduced and made available to the industry. In August 2003, service sire and daughter CE were included in the AIPL net merit index (VanRaden and Seykora, 2003), and each CE trait received an economic weight of 2%. Weights range from 7 to 12% in other countries (VanRaden, 2002). Service sire %DBH should additionally be used for semen allocation decisions to avoid dystocia in first calf heifers (Misztal et al., 1989).

## 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.

Burfening, P. J., D. D. Kress, and R. L. Friedrich. 1981. Calving ease and growth rate of Simmental-sired calves. III. Direct and maternal effects. J. Anim Sci. 53:1210–1216.

Djemali, M., P. J. Berger, and A. E. Freeman. 1987. Ordered categorical sire evaluation for dystocia in Holsteins. J. Dairy Sci. 20:2374–2384.

Ducrocq, V. 2000. Calving ease evaluation of French dairy bulls with a heteroskedastic threshold model with direct and maternal effects. Int. Bull Eval. Serv. Bull. No. 18:123–130.

Gianola, D., and J. L. Foulley. 1983. Sire evaluation for ordered categorical data with a threshold model. Gen. Sel. Evol. 15:201–224.

Harville, D. A., and R. W. Mee. 1984. A mixed-model procedure for analyzing ordered categorical data. Biometrics 40:393–408.

Henderson, C. R. 1975. Inverse of a matrix of relationships due to sires and maternal grandsires. J. Dairy Sci. 58:1917–1921.

Manfredi, E., V. Ducrocq, and J. L. Foulley. 1991. Genetic analysis of dystocia in dairy cattle. J. Dairy Sci. 74:1715–1723.

Misztal, I., D. Gianola, and J. L. Foulley. 1989. Computing aspects of a nonlinear method of sire evaluation for categorical data. J. Dairy Sci. 72:1557–1568.

Pasman, E., Z. Liu, and F. Reinhardt. 2003. An overview of results and current status of MACE for calving traits. Int. Bull Eval. Serv. Bull. No. 30:59–70.

Thompson, J. R., A. E. Freeman, and P. J. Berger. 1981. Age of dam and maternal effects for dystocia in Holsteins. J. Dairy Sci. 64:1603–1609.

Van Tassell, C. P., and C. G. Sattler. 2000. Characterization of data and proposed edits for the national calving ease genetic evaluation. J. Dairy Sci. 83(Suppl. 1):61. (Abstr.)

VanRaden, P. M. 2002. Selection of dairy cattle for lifetime profit. Proc. 7th World Congr. Genet. Appl. Livest. Prod., Montpellier, France 29:127–130.

VanRaden, P. M., and A. J. Seykora. 2003. Net merit as a measure of lifetime profit: 2003 revision. AIPL Res. Rep. NM$2(7-03). Online. Available: http://aipl.arsusda.gov/reference/nmcalc.htm. Accessed July 31, 2003.

Wiggans, G. R., I. Misztal, and C. P. Van Tassell. 2003. Calving ease (co)variance components for a sire-maternal grandsire threshold model with calving ease data. J. Dairy Sci. 86:1845–1848.