ANALYSIS OF GESTATION LENGTH IN AMERICAN SIMMENTAL CATTLE¹

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ABSTRACT

Records of gestation length (71,461) for Simmental cattle were distributed with mean 284.3 d and standard deviation 5.52 d. Gestation length was found to increase with percent Simmental and was 1.9 d longer for calves born to mature dams than for those born to heifer dams. Bull calves experienced gestation lengths 1.5 d longer than heifer calves. Sire, maternal grandsire, residual and total variances were estimated to be 2.42, .58, 22.78 and 25.78 d², respectively, by Henderson's Method III. Heritability of gestation length was calculated to be .374 from the sire variance and .09 from the maternal grandsire variance. Direct additive genetic variance was considered to be of greater importance than maternal additive genetic variance. Correlations between the evaluations of sires for gestation length and heifer calving ease, birth weight and weaning weight were .26, .26 and .13, respectively.

(Key Words: Gestation Period, Heritability, Beef Cattle, Maternal Effects.)

Introduction

There are several reports that gestation length has a moderate to high heritability (see the review of Andersen and Plum, 1965). These estimates imply sizable sire differences in the gestation lengths of progeny. There are two reasons why cattle breeders might wish to use these sire differences in a breeding program. Some breeders might be interested in selecting directly to reduce the length of gestation in order to lengthen the postpartum interval to the breeding season. This would allow more time for cows to return to estrus and increase the likelihood of their becoming pregnant. For example, Bourdon and Brinks (1983) reported an increase in calving interval of 1.17 d for each day increase in gestation length.

Data on gestation length could be used to exploit the relationships between gestation length and birth weight and more importantly the relationship with calving difficulty. One might speculate that selection for shorter gestation lengths might reduce calving problems with less negative impact on growth rate than might be expected, for example, from selection for lower birth weights. Both of these situations

have relevance to breeders of Simmental cattle. Of the Bos taurus beef breeds, Simmental have one of the longer average gestation lengths; Elzo et al. (1987) documented the emphasis that Simmental breeders place on calving ease in sire selection. It was with this background that this study of field data on gestation lengths collected by the American Simmental Association was motivated. The objectives were: to estimate the degree of additive genetic control of gestation length in the Simmental population, to investigate the relationships between gestation length and birth weight and calving ease, and to establish if the former might be useful in improving the accuracy of evaluating the latter traits.

Materials and Methods

Data. The data comprised 426,702 field records of gestation lengths experienced by Simmental-sired calves collected by the American Simmental Association between 1971 and mid-1985. Edits eliminated records from multiple and embryo transfer births and those with gestation lengths outside the range 262 to 306 d, which were considered the result of misrecorded breeding or birth date. Contemporary groups were defined to be records listing the same breeder number, herd number and to have a breeding date within 6-mo year-seasons of April to September and October to March; these correspond to spring and fall birth seasons. Breeding date rather than birth date was used in the definition because the latter is, of course,

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dependent on the trait of interest, gestation length; a simple, yet often disregarded, distinction. Contemporary groups of less than six records were discarded. Gestation lengths of 283 and 285 d were disproportionately represented, e.g., both were several times more frequent than 284 d. This is likely caused by producers reporting a breeding date back-calculated from a birth date using a table of expected calving dates. Tables for beef cattle commonly assume a 283 d gestation length; 285 d tables for Simmentals are also published. To eliminate these standards while minimizing the loss of true records, contemporary groups were discarded by a criterion that if more than 35% of the records in the group were equal that the likelihood of standardization by the producer was high. The final edited data set comprised 71,461 records representing 1,791 sires, 1,771 maternal grandsires and 4,258 contemporary groups of size 6 to 640 records, with an average size of 16.8 records.

Statistical Analysis. Sire, maternal grandsire, residual and total components were estimated assuming the model:

$$Y_{iikmn} = G_i + B_i + S_k + M_m + e_{iikmn},$$

where Yikmn represents the observed gestation length of the nth calf of the kth sire and mth maternal grandsire in the ith contemporary group and the jth category of sex x percent Simmental (50, 75, \geq 87.5) \times age of dam at parturition (12 classes: 1.5 to 2 yr . . . 6.5 to 7 yr, ≥ 7 yr), corrected to a standard gestation length, age at breeding plus 285 d. Sire, maternal grandsire and residual variances were estimated by Henderson's Method III (Henderson, 1953). Sequential sub-models (G_i + B_i, $G_i + B_j + S_j$ and $G_i + B_j + S_k + M_m$) were fitted. Reductions and their expectations were calculated using a direct decomposition method (Gaylor et al., 1970). The direct additive genetic variance and the heritability were estimated.

Evaluations of sires and maternal grandsires were obtained by best linear unbiased prediction (BLUP) procedures, assuming the estimated variances were the true values, using a sire, maternal grandsire model. Base sires and maternal grandsires were added so that the rules for building the inverse of the numerator relationship matrix (Henderson, 1976) could be implemented. Covariances between sires and maternal grandsires were ignored, i.e., treated as

zero. A reduced list of bulls was made comprising those with an effective progeny number greater than 50. The correlation between the evaluation of bulls as sires and as maternal grandsires was estimated. Relationships between sire evaluations for gestation length and birth weight and calving ease were investigated. The evaluations for the latter traits came from the 1986 Simmental Sire Selector (ASA, 1986) obtained using BLUP procedures from a similar sire and maternal grandsire model (Elzo et al., 1987).

Results and Discussion

Gestation lengths in the edited data set were distributed with approximate symmetry, mean 284.3 d and standard deviation 5.52 d, but slightly skewed to the right. This may be due to gestation lengths inaccurate by a factor of 21 d, an estrus cycle, a recording error common in field data whereby the pregnancy results from an insemination at a heat subsequent to the one recorded. Because the range of gestation lengths is so short, it is likely that the analysis of gestation length would be very sensitive to any recording errors of even a few days; hence errors of 21 d are probably of great importance.

The estimated sire (σ_s^2) , maternal grandsire (σ_{mgs}^2) , residual (σ_e^2) and total phenotypic (σ_p^2) variances were 2.42, .58, 22.78 and 25.78 d², respectively. The sire variance is expected to be one-fourth of the direct additive genetic variance, so an estimate of the latter is 9.68 d², resulting in a heritability estimate of .374 $(h_s^2 = 4\sigma_s^2/\sigma_p^2)$. This estimate is in good agreement with others found in the literature (Everitt et al., 1978; Bourdon and Brinks, 1982; Azzam and Nielsen, 1987) and is higher than might have been expected given the initial problems encountered with the standard in these field data.

The heritability estimate calculated from the maternal grandsire variance is .09 ($h_{mgs}^2 = 4\sigma_{mgs}^2/\sigma_p^2$). This estimate is somewhat lower, but is also similar to those found in the literature (e.g., Philipsson, 1976; Azzam and Nielsen, 1987) and demonstrated the greater relative importance of direct over maternal additive genetic effects.

To investigate further the maternal additive genetic component, consider these equations involving the direct additive genetic variance (σ_d^2) , the maternal additive genetic variance (σ_m^2) and the covariance between the direct and

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additive genetic effect (od.m):

$$\begin{split} \sigma_{\rm s}^2 &= (1/4)\sigma_{\rm d}^2 \\ \sigma_{\rm mgs}^2 &= (1/16)\sigma_{\rm d}^2 + (1/4)\sigma_{\rm d.m} + (1/4)\sigma_{\rm m}^2 \\ &= (1/4)\sigma_{\rm s}^2 + (1/4)\sigma_{\rm d.m} + (1/4)\sigma_{\rm m}^2 \,. \end{split}$$

Firstly, it can be noted that $(1/4)\sigma_s^2 = .61$ is very close to $\sigma_{mgs}^2 = .58$, or more explicitly:

$$\sigma_{d.m} + \sigma_m^2 = 4\sigma_{mgs}^2 - \sigma_s^2 = -.09.$$

The σ_m^2 and $\sigma_{d.m}$ terms cannot be separated directly, but since their sum is negative and since by definition the variance σ_m^2 must be greater or equal to zero, $\sigma_{d.m}$ must assume a negative value. To determine what magnitude of $\sigma_{d.m}$ would cause σ_m^2 to be a major component of variance, consider the correlation between direct and maternal components $(r_{d.m})$

$$r_{d,m} = \sigma_{d,m} / \sigma_d \sigma_m$$

such that,

$$\sigma_{\rm m}^2 + \sigma_{\rm d.m} + .09 = 0$$

can be written:

$$\sigma_{\rm m}^2 + r_{\rm d.m} \sigma_{\rm d} \sigma_{\rm m} + .09 = 0$$

resulting in a quadratic in σ_m :

$$\sigma_{\rm m}^2 + (3.11 \, {\rm r_{\rm d} \, m}) \sigma_{\rm m} + .09 = 0.$$

By substituting in various values for r_{d,m}, the quadratic can be solved to find estimates of $\sigma_{\rm m}^2$ (table 1). The correlation would have to be less than -.5 for $\sigma_{\rm m}^2$ to be an appreciable proportion of σ_p^2 . Literature estimates of $r_{d,m}$ derived by indirect methods are mostly negative (-.56, -.38, -.51; Philipsson, 1976; Burfening et al., 1981; Gaillard and Chavaz, 1982, respectively). Azzam and Nielsen (1987) reported -.72 and -.46 for first- and second-parity cows, but a positive .68 for older cows. Thus, the maternal variance might be of some importance, but it is likely that the direct variance is relatively more substantial. This emphasizes the gestation length is dictated by the calf rather than by the dam and supports the physiological evidence of the control of parturition (Alexander et al.,

TABLE 1. THE POSSIBLE MAGNITUDES OF THE MATERNAL VARIANCE (σ_m^2) AND ITS IMPORTANCE RELATIVE TO THE TOTAL PHENOTYPIC VARIANCE (σ_p^2) FOR DIFFERENT VALUES OF THE CORRELATION BETWEEN DIRECT AND MATERNAL ADDITIVE GENETIC EFFECT $(r_{d,m})$

rd.m	$\sigma_{\mathbf{m}}^{2}$	$\sigma_{\rm m}^2/\sigma_{\rm p}^2$
2	.150	.006
3	.676	.026
4	1.359	.053
5	2.231	.087
6	3.295	.128
7	4.553	.177
8	6.366	.247
9	9.009	.311
-1.0	9.481	.368

1968; Anderson et al., 1972; Comline et al., 1974).

Solutions to the fixed effects in the mixed model displayed no interaction between sex-ofcalf, percent-Simmental-of-calf and age-of-dam factors; figure 1 illustrates solutions for 75% Simmental calves. In this figure, solutions for categories 1.5 to 2 and 2 to 2.5, 2.5 to 3 and 3 to $3.5, \ldots, 6.5$ to 7 and $\geqslant 7$ were averaged and denoted 2, 3, ..., 6, respectively. Averaging the solutions over effects demonstrated 1) gestation length increases with age of dam (calves born to primiparous dams experience gestation lengths on average 1.9 d shorter than those born to mature dams), 2) gestation length increases with percent Simmental (1.1 d difference on average between 50% and purebred Simmental calves) and 3) bull calves have a consistently longer gestation length (1.5 d on average) than heifer calves.

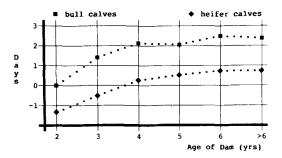


Figure 1. Age-of-dam × sex-of-calf effects on gestation length for 75% Simmental bull and heifer calves (as deviations from bull calves out of 2-yr-old dams).

Evaluations of the sires ranged from -4.55 to 4.44 d and of the maternal grandsires from -1.16 to 1.34 d. One hundred seventy-one of the 1,791 sires and 97 of the 1,771 maternal grandsires had an effective progeny number greater than 50 and so were included on the reduced lists. Of these bulls, 92 were found on both lists and thus had reliable sire and maternal grandsire evaluations. The evaluations for these 92 bulls ranged from -2.97 to 3.58 d for sires and -1.16 to 1.34 d for maternal grandsires. The mean evaluations for gestation length, birth weight and calving ease for the 10 sires with the shortest gestation length evaluations vs the 10 bulls evaluated to have the longest gestation length evaluations were respectively: -2.6 vs 2.5 d, -.004 vs 1.2 kg and 101.0 vs 91.8 calving ease ratio (where a ratio >100 represents easier than average calvings). The high representation in the gestation length data of sires from early importations is likely to explain the asymmetry of the birth weight evaluations about 0 and calving ease evaluations about 100. Those early bulls, as a group, were not known for light birth weights and easy calvings (Elzo et al., 1986).

The correlation between the gestation length evaluations of bulls as sires and as maternal grandsires is .482. This positive correlation suggests that even if the maternal additive genetic component were substantial, that the direct additive component is more influential. Selection for reducing gestation length could be accomplished by concentrating on selection of sires evaluated through their progeny to have short gestation lengths.

The correlations between sire proofs for gestation length with evaluations for genetic component of sires for heifer calving ease, birth weight and weaning weight were .26, .26 and .13, respectively. These are lower than the correlation (.4) between calving ease and birth weight (M. A. Elzo, personal communication). Figure 2 demonstrates the distribution of calving ease evaluations of sires within classes of the bottom 30, the middle 30 and the top 30 gestation length sire evaluations. Clearly, some trend is evident, but the degree of overlap is high; for instance, the seventh ranked sire with a gestation length evaluation of -2.4 d has a birth weight evaluation of 1.7 kg. These outliers might suggest that the relationship between birth weight and gestation length is perhaps due to them both being time-related traits, whilst their genetic control may be more

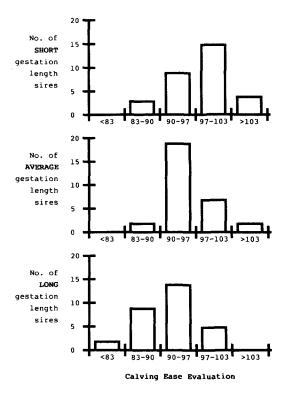


Figure 2. Distribution of calving ease evaluations for sires classified as sires of progeny with short, average or long gestation lengths.

independent.

The results of this study document the existence of potentially exploitable sire differences in gestation length that are detectable from routinely collected field data. It does not seem, however, that these differences are particularly useful predictors of differences in calving ease. Birth weight is a better, and more frequently recorded, predictor and virtually all sires with gestation length data also have progeny calving ease scores recorded. It is likely that gestation length information would be more effective as a selection criterion in its own right, i.e., to shorten average gestation length in the breed. The consequences (e.g., calf mortality, reduced selection pressure) and expected benefits (e.g., improved rebreeding performance) of this option warrant detailed study.

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