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# Simulation study of teat score in first-parity Gelbvieh cows: Parameter estimation<sup>1</sup>

R. L. Sapp<sup>2</sup>, R. Rekaya, and J. K. Bertrand

Animal and Dairy Science Department, University of Georgia, Athens 30602-2771

**ABSTRACT:** Teat scores from 9,598 first-parity Gelbvieh cows were used to investigate the adequacy of grouping approaches to decrease score misclassifications or inconsistencies as well as to simplify the data collection process. The procedure was tested using simulated data and then validated using teat score records of Gelbvieh cattle. First-parity cows were considered to be 4 yr of age or younger at first calving, did not have multiple records within 280 d, and were at least 50% Gelbvieh. Producers scored cows within 24 h of parturition. Teat score, a subjective measure of teat size, ranged from 0 (very large) to 50 (very small). A linear mixed model that included herd-year, month of calving, and age at calving as systematic effects; regression on the percentage of Gelbvieh; and additive breeding values (BV) and residual as random effects was used to generate the data. Simulated data were analyzed using one of three scoring methods: all values (S50), 10 classes (S10), and five classes (S5). The 10 classes were formed by subdividing every five scores into a single class starting at score zero. Similarly, the five classes were formed by combining every 10 scores into one class. The average

Pearson correlations, based on five replicates, between the true and estimated BV (systematic effects) were 0.36 (0.85), 0.35 (0.89), and 0.32 (0.87) using S50, S10, and S5, respectively. Average correlations between estimated BV (systematic effects) were 0.97 (0.95), 0.89 (0.92), and 0.92 (0.97) based on S50 and S10, S50 and S5, and S10 and S5, respectively. Field data were used to validate the simulation procedure. The field data were categorized into 10 classes (F10) and five classes (F5) as described for the simulated data. Pearson correlations between estimated BV (systematic effects) were 0.99 (0.93), 0.93 (0.88), and 0.93 (0.96), based on F50 with F10, F50 with F5, and F10 with F5, respectively. The extremely high correlations between predicted BV based on S50, S10, S5, F50, F10, with F5 suggest that a simplified score classification method could be adopted without compromising the expected genetic progress for the trait under consideration. Furthermore, the difference in corresponding Pearson correlations across the field and simulated data might suggest the presence of some inconsistencies or misclassifications of the actual scoring system.

Key Words: Beef Cattle, Data Simulation, Teat Score

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## Introduction

One of the most important influences on calf growth performance is the milk production of the cow. It has been shown that the weight gain of calves to weaning is correlated with dam milk production (Christian et al., 1965; Gleddie and Berg, 1968), and the actual amount of milk that a calf receives may depend on the size and shape of the teats (Frisch, 1982). Correlations between udder traits and milk production vary in magnitude

and direction (Harris et al., 1992; Brotherstone, 1994; Cruickshank et al., 2002).

The American Gelbvieh Association, along with other breed associations, has implemented an udder scoring system. The current scoring system is based on linear scoring ranging from 0 (very large) to 50 (very small) developed by the American Holstein Association for teat size (AGA, 1999). Scores were assigned by producers within 24 h of parturition.

It has been recognized that several environmental effects and the subjective nature of the trait are the major sources of variation affecting teat score (White, 1974). Although the majority of environmental effects can be accommodated and accounted for within the statistical model, subjectivity is hard to deal with given the lack of information (i.e., classifier) in the data sets. Thus, a large number of subjective score classes could lead to a higher rate of inconsistency across herds and

<sup>1</sup>Appreciation is expressed to the American Gelbvieh Association for the use of their data.

<sup>2</sup>Correspondence: Edgar L. Rhodes Center for Animal and Dairy Science (phone: 705-542-0965; fax: 706-583-0274; E-mail: rsapp@uga.edu).

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**Table 1.** Summary of teat score data used in the analysis of simulated and field data

Item	Number
Animals	
With records	9,598
Pedigree file	34,327
Sires	2,157
Herds	677
Herd-year	2,156

classifiers within a herd. An alternative approach would be to decrease the number of classes. Such an approach would decrease the inconsistency of the subjective classification by enabling classifiers to better distinguish between or among various classes, and perhaps the burden and cost of data collection would also be reduced.

The objective of this study was to investigate the adequacy of various grouping approaches to reduce score misclassifications or inconsistencies as well as to simplify the data collection process. The procedure was tested using simulated data and then validated using teat score records of Gelbvieh cattle.

## Materials and Methods

### Field Data

The data provided by the American Gelbvieh Association were 45,121 teat score records for 25,014 cows, collected from 1981 through 2001. Cows ranged from 2 to 13 yr of age at the time of measurement. Animals were assumed to be scored within 24 h of parturition as recommended by the American Gelbvieh Association (AGA, 1999). Animals were evaluated by a member of the farm or ranch staff. Teat score was a subjective assessment of teat size and ranged from 0 (very large) to 50 (very small). Udder support was also subjectively scored but was not used in this study. Teat size was a combination of length and circumference, with more emphasis on circumference when scoring (AGA, 1999). This study concentrated solely on the teat scores of first-parity animals.

The data set contained multiple records for some cows that had scores within a few days, weeks, or months (less than 8 mo apart) of one another. If the cow was scored at parturition, then at least 9 mo should separate her multiple score records unless she gave birth to twins or triplets. In order to decrease the bias when selecting first-parity records, cows with multiple scores within 280 d were removed. The first score of each cow, 4 yr of age or younger at the time of first measurement and at least 50% Gelbvieh, was retained as the first-parity score for analysis. Further editing involved deleting herds with less than four records. After editing, 9,598 first-parity teat scores remained for analysis. The number of animals in the pedigree file was 34,327. The number of sires, herds, and herd-years are listed in Table 1.

### Simulated Data

A simulation with a structure similar to the field data set was carried out to investigate the adequacy of several grouping approaches. A linear mixed model that included herd-year, month of calving, and age at calving as systematic effects; regression on the percentage Gelbvieh; and additive breeding values (**BV**) and residual as random effects was used to generate the data. Two thousand one hundred fifty-six herd-year effects were drawn from the uniform distribution,  $U[11.5, 33.5]$ . Month-of-calving and age-of-calving effects were drawn from normal distributions with means 4 and 2 and standard deviation 2, respectively. The regression coefficient on the percentage Gelbvieh was set equal to 0.01. There were 2,157 sires having a total of 9,598 progeny with teat scores. Additive BV for all animals in pedigree file were simulated from  $N(0, A\sigma_u^2)$ , where  $\sigma_u^2 = 4.5$ . The residual variance was set equal to 15.5. Five replicates were generated.

### Score Classes

The teat scores in the field and simulated data were categorized into 10 classes and 5 classes. The 10 (or 5) classes were formed by subdividing score 0 to 5 (or score 0 to 10) into the first class, and the remaining classes contain five (or 10) scores each. As a result, three data sets, S50, S10, and S5, were formed from the simulated records based on using all values (0 to 50), 10 classes, and 5 classes as phenotypic observations, respectively. Similarly, three data sets were formed from the field data: F50, F10, and F5.

### Statistical Analysis and Computations

The following linear mixed model was employed for the analysis of all six data sets (S50, S10, S5, F50, F10, and F5):

$$y_{ijklm} = HY_i + M_j + A_k + b(PG)_{ijklm} + u_l + e_{ijklm}$$

where  $y_{ijklm}$  was the teat score or class for cow  $l$ ,  $HY_i$  was the fixed effect of herd-year class  $i$ ,  $M_j$  was the fixed effect of month of calving  $j$ ,  $A_k$  was the fixed effect of age (in years) of cow at calving  $k$ ,  $b$  was the fixed regression coefficient on percentage Gelbvieh  $(PG)_{ijklm}$ ,  $u_l$  was the random additive effect of cow  $l$ , and  $e_{ijklm}$  was the random residual term.

In matrix notation, the model can be expressed as

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

where  $\mathbf{y}$  was an  $N \times 1$  vector,  $\boldsymbol{\beta}$  was the vector of systematic effects of order  $\mathbf{p}$ ,  $\mathbf{u}$  was the vector of animal effects with order  $\mathbf{q}$ , and  $\mathbf{e}$  was the vector of residual effects. Furthermore,  $\mathbf{X}$  and  $\mathbf{Z}$  were the corresponding incidence matrices with the appropriate dimensions.

A Bayesian implementation via Gibbs sampling was adopted. Conditionally on the parameter vector,  $\boldsymbol{\theta} =$

**Table 2.** Summary of the posterior distribution for the simulated data using three scoring methods<sup>a</sup>

Item <sup>c</sup>	True value	S50 <sup>b</sup>				S10				S5			
		PM <sup>d</sup>	PSD	HL	HU	PM	PSD	HL	HU	PM	PSD	HL	HU
$\sigma_u^2$	4.50	4.84	0.70	3.52	6.25	0.19	0.03	0.13	0.24	0.04	0.01	0.03	0.06
$\sigma_e^2$	15.50	15.17	0.61	13.97	16.37	0.69	0.03	0.64	0.74	0.24	0.01	0.22	0.25
b	0.01	0.012	0.005	0.003	0.022	0.002	0.001	0.000	0.004	0.001	0.001	0.000	0.002
$h^2$	0.23	0.24	0.03	0.18	0.31	0.21	0.03	0.15	0.27	0.15	0.03	0.10	0.21

<sup>a</sup>The values for the simulated data are reported as the average of five replicates.

<sup>b</sup>S50 = all score values; S10 = 10 classes, five scores per class; and S5 = 5 classes, 10 scores per class.

<sup>c</sup> $\sigma_u^2$  = additive variance;  $\sigma_e^2$  = residual variance; b = regression coefficient on the percentage of Gelbvieh; and  $h^2$  = heritability.

<sup>d</sup>PM = posterior mean; PSD = posterior standard deviation; HL = the lower bound of the high posterior density 95% interval; and HU = the upper bound of the high posterior density 95% interval.

$(\beta', \mathbf{u}', \sigma_e^2)'$ , the observed responses were assumed to be normally distributed:

$$p(\mathbf{y} | \theta) = N(\mathbf{X}\beta + \mathbf{Z}\mathbf{u}, \mathbf{R}) \quad [1]$$

with  $\mathbf{R} = \mathbf{I}\sigma_e^2$ .

To ensure proper posterior distribution, the following prior distributions were assumed for the parameters in the model.

A normal distribution with 0 mean and a large variance was assumed as the prior for the vector  $\beta$

$$p(\beta) \sim N(\mathbf{0}, 10^6) \quad [2]$$

Multivariate normal distributions were assumed as priors for animal effects

$$p(\mathbf{u} | \mathbf{A}, \sigma_u^2) \sim N(\mathbf{0}, \mathbf{A}\sigma_u^2) \quad [3]$$

For the dispersion parameters,  $\sigma_e^2$  and  $\sigma_u^2$ , uniform bounded priors were assumed

$$p(\sigma_e^2) \sim U[0, 5,000] \quad [4]$$

and

$$p(\sigma_u^2) \sim U[0, 1,000] \quad [5]$$

The joint posterior density was obtained by the product of densities in Expressions [1] through [5].

$$p(\beta, \mathbf{u}, \sigma_u^2, \sigma_e^2 | \mathbf{y}) \propto p(\mathbf{y} | \beta, \mathbf{u}, \sigma_e^2)p(\beta)p(\mathbf{u} | \mathbf{A}, \sigma_u^2)p(\sigma_e^2)p(\sigma_u^2) \quad [6]$$

defined only within the boundary of the bounded priors.

The joint posterior distribution in [6] was in closed form, and the conditional posterior distribution of all the parameters of the model can be derived as described by Wang et al. (1993) and Sorensen et al. (1995), with normal and scaled-inverted chi-squared distributions, respectively, for the position parameters and residual and additive variances.

Convergence diagnostics were based on the method of Raftery and Lewis (1992) as implemented in the CODA software (Best et al., 1995). The first 5,000 iterations of Gibbs sampling were used for convergence diagnostics. A total chain length of 50,000 iterations was indicated, after a “burn in” of 5,000 rounds. This gave an expected accuracy of at least  $\pm 0.05$  for the posterior median of heritability in all analyses.

## Results and Discussion

### Analyses of Simulated Data

A summary of the posterior distribution of genetic parameters using S50, S10, and S5 are presented in Table 2. For S50, point estimates for the variance components, regression coefficient and heritability, based on five replicates, were similar to the corresponding true values used in the simulation and no bias was noted. For S10 and S5, point estimates of genetic and residual variances and the regression coefficient were not on the same scale as the true values, preventing direct comparison. Heritability estimates tended to be smaller than the true value and decreased with the number of categories. For S50 and S10, the true value of the parameter (0.23) was well within the high posterior density interval (HPD [95%]), and the difference between the true and estimated values was not beyond the expected Monte Carlo error. However, for S5, the estimated heritability (0.15) was significantly smaller than the true value. In fact, the true parameter was outside the HPD (95%) interval.

Pearson correlations between true and predicted BV for animals in the pedigree file were 0.36, 0.35, and 0.32 using S50, S10, and S5, respectively. As the number of categories decreased, the correlations between true and predicted BV decreased, which was expected because the amount of information used to predict the BV also decreased. Pearson correlations between true and estimated values for the systematic effects ranged between 0.85 and 0.89 for the three scoring methods. These high correlations were expected given the large amount of information available in the data set from which to infer fixed effects.

**Table 3.** Summary of the posterior distribution for the field data using three scoring methods

Item <sup>b</sup>	F50 <sup>a</sup>				F10				F5			
	PM <sup>c</sup>	PSD	HL	HU	PM	PSD	HL	HU	PM	PSD	HL	HU
$\sigma_u^2$	4.72	0.82	3.12	6.19	0.19	0.03	0.12	0.24	0.04	0.01	0.03	0.06
$\sigma_e^2$	17.06	0.72	15.65	18.45	0.70	0.03	0.64	0.76	0.22	0.01	0.20	0.24
b	-0.022	0.005	-0.032	-0.012	-0.004	0.001	-0.006	-0.002	-0.002	0.001	-0.003	-0.001
$h^2$	0.22	0.04	0.14	0.28	0.21	0.04	0.14	0.27	0.16	0.03	0.10	0.22

<sup>a</sup>F50 = all score values; F10 = 10 classes, five scores per class; and F5 = 5 classes, 10 scores per class.

<sup>b</sup> $\sigma_u^2$  = additive variance;  $\sigma_e^2$  = residual variance; b = regression coefficient on the percentage of Gelbvieh; and  $h^2$  = heritability.

<sup>c</sup>PM = posterior mean; PSD = posterior standard deviation; HL = the lower bound of the high posterior density 95% interval; and HU = the upper bound of the high posterior density 95% interval.

Pearson correlations between predicted BV obtained using the three scoring methods were very high, especially between S50 and S10 (0.97). The correlations between predicted BV using S50 with S5 and S10 with S5 were 0.89 and 0.92, respectively. Therefore, little reranking is expected between S50 and S10. However, greater reranking could occur using S5. For S50 and S10, S50 and S5, and S10 and S5, the Pearson correlations between estimated systematic effects were 0.95, 0.92, and 0.97, respectively. This result suggests that S5 may have some difficulty estimating the systematic effects.

#### Analyses of Field Data

Analyses of the field data were conducted to validate the results of the three scoring methods used in the simulation study. A summary of the posterior distribution of the genetic and residual variances, the regression coefficient and heritability using the field data, and three scoring methods are presented in Table 3. The point estimate of the regression coefficient was slightly negative and significantly different from zero; zero was not included in the HPD (95%) interval for any of the three scoring methods. However, the regression coefficient has virtually no effect on teat score. The heritability estimates decreased as the number of categories decreased. As with the simulated data, there was no difference between the point estimates of heritability obtained using F50 and F10. However, the estimated heritability was smaller (0.16) using F5. The estimates of heritability in F50 and F10 were similar to an estimate for teat length heritability, using a 9-point scale, of 0.18 in Churra sheep (Fernández et al., 1997) and are lower than reported estimates for dairy cattle using a 9- or 50-point scale. Reported heritabilities for teat length estimated in first-lactation Holsteins ranged from 0.26 to 0.44 (Meyer et al., 1987; Brotherstone, 1994; Rupp and Boichard, 1999) when animals were evaluated on a 9-point scale. Heritabilities for teat length, scored on a 50-point scale, in dairy cattle ranged from 0.26 to 0.34 (Short et al., 1991; Cruickshank et al., 2002; DeGroot et al., 2002).

The American Gelbvieh Association considers teat score to be a subjective score of the teat size, where

teat size is considered a combination of length and circumference. The heritability estimate (0.22) for F50 using an animal model tends to be lower than the few reported estimates for teat diameter in the literature. Luo et al. (1997) reported a heritability estimate for teat diameter of 0.38 in dairy goats based on a 50-point scale using an animal model and an estimate of 0.12 when a sire model was used. Heritability estimates of actual teat diameter measurements were 0.39 and 0.37 in Holsteins using a sire model and cow-dam regression, respectively (Seykora and McDaniel, 1985).

Pearson correlations between predicted BV obtained using the three scoring methods were very high, especially between F50 and F10 (0.99). The correlations between predicted BV using F50 with F5 and F10 with F5 were both 0.93. This result suggests that virtually no reranking is expected between F50 and F10. However, a small reranking may occur when using F5. For the systematic effects, Pearson correlations between estimated effects were 0.93, 0.88, and 0.96 for F50 with F10, F50 with F5, and F10 with F5, respectively. This result suggests that F5 may not be adequate for estimating the systematic effects.

#### Miscoding

The Pearson correlations between different scoring methods were higher in the field data compared to the simulated data, which might suggest the presence of some inconsistencies or misclassification of the actual scoring system. A simulation was conducted to investigate the possible source of inconsistencies and score misclassifications and to evaluate the 50 class and 10 class scoring systems in handling miscoded data. Miscoding was introduced into the true data (S50) for each herd-year at a rate of 55%. The miscoding was introduced by adding a random quantity from a normal distribution with mean 2 and standard deviation of 1 to the true scores. The miscoded data (S50M) was then subdivided into 10 classes (S10M) by the method previously described. For both scoring systems, no significant changes were observed for the genetic variance. The genetic variance was 4.84 vs. 4.85 using the true scores (S50) vs. the miscoded data (S50M) and 0.187 vs. 0.194 using true (S10) vs. miscoded (S10M) data

based on 50 and 10 class scoring systems, respectively. Although there were no observable differences between estimates of the residual variance obtained using S10 and S10M (0.69 vs. 0.69), some differences were observed using the 50 class approach. In fact, the residual variance increased from 15.17 using S50 to 16.55 using S50M. As a consequence, heritability estimates decreased from 0.24 (true data) to 0.22 (miscoded data) under the 50 class system. Under the 10 class method, heritability estimates were the same. Although it seems that the 10 class approach is more robust when handling miscoded or contaminated data, it does not look like those differences will induce major differences in the genetic evaluations based on either of the two approaches. No differences were observed in the Pearson correlations between the true and predicted BV based on 50 or 10 classes.

### Implications

The correlations between cow teat size scoring methods for simulated and field data indicate that score misclassification or inconsistency may be present. Differences suggest that the original scoring system (50 scores) could be grouped into 5 or 10 classes. The results indicate that the 10 class method is better at estimating parameters in the model than the 5 class method. The 10 class method is more descriptive and may decrease the frequency of potential score misclassification, without the expected reranking of animals when compared with the full scale. Heritability estimates suggest that teat size evaluated by scoring will respond to selection; however, the relationship between teat score and weight gain of calves, from birth to weaning, is unclear. This relationship may be of some use to cow-calf producers when evaluating cows for rebreeding. Further research is needed to investigate this relationship.

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