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INTERACTION OF MATERNAL GRANDSIRE WITH REGION OF UNITED STATES AND HERD FOR CALVING EASE, BIRTH WEIGHT AND 205-DAY WEIGHT¹

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ABSTRACT

Field records supplied by the American Simmental Association from 2-yr-old dams were used to study maternal grandsire x region of the U.S. and maternal grandsire x herd within region (herd/region) interactions. Regions were 1) Montana, North Dakota and South Dakota, 2) Kansas and Nebraska, 3) Texas and Oklahoma and 4) Alabama, Florida, Georgia, Louisiana and Mississippi. Analyses were conducted pairwise with respect to region with the following number of animals in each comparison: 1 (3,964) vs 2 (2,239), 1 (3,996) vs 3 (1,660), 1 (3,418) vs 4 (474), 2 (2,033) vs 3 (1,709), 2 (1,666) vs 4 (443) and 3 (1,372) vs 4 (430). Independent variables were the fixed effects of region, sex of calf, Simmental percentage of the calf (75 to 88%) and the random effects of herd/region, maternal grandsire, maternal grandsire × region and maternal grandsire × herd/ region. Records were adjusted to account for the direct effect of maternal grandsire in the maternal grandsire component. Dependent variables were calving ease score, birth weight and 205-d weight. Region was significant in all analyses except for 1 vs 2, 1 vs 3 and 2 vs 3 for calving ease score and 2 vs 3 for birth weight and 205-d weight. Herd/region was significant in all analyses. Maternal grandsire was significant in all analyses for calving ease score and birth weight and for 1 vs 2 for 205-d weight. Maternal grandsire X region was not significant in any analysis. Maternal grandsire X herd/region was significant in four of six analyses for birth weight and 205-d weight, but was not significant in any analysis for calving ease score. Maternal grandsire, maternal grandsire X region interaction and maternal grandsire X herd/region interaction accounted for an average of 4, 0 and 1%; 3, 0 and 5%; and 0, 0 and 3% of the total variation for calving ease, birth weight and 205-d weight, respectively. Genetic correlations of maternal grandsires' progeny performance in different herds ranged from .20 to .74 for birth weight and from .05 to .34 for 205-d weight, indicating significant changes in rank from herd to herd.

(Key Words: Interactions, Regions, Calving, Growth Rate, Maternal Effects.)

Introduction

The effect of genotype \times environment interactions on the estimation of breeding values for direct effects in growth rate and calving ease in bulls used widely in artificial insemination has been studied. Nunn et al. (1978) and Buchanan and Nielsen (1979) reported significant sire \times region of the U.S. interactions for weaning weight. However, when Tess et al. (1979) included sire \times herd within region (herd/region) along with sire \times region in the model, sire \times region no longer was

important, but sire x herd/region was a significant source of variation for weaning weight. Burfening et al. (1982) also observed that sire \times region was not a significant source of variation for calving ease score or birth weight, but sire \times herd/region was significant when both interactions were included in the model. Sire \times herd interaction (Legates et al., 1956; Mao and Burnside, 1969) and sire \times region interaction (Lytton and Legates, 1966) have been studied in dairy cattle for milk production traits of sire's daughters. Those interactions reported were essentially zero. In beef cattle, no information is available on genotype x environment interactions involving breeding values for maternal effects (growth rates and calving ease of sire's daughter's calves) and how these may influence the ranking of sires for these maternally influenced traits. One approach to evaluating the sire ranking for maternal effect is by evaluating the maternal grandsire of the calf

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and the maternal grandsire \times environment interactions.

The objectives of this study were to evaluate the importance of maternal grandsire, maternal grandsire \times region interaction and maternal grandsire \times herd/region interaction for calving ease, birth weight and 205-d weight.

Materials and Methods

Records supplied by the American Simmental Association from 2-yr-old dams were used in these analyses. Only records from 2-yr-old (1 yr, 9 mo to 2 yr, 9 mo of age) dams were used because when calving ease was studied as a trait of the calf, variation of age of dam groups was heterogeneous (Burfening et al., 1979) and because selection of dams may have been practiced based on their calving and weaning performance as 2-yr-olds. Contemporary groups or herds were classified according to the procedure outlined by Burfening et al. (1982). Calves within a breeder's herd were sorted on the basis of birth date, and calves born within 90 d of the first birth date were assigned to the same contemporary group. Calves with consecutive birth dates with more than 45 d between their birth dates were assigned to different contemporary groups. Regions, representing a broad cross-section of environments, were formed on the basis of geographic location and number of records in a region. The regions were 1) Montana, North Dakota and South Dakota, 2) Kansas and Nebraska, 3) Texas and Oklahoma and 4) Alabama, Florida, Georgia, Louisiana and Mississippi.

Analyses were conducted pairwise with respect to region due to the limited capacity of the least squares mixed-model program (Harvey, 1977). This was necessary in order to fit both maternal grandsire and maternal grandsire \times region interaction effects.

Each herd was required to have grandprogeny of at least two maternal grandsires. Further restrictions on number of progeny per maternal grandsire \times region subclass were made for each of the comparisons in order to reduce the number of maternal grandsires to the capacity of the program. The number of records, minimum progeny per maternal grandsire \times region subclass, number of maternal grandsires and number of herds for each pair of analyses are shown in Table 1. Each maternal grandsire was required to have records in both regions for the pairwise analyses.

Traits such as calving ease, birth weight and 205-d weight are influenced by both the genes the cow transmits and by the maternal environment she provides (Koch and Clark, 1955). Half the genes that influence the direct effect associated with the maternal traits are contributed by the cow's sire (the offspring's maternal grandsire). These genes also may influence the maternal environment. In order to ensure that the maternal grandsire variance component more precisely estimated the maternal environmental component, each record was adjusted to account for the maternal grandsire's influence on the direct effect associated with the maternal traits. This adjustment was accomplished by calculating a correction factor (CF) for each trait for

			Regional c	omparisons ^a		
Item	1 vs 2	1 vs 3	1 vs 4	2 vs 3	2 vs 4	3 vs 4
Total progeny	6,203	5,656	3,892	3,742	2,109	1,802
Region A	3,964	3,996	3,418	2,033	1,666	1,372
Region B	2,239	1,660	474	1,709	443	430
No. of MGSire	39	35	30	39	29	28
No. of herds	800	737	468	605	388	315
Min. no. of progeny/MGSire						
× region subclass	15	10	5	8	5	5
K-values						
MGSire (k_{a})	95.8	99.3	76.0	60.0	42.1	40.3
MGSire \times region (k_{\star})	46.6	52.1	31.4	30.6	28.2	20.2
MGSire \times herd/region (k_3)	2.2	2.2	2.3	1.8	1.8	1.8

TABLE 1. NUMBER OF PROGENY, NUMBER OF MATERNAL GRANDSIRES (MGSIRE), NUMBER OF HERDS AND K-VALUES FOR EACH ANALYSIS

^aRegion 1 = MT, ND, SD; region 2 = KS, NE; region 3 = TX, OK; region 4 = AL, FL, GA, LA, MS.

each maternal grandsire. Expected progeny differences (American Simmental Association, 1983) were reported in ratios. Because low scores for calving ease and low birth weights were considered to be desirable, ratios for values of calving ease scores and birth weights below the breed average were above 100. Whereas heavy 205-d weights were considered to be desirable, ratios for values of 205-d weights above the breed average were above 100. The following equation was used to convert the ratios to the units of measure used in these analyses and to calculate CF:

$$CF = ((100 - BVR) \cdot EPDU)/2$$

where CF = the correction factor to adjust each calf's record for its maternal grandsire's direct effect for the traits under consideration, BVR =the breeding value ratio for the direct effect of calving ease score, birth weight or 205-d weight for the calf's maternal grandsire and EPDU = the value in the units of measure for a one percentage point change in ratio for that trait (.016 for calving ease score for first calf, .38 kg for age of dam adjusted birth weight and 2.33 kg for 205-d weight).

All analyses were conducted by the mixedmodel least squares procedure (Harvey, 1977; W. R. Harvey, personal communication). Dependent variables were calving ease, birth weight and 205-d weight. Calving ease was scored as follows: 1 = no assistance; 2 = easy pull; 3 = hard pull (usually with a mechanical

puller), and 4 = Caesarean. The model included the fixed effects of region, Simmental percentage of calf (75 or 88%) and sex of calf. Random effects were herd/region, maternal grandsire, maternal grandsire x region interaction, maternal grandsire x herd/region interaction and residual. The variance-covariance matrix for maternal grandsire effects was assumed to be $I\sigma^2$. The expected mean squares for the model with unequal subclass numbers are shown in Table 2. As can be seen from Table 2, there was no appropriate mean square for testing the statistical significance of region. However, estimates of the maternal grandsire x region variance component were either close to zero or negative for all analyses. Therefore, the maternal grandsire \times region variance component was assumed to be zero, and the herd/region mean square was used for testing region because the maternal grandsire x region variance component was the only additional variance component present in the expected mean squares for region. If the maternal grandsire x region variance component actually was not zero, then the test conducted would cause region to test significant more often than if an exact test were possible, due to the underestimation of the error term used. Herd/region and maternal grandsire \times region were tested over maternal grandsire \times herd/region. Maternal grandsire was tested over maternal grandsire x herd/region. Maternal grandsire × herd/region, sex of calf and Simmental percentage of calf were tested over residual.

Variance components and their coefficients were estimated for each random effect (Harvey,

Source	EMS
Region Herd/region MGSire ⁵ MGSire × region MGSire × herd/region Sex of calf Simmental percentage of calf Residual	$\sigma_{e}^{2} + k_{11}\sigma^{2}_{MH/R} + k_{12}\sigma^{2}_{MR} + k_{13}\sigma^{2}_{H/R} + k_{14}\sigma^{2}_{R}$ $\sigma_{e}^{2} + k_{9}\sigma^{2}_{MH/R} + k_{10}\sigma^{2}_{H/R}$ $\sigma_{e}^{2} + k_{6}\sigma^{2}_{MH/R} + k_{7}\sigma^{2}_{MR}^{3}_{MR} + k_{8}\sigma^{2}_{M}$ $\sigma_{e}^{2} + k_{4}\sigma^{2}_{MH/R} + k_{5}\sigma^{2}_{MR}$ $\sigma_{e}^{2} + k_{3}\sigma^{2}_{X} + k_{5}\sigma^{2}_{R}$ $\sigma_{e}^{2} + k_{3}\sigma^{2}_{R}$

TABLE 2. EXPECTED MEAN SQUARES (EMS)

^aNot in expectation with equal subclass numbers.

^bMaternal grandsire.

1977; W. R. Harvey, personal communication). Total variance was estimated as the sum of the variance components for maternal grandsire, herd/region, maternal grandsire \times region interaction, maternal grandsire \times herd/region interaction and residual. Percentage of the total variation attributed to these different variance components was calculated using a weighted average based on the total number of progeny in each analysis presented in Table 1. Genetic correlations (Yamada, 1962) between maternal grandsire's progeny performance in different herds within region were calculated according to:

$$r_{g}_{MH/R} = \frac{\hat{\sigma}_{M}^{2}}{\hat{\sigma}_{M}^{2} + \hat{\sigma}_{MH/R}^{2}}$$

which assumes that the maternal grandsire by region variance component is zero.

Results and Discussion

Region was a significant source of variation in three analyses for calving ease score and in all but one analysis for both birth weight and 205-d weight (Table 3). The least square means for the three traits for each region in each pair of analyses are shown in Table 4. Adjusting for the maternal grandsire's influence on the direct effect did not appreciably change the least square means for the effect of region for the three traits from those reported in Hanford et al. (1985) with the same data. There was a trend for calving ease, birth weight and 205-d weight to decrease from northern to southern regions; region 4 had the lowest calving ease, birth weight and 205-d weight. These results are similar to those reported by Burfening et al. (1982) in which sire \times location interactions were analyzed, except that the least square means for calving ease score were larger than those shown in Table 4.

Simmental percentage of the calf (Table 3) was not a significant source of variation in any analysis for calving ease or 205-d weight. However, it was significant in three of six analyses for birth weight. These results are different from those reported earlier (Burfening et al., 1979; Burfening et al., 1982) in which Simmental percentage was significant in all comparisons for calving ease. However, the Simmental percentage of the calves in those studies was 50 and 75%, respectively. Sex was a significant source of variation in all analyses, which is similar to the findings of Burfening et al. (1982).

Herd/region was a significant source of variation in all analyses (Table 3); the variance component for herd/region (weighted average over all comparisons) accounted for 17, 28 and 51% of the total variation for calving ease score, birth weight and 205-d weight, respectively (Table 5). These results are similar to those given for calving ease score and birth weight by Burfening et al. (1982).

Maternal grandsire was significant in all analyses for calving ease score and birth weight and for 1 vs 2 for 205-d weight. These results are similar to those reported by Hanford et al. (1985) in which the maternal grandsire component was not adjusted for the direct effect. This indicates that the adjustment of the traits for the direct effect of maternal grandsire probably is not necessary in order to evaluate effectively the three traits in this study. Maternal grandsire accounted for 4, 3 and 0% of the total variation for calving ease score, birth weight and 205-d weight, respectively. These results again are similar to those reported by Hanford et al. (1985) of 4% and 0% for calving ease score and 205-d weight, respectively, but are slightly higher than the 2% for birth weight. The maternal grandsire percentage was higher for calving ease and similar for birth weight percentages reported for the sire component for 2-yr-old dams (Burfening et al., 1979; Burfening et al., 1982).

The maternal grandsire \times region interaction was not significant in any analysis. Its variance components were essentially zero for all three traits, which agrees with earlier findings for the sire \times region interaction variance component in which the sire \times herd/region interaction effect also was in the model (Tess et al., 1979; Burfening et al., 1982).

The maternal grandsire \times herd/region interaction was not a significant source of variation in any analysis for calving ease score, but it was significant in four of six analyses for birth weight and 205-d weight. This interaction accounted for 1, 5 and 3% of the total of the weighted average variance components for calving ease, birth weight and 205-d weight, respectively. The genetic correlations between maternal grandsire's progeny performance in different herds within region (Table 6) ranged from .55 to .90 for calving ease score, .20 to .74 for birth weight and from .05 to .34 for 205-d weight. The significant maternal grand-

$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$							Regional com	parisons					
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$		1	s 2	1 vs		1 vs	4	2 vs		2 vs	4		3 vs 4
Region 1 01 110 1	ltem	qfa	мSb	df	WS	đf	WS	df	WS	đţ	SM	df	SM
Region 1 91 1 1 1 21 3241 1 94 Region Hedrice 33 393 29 11.27 36 12.91 3241 1 3241 1 94 Rickine 38 3.99 3.9 1.72 46 1.10 36 1.10 31 1.3 31 32 31 32 31 32 32 33 32 33 32 33 33 33 34 34 34 34 34 33 34 34 34 34 34							Calving ease	(score) ^d —					
Heid/region 798 1,46 ¹⁰ 735 1,72 ¹⁰ 466 1,66 ¹⁰ 603 1,39 ¹⁰ 336 1,08 ¹⁰ 311 1,39 ¹⁰ 311 301 311 301	Region	1	.91	1	8.36	1	51.53		.72	1	32.41**	-	19.43**
	Herd/region	798	1.46	735	1.72**	466	1.66	603	1.39**	336	1.08	313	1.39**
Region 138 75 34 56 29 33 38 56 28 37 23 37 <t< td=""><td>MGSire^c</td><td>38</td><td>3.95**</td><td>34</td><td>3.85</td><td>29</td><td>3.12**</td><td>38</td><td>2.29</td><td>28</td><td>1.66</td><td>27</td><td>1.55**</td></t<>	MGSire ^c	38	3.95**	34	3.85	29	3.12**	38	2.29	28	1.66	27	1.55**
MGSire X hed/region 1,28 6.2 1,425 6.4 865 1,03 5,4 555 539 5,5 Simmenual percentage 1 2 6/77** 2 4,73 2 6/77** 2 6/23** 2 6/3 5,9 1,47 2 6/23** 2 6/3 5,9 1,47 5,6 891 5,5 5	MGSire × region	38	.75	34	.56	29	.33	38	.56	28	.37	27	48
Sax of alf 2 6777* 2 42.70* 2 37.51* 2 37.51* 2 37.51* 2 6.21 3.75 3.76 3.76 3.76 3.75 3.	MGSire X herd/region	1,528	.62	1,425	.64	865	.66	1,103	.54	565	.52	539	.54
Region 1 2.81 1 2.83 1 3.23 1 2.3 1 2.2 1 0.0 Region 379 6 61 3,423 61 3,423 55 59 1,955 59 1,147 56 91 55 9 1,56 91 55 9 1,56 91 55 9 1,55 59 1,451 56 1 1 345 56 91 35 56 1 345 56 1 345 56 1 345 56 1 345 57 56 31 57 27 1 345 56 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36 31 36	Sex of calf	2	67.77	7	42.79**	7	37.51**	2	34.52**	2	20.63**	2	6.21
Residual 3,796 .61 3,423 .61 2,498 .59 1,955 .59 1,47 .56 891 .53 Region 1 1,624.2* 1 3,132.9** 1 3,570.5** 1 49.1 1 711.0** 1 345.6* Herdregion 38 53,7** 466 58,1** 603 58,4** 336 59,1** 313 508 MGSire 38 15,5** 466 58,1** 603 58,4** 336 59,1** 313 508 MGSire 38 15,5** 1,40 29 12,1** 1103 17,5* 563 16,6** 337,7** 27 544 159 15,5 11,47 14,1 15,3 15,4 15,5 11,47 15,1 15,4 15,4 15,5 11,47 14,1 16,8** 339 15,5 11,47 14,1 15,3 15,4 15,4 15,4 15,4 15,4,4,3** 15,4,4,3** <td< td=""><td>Simmental percentage</td><td>1</td><td>2.81</td><td>-</td><td>2.83</td><td>1</td><td>3.23</td><td>1</td><td>.23</td><td>1</td><td>.22</td><td>-</td><td>•</td></td<>	Simmental percentage	1	2.81	-	2.83	1	3.23	1	.23	1	.22	-	•
Region 1 1.6242** 1 3,152.9** 1 3,570.5** 1 49.1 1 711.0** 1 345.6* Herdregion 78 58,7** 735 35,7** 466 38.1.5 58.4** 336 59.1** 313 50.8* Herdregion 798 58,7*** 746 3,70.5** 1 49.1 1 711.0** 1 345.6* MGSire 38 58,1** 466 3,87.9** 38 51.9** 28 37.7** 27 54.8 MGSire 38 15.7 34 70.4** 29 12.7 38 51.9** 27 411.4 11.4	Residual	3,796	61	3,423	.61	2,498	.59	1,955	.59	1,147	.56	891	.52
Region11.624.2**13.152.9**1 $3.570.5^{**}$ 49.11711.0**1 345.6^{*} Herd/region3858.7**73555.7**46658.1**60358.4**33659.1**31350.8*MGSire region3815.73419.02919.3**3815.62711.4MGSire region3815.23419.02914.1021.73815.6*13.62711.4MGSire region3815.21.42515.9**86515.1**1.10317.556316.8**53915.9MGSire region3.815.0**119.02914.02.4432*214.4241**21.019.7***2558.2***24432*Ser of calf22.005.4***1195.7***139.5111.12.2***114.4Simmenal percentage13.79614.02.448419.002.443***********************************							Birth wt,	, kg					
Herdregion 798 58,7** 735 55,7** 466 58,1** 53,6 59,1** 313 50,1** 313 40,2** 31,2** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1** 31,1**<	Region	1	1,624.2**	7	3,152.9**	1	3,570.5**	1	49.1	1	711.0**	1	345.6**
MGSire 38 63.8 ^{••} 34 $70.4^{••}$ 29 $49.3^{••}$ 38 51.9 ^{••} 28 37.7 ^{••} 27 54.8 [±] MGSire × region 38 15.7 34 19.0 29 12.7 38 15.6 27 11.4 MGSire × region 152 15.9 ^{••} 15.9 103 75 565 16.8 ^{••} 59 11.4 MGSire × region 1.52 1.904.4 ^{••} 2 1,904.4 ^{••} 2 1,917.5 565 16.8 ^{••} 59 15.4 14.1 891 15.3 Simmental percentage 1 240.9 ^{••} 1 105.7 ^{••} 1 919 15.3 14.1 891 15.3 14.1 14.4 Region 796 14.0 3,423 14.0 2,495 15.6 1,147 14.1 891 15.3 15.3 15.6 14.1 15.3 15.5 15.1 15.3 15.5 15.5 15.5 15.5 15.5 15.5 <td>Herd/region</td> <td>798</td> <td>58.7**</td> <td>735</td> <td>55.7**</td> <td>466</td> <td>58.1.</td> <td>603</td> <td>58.4</td> <td>336</td> <td>59.1**</td> <td>313</td> <td>50.8**</td>	Herd/region	798	58.7**	735	55.7**	466	58.1.	603	58.4	336	59.1**	313	50.8**
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	MGSire	38	63.8**	34	70.4	29	49.3	38	51.9**	28	37.7**	27	54.8
MGSire × herd/region 1,528 16.6* 1,425 15,0* 865 15,1* 1,03 17,5 565 16.8* 539 15,9 Sex of calf 2 2,00.5** 2 1,004,4** 2 1,019,7** 2 443.2 14,43 14,43 2 1,447 14,1 891 15,4 14,1 891 15,5 1,447 14,1 891 15,3 15,6 1,447 14,1 891 15,3 15,6 1,447 14,1 891 15,4 15,4 15,5 1,417 14,1 891 15,1 15,4 1,1,3 15,3 15,3 1,4,1 891 15,1 15,4 1,1,3 15,3 15,3 1,1,4 1,1 15,3 15,3 1,1,4 1,1 15,3 1,2,3 1,3 4,2,65,4 15,3 1,1,3 1,3 1,2,65,4 1,3 1,3 1,3,4 1,3 1,3 1,3,5 1,3 1,3,5 1,3 1,3,55 1,3 1,3 1,3,5	MGSire × region	38	15.7	34	19.0	29	12.7	38	15.6	28	13.6	27	11.4
Sex of calf 2 2.026,5** 2 1,904,4** 2 1,424,1** 2 1,019,7** 2 558,2** 2 443,2* Simmenal percentage 1 240,9** 1 105,7** 1 555 1 112,2** 1 31.6 1 14,4 Simmenal percentage 3,796 14,0 3,423 14,0 2,498 13.0 1,955 15.6 1,147 14.1 891 15.3 Region 1 50,293.6** 1 118,776.9** 1 193,995.9** 16.0 2,493.0 1 14.1 891 15.5 1,147 14.1 891 15.3 1,21.7 14.1 38,121.7** 138,121.7* 138,121.7* 138,121.7* 138,121.7* 138,121.7** 138,121.7** 138,121.7* 138,121.7* 138,121.7* 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121.7** 138,121	MGSire × herd/region	1,528	16.6	1,425	15.9**	865	15.1**	1,103	17.5	565	16.8	539	15.9
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	Sex of calf	2	2,026.5**	7	1,904.4**	7	1,424.1**	5	1,019.7**	2	558.2**	7	443.2**
Residual 3,796 14.0 3,423 14.0 2,498 13.0 1,955 15.6 1,147 14.1 891 15.3 Region 1 50,293.6** 1 118,776.9** 1 193,990.2** 1 3,483.0 1 117,234.7** 1 38,121.7* Region 78 4,321.1** 735 3,809.5** 466 3,528.6** 603 4,627.3** 336 5,381.3** 313 4,265.4* MGSire 38 13,40.4*** 34 7,69.5* 36 5,381.3** 313 4,265.4* 613.4* MGSire 38 1,34,10** 34 7,69.5* 36 7,34,5 734,5 734,5 MGSire 38 270,5 34 7,06.5 35,28.6* 613,8* 724,1 28 863,7 7734,5 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734,50.1* 734	Simmental percentage	-	240.9**	1	105.7**	1	59.5	1	112.2**	T	31.6	1	14.4
Region 1 50,293.6** 1 118,776.9** 1 193,990.2** 1 3,483.0 1 117,234.7** 1 38,121.7* Herd/regin 78 4,321.1** 735 3,805.5** 466 3,528.6** 603 4,627.3** 336 5,381.3** 313 4,265.4* MGSire 38 1,340.4** 34 7,098.2 29 1,094.4 38 743.0 27 734.9 MGSire 38 270.5 34 7,095.2 29 1,094.4 38 724.1 28 823.9 27 734.9 MGSire × region 38 724.1 28 823.9 27 734.9 863.2 MGSire × region 38 724.1 28 724.1 28 863.7 27 863.13.8 MGSire × red/region 1,528 532.7** 1,425 568.2** 865 544.5** 1,103 578.8 565 572.5 539 613.8 551.1 1 351.3 <td>Residual</td> <td>3,796</td> <td>14.0</td> <td>3,423</td> <td>14.0</td> <td>2,498</td> <td>13.0</td> <td>1,955</td> <td>15.6</td> <td>1,147</td> <td>14.1</td> <td>891</td> <td>15.3</td>	Residual	3,796	14.0	3,423	14.0	2,498	13.0	1,955	15.6	1,147	14.1	891	15.3
Region 1 50.293.6** 1 118,776.9** 1 193.990.2** 1 3,483.0 1 117,234.7** 1 38,121.7* Herd/region 798 4,321.1** 735 3,809.5*** 466 3,238.6*** 603 4,627.3*** 336 5,381.3*** 313 4,265.4* MGSire 38 1,404.**** 34 1,098.2 29 1,094.4 38 734.9 27 734.9 MGSire × region 38 2743.0 28 823.9 27 734.9 853.7 734.9 MGSire × region 38 724.1 28 858.7 27 734.9 853.7 734.9 863.7 734.9 863.7 734.9 863.134 863.7 734.9 863.7 734.9 863.7 734.9 863.7 734.9 863.134 734.9 863.7 734.9 863.7 734.9 863.7 734.9 863.7 734.9 863.7 734.9 863.7 734.9 863.7 734.9 <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td> 205-d wt</td> <td>ko –</td> <td></td> <td></td> <td></td> <td></td> <td></td>							205-d wt	ko –					
Herd/region 798 4,321.1* 735 3,809.5** 466 3,528.6** 603 4,627.3** 336 5,381.3** 313 4,265.4* MGSire 38 1,340.4** 34 1,098.2 29 1,094.4 38 9,43.0 28 823.9 27 734.9 MGSire 38 1,340.4** 34 762.6 29 1,094.4 38 724.1 28 823.9 27 734.9 MGSire 38 270.5 34 762.6 29 590.5 38 724.1 28 863.5 572.5 539 613.8* 27 863.5 544.5** 1,103 557.8.8 55 572.5 539 613.6* 613.8* 265.5 539 613.8* 265.5 539 613.8* 265.66.5** 265.55.5 545.55.5 545.55.5 545.55.5 545.55.5 545.55.5 545.52.75* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* 265.35.27.5* <td< td=""><td>Region</td><td></td><td>50,293.6**</td><td>1</td><td>118,776.9**</td><td>1</td><td>193,990.2</td><td>1</td><td>3,483.0</td><td>-</td><td>117,234.7**</td><td>-</td><td>38,121.7**</td></td<>	Region		50,293.6**	1	118,776.9**	1	193,990.2	1	3,483.0	-	117,234.7**	-	38,121.7**
MGSire 38 1,340,4** 34 1,098.2 29 1,094.4 38 943.0 28 823.9 27 734.9 MGSire X region 38 2.70.5 34 76.26 29 590.5 38 724.1 28 858.7 27 863.5 MGSire X region 1,528 532.7** 1,425 568.2*** 865 544.5*** 1,103 578.8 565 572.5 599 613.8* 565 613.8*** 1,22 73,618.3*** 2 5,5215.9*** 2 14,362.1*** 2 5,5217.5*** 2 14,362.1*** 2 14,362.1**** 1,103 578.8 565 572.5 599 613.8************************************	Herd/region	798	4,321.1**	735	3,809.5**	466	3,528.6**	603	4,627.3**	336	5,381.3**	313	4,265.4**
MGSire × region 38 270.5 34 762.6 29 590.5 38 724.1 28 858.7 27 863.5 MGSire × region 38 724.1 28 858.7 27 863.5 MGSire × herd/region 1,528 532.7*** 1,425 568.2**** 865 544.5**** 1,103 578.8 565 572.5 539 613.8* 555 572.5 539 613.8* 555 572.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 555 572.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 613.8* 555 575.5 539 555.5 555 575.5 539 555.5 555 575.5 539 555.5 555 575.5 539 555.5 555 575.5 539 555.5 555 575.5 539 555.5 555.5 555 575.5 539 555.5 555.5 555 575.5 530 555.5 555.5 555 575.5 530 555.5 555 575.5 531 555 575.5 538.5 555.5	MGSire	38	1,340.4**	34	1,098.2	29	1,094.4	38	943.0	28	823.9	27	734.9
MGSire X herd/region 1,528 532.7* 1,425 568.2* 865 544.5* 1,103 578.8 565 572.5 539 613.8* Sex of calf 2 73,618.3** 2 55,215.9** 2 46,611.0** 2 32,686.6** 2 26,322.7** 2 14,362.1* Simmental percentage 3,796 484.3 3,423 1,200.8 1 47,7 1,955 521.7 1,147 538.1 891 510.9 Residual	MGSire × region	38	270.5	34	762.6	29	590.5	38	724.1	28	858.7	27	863.5
Sex of calf 2 73,618.3** 2 55,215.9** 2 46,611,0** 2 32,686,6** 2 26,322.7** 2 14,362.1 Simmental percentage 1 638.8 1 1,290.8 1 77.0 1 996.2 1 9.1 1 85.1 Residual 3,796 484.3 3,423 460.8 2,498 448.7 1,955 521.7 1,147 538.1 891 510.9	MGSire × herd/region	1,528	532.7**	1,425	568.2**	865	544.5**	1,103	578.8	565	572.5	539	613.8**
Simmental percentage 1 638.8 1 1,290.8 1 77.0 1 996.2 1 9.1 1 85.1 Residual 3.796 484.3 3,423 460.8 2,498 448.7 1,955 521.7 1,147 538.1 891 510.9	Sex of calf	7	73,618.3**	2	55,215.9**	2	46,611.0**	7	32,686.6	7	26,322.7**	6	14,362.1**
Residual 3,796 484.3 3,423 460.8 2,498 448.7 1,955 521.7 1,147 538.1 891 510.9	Simmental percentage	1	638.8	1	1,290.8	1	77.0	1	996.2	1	9.1	1	85.1
	Residual	3,796	484.3	3,423	460.8	2,498	448.7	1,955	521.7	1,147	538.1	891	510.9
	^D Mean squares.												

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^GMaternal grandsire. dCalving ease scores: 1 = no assistance; 2 ≈ easy pull; 3 = hard pull (usually with a mechanical puller); 4 = caesarean. ••• < .01.

TABLE 4. LEAST SQUARES MEANS ± SE FOR THE EFFECT OF REGION OF THE UNITED STATES^a ON CALVING EASE, BIRTH WEIGHT AND 205-D WEIGHT

			Regional compariso	Su		
Region A vs Region B	1 vs 2	1 vs 3	1 vs 4	2 vs 3	2 vs 4	3 vs 4
			Calving	ease (score)d		
¢،	1.76 ± .02 1.78 ± .02 ^b	$1.79 \pm .02$ $1.83 \pm .02b$	1.63 ± .03 1.81 ± .02 ^b	1.74 ± .02 1.76 ± .03b	$1.60 \pm .03$ $1.77 \pm .03b$	1.54 ± .03 1.67 ± .04 ^b
B	1.75 ± .02 ^b	1.74 ± .03 ^c	1.44 ± .04 ^c	1.73 ± .03 ^b	1.43 ± .04 ^c	1.41 ± .05 ^c
			Birt	h wt, kg		
Û	37.0 ±.1	37.0 ± .1	36.2 ± .1	36.4 ± .1.	35.4 ± .2	$35.2 \pm .2$
- V	37.6 ±.1 ^b	37.9 ±.1 ^b	37.7 ± .1 ^b	36.5 ± .2 ^b	$36.2 \pm .2^{D}$	$35.8 \pm .2^{D}$
B	36.4 ± .1 ^c	36.2 ± .1 ^c	34.6 ± .2 ^c	36.3 ± .2 ^b	34.6 ± .3 ^c	34.7 ± .3°
			205	-d wt, kg		
<=	221.7 ± .6	218.8 ± .6	212.8 ± .9	216.2 ± .9	209.1 ± 1.4	205.3 ± 1.4
•	$225.0 \pm .7^{b}$	$224.0 \pm .7^{b}$	224.2 ± .8 ^b	217.3 ± 1.1^{b}	219.2 ± 1.5^{b}	$211.2 \pm 1.5^{\text{D}}$
B	218.5 ± .8 ^c	213.6 ± .9 ^c	$201.4 \pm 1.5^{\circ}$	215.1 ± 1.2 ^b	199.0 ± 2.0 ^c	$199.4 \pm 2.0^{\circ}$
^a Region 1 = M ^b , ^c Means with	T, ND, SD; region 2 = K different superscripts w	(S, NE; region 3 = TX, OK (S) NE; region 3 = TX, OK (S) thin each column for each	; region 4 = AL, FL, GA, I h dependent variable differ	A, MS. (P < .05). al miliar). 4 = concernent		
Calving case s	COLES: I = NO ESSISTATICC	; z = casy punt, z - maru pu	winner a mich wire anno 111			

MATERNAL GRANDSIRE × REGION AND HERD INTERACTIONS

				R	egional compa	risons ^a							Weighted	
	1 vs 2		1 vs 3		1 vs 4		2 vs 3		2 vs 4		3 vs 4		average	
Item	Comp	*	Сотр	*	Comp	*	Сотр	*	Comp	*	Сотр	*	Comp	*
							Coluina nor)()						
Herd/region	.117	15	.150	19	.125	16	.141	19	.094	14	.165	23	132	17
MGSire	.033	4	.033	4	.038	Ś	.029	4	.029	4	.026	4	.032	4
MGSire X region	.003	•	002	0	011	ī	001	0	005	1	004	-	- 002	· c
MGSire × herd/region	004	1	.012	7	.031	4	025	ŝ	023	4	015		100	
Residual	.607	80	.613	76	.590	76	.589	80	.560	85	.518	- 72	592	79
							Birch w	νt, kg						
Herd/region	5.67	27	5.48	26	5 48	28	7 14	06	7 20		01 7			ç
MGSire	.50	7	-51	0	84	2	05	; ,	9	, ,	0.17	× 1	0.0	9
MGSire × region	- 05	c	10	c				4 6	, .	4 •	1.0.1	. .	6.	n
MGSire × herd region	118	v	20	94	9 1	.	01'-	5 •	CT	1,	24	7	06	0
Recidinal	1 2 00			r i	t , :	יי	CO'T	4	1.4/	•	.37	1	1.00	Ś
12 DICOV	19.74	8	14.03	10	12,92	6 6	15.57	64	14.09	60	15.26	66	14.18	65
							205-d v	vt, kg						
Herd/region	520.03	50	448.41	47	383.12	44	711.31	56	858.92	ψ	709 91	2 2	655 70	15
MGSire	91.11	7	3.08	•	5.53	T	3.46	0	2.21	3 0	4.06	ç -	20.2	; •
MGSire × region	-6.20	ī	2.61	0	1.14	0	3.66	0	9.72) -	10.57	o	1 45	,
MGSire × herd/region	22.01	2	48.94	ŝ	41.15	Ś	30.90	. 6	18.88		58.67	• •	35.67	, ,
Residual	484.26	47	460.80	48	448.66	51	521.70	41	538.14	38	510.90	, 6	485.56	45,
^a Region 1 = MT, ND,	SD: region 2 = 1	KS, NE; re	zion 3 = TX. OK.	: region 4 =	AL FL GA	LA MS								
b _M aternal grandsire.)			0										
Calving esce scores: 1	and activity of a		line bend - 6 - 11ma	11 2	•	:								
T IST STORE STORE	- IIU assistante	Keps = 7 (s	puit; s = naro pu	in (usuany u	with a mechan	ical puller); 4 = caesarean							

TABLE 5. ESTIMATED VARIANCE COMPONENTS AND PERCENTAGE OF THE TOTAL VARIATION FOR CALVING EASE, BIRTH WEIGHT AND 205-D WEIGHT

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			Regional c	Regional comparisons ^a							
Trait	1 vs 2	1 vs 3	1 vs 4	2 vs 3	2 vs 4	3 vs 4					
Calving ease scoreb	.90	.73	.55	NCc	NC	.64					
Birth weight, kg	.30	.37	.34	.37	.20	.74					
205-d weight, kg	.34	.06	.12	.10	.05	NCC					

TABLE 6. GENETIC CORRELATIONS BETWEEN MATERNAL GRANDSIRES' PROGENY PERFORMANCE IN DIFFERENT HERDS WITHIN REGION FOR CALVING EASE SCORE, BIRTH WEIGHT AND 205-D WEIGHT

^aRegion 1 = MT, ND, SD; region 2 = KS, NE; region 3 = TX, OK; region 4 = AL, FL, GA, LA, MS.

^bCalving ease scores: 1 = no assistance; 2 = easy pull; 3 = hard pull (usually with a mechanical puller); <math>4 = caesarean.

^CNC = Not calculated due to negative variance component estimates.

sire \times herd/region interaction and the low genetic correlations indicated that different maternal grandsire progeny did not rank the same in different herds for birth weight and 205-d weight. Differences between herds in management, nutrition and other environmental factors may account for this result. If the factors that created this interaction can be identified, it should be possible to predict more accurately the genetic worth of a potential sire in a particular herd.

In these analyses, the maternal grandsire effect was adjusted to account for half the direct effect associated with the maternal traits of calving ease score, birth weight and 205-d weight. However, these adjustments did not significantly change the results compared with analyses in which the maternal grandsire effect was not adjusted. The producer sees and evaluates unadjusted maternal traits. Because no maternal grandsire x region of the U.S. interaction was observed in the evaluation of breeding values for these maternally influenced traits, maternal grandsire rankings are not expected to differ among regional environments studied, even though differences existed among regions of the U.S.

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