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Breed effects and genetic parameter estimates for calving difficulty and birth weight in a multibreed population¹

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ABSTRACT: Birth weight (BWT) and calving difficulty (CD) were recorded on 4,579 first-parity females from the Germplasm Evaluation Program at the U.S. Meat Animal Research Center (USMARC). Both traits were analyzed using a bivariate animal model with direct and maternal effects. Calving difficulty was transformed from the USMARC scores to corresponding Z-scores from the standard normal distribution based on the incidence rate of the USMARC scores. Breed fraction covariates were included to estimate breed differences. Heritability estimates (SE) for BWT direct, CD direct, BWT maternal, and CD maternal were 0.34 (0.10), 0.29 (0.10), 0.15 (0.08), and 0.13 (0.08), respectively. Calving difficulty direct breed effects deviated

from Angus ranged from –0.13 to 0.77 and maternal breed effects deviated from Angus ranged from –0.27 to 0.36. Hereford-, Angus-, Gelbvieh-, and Brangus-sired calves would be the least likely to require assistance at birth, whereas Chiangus-, Charolais-, and Limousin-sired calves would be the most likely to require assistance at birth. Maternal breed effects for CD were least for Simmental and Charolais and greatest for Red Angus and Chiangus. Results showed that the diverse biological types of cattle have different effects on both BWT and CD. Furthermore, results provide a mechanism whereby beef cattle producers can compare EBV for CD direct and maternal arising from disjointed and breed-specific genetic evaluations.

Key words: beef cattle, breed effects, calving difficulty

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INTRODUCTION

Calving difficulty (CD; dystocia) is a significant cost to beef production and is most prevalent in first-calf heifers. Dystocia increases the likelihood of calf and dam mortality, postpartum interval, and labor and veterinarian costs (Bennett and Gregory, 2001). Expression of CD is affected by both direct (calf) and maternal (dam) genotypes. Factors affecting CD include age of dam, sex of calf, shape and weight of calf,

gestation length, breed, sire of calf, pelvic area of dam, and weight of dam (Brinks et al., 1973). The genetic correlation between CD and birth weight (BWT) is positive and moderate to high in magnitude; therefore, selection to decrease BWT can be used to reduce CD (Bennett and Gregory, 2001). However, assuming the same selection accuracy, direct selection on the economically relevant trait of CD would be more efficient. Unfortunately, an antagonistic relationship between CD direct and maternal genetic effects has been reported (–0.26; Bennett and Gregory, 2001); therefore, the inclusion of both CD direct and maternal EBV in a breeding objective is warranted.

Breed utilization allows for the exploitation of heterosis and complementarity to match genetic potential with markets, feed resources, and climates (Cundiff et al., 1998). However, in the current U.S. beef industry, it is generally not possible to directly compare EBV of animals across breeds without the aid of adjustment

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factors. Across-breed adjustments were first developed by Notter and Cundiff (1991) and are updated annually given changes in genetic trends and base adjustments (Van Vleck et al., 2007). Across-breed adjustment factors have most recently been estimated by Kuehn and Thallman (2014) for BWT, weaning weight, yearling weight, maternal milk, marbling score, rib eye area, fat thickness, and carcass weight. Unfortunately, across-breed adjustment factors do not exist for CD.

Consequently, the objectives of this study were to estimate breed differences for direct and maternal CD for first calf heifers in the U.S. Meat Animal Research Center (USMARC) Germplasm Evaluation (GPE) Program as a first step toward the development of across-breed adjustment factors for CD.

MATERIALS AND METHODS

Animals

All animal procedures followed USMARC standard operating procedure (as no experimental protocols were applied) and cattle were treated according to Federation of Animal Science Societies guidelines (FASS, 1999). Pedigree and performance data originated from the GPE Program at the USMARC (Clay Center, NE; 1970–2012). The breeds used and the mating procedures used for each of the 8 cycles were previously reported by Smith et al. (1976; Cycle I), Gregory et al. (1978; Cycle II), Arango et al. (2002; Cycle III), Cundiff et al. (1998; Cycle IV), Wheeler et al. (2001; Cycle V), Wheeler et al. (2004; Cycle VI), Cushman et al. (2007; Cycle VII), and Wheeler et al. (2010; Cycle VIII). Briefly, in each cycle, 5 to 7 breeds of sire, sampled to represent industry germplasm, were mated to base Angus, Hereford, or MARC III (one-fourth Angus, one-fourth Hereford, one-fourth Pinzgauer, and one-fourth Red Poll) cows. Hereford and Angus bulls were used in each cycle as a base comparison. Comparisons of the breeds in this project were primarily facilitated through data from Cycle VII and from more recent continuous sampling of industry bulls (continuous GPE). In Cycle VII of the USMARC GPE project, purebred Angus, Hereford, Red Angus, Charolais, Gelbvieh, Simmental, and Limousin sires were mated by AI to Angus, Hereford, and composite MARC III cows to produce progeny designated as F_1 , born in 1999, 2000, and 2001. The 1999- and 2000-born male calves were castrated and fed for harvest. Female F_1 and the 2001-born F_1 males were kept for breeding and mated in multiple-sire pastures to produce 2-, 3-, and 4-breed cross progeny designated F_1^2 . The F_1^2 calves were born from 2003 to 2007 from 3-yr-old and older dams (Snelling et al., 2010). More recent GPE records were included from individuals that were of varying proportions of the 7 breeds used

in Cycle VII produced through continuous sampling of industry sires from these breeds. For the more recent GPE generations (continuous GPE), purebred AI sires were mated to purebred or crossbred dams to generate purebred and crossbred steers and heifers and purebred and F_1 bulls. The F_1 bulls were mated to the purebred and half-blood females to produce purebred, half-blood, and F_1^2 steers and heifers. All germplasm introduced into the population entered through AI. Animals from the 8 cycles included only spring-born records whereas the advanced generations of GPE included spring and fall calving records. All heifers were bred via natural service during GPE cycles. During continuous evaluation, heifers were bred via AI to sires that were minimally in the top half of their respective breed for either calving ease direct or BWT direct EBV, had high accuracy EBV, and represented heavily used sires in the U.S. industry. Those that did not conceive via AI were exposed to natural service Angus sires selected for calving ease direct EBV. The 18 breeds (number of AI sires) involved in the evaluation were Angus (131), Hereford (140), Red Angus (43), Shorthorn (52), South Devon (25), Beefmaster (44), Brangus (47), Brahman (57), Santa Gertrudis (21), Braunvieh (30), Charolais (100), Chiangus (24), Gelbvieh (73), Limousin (62), Maine-Anjou (38), Salers (50), Simmental (71), and Tarentaise (17).

Data were recorded for CD and BWT on 5,795 calves born to first-parity females in the GPE project. Reasons for removal from the final data set (proportion of those removed) were born with an abnormal presentation (12.2%; e.g., breach), presented with cryptorchidism (0.2%), born to a founder female or a twin (72.6%), and born before 1970 (spring born; 0.6%) or before 2007 (fall born; 14.4%). These cutoffs represent the start dates of different phases of evaluation of GPE progeny. After edits, there were a total of 4,579 records. Cows were closely monitored for CD and were assigned a CD score as outlined in Table 1. Birth weights were recorded within 24 h after calving.

Statistical Analysis

Calving difficulty was transformed from the USMARC scores to the corresponding Z -scores from the standard normal distribution (Table 1) based on incidence rate of the USMARC scores. The midpoint value of the incidence rate between each subsequent USMARC score was used to assign Z -scores. For example, the incidence rate for category 1 was 74% and the incidence rate for category 2 was 2.3%, making the midpoint value for category 1 37% (half of the incidence rate) and the midpoint value for category 2 75.1% (the midpoint between category 1 and category 2). The corresponding Z -scores for the first 2 categories were the 37th and 75th percentiles of

Table 1. Description of calving difficulty score

USMARC ¹ score	Z-score ²	Difficulty level	Incidence rate	Midpoint value ³
1	-0.33	No assistance given	74%	37.0%
2	0.68	Little difficulty, assisted by hand	2.3%	75.1%
3	0.81	Little difficulty, assisted by calf jack	5.7%	79.2%
4	1.18	Slight difficulty, assisted by calf jack	12%	88.0%
5	1.62	Moderate difficulty, assisted by calf jack	1.5%	94.8%
6	1.86	Major difficulty, assisted by calf jack	2.7%	96.9%
7	2.35	Caesarean birth	1.8%	99.1%

¹USMARC = U.S. Meat Animal Research Center.

²The Z-score is the percentile of standard normal distribution corresponding to the midpoint value.

³The midpoint value is the middle value of the incidence rates between 2 subsequent USMARC scores.

the standard normal distribution. Variance components and fixed effects were estimated using ASReml version 3.0 (Gilmour et al., 2009). The linear-linear animal model used to jointly analyze BWT and CD included fixed effects of sex, contemporary group (concatenation of year and season of birth and location of birth at the USMARC; $n = 35$), and covariates for breed fractions, direct, and maternal heterosis. Random effects included direct and maternal additive genetic effects, and residual. The covariates for direct and maternal heterosis were allocated as the regression on expected breed heterozygosity fraction. For heterosis calculation, AI sires and commercial cows of the same breed were considered the same breed, Red Angus was assumed the same as Angus, and composite breeds were considered according to their nominal breed composition. Composite breeds consisted of MARC II (one-fourth Angus, one-fourth Hereford, one-fourth Simmental, and one-fourth Gelbvieh), MARC III (one-fourth Angus, one-fourth Hereford, one-fourth Red Poll, and one-fourth Pinzgauer), Brangus (three-eighths Brahman and five-eighths Angus), Santa Gertrudis (three-eighths Brahman and five-eighths Shorthorn), Beefmaster (one-half Brahman, one-fourth Angus, and one-fourth Shorthorn), Chiangus (one-half Chianina and one-half Angus), and one-half Red Angus– and one-half Simmental–cross cows. Breed fractions were determined based on pedigree information; each animal was assigned half of its sire breed and half of its dam breed. Founder animals, sires or dams with known breed but unknown parentage, were assigned to their respective breeds and used to assign breed fractions throughout the pedigree; for breed fraction covariates, AI sires and commercial cows of the same breed were considered different breeds. Breed fractions were then assigned for each individual and fit as covariates for the estimation of breed effects.

Birth weight and CD breed differences were deviated from Angus. Birth weight breed differences were adjusted to current (2012) breed mean EBV by accounting for the sampled AI sires through adding the sampling effect of sires to estimated breed effects. The sampling effect of sires was accounted for by estimat-

ing the weighted (using average relationship to phenotyped progeny) average EBV of AI sires that had descendants with records, deviated from the mean EBV of their respective breed for calves born in 2012 using the following: $EBV(i)_{YY} - EBV(i)_{USMARC}$, which is the difference between the average within-breed EBV for breed i to a base year (YY) of 2012 and the weighted average EBV for sires of breed i that have descendants with records at the USMARC.

Calving difficulty breed differences were standardized by the following: $BreedSoln/\sigma_a$, in which $BreedSoln$ is the estimated breed effect solutions and σ_a is the additive genetic SD estimated from the current analysis using GPE data from the USMARC. The standardized estimated breed effects were then corrected for sampling of AI sires. Sampling of AI sires were standardized to account for the differences in models used by breed associations in generating calving ease EBV by the following: $\{[EBV(i)_{YY} - EBV(i)_{USMARC}] \times -1\}/\sigma_{a(i)}$. Multiplication by -1 is necessary to convert calving ease EBV reported by beef cattle breeds in the United States report to CD EBV. The additive genetic SD ($\sigma_{a(i)}$) was obtained from the SE of prediction and corresponding accuracy from each breed for calving ease direct and maternal EBV of each breed association. To put all breed estimates on the same scale, breed effects were then multiplied by either the direct (e.g., σ_a) or maternal additive SD from the current analysis for direct and maternal breed estimates, respectively.

RESULTS AND DISCUSSION

Genetic Parameters

Although not the primary aim, estimates of variance components for BWT and CD were obtained as a necessary step in estimating breed effects and developing across-breed adjustment factors for BWT and CD EBV. These variance components are presented in Table 2. Estimates of direct and maternal heritabil-

Table 2. Residual, direct, and maternal (co)variance estimates for birth weight and calving difficulty

Trait ^{1,2}	BWT _r , kg	CD _r	BWT _d , kg	CD _d	BWT _m , kg	CD _m
BWT _r , kg	10.68 (1.55)					
CD _r	0.37 (0.17)	0.23 (0.03)				
BWT _d , kg			6.91 (1.93)			
CD _d			0.58 (0.21)	0.12 (0.04)		
BWT _m , kg			-0.75 (1.52)	0.26 (0.19)	3.03 (1.59)	
CD _m			0.07 (0.21)	0.01 (0.03)	-0.17 (0.17)	0.05 (0.03)

¹BWT_r = birth weight residual; CD_r = calving difficulty residual; BWT_d = birth weight direct; CD_d = calving difficulty direct; BWT_m = birth weight maternal; CD_m = calving difficulty maternal.

²Variances (SE) are on the diagonal and covariances are on the off diagonal.

ity for BWT and CD and their correlations are presented in Table 3. Mujibi and Crews (2009) reported a higher direct heritability estimate (0.46) and a similar maternal heritability estimate (0.14) for BWT. Bennett and Gregory (2001) reported larger direct (0.43) and maternal (0.23) heritability estimates for CD using a linear-linear model in 2-yr-old females where CD was scored using 7 categories.

The genetic correlation between direct and maternal BWT from the present study (-0.16) was similar to the correlation (-0.27) obtained by Mujibi and Crews (2009), who used a 3-trait linear model including BWT, percent unassisted calving, and gestation length. Bennett and Gregory (2001) reported higher genetic correlations between CD and BWT direct (0.81) than reported in the present study (0.64) from a linear-linear model using 7 categories for CD. The positive correlation between BWT direct and CD direct suggests that as BWT increases, CD score also increases, and the magnitude suggests that BWT breeding values explain approximately 41% of the genetic differences in CD. Bennett and Gregory (2001) reported a similar strength in correlation between BWT direct and CD maternal (-0.16) but it differed in direction compared with the estimate from the current study (0.11); however, the estimate from the current study is not different from zero. Bennett and Gregory (2001) reported a stronger negative correlation between direct CD and maternal CD (-0.26) as opposed to the estimate of 0.10 from the current study. Both estimates were not significantly different from zero. A negative correlation between CD direct and maternal would be anticipated because calves born without difficulty tend to be smaller (evidenced by the 0.64 genetic correlation from the current study) and therefore are more likely to be smaller in mature size because the genetic correlation between BWT and mature weight has been estimated as moderate (0.57; Northcutt and Wilson, 1993). Moderate-size cows tend to have a smaller pelvis area and therefore have more difficulty when they calve during their first parity (Bellows et al., 1971). The antagonistic relationship between CD direct

and maternal reported by Bennett and Gregory (2001) is supported by others (e.g., Mujibi and Crews, 2009; Eriksson et al., 2004) and suggests that direct selection for reduced CD could result in female progeny that have increased CD when they become dams. The unexpected positive estimate report herein, although not different from zero, could be an artifact of a mating design whereby sires were selected based on their genetic potential to reduce dystocia when bred to virgin heifers. The genetic correlation reported here between CD maternal and BWT maternal (-0.42) suggests that females that have less CD will also have lighter calves. Eriksson et al. (2004) reported a positive correlation between CD maternal and BWT maternal for Charolais cattle (0.46) and a slightly negative correlation using Hereford data (-0.28). Calves born with lighter BWT are smaller in size, having a higher probability of fitting through the cow's pelvis, and therefore are born with less difficulty. Bennett and Gregory (1996) reported a genetic correlation estimate of 0.14 between BWT direct and BWT maternal for composite breeds (MARC II and MARC III) and 0.08 for the purebreds that formed the composites compared with the estimate of -0.16 from the current study.

Breed Effects for Birth Weight

Adjusted breed effects for BWT are presented in Table 4. The breed solutions for BWT presented here

Table 3. Heritability and direct and maternal correlation estimates for birth weight and calving difficulty

Trait ^{1,2}	BWT _d , kg	CD _d	BWT _m , kg	CD _m
BWT _d , kg	0.34 (0.10)			
CD _d	0.64 (0.17)	0.29 (0.10)		
BWT _m , kg	-0.16 (0.29)	0.43 (0.38)	0.15 (0.08)	
CD _m	0.11 (0.37)	0.10 (0.42)	-0.42 (0.53)	0.13 (0.08)

¹BWT_r = birth weight residual; CD_r = calving difficulty residual; BWT_d = birth weight direct; CD_d = calving difficulty direct; BWT_m = birth weight maternal; CD_m = calving difficulty maternal.

²Heritability (SE) are on the diagonal and correlations are on the off diagonal.

Table 4. Birth weight breed differences estimated from USMARC data adjusted for sire sampling

Breed	Average base EBV		BreedSoln ³ at USMARC (vs. Angus)	BY 2012 breed difference ⁴
	Breed 2012 ¹	USMARC bulls ²		
	(1)	(2)	(3)	(4)
Angus	1.5	1.4	0	0.0
Hereford	3.2	1.9	0.62	1.8 (1.27)
Red Angus	-1.1	-2.2	-2.71	-1.8 (1.89)
Shorthorn	2.0	0.8	3.77	4.8(2.13)
South Devon	2.4	2.0	1.49	1.7 (2.03)
Beefmaster	0.3	0.7	1.42	0.8 (3.34)
Brahman	1.5	0.5	6.17	7.0 (2.68)
Brangus	0.7	0.4	-3.13	-3.0 (4.24)
Santa Gertrudis	0.2	0.3	6.53	6.2 (2.71)
Braunvieh	2.5	3.3	4.91	4.0 (2.42)
Charolais	0.5	-0.4	2.99	3.6 (1.32)
Chiangus	3.4	2.6	0.61	1.2 (2.66)
Gelbvieh	0.7	1.3	-0.75	-1.5 (1.83)
Limousin	1.5	0.9	1.95	2.4 (1.28)
Maine-Anjou	1.5	1.7	-3.11	-3.40 (2.63)
Salers	1.5	1.5	-5.17	-5.40 (2.45)
Simmental	2.0	2.8	3.10	2.1 (1.41)
Tarentaise	1.7	1.6	-4.72	-4.8 (4.71)

¹The average within-breed EBV for birth year 2012.

²The weighted average EBV of bulls with descendants with records at the U.S. Meat Animal Research Center (USMARC).

³BreedSoln = estimated breed effect solutions from analysis of USMARC data with Angus set as the base.

⁴Estimated breed effects (SE) corrected for sire sampling for birth year (BY) 2012 as calculated by (4) = (3) + [(1) - (2)]. Standard errors are equal to those from the breed solutions from the current analysis.

differ from those previously reported by Kuehn and Thallman (2014). There are several likely reasons for this discrepancy. The primary reason for this is because Kuehn and Thallman (2014) used mature cow data as well as the heifer data from this study for a total of over 30,000 BWT records. Additionally, the breeds with the largest changes between the studies included those in which over half of the phenotypes in the present study were generated from continuous GPE where heifers were bred back to their breed of sire from selected bulls chosen based on high (desirable) EBV for calving ease via AI, potentially creating partial confounding between direct and maternal breed effects. On the other hand, Kuehn and Thallman (2014) did not fit a maternal effect for BWT, and that may have biased some of the estimates, especially as the number of cows bred back to their breed of sire has increased in the GPE population. Yet another difference between the 2 analyses is that Kuehn and Thallman (2014) did not fit CD (direct and maternal) as a correlated trait.

Estimates of maternal breed effects on BWT were not reported because EBV of sampled sires (with which to adjust for sampling bias between breeds) were not available. Nonetheless, significant maternal breed effects on BWT have been previously reported. *Bos indicus* breeds have an especially important advantage

in maternal effect on BWT (Freetly and Cundiff, 1998; Jenkins et al., 2000; Dillon et al., 2015).

Among the British breeds, Shorthorn calves were estimated to have the heaviest BWT whereas Red Angus calves were estimated to have the lightest BWT. Among the *B. indicus*-influenced breeds, Brahman were estimated to have the heaviest BWT and Brangus calves were estimated to have the lightest BWT. Roberson et al. (1986) and Comerford et al. (1987) reported that *B. indicus* sires increased BWT compared with *Bos taurus* sires when bred to *B. taurus* cows. Among the Continental breeds, Charolais calves were estimated to have the heaviest BWT and Salers and Tarentaise calves were estimated to have the lightest BWT. Cundiff et al. (1986) reported that high-growth-rate breeds (Simmental, Maine-Anjou, Brahman, and Charolais) had heavier BWT whereas low-growth-rate breeds (Hereford, Angus, and South Devon) had lighter BWT. Estimates of breed effects show similar results except for Hereford, Simmental, and Maine-Anjou, where estimates suggest that Hereford have larger BWT than Simmental and Maine-Anjou in contrast to Cundiff et al. (1986) These differences reflect the changes in selection pressure by both Continental and British breeds that have occurred over time since Cundiff et al. (1986).

Table 5. Calving difficulty score direct breed differences estimated from USMARC data adjusted for sire sampling

Breed	Average base EBV		Additive genetic SD ³	BreedSoln at USMARC	BY 2012 breed difference ⁵
	Breed 2012 ¹	USMARC bulls ²		(vs. Angus) ⁴	
	(1)	(2)	(3)	(4)	(5)
Angus	-10.0	-4.1	9.4	0.00	0.00
Hereford	-1.6	8.1	8.3	0.06 (0.18)	-0.13 (0.06)
Red Angus	-8.0	-10.5	9.0	0.12 (0.26)	0.43 (0.09)
Brangus	-10.2	-9.8	8.4	-0.04 (0.60)	0.16 (0.21)
Charolais	-6.0	-3.9	14.2	0.59 (0.18)	0.76 (0.06)
Chiangus	-11.0	-14.4	7.8	0.27 (0.38)	0.64 (0.13)
Gelbvieh	-19.4	-14.2	7.8	0.17 (0.26)	0.16 (0.09)
Limousin	-18	-18.8	8.6	0.52 (0.18)	0.77 (0.06)
Maine-Anjou	-18.4	-13.7	7.8	0.40 (0.37)	0.41 (0.13)
Simmental	-18.6	-10.5	7.8	0.41 (0.20)	0.27 (0.07)

¹The average within-breed EBV for each breed for birth year 2012 as reported by each respective breed association.

²The weighted average EBV as reported by each respective breed association of bulls for each breed having descendants with records at the U.S. Meat Animal Research Center (USMARC).

³The additive genetic SD for calving difficulty direct for each breed.

⁴BreedSoln = estimated breed effect solutions (SE) from analysis of USMARC data (Z-scores) with Angus set as the base.

⁵Estimated breed effects (SE) corrected for sire sampling and reported on the USMARC scale (Z-scores) for birth year (BY) 2012. Calculations: (5) = $((4)/\sigma_a + \{[(1) - (2)]/(3)\}) - \{[(1) - (2)]/(3)\}_{Angus} \times \sigma_a$, in which σ_a is the direct additive genetic SD for calving difficulty estimated from the current analysis. Standard errors are the scaled SE from (4).

Breed Effects for Calving Difficulty

Breed effects for CD direct and maternal are presented in Tables 5 and 6, respectively. Breeds without estimates reflect breed associations that do not have CD direct and CD maternal EBV and include Shorthorn, South Devon, Beefmaster, Brahman, Santa Gertrudis, Braunvieh, Salers, and Tarentaise. Two Continental breeds, Limousin and Charolais, were estimated to have the largest breed effects for CD direct of 0.77 and 0.76, respectively. Of the British breeds, Red Angus was estimated to have the greatest degree of CD direct (0.43) whereas Hereford- and Angus-sired calves were estimated to require the least assistance at birth of all breeds analyzed. In terms of CD maternal, Red Angus- and Chiangus-sired heifers were estimated to have the most difficulty calving. However, larger Continental breeds such as Simmental-, Charolais-, Limousin-, and Maine-Anjou-sired heifers were estimated to have a fewer calving difficulties. Cundiff et al. (1986) reported that high-growth-rate breeds (Simmental, Maine-Anjou, and Charolais) experience more CD direct than low-growth-rate breeds (Hereford and Angus); the estimates of breed effects show similar results. Reynolds et al. (1990) reported that dams bred to large-size sire breeds experience more CD than dams bred to medium-size sire breeds.

Brangus is the only *B. indicus*-influenced breed in this study with EBV for CD. However, previous research has shown strong direct breed effects increasing CD in progeny of Brahman, Nellore, and

Boran sires bred to *B. taurus* cows but strong favorable maternal effects reducing CD in cows sired by these breeds (Cundiff et al., 1998; Freetly and Cundiff, 1998; Jenkins et al., 2000; Casas et al., 2011; Dillon et al., 2015).

Challenges for Developing Across-Breed EBV Adjustments for Calving Difficulty

An underlying issue relative to the development of across-breed EBV for CD direct and maternal is correctly accommodating the differences in models used by various beef breed associations in the estimation of EBV for these traits. All breeds use a multitrait model fitting BWT, but some use a linear-linear model and others use a threshold-linear model. Even within these 2 broad categories of model specification, other differences exist. Some breeds combine categories, thus shrinking the number of potential scores on a linear scale. For breeds that use a probit function treating CD as a threshold character, the point at which CD is centered on the underlying scale differs. Also, the mean incidence of difficulty (e.g., 50%, 80%, etc.) at which the back-transformed EBV is calculated from the underlying EBV can be different. To correctly estimate breed differences toward the development of adjustment factors for breeders to use when comparing animals of different breeds for CD direct and maternal, this larger issue of scaling must be addressed. Differences due to sire sampling undoubtedly impact these estimates. For breeds where sampled sires

Table 6. Calving difficulty score maternal breed differences estimated from USMARC data adjusted for sire sampling

Breed	Average base EBV		Additive genetic SD ³	BreedSoln at USMARC (vs. Angus) ⁴	BY 2012 breed difference ⁵
	Breed 2012 ¹	USMARC bulls ²			
	(1)	(2)	(3)	(4)	(5)
Angus	-16.0	-7.5	11.2	0.00 (0.00)	0.00 (0.00)
Hereford	-2.2	9.8	9.1	0.17 (0.13)	0.04 (0.03)
Red Angus	-10.0	-15.6	9.0	0.01 (0.22)	0.32 (0.05)
Brangus	-14.2	-14.1	6.5	-0.08 (0.41)	0.09 (0.09)
Charolais	-7.4	-3.9	13.4	-0.33 (0.16)	-0.22 (0.04)
Chiangus	4.4	-7.6	7.9	-0.15 (0.42)	0.36 (0.09)
Gelbvieh	-13.6	-8.3	7.9	0.14 (0.20)	0.16 (0.04)
Limousin	-9.0	-6.9	8.9	-0.29 (0.16)	-0.17 (0.04)
Maine-Anjou	-7.0	-1.7	7.9	-0.17 (0.31)	-0.15 (0.07)
Simmental	-21.2	-13.0	7.9	-0.21 (0.34)	-0.27 (0.08)

¹The average within-breed EBV for each breed for birth year 2012 as reported by each respective breed association.

²The weighted average EBV as reported by each respective breed association of bulls for each breed having descendants with records at the U.S. Meat Animal Research Center (USMARC).

³The additive genetic SD for calving difficulty maternal for each breed

⁴BreedSoln = estimated breed effect solutions (SE) from analysis of USMARC data (Z-scores) with Angus set as the base.

⁵Estimated breed effects (SE) corrected for sire sampling and reported on the USMARC scale (Z-scores) for birth year (BY) 2012. Calculations: (5) = (5) = $((4)/\sigma_a + \{[(1) - (2)]/(3)\}) - \{[(1) - (2)]/(3)\}_{Angus} \times \sigma_a$, in which σ_a is the maternal additive genetic SD for calving difficulty from the current analysis. Standard errors are the scaled SE from (4).

EBV deviated from their breed's mean, EBV of calves born in a reference year (e.g., 2011), estimates should be adjusted for the sampling bias. However, this requires rescaling. Furthermore, sires that were born several decades ago may have had CD recorded in some breeds but not in others. Genetic trend will be underestimated in breeds that began recording CD more recently, and the disparity in data between breeds could bias estimates of breed differences.

Implementation of existing across-breed EBV has been through a table of additive adjustment factors. The scaling differences between breeds make this approach problematic for CD. An updated delivery model (perhaps web based), using a similar method of scale by variance as reported in this study, would be required to effectively implement across-breed EBV for CD.

Conclusions

Both BWT and CD direct are moderately heritable and, therefore, would favorably respond to direct selection. However, maternal effects are less heritable. Birth weight explained 41% of the genetic variation in CD, suggesting that BWT is a valuable indicator trait, but does not explain all of the genetic variation of the economically relevant trait of CD. Selecting bulls to reduce dystocia in their calves will have little effect on difficulty their daughters may experience when they calve. Therefore, both CD direct and maternal should be included in the breeding objective. Angus-, Hereford-,

Simmental-, Gelbvieh-, and Tarentaise-sired calves would be the least likely to experience CD, whereas Braunvieh-, Shorthorn-, Salers-, and Limousin-sired calves would be the most likely to have dystocia issues. Hereford-, Salers-, and Tarentaise-sired heifers would be the most likely to have calves born unassisted, whereas Braunvieh-, Red Angus-, and Chiangus-sired heifers would be the most likely to have dystocia problems. Results show that the diverse biological types of cattle have different effects on both BWT and CD. Clearly, biological type delineation (British and Continental) is not the sole predictor in determining calving ease. Breeds with the most favorable effects for CD direct and maternal represent a mixture of biological types. These differences can be used to match breeds to complement needs of production systems. Issues to be resolved to develop an across-breed adjustment for CD direct and maternal includes accounting for different models used by breed associations. Some breed associations use a linear model and some use a threshold model. Among breed associations that use linear models, there can be differences between the number of categories that are used and the incidence rates for each category. Among breed associations using a threshold model, there are differences in the incidence rates, where centering occurred on the underlying scale, and the number of categories used. Scaling factors need to be developed to account for these differences. This work will serve as the foundation for the estimation of across-breed EBV for CD in the United States.

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