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Summary

Eighteen breeds were utilized to estimate genetic parameters for birth weight and calving difficulty on first-parity females. Birth weight and calving difficulty were moderately heritable allowing for genetic selection to decrease calving difficulty. Genetic correlation estimates were positive between direct effects for birth weight and calving difficulty. This work will serve as the foundation for estimating across-breed EPD for calving difficulty in the U.S.

Introduction

Calving difficulty (CD), also known as dystocia, is a significant cost to beef production and is more prevalent in first-calf heifers. Dystocia increases the likelihood of calf and dam mortality, increases the postpartum interval, and increases labor and veterinarian costs (*Journal of Animal Science,* 2001, 79:45-51). Calving ease (CE) EPD predicts the ability of calves to be born unassisted and typically includes birth weight (BWT) as an indicator trait.

Different breeds present the opportunity for the exploitation of heterosis and complementarity to match genetic potential with markets, feed resources, and climates. However, in the current U.S. beef industry, it is generally not possible to directly compare the EPD of animals across breeds without the aid of adjustment factors. Across-breed adjustment factors have been estimated by Kuehn and Thallman (*Proceedings, Beef Improvement Federation, Annual Research Symposium and Annual Meeting,* 2014, pp. 134-154) for birth weight and several growth and carcass traits. Unfortunately, across-breed adjustment factors do not exist for CE.

Consequently, the objectives of this study were to estimate genetic parameters for calving ease and birth weight in a multibreed population as a first step towards the development of across-breed adjustment factors for CE.

Procedure

Animals

Pedigree and performance data used in this study originated from the Germplasm Evaluation (GPE) program at the U.S. Meat Animal Research Center (USMARC) in Clay Center, Neb. The breeds utilized in each GPE cycle are listed in Table 1. These breeds were used as A.I. sires and mated to Angus, Hereford, and MARC III females (¼ Angus, ¼ Hereford, ¼ Pinzgauer, ¼ Red Poll). Data from continuous evaluation of 18 breeds in GPE were also included.

Data

Data were recorded for calving difficulty (CD; the inverse of calving ease) and BWT on 5,795 calves born to first-parity females. Animals were removed from the data set if they were born with an abnormal presentation (e.g., breach), presented with cryptorchidism, born to a founder female (known breed with unknown parents), or a twin. Only animals born after 1970 (spring born) or after 2007

Table 1. Breeds of sires utilized in each Gerplasm Evaluation Program cycle.

Cycle	Breeds used in cycle
I	Angus, Hereford, South Devon, Limousin, Simmental, and Charolais
II	Angus, Hereford, Gelbvieh, Maine-Anjou, Chianina, and Santa Gertrudis
III	Angus, Hereford, Tarentaise, and Brahman
IV	Angus, Hereford, Shorthorn, Salers, and Charolais
V	Angus, Hereford, and Brahman
VI	Angus and Herford
VII	Angus, Hereford, Red Angus, Simmental, Charolais, Limousin, and Gelbvieh
VIII	Angus, Hereford, Brangus, and Beefmaster

Table 2. Description of calving difficulty scores.[1]

Score	Difficulty Level
1	No assistance given
2	Little difficulty, assisted by hand
3	Little difficulty, assisted by calf jack
4	Slight difficulty, assisted by calf jack
5	Moderate difficulty, assisted by calf jack
6	Major difficulty, assisted by calf jack
7	Caesarean birth
8	Malpresentation

[1]Records with scores of 8 were removed from the analysis.

(fall born) were retained for analysis. After edits there were a total of 4,580 records. Cows were monitored closely for calving difficulty and were assigned a calving difficulty score as outlined in Table 2. Birth weights were recorded within the first 24 hours of calving.

Statistical Analysis

A bivariate linear-linear animal model was fitted with breed effects represented as genetic groups. All industry artificial insemination (AI) sires were assigned a genetic group according to their breed of origin. Dams mated to AI sires and natural service sires mated to F_1 females were also assigned to different genetic groups (i.e., Hereford dams were assigned to different genetic groups than Hereford AI sires). Herefords from selection lines were also assigned their own genetic groups. Most dams were Angus, Hereford, and MARC III (¼ Angus, ¼ Hereford, ¼ Pinzgauer, ¼ Red Poll) composite lines through Cycle VIII.

Table 3. Estimates of direct and maternal heritability and genetic correlations (SE) for birth weight (BWT) and calving difficulty (CD).[1]

Trait [2]	Trait			
	BWT_d	CD_d	BWT_m	CD_m
BWT_d	0.35 (0.09)			
CD_d	0.63 (0.10)	0.29 (0.09)		
BWT_m	-0.16 (0.29)	0.41 (0.39)	0.15 (0.07)	
CD_m	0.18 (0.36)	0.17 (0.42)	-0.44 (0.51)	0.14 (0.07)

[1]Heritabilities (SE) are on the diagonal and genetic correlations (SE) are on the off diagonal.
[2]Birth weight direct (BWT_d), calving difficulty direct (CD_d), birth weight maternal (BWT_m), and calving difficulty maternal (CD_m)

Systematic effects fitted in the model included sex, breed (fitted as genetic group), contemporary group (concatenation of year and season of birth and location of birth at USMARC), and covariates for direct and maternal heterosis. Random effects included animal, maternal effect, and a residual. The covariates for heterosis direct and maternal were estimated as the regression on expected breed heterozygosity fraction. For heterosis calculation, AI sires and commercial cows of the same breed were considered the same, Red Angus was assumed the same as Angus, and composite breeds were considered according to their nominal breed composition.

Variance components and fixed effects were estimated using ASReml version 3.0 (*ASReml User Guide Release 3.0,* 2009). Breed differences were adjusted to current (2012) breed breeding value levels by accounting for the weighted (using average relationship to phenotyped progeny) average EPD of AI sires that had descendants, with records, deviated from the mean EPD of their breed for calves born in 2012. Calving difficulty scores were scaled by a factor of 10 for analysis to reduce numerical problems.

Results

Genetic Parameters

Estimates of direct and maternal heritability for BWT and CD and their correlations are presented in Table 3. Even though there is a high positive correlation between BWT and CD direct, birth weight only explains 40% of the genetic variation in calving difficulty.

Challenges in Across-Breed EPD for CE Breed Effects

An underlying issue relative to the development of across-breed EPD for CE direct and maternal is correctly accommodating the differences in models used by various beef breed associations in the estimation of EPD for these traits. All breeds use a multi-trait model fitting BWT, but some use a linear-linear model while others use a threshold-linear model. Additionally, some breeds combine categories, thus shrinking the number of potential scores on a linear scale. For breeds that treat CE as a threshold character, the point at which CE is centered on the underlying scale differs. Also, the mean incidence of difficulty (e.g., 50%, 80%, etc.) at which the back-transformed EPD is calculated from the underlying EPD can be different.

Implementation of existing across-breed EPD has been through a table of additive adjustment factors. Due to many of the issues above, this approach becomes problematic for CE. An updated delivery model (perhaps web-based) would be required to effectively implement across-breed EPD for CE. It would also allow substantial improvements to the system for other traits.

Although BWT is a good indicator of CE, it does not explain all of the variation in CE. Consequently, producers should place selection pressure on CE (direct) and not BWT to decrease dystocia. Selection for both EPD simultaneously would essentially place undue additional selection for BWT. Although the genetic correlation between CD direct and maternal was slightly positive in the current study, it is associated with a large standard error. Caution should be used so that continued selection for CE direct does not lead to maternal CE issues.

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