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Evaluation of Commercial Genomic Tests for Maternal Traits in Crossbred Beef Cattle

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Summary with Implications

DNA samples were collected from beef heifers born at the Gudmundsen Sandhills Laboratory and analyzed with a genomic test. Phenotypic data from these females were compiled and used in a regression analysis to evaluate the utility of these genomic scores as predictors for phenotypic outcomes. The genomic score for birth body weight (BW) was significantly associated with animal birth BW. The genomic score for heifer pregnancy was not a statistically significant predictor of actual pregnancy. Neither dam age or the genomic score for stayability were significant predictors of actual reproductive longevity.

Introduction

Raising a replacement female can be a significant cost for cow-calf producers. Replacement females require inputs and management, which can be seen as an investment if that female remains in the herd producing a calf year after year until she has paid for those investments and more. Reproductive failure can result from many factors, but regardless, many producers will disqualify a female from remaining in the herd after just one failure to produce a calf. If this happens early in the female's life, then significant investment value is lost. Determining which females to retain as replacements can challenge many producers. Knowing pedigrees may increase confidence in the decision process, but newer technology available in the field of genomic testing may allow producers to make a more informed decision about keeping heifers with a higher probability of staying in the herd longer. Genomic predictors for

longevity or stayability may help producers identify and select these females earlier and thereby reduce inputs into unwanted, inferior females.

The objective of this study was to evaluate the predictive ability of a commercial DNA test designed to predict genetic merit of crossbred females for stayability and other traits.

Procedure

Phenotypic data were collected from heifer calves born at the Gudmundsen Sandhills Laboratory (GSL), Whitman, from 2009 to 2012. In 2009, all calves were born in a March calving season and a May calving herd was initiated. In 2010 and 2011, hair samples were taken from both March and May calves. In 2012, hair samples were only taken from the March calving herd. Samples were collected as hair pulled from the tail with follicles and placed in a DNA hair sample card. This occurred at birth of each calf as birth body weight (BW) was measured and recorded.

After weaning, heifer calves were developed until first breeding at approximately 15 months of age. Each female was kept within the calving system (March or May) it was born in. All female calves were retained on the ranch and only removed for reproductive failure. Records were kept on all females and calving information taken each year for 5 subsequent years to determine their longevity in the herd. If a female never became pregnant as a yearling then it received a 0 for heifer pregnancy, and subsequently received a 0 from that point forward as it was removed from the herd. Stayability was calculated as the number of calves produced in a 5-year period for a maximum of 5 calves. Any calving data past 5 years was not included in this study.

DNA samples from 414 crossbred, female, beef calves were analyzed with the Ignity Gold panel (Neogen GeneSeek Operations, Lincoln, NE; Neogen Corporation, Lansing, MI). This panel uses gene markers

to report the genomic value for 13 traits; 7 maternal traits: birth weight, calving ease direct, calving ease maternal, docility, heifer pregnancy, milk, and stayability; 2 performance traits: average daily gain and residual feed intake; and 4 carcass traits: tenderness, USDA marbling score, ribeye area, and fat thickness. Upon analyzing the DNA samples each female was assigned a score between 1 and 10 (10 being the best) for each of the 13 traits.

The heifer was the experimental unit in this design. The GLIMMIX procedure of SAS Software (SAS Institute, Inc., Cary, N.C.) was used to perform the regression analysis to evaluate the efficacy of the genomic test scores as predictors of the observed phenotypic traits. All models included calving season, age of dam, and birth year as independent variables along with the genomic scores corresponding to the dependent variable for that model. A P-value ≤ 0.05 was considered significant. A P-value > 0.05, but ≤ 0.10 would be considered a tendency.

The regression analysis was performed using 4 phenotypic traits as dependent variables: birth BW, weaning BW, heifer pregnancy, and stayability (total pregnancies out of a possible 5 years).

Results

The genomic score for birth BW was significant in explaining variation in the heifer's own birth BW ($P < 0.01$). Within the same model, dam age and birth year affected ($P \leq 0.01$) birth BW. Birth BW tended ($P = 0.09$) to differ between calving season with calves born slightly heavier (76 lb vs. 74 lb; May vs. March respectively) in the May calving season. Weaning BW was broken into 4 separate models to analyze 3 different genomic scores, one for each genomic score and one with all genomic scores together (combined). The genomic predictor scores used with weaning BW regression were milk score, calving-ease direct, and calving-ease maternal. Dam age

Table 1 Average of phenotypic traits of heifer calves born in each production year in two different calving seasons[1]

	n	Birth WT[2]	Wean WT[3]	Total Preg[4]	Heifer PG[5]
March 2009	61	75.7	465.1	2.2	0.64
March 2010	68	73.2	465.9	2.8	0.74
May 2010	58	77.2	411.8	1.6	0.58
March 2011	67	75.3	487.5	2.5	0.78
May 2011	66	74.7	433.7	1.7	0.65
March 2012	94	70.0	437.3	1.7	0.78
All March	290	73.6	464.0	2.3	0.74
All May	124	75.9	422.8	1.7	0.62

[1]Location managed two separate calving herds; March and May

[2]Birth body weight (BW) average of females in the contemporary group in lb

[3]Weaning BW average of females in the contemporary group in lb

[4]Average of number of pregnancies per female out of possible 5 years

[5]Average number of females (as percentage) successfully pregnant at first opportunity (yearling heifer)

and calving season had a strong impact ($P < 0.01$) on weaning BW with March-born calves heavier at weaning (464 lb vs. 423 lb; March vs. May, respectively; March calves weaned 8 d older than May calves, 224 d old vs. 216 d old) for all 4 models analyzed. Birth year impacted ($P < 0.05$) all 4 models. The combined model containing all 3 genomic predictor scores for weaning BW demonstrated calving-ease direct as a valid ($P < 0.01$) predictor for weaning BW and milk score tending ($P = 0.06$) to predict weaning BW. Calving-ease maternal was not ($P = 0.35$) a valid predictor for weaning BW within this model; however, when put in the model with calving season, dam age, and birth year it was a valid ($P = 0.01$) predictor of weaning BW. Calving-ease direct was a predictor ($P < 0.01$) within the model of its own, and the genomic score for milk was not ($P = 0.27$) a predictor of weaning BW when in a model on its own. It is important to note that the weaning BW used was the female's own weaning BW, not the weaning BW of her offspring. This needs to be recognized when interpreting the data.

The model results for heifer pregnancy showed dam age ($P = 0.31$) and birth year ($P = 0.11$) having slight effect while calving seasons showed difference ($P = 0.01$) in heifer pregnancy with averages of 74% for March and 62% for May born heifers (Table 1). The genomic score for heifer pregnancy was a non-significant ($P = 0.75$) predictor for phenotypic heifer pregnancy. The stayability model showed birth year ($P < 0.01$) and calving season ($P < 0.01$) influencing the longevity of a female and their ability to stay in the herd with March-born heifers averaging 2.3 calves vs. 1.7 for May-born heifers over a 5-year period. Dam age had little effect ($P = 0.16$) on stayability and the genomic score for stayability was not significant ($P = 0.88$) for the longevity of a female.

Conclusion

In summary, the genomic scores for birth BW and calving-ease direct are significant predictors for birth BW and weaning BW respectively. The genomic scores of heifer pregnancy and stayability were not significant predictors for actual heifer pregnancy and female longevity/stayability in this population.

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