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Evaluation of using half-sibling beef cows to increase growth and carcass uniformity of calf crops

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ABSTRACT

Uniformity of growth and carcass traits of calves resulting from commercial beef cows that were either half-siblings (HS) or similar phenotype but unknown genetic relationship (PS) were determined over 5 calf crops. Residuals (n = 853) of 205-d adjusted weaning weight from a repeated-measures ANOVA model were evaluated for homogeneity of variance between cow groups with Levene's test in PROC GLM of SAS. Adjusted weaning-weight SD was not different between cow groups (22.4 and 21.6 kg for HS and PS cows, respectively; P = 0.56). Lifetime weaning-weight production SD was 320 kg for HS cows and 322 kg for PS cows (P = 0.95). Healthy calves from each year were finished in a commercial feedlot. Standard deviation of HCW, LM area, and LM area per unit of HCW of calves from HS cows tended to be less ($P \leq 0.15$) than SD of calves from PS cows, whereas finishing-period ADG tended to be greater. Observed differences in calf-trait SD were small (approximately 1.5%) and overall were similar to expectations calculated from quantitative genetics theory. However, observed differences in SD fluctuated widely from expectations for any given trait, indicating that very large samples may be needed to reliably observe the small differences that are expected. Therefore, preferentially selecting commercial beef cows so that they have half-sibling genetic relationships, over and above phenotypic selection criteria, appears to have limited ability to reduce phenotypic variability of calf crops, especially for traits with low heritabilities.

Key words: calf-crop uniformity, beef cow

INTRODUCTION

Increasing uniformity in beef cattle production has been an industry goal for many years. More uniform lots of cattle bring greater sale prices for cow-calf producers (Zimmerman et al., 2012). The National Beef Quality Audit in 1991 determined that one of the leading quality concerns for packers, purveyors, retailers, and restaurateurs was uniformity. The 2005 National Beef Quality Audit cited improvement in uniformity of beef cuts and carcasses for retailers and purveyors, but lack of uniformity continued to be in the top 2 for quality challenges and concerns according to the industry segments from the packer through the restaurateur (Shook et al., 2008).

Product uniformity in the beef industry begins at the cow-calf level. Management strategies used to reduce phenotypic variation include defined calving seasons, which can be further improved by use of estrous synchronization programs. During the finishing phase, sorting cattle for frame size, weight, age, and level of fatness through ultrasound technology can help decrease variability of carcasses at slaughter. However, genetic selection for uniformity is also considered by producers as a potential means to increase uniformity.

Mating systems and selection schemes were reviewed by Hohenboken (1985) for their effectiveness in reducing phenotypic variation. Hohenboken (1985) concluded that selection for increased genetic relationships among individuals was likely to produce unsubstantial results. Nevertheless, many producers continue to select closely related sires with the intent to increase calf-crop uniformity. Few, however, use this strategy in conjunction with herds of half-sibling females. Our objective was to determine whether growth and carcass performances of calf crops from half-sibling females were less variable

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than those of calf crops from females with similar phenotypes but unknown genetic relationships.

MATERIALS AND METHODS

Animals

All procedures involving animals used in this experiment conformed to the *Guide for the Care and Use of Agricultural Animals in Research and Teaching* (FASS, 2010). In 2003 and 2004, 400 yearling heifers were purchased for use in this study. Two selection schemes were used that mimicked how a commercial producer might select heifers with the goal of producing uniform calves. Two hundred heifers were purchased in November 2003 from 3 different cowherds in Montana. These 200 heifers (**HS**) were sired by a single Angus AI sire and were, therefore, at least half-siblings. An additional 200 heifers (**PS**) were purchased in January 2004 from 11 commercial cowherds in southern Oklahoma and northern Texas and were selected based on phenotype alone. The phenotypic selection criteria were moderate frame, moderate muscle, and visual evidence of Angus ancestry. Actual pedigree of these heifers was unknown, i.e., there may have been some unknown amount of genetic relationship among PS heifers. Heifers of both types were transported to the Noble Foundation's Red River Research and Demonstration Farm in Burneyville, Oklahoma, and were maintained there as a single spring-calving herd through 2009 (5 calf crops).

Management

The research area was composed of primarily bermudagrass (*Cynodon dactylon* L.) pastures, and rotational grazing practices were used. Each year, cows were randomly selected to be AI bred to either an Angus or Limousin sire followed by natural exposure to the AI sire and full brothers of the AI sire. Cows designated for each bull breed were managed in separate breeding pastures until the end of the breeding season, at which point all cows were managed as one herd again until the next breeding season. Because both cow groups were bred to an AI sire and then exposed to clean-up bulls that were full brothers of the AI sire, their resulting calves were more closely related to each other than their dams were. Furthermore, calves from the HS cows were more closely related to each other than were calves from PS cows. However, the objective of the current evaluation was to determine the effect of cow relatedness on calf trait variability.

At calving, calves were weighed, individually tagged, and surgically castrated. At 2 to 3 mo of age, calves were vaccinated for clostridial and respiratory diseases. Calves were weaned approximately October 1 of each year except 2006 when weaning took place in mid-August because of drought. Cows were palpated for pregnancy, vaccinated, and dewormed at calf weaning. After weaning, calves were vaccinated, dewormed, and preconditioned a minimum of 45 d before a subset of healthy cattle chosen at random was transported to a commercial feed yard in northwest Kansas for finishing. Cattle were fed using the ACCU-TRAC Electronic Cattle Management System (Micro Beef Technologies, Amarillo, TX) and scheduled for slaughter when incremental cost of gain exceeded the value of gain, as determined by this system. Cattle were then slaughtered at a commercial packing plant where carcass data were collected.

Beginning in May 2004, 398 females were exposed for breeding. This number declined as unproductive females and females with poor dispositions were sold. The numbers of females exposed for breeding were 322, 294, 250, and 211 in 2005 through 2008, respectively. The breeding season in 2004 lasted 93 d and by 2008 was reduced to 62 d. The beginning of the calving season was January 22 in 2005 and was moved to February 24 to 27 for the remainder of the study. The average calving date for 2005 through 2009 was March 1, March 29, March 25, March 21, and March 21, respectively. In 2005 the average calving day was d 38 of the calving season. Average calving day was reduced each year and by 2009 reached d 22 of the calving season. Percentage of calves born in the first 21 d of the calving season followed a similar trend. In 2005, 34% of calves were born in the first 21 d and increased to approximately 57% by 2009.

Statistical Analysis

Variables of interest in this manuscript were 205-d adjusted weaning weight, lifetime weaning-weight production per cow, finishing-period ADG, days on feed, initial and midpoint backfat during finishing, HCW, LM area, and LM area per kilogram of HCW. Beef Improvement Federation standard adjustment factors for sex of calf and age of dam were used in the calculation of 205-d adjusted weaning weights (BIF, 2010). Lifetime weaning-weight production was calculated for each cow by summing all observed actual weaning weights across all 5 years. Some cows were not in the herd in later years because of culling. However, these cows were included in the calculation of lifetime weaning-weight production. Lifetime weaning-weight production attempted to capture differences between the cow types for variables that might influence culling status, such as reproductive efficiency.

Continuous variables were evaluated in a repeated-measures ANOVA using PROC MIXED in SAS (SAS Institute Inc., Cary, NC). Year, cow group (HS or PS), calf sire breed (Limousin or Angus), calf sex, and their interactions were fixed effects, and cow was the repeated subject. An autoregressive covariance structure was employed to account for decreases in within-cow correlation over time. Residuals from the model were evaluated for homogeneity of variance between cow groups with Levene's test in PROC GLM of SAS.

To quantify variance reductions between populations, decreases in variability were calculated and dis-