Selection for Postweaning Weight and Residual Feed Intake in Nelore Cattle

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ABSTRACT: Sire selection differentials, breeding values for postweaning average daily gain (ADG), dry matter intake (DMI), residual feed intake (RFI), feed conversion rate (FCR), and genetic parameters were evaluated in a herd selected for 0.63 generations for postweaning weight (W378) and RFI. Selection pressures were 0.97 and 0.81 phenotypic standard deviation units for W378 and RFI. The heritability for directly selected traits, W378 and RFI, were 0.38 ± 0.03 and 0.27 ± 0.09, and the genetic correlation between them was zero. The heritabilities for ADG, DMI and FCR were 0.26 ± 0.09, 0.34 ± 0.10 and 0.14 ± 0.07. There was a small trend towards increased breeding values for ADG in the absence of changes in the breeding values for DMI, resulting in a reduction in the breeding values for FCR.

Keywords: beef cattle; feed efficiency; genetic parameters; selection differential

Introduction

Most beef cattle breeding programs in Brazil place emphasis on selection for traits such as weaning and postweaning weight, average daily gain, maternal effect, scrotal circumference, and visual scores of finishing precocity and muscling (Albuquerque et al., 2006). Although selection for higher weight or average daily gain, combined with muscling and fertility, should select for increased production efficiency, this approach does not take into consideration the largest component of beef cattle production costs, i.e., feed costs.

Several studies on the genetic variability of feed efficiency traits in beef cattle have been published in recent years (Arthur et al., 2001; Schenkel et al., 2004; Barwick et al., 2009; Crowley et al., 2010). Except for Barwick et al. (2009) whose results were obtained for Brahman cattle, all studies involved Bos taurus breeds reared in temperate climate. The results of a meta-analysis of genetic parameter estimates for residual feed intake (RFI) confirm that this trait exhibits medium heritability (0.255 ± 0.008) and a genetic correlation of almost zero with average daily gain (ADG) and metabolic weight (Del Claro et al., 2012). Arthur et al. (2001), based on a selection experiment comprising about 1.7 generations of selection, also reported the effectiveness of selecting beef cattle for low RFI in reducing feed intake without altering productive traits such as weight or average daily gain.

Until recently, few results of genetic parameters and response to selection were available for Bos indicus herds, especially Nelore cattle which form the basis of Brazilian meat production, a fact justifying the implementation of projects in Brazil designed to obtain feed efficiency records in cattle. The objective of the present study was to evaluate the selection procedure and response to selection of a Nelore herd selected for postweaning weight and RFI.

Materials and Methods

Herd formation. At Centro APTA Bovinos de Corte, there are three selection lines (including one control line) of Nelore cattle which have been selected since 1981 based on the animals’ own performance for postweaning weight (Mercadante et al., 2003; Mercadante and Razook, 2010). The collection of dry matter intake (DMI) records in postweaning performance tests started in 2004 for females and in 2006 for males (Grion et al., 2014). The present study began in 2008 with 190 cows (from one of the selection lines described above) using bulls selected based on their own performance for postweaning weight adjusted for 378 days of age (W378) and own performance for RFI. Animals with high W378 and low RFI were desired. In addition to selection for these two traits, the bulls selected were required to meet the breed standards of the Brazilian Association of Zebu Cattle Breeders (ABCZ). Starting with the progeny of 2009, all males and females were evaluated regarding RFI in performance tests.

Nine bulls were used annually for natural mating with cows. The bulls were divided randomly into batches of cows, avoiding mating between related animals. Bulls and heifers entered the first breeding season at 24 months of age. The project contemplated the use of bulls for 2 years, with the culling of 50% of them per year. However, although 60 bulls/year (born in 2009 and 2010) and 95 bulls/year (born in 2011 and 2012, part of another line selected for high W378) were evaluated in feed efficiency tests, the number of bulls meeting the selection criteria described above was not sufficient. Therefore, of the 15 bulls used in the breeding seasons from 2008 to 2012, 40% were used for 3 years. In 2009, 22% of the offspring born were from bulls evaluated for RFI. This percentage was 58% in 2010, 78% in 2011, and 100% by 2012. There was no selection pressure on females since about 80% of them were incorporated into the herd.

Performance test. W378 was obtained in a 168-day performance test. The records of DMI and ADG (based
on four weight recordings after fasting or weekly or fortnightly recordings without fasting) were obtained in a test lasting 83 ± 16 days within the longer test period for W378. Before the tests, the animals were submitted to a period of adaptation to the diet and facilities for at least 21 days. During the tests, the animals were kept in individual pens, except for males born in 2011 and 2012 which were tested in collective pens using the GrowSafe System®. The diets offered over the years differed in terms of composition and source of feeds, but were formulated to have isoenergetic and isoprotein levels (62% total digestible nutrients and 13% crude protein). ADG and RFI were estimated as described by Grion et al. (2014). The feed conversion rate (FCR) was calculated by dividing DMI by ADG. For the 458 bulls tested, the mean initial age, initial weight, W378, DMI, ADG, metabolic weight (BW0.75), RFI and FCR were, respectively, 273 ± 27 days, 250 ± 43 kg, 363 ± 44 kg, 7.11 ± 1.21 kg, 1.13 ± 0.242 kg/day, 71.8 ± 8.37 kg, 0.024 ± 0.713 kg, and 6.51 ± 1.46.

Analyses. Selection differentials for sires born after 2006, within year of birth, were weighted by the number of offspring born. The selection differentials for W378 and RFI were considered to be zero for sires without RFI information. The generation interval and generation coefficient (GC) were calculated as described by Koch et al. (1994). The number of generations of selection was defined as GC-1.

Variance components were estimated by the restricted maximum likelihood method. The variance components and BLUP for W378 were estimated using all animals of the three selection lines (n=7,895). The model included direct additive genetic and maternal permanent environmental as random effects and the fixed effects of contemporary group and month of birth, in addition to age of dam (linear and quadratic effects) and age of animal (linear effect) as covariates. The variance components and BLUP for ADG, DMI, RFI and FCR were estimated in single-trait analysis considering animals of the two selection lines (W378 and RFI line and higher W378 line) with RFI performance records (n=681). The pedigree file contained 2,217 animals. The model included random direct additive genetic effects, the fixed effect of test group, and age of dam (linear and quadratic effects) and age of animal at the beginning of the test (linear effect) as covariates. The genetic correlations of W378 with ADG, DMI, RFI and FCR were estimated in two-trait analysis considering all animals of the three selection lines for W378 and all animals with RFI performance records (n=892). The pedigree file contained 9,551 animals.

Results and Discussion

Selection applied and genetic response. The sire selection differentials for W378 and RFI, weighted by the number of offspring born, were 30 kg and -0.291 kg for W378 and RFI, respectively, corresponding to 0.97 and 0.81 units of phenotypic standard deviation. However, since there was no selection of heifers, the selection pressure was lower (0.49 and 0.41 units of standard deviation for W378 and RFI, respectively). Arthur et al. (2001) reported a selection differential of -0.318 kg for RFI in a herd selected exclusively for RFI. The generation interval was 3.84 years for sires and 6.21 for cows (mean interval of 5 years). The mean GC of animals born in 2012 (with RFI records) was 1.63 ± 0.32 and that of animals born in 2013 (still without RFI records) was 1.74 ± 0.25, i.e., the data analyzed refer to 0.63 generations of selection for W378 and RFI.

The estimated breeding values for ADG, DMI, RFI and FCR are shown in Figures 1 and 2, and are expressed as the deviation from the mean breeding values estimated for animals born in 2006. An increase in the variability of breeding values was observed for traits related to DMI. There was a small trend towards increased breeding values for ADG in the absence of changes in the breeding values for DMI, resulting in a reduction in the breeding values for FCR. These changes are desirable from the point of view of the response to selection. However, the mean phenotypic and genetic values for the four traits in the years studied were highly variable, showing no phenotypic or genetic trend. These results were expected since selection was applied to two uncorrelated traits (rg=0 between W378 and RFI), there was no selection of females, and the generation interval was relatively high. The design of the selection lines described by Arthur et al. (2001) permitted the detection of an annual genetic change in RFI of 0.249 kg/day over 5 years of selection for this trait.

Figure 1. Distribution of estimated breeding values (y-axis) for ADG (kg/day, above) and DMI (kg/day, below) by year of birth (x-axis).
Genetic variation. The heritability estimates for the directly selected traits, W378 and RFI, were 0.38 ± 0.03 and 0.27 ± 0.09, and the heritabilities for ADG, BW0.75, DMI and FCR were 0.26 ± 0.09, 0.59 ± 0.11, 0.34 ± 0.10 and 0.14 ± 0.07, respectively. In general, these values are lower than those reported in other studies on Bos taurus or crossbred cattle (Arthur et al., 2001; Schenkel et al., 2004; Crowley et al., 2010). The genetic correlation between W378 and RFI was zero, whereas the correlations of W378 with ADG, DMI and FCR were 0.84, 0.81 and -0.17, respectively. Selection for higher W378 and lower RFI is possible due to the genetic independence between the two traits. However, selection for W378 results in an increase in DMI, whereas selection for lower RFI is selection against DMI without altering ADG. Considering the heritability estimates, it is possible that a greater response to selection will be obtained for W378 and a lower response for RFI, with an increase in W378 and ADG accompanied by a lower increase in DMI, or without an increase in DMI, resulting in a lower value of FCR and higher feed efficiency. However, the results regarding the response to selection are still preliminary and may change if the number of generations of selection analyzed is increased. For 25 years, the Nelore herd of the present study has been selected exclusively based on the animals’ own performance for W378, with a genetic gain of 0.72% of the average per year (Mercadante and Razook, 2010). A lower rate of genetic gain is expected since selection is based on two traits, one of them with heritability lower than that of W378. However, with the increase in the number of animals and generations analyzed, selection will be based on BLUB and not on the animals’ own performance for W378 and RFI.

Conclusion

Six years of selection of a Nelore herd for higher postweaning weight and lower residual feed intake resulted in 0.63 generations of selection without phenotypic or genetic changes in the means of directly selected traits. There was a trend towards increased variability in breeding values for traits related to dry matter intake, increased breeding values for average daily gain, and reduced breeding values for feed conversion rate. Residual feed intake is a moderately heritable trait that is genetically independent of postweaning weight.

Literature Cited