The Effect of United States Versus New Zealand Angus Germplasm on Characteristics of Crossbred Calves

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ABSTRACT: Blood selenium concentration at birth and growth from birth through finishing were analyzed on progeny from two birth years of Angus bulls of United States (US) or New Zealand (NZ) origin. Dams of the calves were Polled Hereford × Angus crossbreds whose sires had been selected divergently from the national sire summary to be superior (+) or inferior (−) for yearling weight EPD (G) and for total maternal effects (M) on weaning weight. There was no evidence of differences attributable to calf paternity or dam genetic group in concentration of blood selenium in calves at birth. For birth year 1988, progeny of US sires grew nonsignificantly more rapidly than progeny of NZ sires in most life-cycle phases. In 1989 calves, NZ-sired offspring grew nonsignificantly more rapidly than US-sired offspring through a year of age. Averaged across years, preweaning and postweaning growth rates were similar for calves of US and NZ paternity. Divergent selection of the calves’ maternal grandsires for yearling weight EPD was successful; calves in +G groups had more rapid gains through 1 yr of age than did calves in −G groups. Also, growth rate through 4.5 mo of age was influenced by divergent selection of maternal grandsires on total maternal weaning weight EPD; calves from +M groups gained more rapidly than calves from −M groups.

Key Words: Beef Cattle, Growth, Angus, Divergent Selection

Introduction

Since early in this century, Angus cattle have contributed importantly to beef production in both New Zealand and the United States. Although there has been periodic emigration of North American Angus germplasm to New Zealand, flow of Angus genes from New Zealand to the United States has been limited. Thus, there has been opportunity for the two populations to diverge genetically, from founder effects and genetic drift and because selection has been conducted under different management and environmental circumstances. Neither commercial nor stud breeders in New Zealand provide concentrate feeding to beef cattle. Thus, animals have undergone natural selection for reproduction and survival and artificial selection for performance strictly under forage feeding systems. Cattle in the United States have been selected for similar traits but in mixed concentrate/forage feeding systems. Selection within these different environments might have favored different genotypes for economically important traits. The primary objective of this experiment was to compare crossbred progeny of New Zealand vs United States Angus paternity for growth traits measured from birth through finishing. Because selection under conditions of Se deficiency in New Zealand may have favored cattle better able to sequester that mineral in the blood, another objective was to quantify differences attributable to sire paternity in blood Se concentration at birth. Additional objectives were to document other genetic and important environmental sources of variation for the growth traits.

Materials and Methods

Cattle. New Zealand (NZ) and United States (US) Angus semen was used in 2 yr. For calves born in 1988 (n = 55), four NZ and five US sires were sampled. New Zealand sires were not a random sample of artificial insemination bulls available to cattle farmers in New Zealand at that time. Rather, they were the only sires with semen eligible for importation into the US. For calves born in 1989 (n = 83), one NZ and one US sire from the 1988 battery were used again, and two new NZ and three new US bulls were sampled.
The new NZ bulls were from a privately owned and from a government-owned group breeding scheme. In both of those breeding programs, selection had been for a combination of growth and maternal traits. Angus sires from the U.S., in both years, were chosen to represent the price and quality of AI bulls readily available to commercial cattle farmers.

Dams of the calves were 4- to 6-y-old Polled Hereford × Angus F₁ crossbreds at the Shenandoah Valley Agricultural Experiment Station, Steeles Tavern, VA. These cows were produced from grade Angus dams, described in greater detail by Hohenboken et al. (1991), mated with semen from Polled Hereford bulls divergently selected for yearling weight and maternal weaning weight EPD, as described by Mahrt et al. (1990). Dams, therefore, were categorized into four genetic groups, according to above or below average predicted merit of their sires for direct and for total maternal genetic effects on growth.

Cows were bred for a 64-d AI season beginning in late May, and calving was predominantly in March and April of each year. Calves were weighed at the end of the breeding season (at an average age of 135 d) and were weaned in October, at an average of 195 d of age. Pastures at the station were predominantly tall fescue with some orchardgrass, white clover, and red clover. Cows were wintered on stockpiled fescue, hay, corn silage, and poultry litter. Nutritional, health, and reproductive management were according to recommendations to commercial Virginia cattle producers at that time.

Statistical Analysis. The following traits, expressed before and through weaning, were measured on all calves: birth weight, (BWT), concentration of Se in the blood at birth (Brodie, 1979), ADG from birth through July (JADG), and ADG from July through weaning (WADG). Blood Se was measured because NZ soils and forages are deficient in that mineral, and we wished to test whether Angus cattle in NZ had responded to that deficiency by evolving enhanced ability to sequester Se. The JADG variable was expected to be responsive to factors affecting milk production of dams (such as cow age and cow genetic group), whereas WADG was expected to be responsive to factors unique to the calf (sex and sire, for example).

The basic mathematical model included fixed main effects for calf paternity (NZ vs US), cow genetic group (four classes), calf sex, birth year, and cow age (4 vs 5 or 6 yr of age). Julian birth date of the calf was a potential covariate for all preweaning traits, and, for analysis of blood Se, the concentration at calving of Se in blood of the dam was an additional covariate. The only interaction included in the model was that of calf paternity × birth year. That interaction was included so that individual sires could be nested within calf-paternity × birth-year subclasses. Other interactions were not included because they were not of particular interest and because the number of observations per subclass would have been small. The mean square for sires was used as the denominator in the F-test for calf paternity. All other sources of variation were tested against the residual mean square.

Calf paternity, cow genetic group, birth year, the interaction of calf paternity × birth year, and the sire effect were retained in all analyses, because the major goal of the experiment was to quantify genetic effects on the traits. Other main effects sequentially were removed to select a final model for each trait that included only effects for which the significance level exceeded .20, plus those that were necessary for hypothesis testing. In a final series of analyses, all variables were analyzed simultaneously with the basic model described above to compute residual correlations among the traits.

Postweaning growth data were available only on steer calves. For each birth-year group, the steers first entered a wintering phase. The 1988 steers were treated uniformly during this phase, but 1989 calves were randomized, within calf paternity, to four dietary treatments: 1) ad libitum grass hay, 2) 80% poultry litter plus 20% whole shelled corn, 3) 70% poultry litter plus 30% shelled corn, or 4) grazed stockpiled tall fescue.

Steers from both years then participated in a summer grazing study, during which they were randomized within calf paternity to two replicates of two dietary treatments: orchardgrass pastures grazed either continuously or in rotation. Finally, they entered a finishing phase in which they were randomized within calf paternity to nutritional treatments of 1) corn plus a commercial protein supplement, 2) corn plus poultry litter, and 3) and 4) corn silage plus poultry litter plus either 1 or 2% of BW of corn grain per day.

Potential sources of variation for growth during the postweaning phases were calf paternity, sire nested within calf paternity group, cow genetic group, age of a calf's dam, birth date, and dietary treatment. Because of differences between years in duration of the phases, all postweaning data were analyzed on a within birth-year basis. Nonsignificant environmental effects were sequentially eliminated to build a final model for each phase. The calf paternity mean square was tested against the sire within calf paternity mean square, and all other effects were tested against the residual.

For calves born in 1988, growth was expressed as ADG from weaning until summer grazing trials began, a period of 181 d. The 1989 calves were weighed biweekly during the wintering trial, as were calves from both birth years in the remaining phases. To use the information provided by those data, growth for each steer was expressed as the regression coefficient of its weight on days on feed.
Results and Discussion

Traits Measured through Weaning. Analysis of variance results for traits measured through weaning are presented in Table 1, and least squares means of genetic effects are presented in Table 2.

The only effect that approached statistical significance in explaining variability in blood Se of the calf was blood Se level of the dam (P = .07). The regression coefficient was .65 ± .35 unit/unit. Neither calf paternity nor genetic group of the dam influenced calf Se. Least squares means for paternal half sib (PHS) groups ranged from 117 to 205 ppb; but with an average of only eight offspring per sire, standard errors of the estimates ranged from 14 to 43 ppb. The NZ and US sire groups ranked throughout the range of observed values in both years. Whereas the NZ sire used in both years produced progeny near average in Se level in both 1988 and 1989, progeny of the reused US sire ranked highest for Se in 1988 but lowest in 1989.

Analysis of variance of cow blood Se concentrations revealed that genetic group of the cow did not significantly affect that trait, neither did cow age. Birth year was an important source of variation; least squares means for 1988 and 1989 were 34.3 to 38.5 kg. Differences attributable to cow genetic group of the dam influenced calf paternity nor genetic group of the dam affected BWT of calves, although progeny of US sires averaged 1.1 kg heavier than progeny of NZ sires (P = .13) by .4 ± .1 ppb.

Neither sire paternity nor its interaction with birth year affected BWT of calves, although progeny of US sires averaged 1.5 kg heavier than progeny of NZ sires (P = .16), a difference that was consistent across the 2 yr. The range in PHS group least squares means was 34.3 to 38.5 kg. Differences attributable to cow genetic groups approached statistical significance. Progeny of the two groups whose sires had above average EPD for yearling weight were 1.5 kg heavier than progeny of the two groups whose sires had below average yearling weight EPD. The difference was only +.5 kg, however, between grandprogeny of sires with above average vs below average total maternal effect EPD. Bull calves averaged 4 kg heavier than heifers. The effect of birth date was not important, and it was not included in the final model.

In 1988, calves from US sires grew more rapidly from birth through 4.5 mo of age than did calves from NZ sires; in 1989, this difference was reversed. Because of this interaction (P < .01), the main effect of calf paternity on JADG was not significant. The ranges from lowest to highest PHS group least squares mean were .13 kg/d in 1988 and .20 kg/d in 1989, and standard errors of PHS group averages ranged from .01 to .08 kg/d.

Coequal sire genetic group was not a significant source of variation in JADG, calves whose grandsires were above average for total maternal EPD averaged .86 kg/d, whereas calves whose grandsires were below average for that trait averaged .83 kg/d for JADG. Thus, differences were in the expected direction. The EPD of maternal grandsires for yearling weight had little effect on JADG; averages for grandprogeny of above and below average sires were .85 and .84 kg/d, respectively.

Calves from 5- and 6-yr old dams grew more rapidly than calves from 4-yr-old dams (.90 vs .78 kg/d), and there was a .12 kg/d difference in average JADG between birth years. For each 1 d later in the season that a calf was born, JADG increased by .0022 kg/d.

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In both 1988 and 1989, progeny of US sires grew more rapidly than progeny of NZ sires between 4.5 mo of age and weaning; the main effect of calf paternity was significant at P = .05. Ranges of PHS group least squares means were .21 and .11 kg/d in 1988 and
1989, respectively. Standard errors of PHS group averages ranged from .02 to .07 kg/d. The effect of cow genetic group on WADG was not significant, although calves whose maternal grandsires were above average for yearling weight EPD grew slightly more rapidly than calves whose maternal grandsires were below average for that trait (.66 vs .64 kg/d).

Calves born in 1988 had .05 kg/d higher WADG than calves born in 1989. For each 1 d later that a calf was born in the season, its WADG increased by .0016 ± .0007 kg/d.

Residual correlations among variables measured through weaning were as follows: Se with BWT, JADG, and WADG equalled -.03, .02, and -.11, respectively; BWT with JADG and WADG equalled .33 and -.05, respectively; JADG with WADG equalled .20. Thus, rates of prenatal growth, growth to 4.5 mo of age, and growth from then through weaning were not closely correlated in this experimental population.

Postweaning Gain. In both birth-year groups, birth date and age of a steer’s dam did not affect gain in any of the postweaning phases. These effects were therefore eliminated from final models. Least squares means for genetic effects on postweaning growth traits are presented in Table 3.

Although the differences were not significant, calves from NZ sires had more rapid winter gains than calves from US sires in both years. For 1988, this may have been a manifestation of compensatory gain, because US-sired calves from that year had moderately higher JADG and WADG than did NZ-sired calves. Compensatory gain would not, however, have accounted for the difference in 1989. Variation attributable to genetic group of a steer’s dam approached statistical significance only in 1989; gain was highest for steers whose maternal grandsires were above average both for growth and maternal effects on weaning weight.

Dietary effects on winter gain were important for 1989 calves (P < .01); the regression coefficients of weight on days on feed were .42 ± .03 kg/d for ad libitum grass hay, .32 ± .03 kg/d for 80% poultry litter/20% whole shelled corn, .26 ± .03 kg/d for 70% poultry litter/30% whole shelled corn, and .45 ± .03 kg/d for stockpiled tall fescue pasture.

In 1988, calves from US sires grew 11% more rapidly during the summer grazing season than calves from NZ sires, although the difference was not significant. In 1989, steers from the two paternity groups grew at nearly equal rates. In both years, differences in summer gain attributable to genetic group of the dam did not approach statistical significance.

In the 1988 summer grazing trial, there was a highly significant nutritional treatment × replicate interaction. At one site, calves continuously grazing orchardgrass grew more rapidly than calves rotationally grazing adjacent orchardgrass pastures; at the other site on the same experiment station, the reverse was true. In 1989, treatment and replicate did not interact; the average regression coefficients of weight on days on feed were .88 ± .03 and .80 ± .04 kg/d for rotationally grazed and continuously grazed groups, respectively.

Neither steer paternity nor genetic group of the steers’ dams was a significant source of variation (Table 3) for gain during the finishing period in either year. Dietary treatment was, however, an important effect in 1988. Steers fed corn plus a commercial protein supplement and corn plus poultry litter gained 2.17 ± .13 and 1.78 ± .09 kg/d, respectively; whereas groups receiving corn silage plus poultry litter plus 1 or 2% of BW of whole shelled corn per day gained 1.08 ± .10 and 1.09 ± .09 kg/d, respectively. Dietary treatment also influenced growth rate in 1989 (P < .01). Least squares means for the average regression of weight on days on feed were 2.02 ± .10 kg/d for corn plus the commercial supplement, 1.81 ± .09 kg/d for corn plus poultry litter, 1.36 ± .11 kg/d for corn silage plus poultry litter plus 1% of whole

<table>
<thead>
<tr>
<th>Least squares means</th>
<th>Se, ppb</th>
<th>BWT, kg</th>
<th>JADG, kg</th>
<th>WADG, kg</th>
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<tbody>
<tr>
<td>Calf paternity</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>US</td>
<td>154 ± 9</td>
<td>37.3 ± .5</td>
<td>.64 ± .02</td>
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<tr>
<td>NZ</td>
<td>159 ± 8</td>
<td>36.2 ± .5</td>
<td>.64 ± .02</td>
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<tr>
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<tr>
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<td>US 1989</td>
<td>165 ± 13</td>
<td>37.0 ± .7</td>
<td>.75 ± .02</td>
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<tr>
<td>NZ 1989</td>
<td>184 ± 13</td>
<td>36.1 ± .7</td>
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<td></td>
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<tr>
<td>+ Growth; + maternal</td>
<td>156 ± 11</td>
<td>31.8 ± .7</td>
<td>.86 ± .02</td>
<td>.65 ± .02</td>
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<td>+ Growth; - maternal</td>
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<td>36.8 ± .8</td>
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<td>- Growth; - maternal</td>
<td>156 ± 10</td>
<td>36.1 ± .6</td>
<td>.81 ± .03</td>
<td>.63 ± .02</td>
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</table>

*BWT is birth weight, JADG is average daily gain from birth through 4.5 mo of age, and WADG is average daily gain from 4.5 mo of age through weaning.
UNITED STATES VS NEW ZEALAND ANGUS GERMPLASM

Table 3. Genetic effects on postweaning growth

<table>
<thead>
<tr>
<th>Least squares means</th>
<th>Winter gains, kg/d&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Summer gains, kg/d</th>
<th>Feedlot gains, kg/d</th>
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<tr>
<td>Calf paternity</td>
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<td></td>
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<tr>
<td>US</td>
<td>.16 ± .02</td>
<td>.34 ± .02</td>
<td>.82 ± .02</td>
</tr>
<tr>
<td>NZ</td>
<td>.22 ± .03</td>
<td>.39 ± .02</td>
<td>.74 ± .04</td>
</tr>
<tr>
<td>Probability of larger F</td>
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<td>.47</td>
<td>.26</td>
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<tr>
<td>Cow genetic group</td>
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</tr>
<tr>
<td>+ Growth; + maternal</td>
<td>.18 ± .03</td>
<td>.43 ± .03</td>
<td>.79 ± .04</td>
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<td>- Growth; + maternal</td>
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<td>.77 ± .05</td>
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<tr>
<td>- Growth; - maternal</td>
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<td>.38 ± .03</td>
<td>.75 ± .03</td>
</tr>
<tr>
<td>Probability of larger F</td>
<td>.89</td>
<td>.07</td>
<td>.64</td>
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</tbody>
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<sup>a</sup>Average daily gain during the wintering phase. All postweaning growth variables are the regression coefficient of weight on days on feed except winter gain in 1988, which is ADG.

shelled corn of BW per day, and 1.43 ± .09 kg/d for silage plus litter plus 2% of BW of whole shelled corn per day.

Discussion and Conclusions. As reviewed by Oldfield (1987), dietary Se is necessary in minute amounts to prevent various metabolic disorders and to support normal growth and reproduction in cattle. Wiener and Woolliams (1983) reviewed four experiments that documented the existence of genetic variation in Se metabolism among and within breeds of sheep. One of those experiments (Langlands et al., 1980) also documented variation between Australian cattle breeds in glutathione peroxidase activity (an enzyme containing Se and indicative of Se status of the individual). Our experiment did not provide evidence of genetic variation among newborn calves in their ability to concentrate Se in the blood.

We are not aware of published accounts comparing growth performance of NZ and US beef cattle strains. Dairy cattle germplasm from New Zealand and North America has, however, been evaluated under standard environmental conditions. Holstein-Friesian semen from the US, Canada, NZ, and seven other countries was used to produce F<sub>1</sub> and backcross offspring of the local strain of Black and White dairy cattle in Poland. In that experiment, bulls descended from NZ sires had lower growth rates through slaughter, poorer feed efficiency, and higher fat content in the carcass than bulls descended from US or Canadian sires (Reklewski et al., 1985), when the animals were intensively fed under experiment station conditions. A later experiment from this Polish project, which included large numbers of bulls and heifers raised under field conditions, confirmed faster growth rates of US and Canadian than of NZ offspring (Stolzman et al., 1988). Two additional publications from that experiment (Jasiorowski et al., 1983, 1988) reported that descendants of the US and Canadian sires had considerably higher fluid milk and total milk solid yields than descendants of NZ sires. The NZ descendants, however, excelled in milk fat percentage, in fat yield, and in fat plus protein yield per unit live weight of the cow.

Canadian, US, and NZ Freisian germplasm also was compared in Israel (Bar-Anan et al., 1987). Results there, using elite, proven bulls from five countries, confirmed higher milk fat percentage of daughters of NZ bulls but greater milk and milk component yields and larger cow size in daughters of the North American sires. Interestingly, the correlations between a sire's proof for milk in the US vs Israel and in Canada vs Israel were .84 and .51, respectively, whereas the correlation between a sire's proof in NZ and Israel was only .01. Sire ranking in extensive, pasture-based systems in NZ, in other words, was unrelated to ranking of those same sires based on daughter performance in intensively fed and managed herds in Israel.

Figure 1. Cumulative weight plotted against age for US- and New Zealand (NZ)-sired calves born in 1988 and 1989.
Figure 2. Cumulative weight through weaning plotted against age for calves whose maternal grandsires were divergently selected (+ or −) for yearling weight expected progeny difference (EPD) \( G \) and EPD for maternal effects on weaning weight \( M \).

In another experiment, semen from highly selected dairy bulls was exchanged between NZ and Canada. In NZ, daughters of Canadian bulls produced more fluid milk and a higher yield of protein, whereas daughters of NZ sires had higher milk fat and protein percentages (Peterson, 1988). Fat yields from the two groups were equal. Canadian sires ranked differently under NZ conditions than from their daughter proofs in Canada, constituting a genotype (sire) \( \times \) environment (country) interaction. When daughters of Friesian bulls of the two nationalities were compared under a concentrate/forage feeding system in Ontario (Graham et al., 1991), Canadian-sired heifers produced more milk, protein, and lactose, consumed more net energy in the feed, and produced a higher output of gross energy in milk. New Zealand daughters equalled Canadian daughters for lactation fat yield and for energetic efficiency of milk production.

Body weights plotted against age, for calf-paternity \( \times \) birth-year subclasses, are presented in Figure 1. In 1988, US-sired calves were heavier at birth and greater than or equal in growth rate to NZ-sired calves in all life-cycle stages except the wintering phase. At the end of the finishing phase, the US-sired calves were 3.6% heavier than their NZ-sired counterparts. For calves born in 1989, those from NZ Angus sires grew approximately equal to or more rapidly than calves from US sires, and the advantage at 20 mo of age of NZ-sired calves was 3.0%. The data do not, therefore, suggest large or important differences in growth traits due to calf paternity, given the US and NZ bulls sampled.

Figure 3. Cumulative weight from weaning through finishing plotted against age for steers whose maternal grandsires were divergently selected (+ or −) for yearling weight expected progeny difference (EPD) \( G \) and EPD for maternal effects on weaning weight \( M \). Upper panel represents data for 1988; lower panel data for 1989.

In Figure 2, the effect of genetic group of the dam on calf growth through weaning is shown. Although differences were not large, divergent selection for yearling weight EPD in the calves' maternal grandsires did seem to influence preweaning growth. Divergent selection of the maternal grandsires for total maternal effects on weaning weight affected primarily growth through 4.5 mo of age, as would be expected.
Growth of the steers from weaning through finishing, according to year of birth and genetic group of their dam, is shown in Figure 3. For calves born in 1988, differences in growth rate attributable to genetic group of the dam emerged most dramatically during the spring/summer grazing phase. By the end of the finishing period, steers from the below average growth/below average maternal effects group were lightest, with little difference among the remaining groups. For 1989 steers, differences emerged during the wintering phase, were maintained during the subsequent grazing season and moderated by the end of the finishing period. Heaviest weights throughout all life-cycle stages were maintained by the calves whose maternal grandsires were above average for EPD both for yearling weight and for total maternal effects on weaning weight; the lightest steers were those whose maternal grandsires were below average for yearling weight EPD.

Implications

Beef cattle in the United States and New Zealand have been selected for similar objectives, but they could have diverged from genetic drift and natural and artificial selection under different physical and management conditions. Selection in New Zealand under forage feeding systems may have favored different genotypes than selection under mixed forage/concentrate feeding in the United States. Calves from U.S and New Zealand Angus sires were similar for growth rate through slaughter under typical management conditions in Virginia. New Zealand Angus germplasm is a potential source of genetic diversity for the United States beef cattle industry.

Literature Cited


