Relationship among GeneSTAR marbling marker, intramuscular fat deposition, and expected progeny differences in early weaned Simmental steers

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ABSTRACT: Research has demonstrated that triiodothyronine and thyroxin are correlated with marbling (MARB) deposition in Wagyu cattle. Polymorphisms in the 5′ region of the thyroglobulin gene have been associated with an improvement in overall fattening and could be used as a gene marker for MARB. The commercially available GeneSTAR MARB test measures the specific thyroglobulin gene polymorphism and identifies cattle as having 0, 1, or 2 copies of the allele; these are identified as 0-STAR, 1-STAR, or 2-STAR, respectfully. Early weaned Simmental steers (n = 192) of known genetics were individually fed over a repeated 4-yr trial period to determine the correlations between GeneSTAR MARB test [Genetic Solutions/Bovigen Pty. Ltd. (Australia) in conjunction with Frontier Beef Systems, LLC (Louisville, CO)] results and intramuscular fat (IMF) deposition. Yearling weight, MARB, percent retail cuts, and carcass weight EPD were calculated for each steer. Steers were weaned at 88.0 ± 1.1 d, pen-fed a high-concentrate diet for 84.5 ± 0.4 d before allotment, and subsequently individually fed a 90% concentrate diet composed primarily of cracked corn and corn silage for 249.7 ± 0.7 d. Steers were slaughtered at 423.3 ± 1.4 d. Deoxyribonucleic acid samples were used by Genetic Solutions/Bovigen (Australia) for GeneSTAR MARB analysis. Steers with allele types of 0-STAR (n = 47), 1-STAR (n = 95), and 2-STAR (n = 33) had no effect ($P > 0.10$) on MARB score, chemically determined IMF percentage, quality grade, or percent low Choice and better. There were no differences ($P > 0.10$) in performance or other carcass parameters among the allele types. GeneSTAR results were not associated with MARB ($P > 0.10$). Conversely, MARB EPD was correlated ($P < 0.01$) with MARB score (r = 0.44) and IMF percentage (r = 0.27). Thus, in this management system, MARB EPD is an accurate predictor of IMF deposition. These data suggest that the GeneSTAR MARB marker was not an efficacious predictor of IMF deposition in early weaned Simmental steers fed a high-energy diet.

Key words: GeneSTAR marbling marker, carcass composition, early weaned steer

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INTRODUCTION

The ability to sort cattle and predict carcass traits is of increased importance as more cattle are priced on a grid-marketing system (Basarab et al., 1999; Koontz et al., 2000). Marbling (**MARB**) can be the greatest factor affecting profits (Forristall et al., 2002), yet only 10% of U.S. cattle are premium Choice or greater (McKenna et al., 2002). There are several tools available to improve and predict MARB and carcass composition including EPD, real-time ultrasound, live-animal evaluation, DNA sequencing of the bovine genome, and marker-assisted selection (Barendse et al., 1997; McPeake, 2003). Several genes affect intramuscular fat (**IMF**) deposition, but none are omnipotent (Barendse et al., 1997, 2001; Genetic Solutions, 2003). Recent research has suggested that DNA markers are related to MARB deposition (Barendse et al., 2001; Jackwood and Fluharty, 2001; Geary et al., 2003). Commercially available DNA markers, including GeneSTAR MARB, evaluate a known QTL polymorphism on the 5′ thyroglobulin gene (**TG5**). Barendse et al. (2001) reported the C to T transition on this gene was highly associated with IMF deposition in long-fed cattle. This knowledge may be useful for several segments of the industry, including identifying elite herd sires or cattle with superior carcass merit genetics and designating those cattle to their optimal grid (e.g., a quality grade or yield grade emphasis). Boleman et al. (1998) noted that only 50% of feedlot cattle are marketed at an optimum quality grade to yield grade level. The objectives of this trial were 1) to study the efficacy of GeneSTAR MARB [Genetic Solutions/Bovigen Pty. Ltd. (Australia) in conjunction with Frontier Beef Systems, LLC (Louisville, CO)] marker as a predictor of IMF deposition, 2) to determine the

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Table 1. Diet composition of the growing diet for early weaned Simmental steers

Ingredient	%, DM basis
Coarse cracked corn	73.1
Soybean meal	13.1
Alfalfa hay	10.3
Rumensin-mineral supplement[1]	3.5

[1]50.0% base mineral, 49.5% ground corn, and 0.05% Rumensin 80 (27.5 g/ton). The mineral supplement was a custom mix containing Ca, 15.1% (minimum) to 17.1% (maximum); P, 8.1% (minimum); NaCl, 18.0% (minimum) to 20.0% (maxiumum); Mg, 2.3% (minimum); K, 2.3% (minimum); Zn, 0.3% (minimum); Cu, 1,486 ppm (minimum); Se, 27 ppm (minimum); vitamin A, 528,000 IU/kg (minimum); vitamin D, 88,000 IU/kg (minimum); and vitamin E, 2,200 IU/kg (minimum).

Table 2. Diet composition of the finishing diet for early weaned Simmental steers

Item	%, DM basis
Coarse cracked corn	67.9
Soybean meal[1]	13.8
Corn silage	9.9
Molasses	4.9
Trace mineral salt	0.5
Calcium carbonate	1.0
Rumensin-mineral supplement[2]	2.0

[1]46.5% protein.
[2]Rumensin was fed at 33 g/ton (Elanco Animal Health, Indianapolis, IN). The mineral supplement was BosBuilder G (Land O'Lakes, Fort Dodge, IA) containing Ca, 13.4% (minimum) to 16.1% (maximum); P, 12.5% (minimum); NaCl, 15.6% (minimum) to 18.7% (maximum); K, 0.7% (minimum); Zn, 4,500 ppm (minimum); Cu, 1,200 ppm (minimum); Se, 35.2 ppm (minimum); vitamin A, 660,000 IU/kg (minimum); vitamin D, 66,000 IU/kg (minimum); and vitamin E, 660 IU/kg (minimum).

effects on other carcass and performance parameters, and 3) to evaluate the relationship among the DNA markers and growth and carcass EPD. We hypothesized that knowledge of genotype along with proper management and nutrition would produce more efficient, profitable beef production and allow for more accurate prediction of carcass composition.

MATERIALS AND METHODS

Experimental Animals

A 4-yr study was conducted utilizing 192 early weaned steers of known genetics (≥¾ Simmental breeding) to test the efficacy of using GeneSTAR MARB test as a sorting and management tool. Animals used in this trial were managed according to the guidelines recommended in the *Guide for the Care and Use of Agriculture Animals in Agriculture Research and Teaching* (Consortium, 1988). Experimental protocols were submitted and approved by the Institutional Animal Care and Use Committee. Calves were a result of AI matings between registered Simmental sires (n = 20) and dams. Cows were managed at the Orr Beef Research Center (Baylis, IL).

EPD

The American Simmental Association (Bozeman, MT) provided sire and dam EPD for growth and carcass EPD such as yearling weight, MARB, percent retail cuts, and carcass weight. These values allowed EPD calculations to be made for each steer via Herd Handler (American Simmental Association, Bozeman, MT). Because EPD are constantly changing as more information is collected, EPD values for each steer were last updated January 9, 2004 for yr 1 thru 4.

Management and Diets

Calves were weaned at 88.0 ± 1.1 d and immediately adapted to a high-concentrate diet (Table 1) for 84.5 ± 0.4 d before entering the feedlot. Steers were shipped to Illinois State University Research Farm located in Normal, Illinois, and randomly allotted to 1 of 12 pens (4 head per pen) so that pen starting weights were similar. Cattle were individually fed using the Calan electronic gate system (American Calan, Northwood, NH). Steers were subsequently fed a 90% concentrate finishing diet (Table 2) balanced to provide 15.5% CP, 0.57% Ca, and 0.38% P. Calves were implanted with Synovex C (100 mg of progesterone and 10 mg of estradiol benzoate, Fort Dodge Animal Health, Fort Dodge, IA) at weaning followed by Synovex S (200 mg of progesterone and 20 mg of estradiol benzoate, Fort Dodge Animal Health) and then Revalor S (120 mg of trenbolone acetate, 24 mg of estradiol, Intervet, Inc., Millsboro, DE) approximately 120 d before slaughter. Cattle were fed for 249.7 ± 0.7 d and slaughtered at 423.3 ± 1.4 d of age.

Performance Analysis

Animal weights were taken every 28 d throughout the finishing period. Dry matter intake and orts were recorded on a daily basis. Gain and feed efficiency (expressed as G:F) were calculated based on carcass-adjusted final weights. Adjusted final weight was calculated by dividing HCW by the average yearly dressing percent. In yr 3, 1 steer was removed from trial as a result of illness. In yr 4, 2 steers died during the feeding period, and 1 steer was slaughtered early because of injury. These contributed to missing observations in the data set.

Carcass Data Analysis

Steers were slaughtered at a commercial processing facility. Steers were stunned via captive bolt pistol and exsanguinated. Carcass weights were taken on the day of harvest. After carcasses had hung at –4°C for 24 h, chromatography paper was used to make an image of the *longissimus dorsi* muscle for each carcass, and grid measurements were taken for the ribeye area. Measurements were made for backfat, and estimates were reported for kidney, pelvic, and heart fat percentages and MARB scores (**MS**) by trained university personnel. Quality grade was established based on subjective MS both by University of Illinois and USDA graders. Yield grades were calculated using the formula reported by Taylor (1994).

Longissimus dorsi Samples

Thin (0.25 cm) slices of the *longissimus dorsi* muscle were removed from the left side of each steer at the 12th–13th rib interface to chemically determine IMF percentage. Samples were stored at –20°C until chemical extraction was completed. Subcutaneous fat surrounding the muscle was removed before homogenization. Ten-gram duplicate samples were dried and repeatedly washed with chloroform:methanol in accordance with the procedures of Riss et al. (1983). Extraction values were used to verify grader-assessed MS as described by Brackebush et al. (1991).

DNA Analysis

Blood (yr 1 and 2) and hair (yr 3 and 4) DNA samples were tested by Genetic Solutions/Bovigen Pty Ltd (Australia) in conjunction with Frontier Beef Systems, LLC (Louisville, CO) for GeneSTAR MARB analysis. The DNA was evaluated for single nucleotide polymorphisms on the TG5 as previously described by Barendse et al. (2001). One hundred seventy-five of the 189 cattle submitted were clearly designated 0-STAR, 1-STAR, or 2-STAR based on the allele types (composition of the C to T polymorphism on the TG5 allele; genotype CC, CT, and TT were identified as 0-STAR, 1-STAR, or 2-STAR, respectively). This marker group was sired by 18 sires.

Statistical Analysis

Differences among means for performance, carcass, and laboratory parameters for the GeneSTAR MARB marker allele types were evaluated using the MIXED procedure of SAS (2000); individual animal was the experimental unit. Dependent variables of yearling weight; MARB; percent retail cuts; carcass weight; adjusted final weight; DMI; ADG; G:F; HCW; backfat; MS; ribeye area; kidney, pelvic, and heart fat; IMF percentage; University of Illinois grader-assessed quality grade, and University of Illinois grader-assessed yield grade were tested against the fixed effects of year and GeneSTAR. Linear and quadratic contrasts were made for GeneSTAR MARB test for dependent variables. Differences in percent low Choice and average Choice or better among allele types were separated using the chi-squared analysis of GENMOD (SAS, 2000). Simple correlation coefficients were calculated using PROC CORR between treatment and dependent variables (SAS, 2000).

RESULTS AND DISCUSSION

Means, standard deviations, and ranges for EPD, performance, and carcass parameters are given in Table 3. The steer population was near the breed average (American Simmental Association, 2004) for growth and carcass EPD with the exception of carcass weight. Eighty-five percent of the early weaned Simmental steers graded low Choice or better, whereas the breed average in the American Simmental Association carcass merit database is 55% (≥75% steers and heifers combined; M. Ropp, 2004, personal communication). At the same time, this population is only slightly above the breed average for yield grade (2.85 vs. 2.50), partially because of heavy carcass weights. This result demonstrates that this population consisted of steers that deposited IMF at a greater rate than the average of the breed, but still maintained a similar backfat.

The relationships among GeneSTAR, EPD, performance, and carcass parameters are given in Table 4. Correlations for these factors are shown on Table 5. Allele frequencies were normally distributed among 0-STAR, 1-STAR, and 2-STAR populations at 26.9, 54.3, and 19.4%, respectively (Table 4). This study had a greater percentage of 2-STAR cattle than studies reported by Genetic Solutions (2002a; 65, 29, and 6%, respectfully), indicating that our data set had a more even distribution. Alternatively, Genetic Solutions (2003) reported that purebred Japanese Waygu steers had a greater proportion of 2-STAR cattle (39%), which is indicative of the breed's inherent genetic predisposition to marble.

EPD

There were no differences ($P > 0.10$) among allele types for MARB (Table 4) and no correlation ($P > 0.10$) between the GeneSTAR MARB marker and MARB (Table 5). This result might have been due to the fact that MARB is polygenic, and the GeneSTAR MARB test only accounts for one gene polymorphism (Genetic Solutions, 2003). Conversely, there was still a correlation ($P < 0.001$) between MARB EPD and MS (r = 0.44) and IMF percentage (0.27; Table 5). Therefore, early weaning management did not mask all genes associated with IMF deposition but might have affected the expression of the specific polymorphism associated with the GeneSTAR MARB marker. When utilizing early weaning management, MARB EPD can be used as an accurate predictor for MARB deposition and to sort cattle for grid-marketing systems.

Marbling is highly heritable ($h^2 = 0.38$; Dikeman et al., 2001); thus, genetic tools such as DNA markers and EPD can facilitate rapid genetic improvement. Genetic Solutions (2003) noted that by utilizing the GeneSTAR MARB marker in conjunction with MARB EPD cattlemen could better select for greater IMF. Previous research showed a positive relationship between MARB EPD and IMF deposition, indicating that it is a useful

Table 3. Means, SD, and minimum and maximum values of EPD and performance and carcass parameters

Item	Mean	SD	Minimum	Maximum
EPD[1]				
Yearling weight EPD	59.74	14.81	17.80	88.00
Marbling EPD	0.10	0.09	–0.15	0.34
Percent retail cuts EPD	–0.03	0.14	–0.41	0.32
Carcass weight EPD	10.23	11.84	–22.20	34.30
Performance parameter				
Birth weight, kg	44.1	6.4	27.3	66.8
Age at weaning, d	88.0	15.6	41.0	126.0
Weaning weight, kg	127.3	20.2	72.7	188.6
Starting weight, kg	246.3	30.7	145.5	316.4
Final weight, kg	657.4	57.5	507.5	759.1
Days on feed, d	249.7	9.6	229.0	259.0
DMI, kg/d	8.82	1.23	6.13	11.60
ADG, kg/d	1.64	0.17	0.98	2.10
G:F	0.193	0.023	0.147	0.253
Carcass parameter				
Age at harvest, d	423.3	19.7	360.0	463.0
HCW, kg	407.9	38.3	296.3	509.1
12th-13th rib fat, cm	1.11	0.35	0.38	2.79
Ribeye area, cm^2	93.89	8.79	72.26	116.80
Kidney, pelvic, and heart fat, %	2.53	0.62	1.00	4.00
University of Illinois grader-assessed yield grade	2.85	0.64	1.35	5.38
Marbling score[2]	581.4	93.4	380.0	850.0
University of Illinois grader-assessed quality grade[3]	5.33	0.99	3.00	8.00
Intramuscular fat, %	5.56	1.65	2.06	11.08

[1]Provided by the American Simmental Association database on January 9, 2004.
[2]400 = Slight^0; 500 = Small^0; 600 = Modest^0.
[3]4 = Select; 5 = low Choice; 6 = average Choice.

indicator of the genetic propensity to marble (Gwartney et al., 1996; Vieselmeyer et al., 1996). More specifically, Vieselmeyer et al. (1996) noted that Angus cattle designated with high MARB EPD graded better ($P < 0.01$) than contemporaries identified as possessing low MARB EPD. Gwartney et al. (1996) noted that by selecting cattle with increased MARB, greater IMF deposition could be achieved without also selecting for increased subcutaneous fat deposition. Conversely, data from the current experiment suggested that there was no relationship ($P > 0.10$) between MARB EPD and backfat (r = –0.04) or yield grade (r = 0.09; Table 5).

There was a linear increase ($P < 0.05$) among the 3 allele types for carcass (Table 4) and a moderate correlation ($P < 0.05$) between the 2 traits (r = 0.27; Table 5). It is unclear why there was an increase in growth and carcass weight potential in relation to the MARB marker. Analogously, there was a relationship ($P < 0.01$) between carcass weight and MARB EPD (r = 0.63), suggesting an association with all genes associated with MARB.

Furthermore, there was a linear decrease ($P < 0.05$) in percent retail cuts EPD among the 3 genetic populations (Table 4). There tended ($P < 0.10$) to be a negative correlation (r = –0.17) between the EPD and the DNA marker (Table 5). These data suggest that selecting for MARB using the GeneSTAR MARB test may reduce retail yield. Within population, there were no relationships ($P > 0.10$) between percent retail cuts EPD and backfat (r = –0.07) and University of Illinois grader-assessed yield grade (r = –0.07; Table 5), demonstrating that the percent retail cuts EPD did not predict subcutaneous fat deposition or slaughtered cutability. Similarly, GeneSTAR MARB had no correlation to University of Illinois grader-assessed yield grade (r = –0.07) or BF (r = –0.09; Table 5). These data suggest that when using an early weaning management system, selecting for either percent retail cuts or the DNA MARB test will have no effect on slaughtered yield grade or backfat. Wertz et al. (2001) noted that early weaned cattle fed a high-concentrate diet had lower numerical yield grades than traditionally weaned cattle at the same MARB level; thus, this management system might have contributed to the nonsignificant ($P > 0.10$) relationship between percent retail cuts and final red meat yield.

Genetic markers may be used by cattle breed associations, resulting in DNA-adjusted EPD (Thallman, 2004), and may be potentially incorporated in the National Cattle Evaluation (Notter, 2004). The DNA markers may be valuable to adjust EPD according to their genotype for increased accuracies. Notter (2004) suggested that the impact of DNA markers can contribute to the additive genetic variation of the trait of inter-

Table 4. The relationship between GeneSTAR marker analysis[1] and EPD, performance, and carcass estimates

Item	0-STAR	1-STAR	2-STAR	SEM	*P*-value Linear	*P*-value Quadratic
n[2]	47	95	33	—	—	—
EPD[3]						
Yearling weight EPD	58.56	59.50	63.27	2.01	0.46	0.33
Marbling EPD	0.10	0.11	0.12	0.02	0.57	0.39
Percent retail cuts EPD	–0.02	–0.03	–0.09	0.03	0.04	0.25
Carcass weight EPD	7.87	11.84	15.92	1.92	0.04	0.69
Performance parameter						
Final weight, kg	663.4	658.2	645.4	10.5	0.57	0.50
DMI, kg/d	8.87	8.78	8.82	0.13	0.14	0.89
ADG, kg/d	1.64	1.64	1.62	0.03	0.83	0.61
G:F	0.187	0.190	0.186	0.003	0.17	0.41
Carcass parameter						
HCW, kg	412.1	408.9	401.0	6.5	0.57	0.50
12th–13th rib fat, cm	1.16	1.13	1.11	0.06	0.52	0.79
Ribeye area, cm^2	94.1	94.4	92.0	1.5	0.42	0.11
Kidney, pelvic, and heart fat, %	2.63	2.48	2.61	0.10	0.86	0.11
University of Illinois grader-assessed yield grade	2.95	2.82	2.90	0.11	0.96	0.04
Marbling score[4]	582.0	584.0	582.7	15.6	0.73	0.91
University of Illinois grader-assessed quality grade[5]	5.36	5.35	5.33	0.17	0.71	0.87
Intramuscular fat, %	5.73	5.58	5.59	0.29	0.72	0.90
Low Choice, %	82.98	87.37	90.91	—	0.40	0.11
Premium Choice, %[e]	42.55	44.21	30.30	—	0.53	0.93

[1]Least squares means. Designations 0-STAR, 1-STAR, or 2-STAR were based on the allele types (composition of the C to T polymorphism on the 5′ region of the thyroglobulin gene allele; genotype CC, CT, and TT were identified as 0-STAR, 1-STAR, or 2-STAR, respectively).
[2]Frequency of allele types tested by Genetic Solutions/Bovigen (Australia).
[3]Provided by the American Simmental Association database on January 9, 2004.
[4]400 = Slight^0; 500 = Small^0; 600 = Modest^0.
[5]4 = Select; 5 = Choice$^-$; 6 = Choice^0.

Table 5. Simple correlation coefficients among carcass EPD,[1] GeneSTAR marbling marker,[2] and actual carcass parameters[3,4]

Item	MARB	PRC	CW	GS	HCW	BF	REA	KPH	MS	IMF%	UI YG	UI QG
YW	0.42	–0.02	0.59	0.13	0.32	–0.25	0.04	–0.01	0.07	–0.09	–0.12	0.06
MARB		–0.14	0.63	0.02	0.23	–0.04	0.00	–0.02	0.44	0.27	0.09	0.40
PRC			–0.55	–0.17	–0.01	–0.07	0.05	0.03	0.01	0.07	–0.07	0.01
CW				0.27	0.27	–0.10	0.01	0.01	0.13	–0.14	0.07	0.13
GS					–0.09	–0.09	–0.05	–0.01	0.01	0.01	–0.07	0.00
HCW						0.21	0.44	0.37	0.29	0.26	0.40	0.26
BF							–0.11	0.32	0.15	0.39	0.70	0.06
REA								0.32	0.11	–0.07	–0.38	0.03
KPH									0.21	0.10	0.38	0.05
MS										0.63	0.20	0.96
IMF%											0.23	0.63
UIYG												0.26

[1]Available from the American Simmental Association on January 9, 2004.
[2]Test performed by Genetic Solutions/Bovigen (Australia).
[3]YW = yearling weight EPD; MARB = marbling EPD; PRC = percent retail cuts EPD; CW = carcass weight EPD; GS = GeneSTAR marbling test; BF = backfat measured at the 12th rib; REA = ribeye area measured between the 12th and 13th ribs; KPH = kidney, pelvic, and heart fat percentage; MS = marbling score estimated by University of Illinois personnel; IMF% = chemically determined intramuscular fat percentage; UIYG = University of Illinois grader-calculated yield grade; UIQG = University of Illinois grader-estimated quality grade.
[4]For the null hypothesis that $|R| = 0$, $P < 0.10$ if $r > 0.19$, $P < 0.05$ if $r > 0.26$, $P < 0.01$ if $r > 0.44$, $P < 0.001$ if $r > 0.60$.

est. When utilizing early weaning management per se, GeneSTAR MARB marker was not an accurate predictor of IMF deposition even though MARB EPD did show a positive relationship ($P < 0.05$). This specific genetic marker might be a more valuable predictor in traditionally weaned scenarios or in a management system where cattle are early weaned but are subsequently fed a high-forage diet as opposed to a high-energy diet.

Performance

There were no differences ($P > 0.10$) among adjusted final weight, DMI, ADG, or G:F among the 3 genotypes (Table 4). This result differed slightly from the results of Barendse et al. (2001), where the TG5 genotype positively affected ($P < 0.001$) live weight gain. Previous research has not addressed the effect of the thyroglobulin gene marker on other performance parameters.

IMF

There were no differences ($P > 0.10$) in MS or IMF among 0-STAR, 1-STAR, and 2-STAR populations (Table 4). There was no correlation ($P > 0.10$) between GeneSTAR MARB and MS or IMF (Table 5). These results indicate the TG5 polymorphism had no effect on MARB deposition in early weaned steers. These results contradict work from Genetic Solutions (2003), who observed an increase ($P < 0.05$) in Japanese beef MARB score, according to the Japan Meat Grading Association, among full-blood Black Wagyu cattle having 0, 1, or 2 copies of the gene, respectively. Similarly, the DNA MARB marker was significantly associated with USDA MS for yearlings and fed calves of the Angus and Angus × Continental breeds (Genetic Solutions, 2002a). However, with Simmental steers, Genetic Solutions also reported no significant differences in MS (2002b).

There were no differences ($P > 0.10$) among the 3 allele types for University of Illinois grader-assessed quality grade percent low Choice or better or percent average Choice or better (Table 4). This result contrasts with preliminary research from Genetics Solutions (2002b), where the researchers noted a significant difference in the percent Choice vs. the percent Select. Additionally, Genetic Solutions (2003) reported 2-STAR Wagyu animals had 50% greater premium Choice carcasses when compared with the 0-STAR populations and had, on average, 14% greater MS.

Barendse et al. (2001) demonstrated that the TG5 gene polymorphism was associated with IMF deposition ($P < 0.05$). Burroughs et al. (1958) and Raun et al. (1960) also observed the TG5 polymorphism was related to the overall fattening of feedlot cattle. The TG5 gene coding affects the molecular stores of thyroid hormones triiodothyronine and thyroxine, which have been shown to affect adipocyte growth and differentiation both in vitro and in vivo (Beato, 1989; Ailhaud et al., 1992; Darimont et al., 1993). These hormones have also been associated with IMF deposition in Wagyu cattle (Mears et al., 2001).

There are several possibilities for why our study did not show a relationship between the TG5 polymorphism and MARB deposition. First, breed type might have affected the efficacy of the gene, as various cattle breeds may express genes differently or at different times in their physiological maturity. Notter (2004) reported that DNA markers are presumptively close to an associated function QTL sequence across the entire species, but evolutionary history suggests that the association may be different among breeds.

British breeds (e.g., Angus and Shorthorn) were used by Barendse et al. (2001), where differences ($P < 0.05$) were noted. Further, Angus and Angus-cross cattle demonstrated significant differences in MS and quality grade among the 3 GeneSTAR populations with work reported by Genetic Solutions (2002a). Furthermore, when using Japanese Black Wagyu steers, research has shown a linear increase ($P < 0.05$) in MS across the 0-STAR, 1-STAR, and 2-STAR populations (Genetic Solutions, 2003).

Alternatively, Genetic Solutions (2002b) reported no differences in MS among Simmental steers, which is similar to our results. In contrast, those researchers did note a significant relationship between percent Choice and percent Select, which was not observed ($P > 0.10$) in our experiment. We did observe a numeric increase in percent low Choice and better among the allele types; however, there were no differences ($P > 0.10$) among the marker populations for percent Premium Choice and better (Table 4).

Second, management could be a factor contributing to the nonsignificant relationship between the genetic marker and MARB deposition in our trial. The days spent on feed may determine how efficacious this DNA marker is for MARB deposition prediction. Research by Genetic Solutions (2002a) showed yearling steers entering the feed yard at 12 to 15 mo. of age that spent 122 to 146 d on feed had greater differences between the 0-STAR and 2-STAR populations than calves entering the feed yard at 10 to 12 mo. of age that spent 155 to 200 d on trial. Those researchers did note that the fed-calf population might not have been fed to a compositional end point for optimum gene expression. However, Barendse et al. (2001) reported that steers fed grain for 160 to 240 d had fewer differences in MARB with the polymorphism than a long-fed study of 300 d (Barendse, 1997), and the researchers hypothesized that this result might have been due to the fact that animals that were fed for a shorter period. In contrast, early weaned steers were fed a high-concentrate diet for a longer overall period (approximately 335 d) and had less variation.

Van Koevering et al. (1995) found a linear relationship ($P = 0.01$) between MS and percent Choice with increased days on feed. Myers et al. (1999b) reported a linear decrease ($P < 0.05$) in MS with fewer days on feed as weaning age increased. Early weaning management allows for more days on feed to permit optimum IMF deposition. These data suggest that when cattle have more time on a high-starch diet, the role of genetics may have less effect on IMF deposition. Previous research with early weaning management systems and creep feeding high-starch diets resulted in increased rates of MARB deposition (Faulkner et al., 1994; Myers et al., 1999a; Wertz et al., 2001). Prior (1983) concluded that the greater ruminal propionate from starch fermentation causes an increase in intramuscular adipogenesis. Wertz et al. (2002) reported that early weaned calves subsequently fed a high-concentrate diet had greater quality grades at any given backfat level than heifers that were early weaned and fed a high-forage diet before entering the feedlot. This type of management and nutrition combination may interact with the expression of the GeneSTAR MARB marker.

Because our cattle were fed a starch-based diet for approximately 335 d, the thyroglobulin gene might not have impacted IMF deposition when compared with steers that were managed differently and spent fewer days on a high-energy diet in previous studies. To rebut this argument, Genetic Solutions (2003) fed Wagyu and Wagyu × Angus steers and heifers for 300 to 350 d and F1 and F2 Wagyu-cross steers and heifers for 527 d and reported a relationship ($P < 0.05$) between MS and the GeneSTAR MARB test. Those researchers did not note the unique feeding strategy used with the long-fed Japanese Black Wagyu breed. Wagyu are anomalous for their ability to marble and have been reported to have the highest frequency of 2-STAR animals when compared with Angus (Black and Red) and Shorthorn breeds (Genetic Solutions, 2003). Therefore, perhaps the breed's single trait selection for MARB has amplified the effects of the TG5 polymorphism compared with our Simmental steer population.

Third, Barendse et al. (2001) hypothesized why variation with the TG5 polymorphism exists. Those researchers noted that the DNA marker could be too far from the casual mutation, resulting in a lack of consistency. They suggested that this variability may partially explain the fact that this gene does not account for a large proportion of IMF deposition. Barendse et al. (2001) did conclude, however, that the TG5 polymorphism is either a causal mutation or is in close proximity to the causal mutation. To date, no research has shown whether the thyroglobulin gene directly affects MARB or if the gene mutations that control triiodothyronine and thyroxin affect IMF deposition. We concluded that in this early weaning management scenario, the thyroglobulin gene is not an accurate marker to estimate genetic propensity to MARB.

Alternative Carcass Parameters

There were no differences ($P > 0.10$) among allele types for carcass parameters (Table 4). GeneSTAR results had no association with HCW, backfat, ribeye area, or kidney, pelvic, and heart fat (Table 5). These data agree with previous research by Genetic Solutions (2002a, 2002b, 2003) and by Barendse et al. (2001). Brethour (1997) noted no relationship between MARB and backfat (r = 0.06), indicating that IMF and subcutaneous fat deposition are independent. We observed a slightly stronger association in our population (r = 0.15) but agree that backfat and MS appear to be controlled by different genes. Consequently, a relationship between the TG5 polymorphism and backfat or yield grade was not observed.

IMPLICATIONS

In the current beef economy, with increasing emphasis on individual carcass merit, more effective sorting can lead to increased efficiency and profits by marketing individual cattle into the grid system that best fits their composition. Cattlemen should evaluate all tools available through technology to increase efficiency and profits. However, the GeneSTAR marbling marker was not associated with intramuscular fat deposition in early weaned steers fed a high-concentrate diet. This polymorphism in the thyroglobulin gene was not associated with other carcass, performance parameters, or marbling expected progeny difference. Marbling expected progeny difference was positively correlated with intramuscular fat deposition and could be used as a valuable selection tool in this type of management program. Marbling expected progeny difference would be a more accurate predictor of marbling and quality grade than the GeneSTAR DNA marker in similarly managed early weaned Simmental steers.

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