Examining Marker-assisted Management as a Strategy in Precision Agriculture to Maximize Carcass Traits and Production Efficiencies in Beef Cattle

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The objective of this study is to assess how different implant strategies interact with the GALR2 genotype and influence carcass characteristics, production efficiencies and feeding behavior. The ultimate goal of this study is to aid in developing marker-assisted management strategies utilizing the GALR2 genotype to improve the profitability of crossbred finishing cattle. Our results show promising potential for the GALR2 SNP to be utilized as a marker-assisted management strategy in feedlot cattle, with further research necessary.

Summary

Crossbred Angus steers (n = 91) from the Central Grasslands Research Extension Center (Streeter, N.D.) were selected at weaning based on their genotype for the galanin receptor 2 (GALR2) single nucleotide polymorphism (SNP): GG (n = 19), TG (n = 37) and TT (n = 35). They then were brought to the Beef Cattle Research Complex (Fargo, N.D.), where they were assigned randomly to one of two implant strategies: conservative vs. aggressive using Revalor-S (Merck Animal Health, Summit, N.J.).

Insentec® Feeders were used to allow for feed intake and behavior data of individual steers to be captured using radio frequency ID tag technology. Feeding intake and behavior data are quantified using three categories: events, eating time and feed intake. Cattle were fed out to 166 or 201 days based on their initial body weight.

Cattle were slaughter at a commercial abattoir, where carcass data was collected and strip loins were collected for further meat quality analysis, which was done at the North Dakota State University Meat Lab.

Results of this study show an effect of the GALR2 genotype on dry-matter intake, with the GG and TG genotypes having increased intake, in comparison with TT. An effect of implant is present for average daily gain, hot carcass weight and back fat, with no adverse influence of genotype.

While this study provides novel insight on the influence of the GALR2 genotype and production efficiencies, more research is needed to determine how the GALR2 SNP could best be targeted for marker-assisted management strategies.

Introduction

Marker-assisted management can be defined a variety of ways. Specifically, in a feedlot setting, marker-assisted management is strategy often combining genetic information of a beef animal using a single nucleotide polymorphism (SNP) of interest with live animal evaluation. The goal of marker-assisted management is to generate decision making based on the genetic background of a beef animal specifically targeting an SNP of interest (Kolath, 2009).

An array of decisions can be made utilizing genetic information and current body conformation of the beef animal upon arrival at the feedlot. Days spent on feed, implant strategy and diet composition are all management decisions that can be influenced by genetic background information. Genetic markers do not directly influence profit, but rather they influence growth and carcass traits that determine profit (Thompson *et al*., 2014).

Galanin has three identified receptors: galanin receptor 1 (GALR1), galanin receptor 2 (GALR2) and galanin receptor 3 (GALR3) (Chen *et al*., 1992). While each receptor is a G-protein coupled receptor, they differ in their response to signaling pathways activated by the galanin peptide.

Using synthetic ligands of the three galanin receptors, researchers discovered the binding of GALR2 leads to increased food consumption in mice (Saar, 2011). The Galanin receptor 2 (GALR2) is associated with feeding behavior, insulin release and growth hormone secretion (Smith *et al*., 1997; Waters and Krause, 2000).

An SNP is the most common type of genetic variation, representing a variation of a nucleotide. In the case of GALR2, this is the mutation of a G in place of a T allele. An SNP identified as *GALR2*c.-199T>G is associated with carcass traits in beef cattle, where a dominant effect of the T allele is exhibited by increasing marbling and rib-eye area (Duncombe, 2016). Because of the previous findings associated with increased feed intake and improved carcass performance, we hypothesized examining the GALR2 genotype as a potential target for maximizing carcass traits and production efficiencies in crossbred Angus cattle.

Procedures

All animal procedures were conducted in accordance with the rules of the Institutional Animal Care and Use Committee at North Dakota State University (Protocol #A18062). Procedures for this study were conducted at the NDSU Central Grasslands Research Extension Center (CGREC) and NDSU Beef Cattle Research Complex (BCRC).

Materials and Methods

Cattle from the crossbred Angus herd at the Central Grasslands Research Extension Center were genotyped for the GALR2 SNP as determined by blood samples collected prior to weaning. At weaning, steers were selected for the study based on weaning weight.

Ninety-three steers were transported to the North Dakota State University Beef Cattle Research Complex. Two steers were taken off the study, resulting in the remaining number of steers for each genotype as GG (n = 19), TG (n = 37) and TT (n = 35).

Upon arrival, steers were assigned randomly to an implant strategy of: 1) Conservative, one implant of Revalor-S (Merck Animal Health, Summit, N.J.) on day 77, or 2) Aggressive, implant of Revalor-S on day 0 and re-implanted on day 77, with even distribution across genotypes. Two-day weights were recorded to collect initial body weight as well as finishing weight of all steers in the study.

Once cattle arrived at the BCRC, they were given two weeks to acclimate to the automated feeders before beginning the study. Cattle began on the study with an average body weight of 254.8 kilograms (kg) ($\pm$80.44 kg) and were fed a 90% concentrate standard finishing ration consisting of 14.3% crude protein, shown in Table 1, proceeding a four-phase step-up diet.

Steers were fed using the Insentec ® Feeders (Hokofarm Group B.V., Netherlands). The Insentec ® Feeders allowed for feed intake and behavior data of individual steers to be captured using radio frequency ID tag technology.

Feeding intake and behavior data are quantified using three categories: events, eating time and feed intake. The categories are further defined as described by Montanholi *et al*. (2010) and Swanson *et al*. (2014). Events include number of visits per day and number of meals per day; eating time as minutes per visit and minutes per meal; and feed intake as kg per visit, kg per meal and kg per minute.

Body weight and blood samples were collected every 28 days of the study to track average daily gain and hormone and metabolite activity throughout the study. Cattle were fed to 166 or 201 days based on initial body weight, with average finishing weights of 595.5 kg and 598.9 kg, respectively.

Table 1. Finishing Diet.

Ingredient	% Inclusion (dry-matter basis)
Corn	60
Dried distillers' grain plus soluble	20
Silage	10
Hay	5
Premix	5

Table 1 contains the ingredients and their percentage inclusion in the diet on a dry-matter basis. The diet was a 90% concentrate, 14.3% crude protein finishing diet.

Cattle then were transported to a commercial abattoir for slaughter. Hot carcass weight was collected at slaughter while quality grade, yield grade and marbling score were collected 24 hours postmortem. Strip loins were collected from the left side of each carcass and brought back to NDSU for further meat quality analysis.

The strip loins were aged for 14 days following slaughter and stored in the carcass cooler (2.5 C) at the NDSU meat lab. Following aging, strip loins were defaced from the lateral side and 2.54-centimeter (cm) steaks were collected for color display and shear force, while 1.27 cm steaks were collected for ether extract values and western blot analysis, respectively. Additionally, a 50-gram (g) meat cube was collected from the lateral and medial sides of the strip loin for drip loss analysis, and pH was collected from the medial side of each strip loin.

Statistical Analysis

All statistical analyses were performed using the MIXED procedure in SAS (version 9.4, 2017) as a 2×3 factorial design where steers were blocked by initial body weight. The model included the interaction of genotype × implant with slaughter date considered as a random effect and significance was set at $P \leq 0.05$.

Results and Discussion

Production Efficiencies and Serum Metabolites

Dry-matter intake was influenced by genotype ($P = 0.05$), with GG and TG steers consuming greater intake levels than TT steers, as illustrated in Figure 1. Average daily gain of the steers was not influenced by genotype; however, an effect of implant was present, with steers assigned to the aggressive (2×) implant strategy gaining 0.03 kg/day greater than steers with the conservative (1×) implant strategy ($P < 0.05$) as depicted in Figure 2.

However, the feed-to-gain ratio was not affected by genotype, implant or the interaction of genotype by implant. Day by implant had a direct effect on serum urea nitrogen and serum glucose levels. Blood serum levels of urea nitrogen differed by implant strategy on day 56, with the conservative strategy having elevated urea nitrogen levels ($P < 0.05$).

Carcass Characteristics and Meat Quality Analysis

Hot carcass weight and back fat were affected directly by implant strategy, with steers receiving the aggressive strategy exhibiting heavier hot carcass weights and increased back fat ($P < 0.05$). Rib-eye area, kidney pelvic and heart fat, yield grade and quality grade were not affected by genotype by implant interaction or the main effect of genotype or implant. Carcass characteristics are displayed in Table 2.

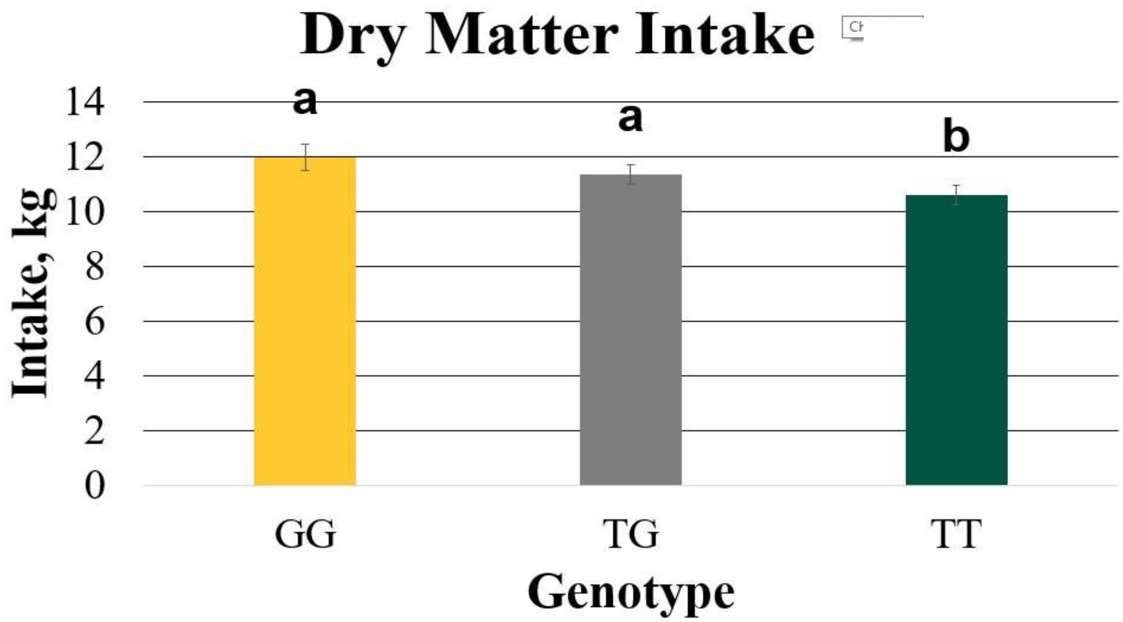

Figure 1. Displays dry-matter intake in kilograms for a daily average for the finishing period. Genotypes significantly different from one another depict a different superscript ($P = 0.05$).

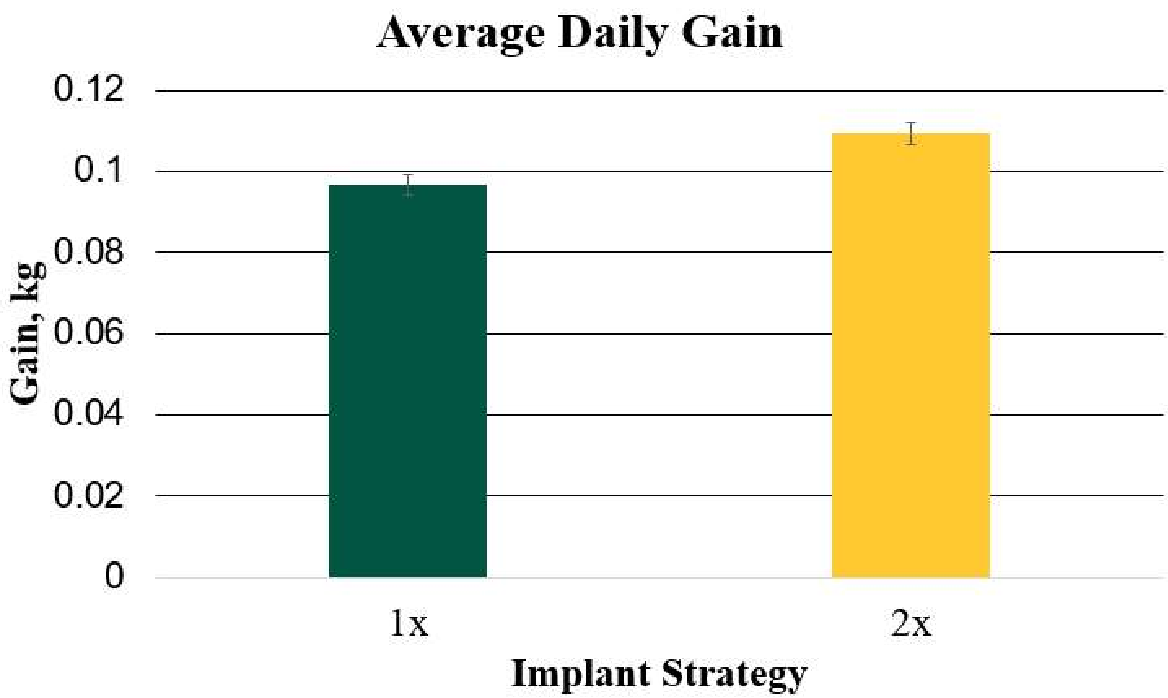

Figure 2. Average daily gain of steers assigned to the two different implant strategies of Revalor-S: conservative (1×) vs. aggressive (2×). ($P < 0.05$).

Table 2. Carcass Characteristics

Item[1]	Conservative (1×) GG	TG	TT	Aggressive (2×) GG	TG	TT	SEM Geno.	Imp.	Geno. × Imp.	P-value Geno.	Imp.	Geno × Imp
HCW, kg	356	358	356	363	373	375	3.43	3.15	4.85	0.47	< 0.05*	0.61
BF, cm	0.58	0.60	0.55	0.60	0.65	0.64	0.01	0.01	0.02	0.40	< 0.05*	0.47
REA, cm^2	75.4	73.2	73.5	75.4	76.3	78.3	0.20	0.18	0.28	0.90	0.12	0.53
KPH%	2.01	1.97	1.98	2.02	2.00	1.93	0.03	0.02	0.04	0.54	0.92	0.58
YG	3.3	3.5	3.4	3.5	3.6	3.6	0.08	0.07	0.12	0.81	0.08	0.91
MARB	490	400	430	420	420	420	13.48	12.3	18.89	0.18	0.23	0.12

[1]Table 2 lists carcass characteristics collected at the commercial abattoir and their SEMs and *P*-values. HCW = hot carcass weight, BF = back fat, REA = rib-eye area, KPH % = kidney, pelvic and heart fat percentage, YG = yield grade, MARB = marbling degree, SEM = standard error of the mean. All significant *P*-values are denoted with an asterisk (*).

Cook loss was influenced by the interaction of genotype by implant strategy with the GG one-implant steers having greater cook loss in comparison with all other steers ($P < 0.05$). Shear force was influenced by the interaction of genotype by implant strategy ($P < 0.05$), as illustrated by Figure 3. The pH and drip loss of the strip loins was not affected by the genotype by implant strategy interaction or main effects of genotype and implant strategy.

The results of this study show an effect of genotype on intake, as shown by increased intake for steers with the GG genotype, with no adverse effects on the improved efficiencies of using implants or on meat quality. Steers assigned to the aggressive implant strategy exhibited heavier carcasses with increased back fat; however, steers assigned to the conservative implant strategy resulted in more tender steaks, as supported by decreased Warner-Bratzler shear force values.

These results indicate the *GALR2*c.-199T>G SNP may serve as a good candidate for developing marker-assisted management strategies in feedlot cattle. However, more research needs to be conducted.

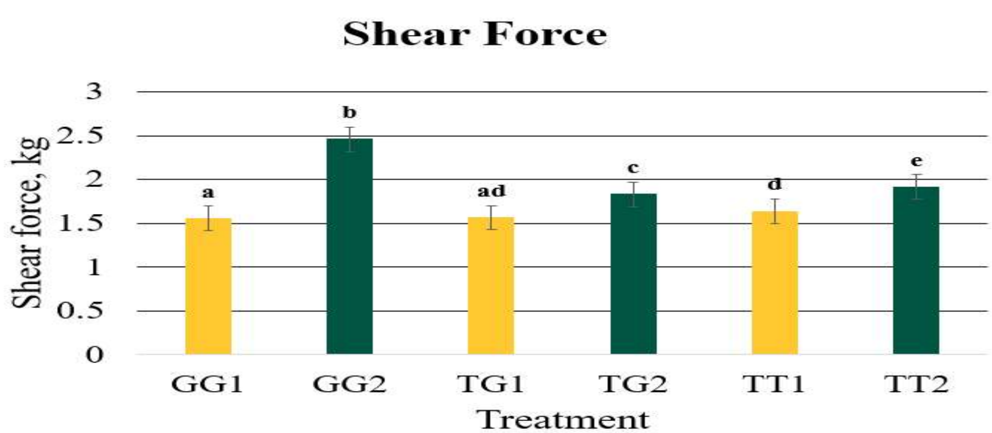

Figure 3. Shear force of longissimus dorsi cores using the Warner-Bratzler protocol showing shear force values for the interaction of genotype × implant when taking an average value of six cores per steak from the longissimus muscle ($P < 0.05$).

Acknowledgments

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