

Pleiotropic effects on carcass and meat quality traits in crossbred beef cattle

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Abstract

Our objective was to identify genomic regions with pleiotropic effects on carcass and meat quality traits in a multibreed Angus-Brahman population. Data included phenotypes from 2,384 steers, of which 1,038 were genotyped. Single-trait genome-wide association studies were first used to investigate the relevance of additive genetic effects. A second analysis was performed to capture genomic regions with pure direct effects on each trait, removing regions with indirect effects. Four pleiotropic (BTA5, BTA7 and BTA18) and two suggestive pleiotropic regions (BTA10 and BTA19) were identified. Candidate genes encode key players in cell growth, muscle development, lipid metabolism and fat deposition. Functional analysis revealed GO terms directly related to carcass quality, meat quality, and tenderness in beef cattle, including calcium-related processes, and modulation of cell-cell adhesion. These results contribute with novel information about the complex genetic architecture of carcass and meat quality traits in crossbred beef cattle.

Introduction

To attenuate the impacts of tropical and subtropical conditions on growth rate and reproductive performance of Taurine (*Bos taurus taurus*) beef breeds, producers use crossbreeding between European Taurine and Zebu (*Bos taurus indicus*) breeds as a strategy to enhance beef production. In subtropical areas of the United States, Angus-Brahman crosses are preferred for beef production over other Taurine-Zebu combinations.

While carcass quality is the primary factor determining the value of a carcass in the beef industry supply chain, consumers evaluate beef products at purchase time based on visual quality and at consumption time based on sensory quality. These traits are of even greater importance in crossbred cattle used in subtropical and tropical regions for their superior adaptability because they tend to underperform compared to their purebred counterparts.

Many of these traits are challenging and expensive to measure and unavailable until late in life or after the animal is harvested, hence unrealistic to improve through traditional phenotypic selection, but perfect candidates for genomic selection. Before genomic selection can be implemented in crossbred populations, it is important to explore if pleiotropic effects exist between carcass, visual meat quality and sensory meat quality traits. Therefore, our objective was to identify genomic regions with pleiotropic effects on carcass and meat quality traits in a multibreed Angus–Brahman population.

Materials & Methods

The cattle population for this study consisted of 2,384 steers from the University of Florida multibreed Angus-Brahman herd born between 1989 and 2018 and raised under very similar management system throughout the years. The breed composition of animals in this unique multibreed population ranged from 100% Angus to 100% Brahman, including all crosses in between them. Phenotypes for marbling (MARB), ribeye area (REA), tenderness (TEND), juiciness (JUIC), color, texture (TEXT) and firmness (FIRM) were analyzed. Genotyping was

carried out on 1,038 of the 2,384 animals using the Bovine GGP F250 array, which contains 221,115 SNP. A total of 125,042 autosomal SNP markers with MAF>0.01 and call rate higher than 90% were included in the genomic analysis.

Variance components, heritabilities, additive genetic correlations, and phenotypic correlations were estimated using single-trait and two-trait single-step genomic best linear unbiased prediction (ssGBLUP). Animal mixed models included the direct additive genetic and residual as random effects, year of birth as a class effect, and age at slaughter as a covariate, except for TEND and FLAV where age at slaughter was not significant. Computations were performed with the *airemlf90* package from the BLUPF90 (Miszta et al., 2009).

Genome-wide scan for pleiotropic effects. Single-trait genome-wide association studies were carried out using the weighted ssGBLUP (WssGBLUP; Wang et al., 2012) procedure to scan for genomic regions with pleiotropic effects on carcass and meat quality traits. First, the relevance of direct additive genetic effects was investigated fitting all fixed and random effects from the variance component models. Second, conditional genome scan fitting all other traits as covariates in the aforementioned model allowed correcting for indirect effects and capturing genomic regions with pure direct effects on the trait under analysis. Genomic windows explaining more than 1% of direct additive genetic variance were considered associated with the analysed trait. Common genomic regions involving overlapping windows associated with two or more phenotypes in both analyses were considered as pleiotropic regions. Additionally, common regions from overlapping windows explaining more than 1% of the direct additive genetic variance for one trait and between 0.9 and 1% of the direct additive genetic variance for another trait were considered as suggestive pleiotropic regions.

Functional analysis. Top 20 SNP markers with the largest absolute estimated effect across two or more traits within each pleiotropic region were used to identify genes with pleiotropic effects. A SNP marker was assigned to a particular gene if it was located within the gene. Genes with a known function directly or indirectly associated with carcass and meat quality traits were defined as candidate pleiotropic genes. Following, GO and pathway enrichment and clustering analyses of all annotated genes within pleiotropic regions were performed.

Results

Estimates of heritabilities, phenotypic and genetic correlations between analyzed traits are presented in Table 1. Heritability estimates for MARB, REA and TEND were moderate, ranging from 0.44 to 0.53, and low estimates were observed for the other sensory panel and visual meat quality traits (0.12-0.19). Ribeye area had consistently the lowest phenotypic correlations with all other traits (-0.01 to 0.10). Positive moderate phenotypic correlations existed between MARB and TEND (0.32), MARB and JUIC (0.32), TEND and JUIC (0.51), and JUIC and COLOR (0.36). Negative moderate phenotypic correlations were estimated between MARB and FIRM (-0.37) and JUIC and FIRM (-0.33). High and favorable additive genetic correlations was observed between MARB and JUIC (0.66) and MARB and FIRM (-0.38), TEND and JUIC (0.64) and TEND and TEXT (-0.53).

The WssGBLUP analyses correcting for indirect effects identified a total of 3,460 non-overlapping 1-Mb genomic windows for MARB, 3,083 for REA, 3,218 for TEND, 3,557 for JUIC, 3,502 for COLOR, 3,315 for TEXT, and 3,341 for FIRM. Out of these, 4, 8, 5, 7, 6, 2, and 5 windows explained more than 1% of the direct additive genetic variance for MARB, REA, TEND, JUIC, COLOR, TEXT, and FIRM, respectively. Four pleiotropic genomic regions and two suggestive pleiotropic regions were identified. The first pleiotropic region on BTA5 (26.7–27.5 Mb) was significantly associated with REA (2.68%) and MARB (1.27%),

while the second region (56.2–56.9 Mb) explained a high proportion of the direct additive genetic variance in REA (4.78%), TEND (2.45%), MARB (2.09%), TEXT (1.55%) and FIRM (1.34%). One genomic region on BTA7 (51.5–52.5 Mb) had effect on MARB (2.24%), TEND (1.63%), and TEXT (1.36%). The genomic region between 61.9 and 62.5 Mb on BTA18 accounted for 2.17 and 1.10% of the genetic variance for COLOR and TEND, respectively. A suggestive pleiotropic region on BTA10 (76.2–77.2 Mb) explained 1.04 and 0.99% of the genetic variance for JUIC and MARB. The suggestive pleiotropic region on BTA19 (27.0–28.0 Mb) explained 1.12 and 0.96% of the genetic variance for TEND and TEXT.

Table 1. Heritabilities (h^2 , diagonal), phenotypic (above diagonal) and direct additive genetic (cor, below diagonal) correlations between carcass and meat quality traits in a multibreed Angus-Brahman population.

Trait	MARB	REA	TEND	JUIC	COLOR	TEXT	FIRM
MARB	0.49	0.19	0.32	0.32	0.03	-0.22	-0.37
REA	-0.03	0.53	0.10	-0.03	0	-0.01	0.04
TEND	0.21	0	0.44	0.51	0.16	-0.08	-0.17
JUIC	0.66	-0.15	0.64	0.15	0.36	-0.01	-0.33
COLOR	-0.19	0.02	0	-0.54	0.15	0.23	-0.19
TEXT	-0.30	0.24	-0.53	-0.99	0.02	0.12	0.16
FIRM	-0.38	0.24	-0.16	-0.32	-0.22	-0.24	0.19

Standard error (SE): $0.04 < SE_{h^2} < 0.07$ and $0.06 < SE_{cor} < 0.5$

These pleiotropic genomic regions contained about 260 genes with effect across two or more traits. Two candidate genes were identified in the first pleiotropic region on BTA5, seven in the second region on BTA5, one gene in the pleiotropic window on BTA7, and two genes in the pleiotropic region on BTA18. In addition, two genes were mapped in the suggestive pleiotropic region of BTA10, and the region on BTA19 contain four candidate genes. Overrepresented terms for GO Biological Processes within pleiotropic regions included “Regulation of Apoptotic Process”, “Regulation of Cell Proliferation”, “Linoleic Acid Metabolic Process”, and “Cell Adhesion via Plasma Membrane Adhesion Molecules”. Moreover, overrepresented terms for GO Molecular Functions included “Iron Ion Binding”, “Calcium Ion Binding”, “Steroid Hormone Receptor Activity”, “DNA Binding”, “Translation Initiation Factor Activity”, and “Transcription Factor Activity”.

Discussion

Heritability estimates for carcass and meat quality traits in the multibreed Angus–Brahman population were generally consistent with values reported in the literature (Mateescu et al., 2014). Examination of direct additive genetic correlations between traits in this study is important to understand the challenges and limitations that could result from the inclusion of any of these traits in selection schemes. The moderate favorable direct additive genetic correlation observed between MARB and TEND was lower than other estimates of 0.40 (Reverter et al., 2003) and 0.61 (Wheeler et al., 2010), but comparable to estimates for purebred Brahman (Riley et al., 2003), reinforcing the long-held belief of a unique fat-tenderness relationship in *B. t. indicus* versus *B. t. taurus* cattle.

The two candidate genes (*CSAD* and *TNS2*) in the first pleiotropic region on BTA5 are directly involved in muscle physiology and lipid metabolism (Wen et al., 2019; Ishii et al., 2013). The second BTA5 region is of particular importance because of its pleiotropic effects

on most of the traits under investigation. This region harbors three candidate genes (*LRPI*, *MYOIA*, *NACA*) involved in muscle development, myoblast proliferation, and lipid metabolism (Dato & Chiabrand, 2018; Lv et al., 2019, Berger et al., 2012). Besides the obvious effect on MARB and REA, these genes could also affect TEND, TEXT and FIRM given the impact of muscle fiber diameter and density on these traits (Pearson, 1990, Lv et al., 2019). The region on BTA7 contains *Protocadherin Beta 1 (PCDHBI)*, which may directly impact marbling, tenderness, and texture. Cadherins are structural proteins that play important roles in cell adhesion and differentiation in several bovine tissues (Martignani et al., 2020), thus could be involved in processes that lead to less tender and visually coarser meat. The suggestive pleiotropic region on BTA10 harbors *SYNE2*, and obvious candidate gene due to its possible role in proteolysis and cell compartmentalization (Zhang et al., 2007).

Many of the biological pathways enriched within these regions were previously reported to be important for carcass quality, meat quality, and tenderness in beef cattle (Leal-Gutiérrez et al., 2019). Numerous genes identified in pleiotropic regions are involved in calcium-related processes such as calcium ion binding, calcium channel, and calcium channel regulator. It was anticipated that calcium and potassium play a major role in meat tenderness because of their contribution to the proteolytic system responsible for muscle contraction and postmortem tenderization. Taken together, our results contribute with novel information on the complex architecture of direct additive genetic correlation between carcass and meat quality traits in crossbred beef cattle.

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