Genome Scan for Beef Tenderness in an Angus-Brahman Crossbred Population in Florida

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Synopsis
Potential chromosomal regions containing 22 genes could explain phenotypic variation in traits related to tenderness in Angus-Brahman steers.

Summary
Consumers develop perceptions that will directly contribute to subsequent market demand for beef; however, inconsistencies in meat tenderness have been widely reported. Genetic markers have been used as the most suitable strategy to uncover genomic regions able to explain the phenotypic variability present in meat quality. One steak from the longissimus dorsi muscle of 673 steers was used to determine tenderness by Warner-Bratzler shear force and 496 steaks were used in a trained sensory panel to assess tenderness and connective tissue amount. A total number of 22 genes were determine as potential chromosomal regions able to explain phenotypic variation in traits related to tenderness in the present population.

Introduction
Meat quality is determined by multiple factors, including tenderness, water-holding capacity, color, nutritional value and safety, and importance of these traits varies depending on both the type of product and the consumer profile (Koohmaraie & Geesink, 2006). Tenderness has been established as the most important quality trait in beef, and it depends on the amount of connective tissue, myofibrillar protein degradation (Houbak, et al., 2008) and intramuscular fat content. In a few seconds, a consumer develops perceptions that will directly contribute to subsequent market demand for beef (Harper, 1999), but a big problem of inconsistent meat tenderness has been reported, and this inconsistency must be a top priority of the beef cattle industry (Mohammad Koohmaraie, 1996). This requires a greater understanding of the processes that affect meat tenderness and the adoption of such information by the beef cattle industry (Mohammad Koohmaraie, 1996). The assessment of meat quality by trained panels or even physical measures is costly, and direct selection on sensory tests is not feasible (Renand, et al., 2001). Accordingly, it is important to find biological components related to sensory attributes which are easy to measure and sufficiently heritable to be selected for (Renand et al., 2001), because the consumer dissatisfaction will be addressed only when the problem of unacceptable variation in meat tenderness is solved (Mohammad Koohmaraie, 1996). Genetic markers such as single nucleotide polymorphisms (SNPs) have been used as the most suitable strategy to uncover genomic regions able to explain the phenotypic variability in traits like meat quality. The objective of this study was to perform a whole genome scan (WGS) to find genes and genomic regions associated with meat quality traits related to beef tenderness.

Materials and Methods
Population and phenotypic data
Animals used in the study belong to the multibreed Angus-Brahman herd from University of Florida (Elzo et al., 2012) born between 2007 and 2014. This population has animals with different percentages of Angus-Brahman blood. When steers reached 0.5 in over the ribeye, they were transported to a commercial packing plant and harvested. The average slaughter weight was 1186 ± 721 lb at 17 ± 1.2 months. Two 1.0 in steaks from the longissimus dorsi muscle at the 12th/13th rib interface were sampled from each animal, transported to the Meat Science laboratory at University of Florida, aged for 14 d at 1-4°C, and then stored at −20°C. Thawed steaks were cooked to an internal temperature of 71°C in an open-hearth grill. Objective tenderness was measured by Warner-Bratzler Shear Force (WBSF) on 673 steaks,

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and sensory tenderness (TEND) and sensory connective tissue amount (CT) were measured through a trained sensory panel on 496 steaks.

Genome-wide association analysis
Genomic DNA was extracted from blood using the DNeasy Blood & Tissue kit (Qiagen, Valencia, California) and stored at −20°C. Animals were genotyped with the Bovine GGP F250 array (GeneSeek, Inc., Lincoln, NE, USA) which contains approximately 250,000 SNPs or genetic markers. Data processing and analysis were performed using the Genetics Q-K analysis workflow of JMP-Genomics 6.0 software (SAS Institute). Only animals with a calling rate higher that 85%, and autosomal markers with minor allele frequency higher that 5% were included in the analysis. The mixed model K method including the genomic relationship matrix and fixed effects SNP and birth year was applied (Stich et al., 2008; Stich & Melchinger, 2009; Yu et al., 2006). The genome wide significance threshold was equal to 0.0001.

Results
The means and standard deviations for WBSF, TEND and CT in this population were 9.48 ± 3.31 lb, 5.5±0.84 and 6.1±0.82, respectively. Out of 221,077 SNPs, 115,287 were included in the WGS analysis. Figure 1 shows the six significant SNPs identified by the WGS for TEND. Figure 2 presents the association results for the WGS for CT and Figure 3 the association results for the WGS for WBSF. Thirteen SNPs were associated with CT and seven with WBSF. Table 1 reports the chromosomal location of the associated SNPs by trait.

In the present population 22 genes were identified as potential chromosomal regions able to explain phenotypic variation in traits related to tenderness, and 32% of these genes have been reported as involved in gene expression, 27% play a role in cell differentiation and 9% in apoptosis (Table 1). Further research is necessary in order to be able to identify the causative polymorphisms located in the chromosomal regions mapped in the present population.

Literature Cited
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Table 1. Genomic location of the significant SNPs for connective tissue, (CT), sensory tenderness (TEND) and Warner-Bratzler Shear Force (WBSF) in longissimus dorsi muscle in an Angus-Brahman crossbred population

Trait	SNP name	Alleles	Chr.$	Position	SNP location*	Gene+	Gene name	Cellular pathway#				
								A	B	C	D	E
CT	rs382798063	T_C	4	82104475	Genic	POU6F2	POU class 6 homeobox 2	+	+			
CT	BTB_00285418	A_G	8	30235048	Intergeneic	NFIB	Nuclear factor I B	+				
CT	rs383284205	G_A	18	62448201	Genic	SSC5D	Scavenger receptor cysteine rich family member with 5 domains					+
CT	rs383370400	C_T	18	63380534	Intergeneic	RPS9	Ribosomal protein S9					+
CT	rs208269561	G_A	18	63435414	Genic	CNOT3	CCR4-NOT transcription complex subunit 3	+				
CT	rs445139035	C_G	18	63470710	Genic	OSCAR	Osteoclast associated, immunoglobulin-like receptor	+	+			
CT	rs448356139	C_T	18	63672844	Genic	NLRP5	NLR family pyrin domain containing 5		+			
CT	BovineHD1900010142	A_G	19	34574420	Intergeneic	SLC47A1	Solute carrier family 47 member 1					+
CT	BovineHD2600009820	T_G	26	35914815	Genic	ATRNL1	Attractin like 1			+		
CT	ARS_BFGL_NGS_107801	A_G	26	51376213	Intergeneic	BNIP3	BCL2 interacting protein 3				+	
CT	UA_IFASA_7512	A_C	29	10172197	Intergeneic	CREBZF	CREB/ATF bZIP transcription factor	+				
CT	rs109360347	C_T	29	42358775	Intergeneic	LGALS12	Galectin 12				+	
CT	rs518993704	G_A	29	43708126	Genic	EHD1	EH-domain containing 1					+
TEND	rs480097065	G_A	5	61135263	Genic	CFAP54	Cilia and flagella associated protein 54		+			
TEND	rs447190111	G_A	5	61135331	Genic	CFAP54	Cilia and flagella associated protein 54		+			
TEND	rs379508103	A_G	7	92551652	Genic	GPR98	Adhesion G protein-coupled receptor V1			+		
TEND	rs208253598	T_C	7	92552466	Genic	GPR98	Adhesion G protein-coupled receptor V1			+		
TEND	rs209170989	A_G	7	92553285	Genic	GPR98	Adhesion G protein-coupled receptor V1			+		

TEND	BovineHD1900010142	A_G	19	34574420	Intergeneic	SLC47A1	Solute carrier family 47 member 1				+
TEND	rs432203649	A_C	29	41625731	Genic	TUT1	Terminal uridylyl transferase 1, U6 snRNA-specific	+			
WBSF	BovineHD1800014522	A_G	18	49284695	Intergeneic	IFNL1	Interferon lambda 1		+		
WBSF	rs210713737	A_C	18	50230181	Genic	NUMBL	NUMB like, endocytic adaptor protein			+	
WBSF	BovineHD1900006277	T_C	19	21923008	Genic	BLMH	Bleomycin hydrolase				+
WBSF	rs468455600	C_T	19	23851770	Genic	SMG6	SMG6, nonsense mediated mRNA decay factor	+			
WBSF	rs41806416	C_T	27	13375105	Intergeneic	RWDD4A	RWD domain containing 4				+
WBSF	rs41806411	A_G	27	13385809	Intergeneic	RWDD4A	RWD domain containing 4				+
WBSF	ARS_BFGL_NGS_42803	T_C	29	46527676	Genic	LRP5	LDL receptor related protein 5		+		

$Chromosome number

*Location of the SNP relative to the gene (genic = inside the gene, intergenic = outside the gene).

+The gene where the SNP is located or the closest gene for SNPs located outside a gene.

#The cellular pathways involving the genes: A = Gene-expression; B= Cell-differentiation; C= Cell-signaling; D= Apoptosis; E= other pathway.

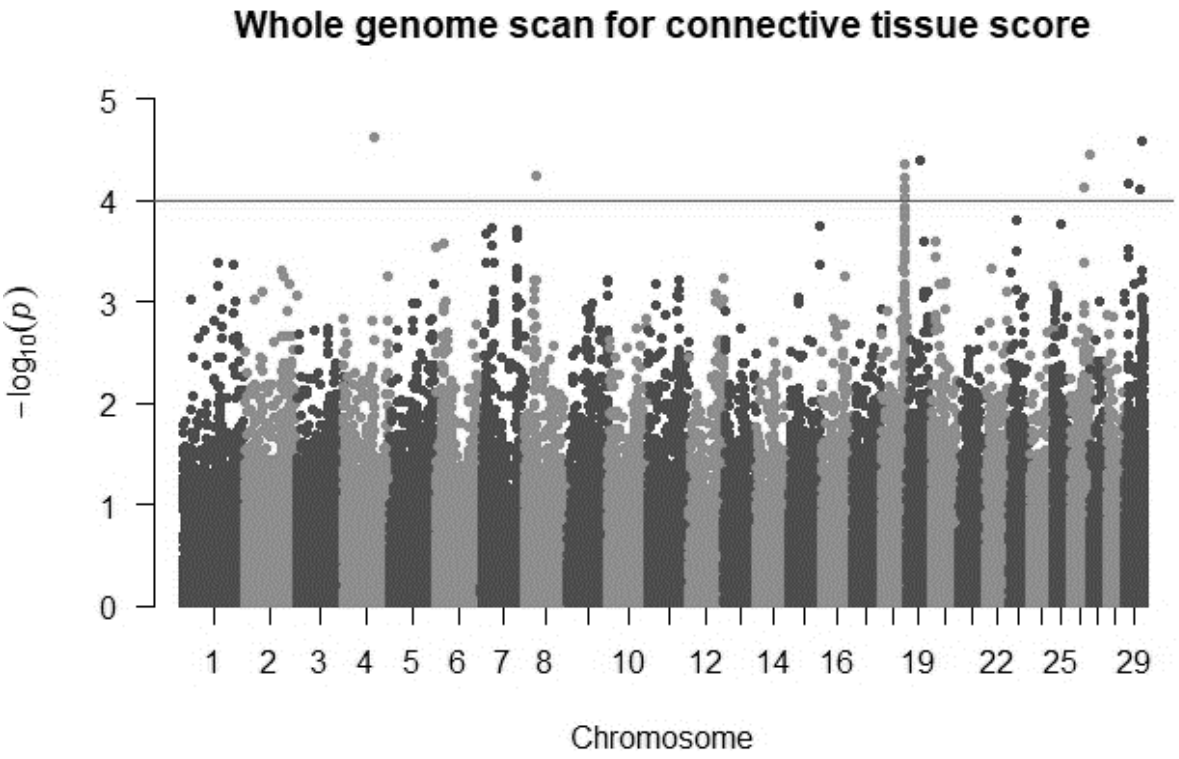

Figure 1. Plot of the genome-scan results for connective tissue in longissimus dorsi muscle in an Angus-Brahman crossbred population. Each dot corresponds to a SNP having its chromosomal location in the X axis and its significance level in the Y axis. The red line represents the genome wide significance threshold (any SNP above this line has a significant effect on the trait).

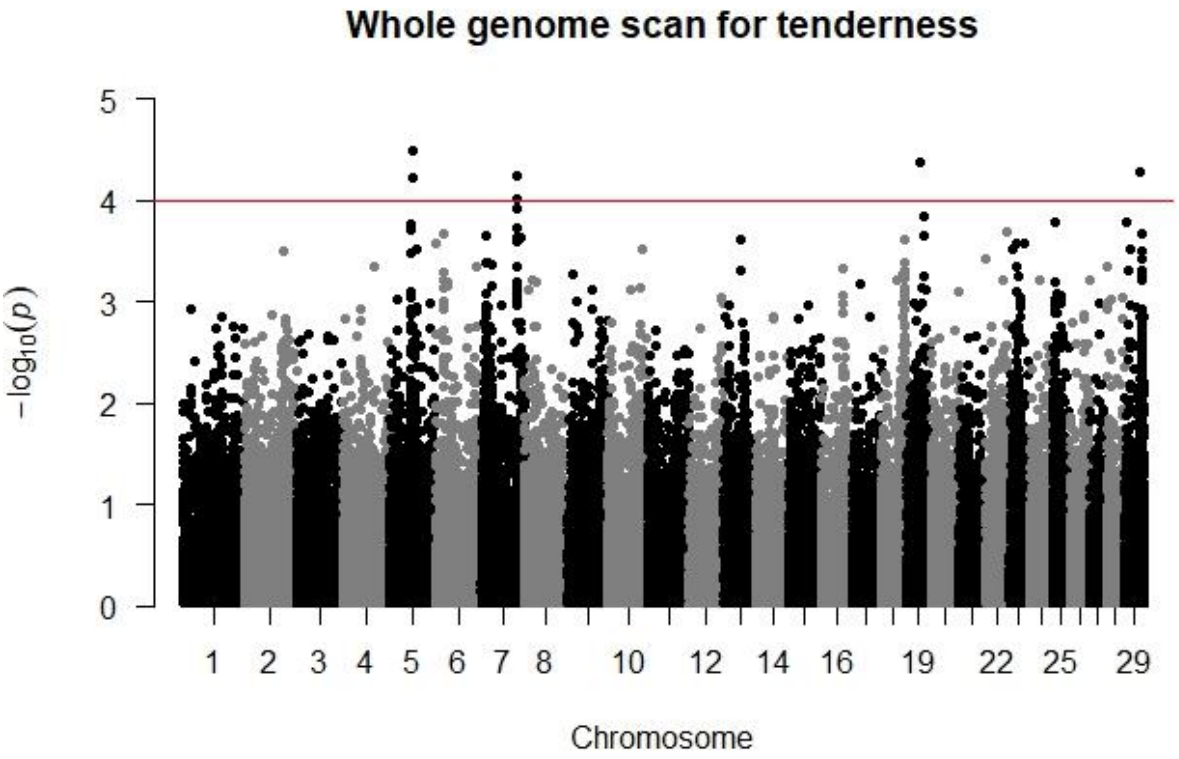

Figure 2. Plot of the genome-scan results for sensory tenderness in longissimus dorsi muscle in an Angus-Brahman crossbred population. Each dot corresponds to a SNP having its chromosomal location in the X axis and its significance level in the Y axis. The red line determine the genome wide significance threshold (any SNP above this line has a significant effect on the trait).

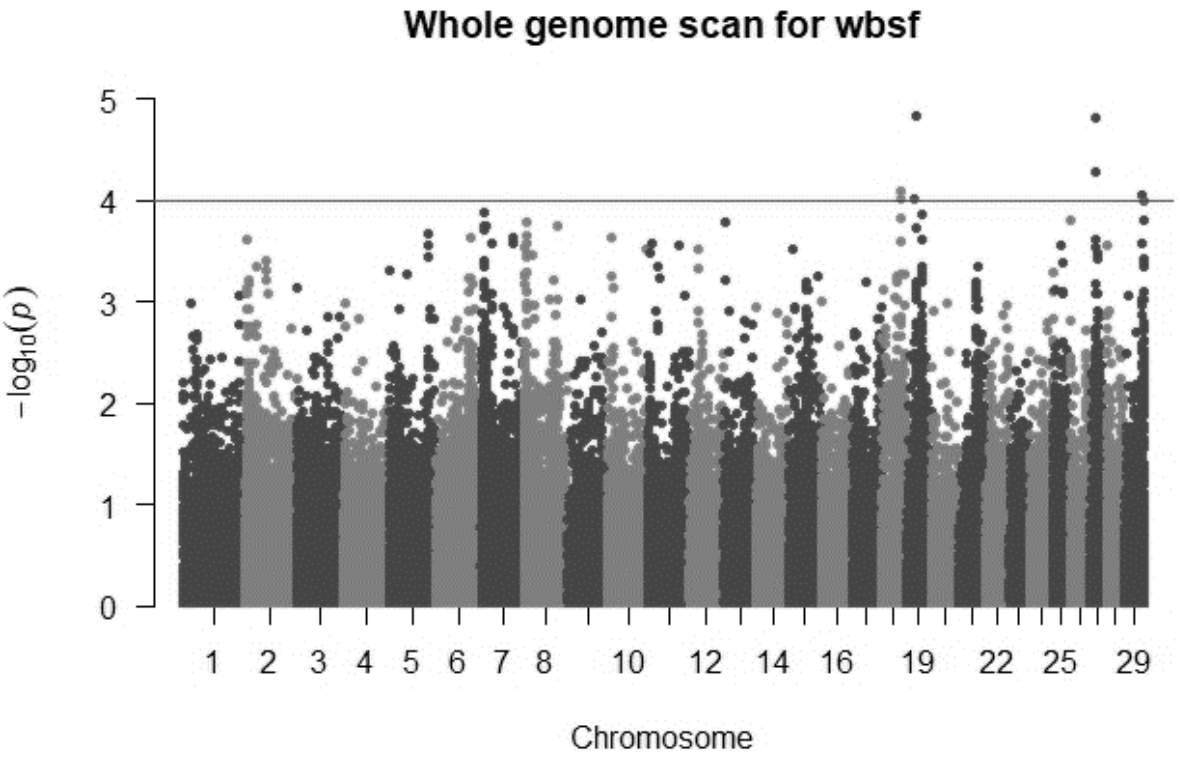

Figure 3. Plot of the genome-scan results for Warner-Bratzler shear force (WBSF) in longissimus dorsi muscle in an Angus-Brahman crossbred population. Each dot corresponds to a SNP having its chromosomal location in the X axis and its significance level in the Y axis. The red line determine the genome wide significance threshold (any SNP above this line has a significant effect on the trait).