Genome-wide association and gene enrichment analyses of meat sensory traits in a crossbred Brahman-Angus population

J. D. Leal, M. A. Elzo, D. Johnson and R. G. Mateescu

Department of Animal Sciences, University of Florida, Gainesville, FL, USA

INTRODUCTION

Given a large enough population and a dense coverage of the genome, a genome-wide association study (GWAS) is usually successful in uncovering major genes and QTLs with large and medium effect on traits such as meat tenderness. Several GWA studies on *Bos indicus* (Magalhães et al., 2016; Tizioto et al., 2013) or crossbred beef cattle breeds (Bolormaa et al., 2011b; Hulsman Hanna et al., 2014; Lu et al., 2013) were successful at identifying QTL for meat tenderness; and most of them include the traditional candidate genes μ-calpain and calpastatin. Genome wide association combined with gene enrichment analyses (GEA) will not only identify genomic regions of large effect but have also the potential to help with the challenging small effect regions. The objective of this study was to apply this methodology to meat tenderness related traits in an Angus-Brahman cattle population.

MATERIALS AND METHIDS

Tenderness (TN), connective tissue amount (CT), juiciness (JC), marbling (MR) and flavor (FL) were measured through a trained sensory panel on 496 steaks in an Angus-Brahman cattle population. Animals were genotyped with the Bovine GGP-F250 array. Data processing and analysis were performed using the Genetics Q-K workflow of JMP-Genomics 6.0 software, applying the mixed model K method. The GEA was carried out using an in-house scripts written in JAVA. All SNPs with uncorrected p-value ≤ 0.05 were included in the GEA. Gene enrichment was performed using the hypergeometric test. A total of 95, 86, 89, 81, and 92 pathways for FL, CT, MR, JC, and TN, respectively, were included in the analysis.

RESULTS

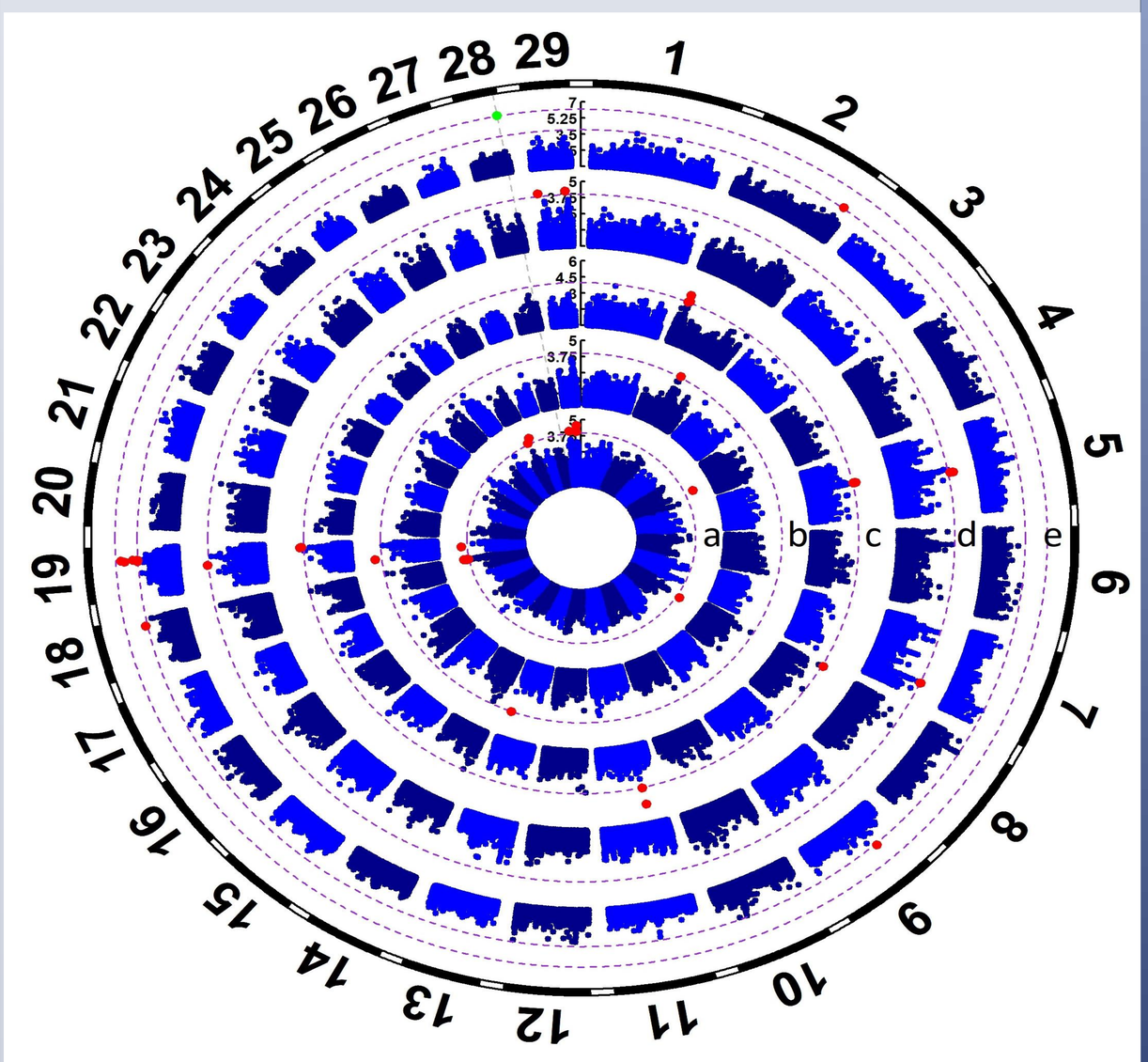

Figure 1. Circular Manhattan plot for: a. connective tissue, b. flavor, c. marbling, d. tenderness, and e. juiciness. Red dots are SNPs with p-value ≤ $1*10^{-4}$; green dots are SNPs with p-value ≤ $6*10^{-7}$

Figure 1 shows GWAS results for CT, FL, MR, TN, and JC. Forty five SNPs, mapping 38 genes were determine as associated (p-value < 0.0001) with at least one trait, and 30% of these genes were related with gene expression, 17% with cell-signaling, and 11% with cell differentiation. One polymorphism in MMRN2 gene reached the genome wide adjusted significance (p-value ≤ $6*10^{-7}$) for JC.

In the GEA, three pathways were identified as enriched: the "Negative regulation of transcription from RNA polymerase II promoter" pathway in FL, "Endoplasmic reticulum membrane" in TN, JC, and CT, and "Positive regulation of transcription from RNA polymerase II promoter" in MR and CT. Figure 2 shows the number of genes identified by trait in each enriched GO-terms. A total number of 35 genes were found as enriched for FL in the "Negative regulation of transcription from RNA polymerase II promoter" GO-term.

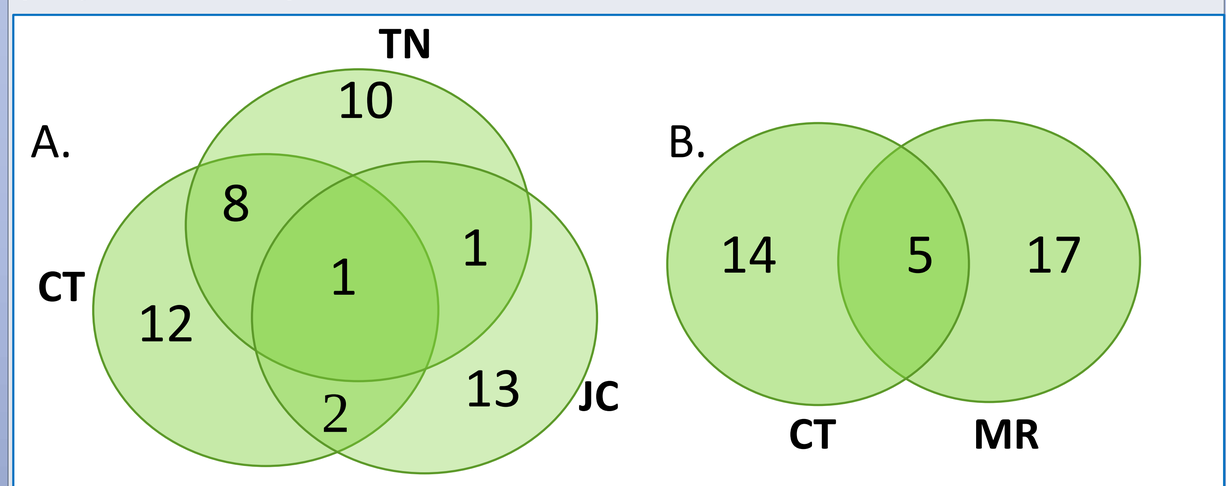

Figure 2. Number of enriched genes identified in an Angus-Brahman population.
A. "Endoplasmic reticulum membrane" GO -term for connective tissue (CT), tenderness (TN) and juiciness (JC).
B. "Negative regulation of transcription from RNA polymerase II promoter" GO-term for connective tissue (CT) and marbling (MR).

The Receptor Accessory Protein 1 (REEP1) gene was identified in the gene enrichment analysis for CT, JC and TN simultaneously (Figure 2A). REEP1 is required for endoplasmic reticulum (ER) network formation, shaping and remodeling. This protein links ER tubules to the cytoskeleton (www.genecards.org).

CONCLUSIONS

This study found 45 associated SNPs, mapping 38 genes by a GWAS approach, and three enriched GO-terms identified by the GEA analyses. Some of these genes are involved in negative regulation of transcription, and cell growth and proliferation. These genes are related to phenotypic variation in sensory panel traits in beef in the present population.

REFERENCES

Baranzini, S.E., et al., 2009. Hum Mol Genet. 18(11):2078-2090.
Bolormaa, S. et al., 2011. J Anim Sci. 89(6):1684-1697.
Elzo, M. A., et al., 2012. Meat Sci. 90: 87-92.
Gao, X., et al., 2008. Genet Epidemiol. 32(4):361-69.
Hulsman Hanna, L. L., et al., 2014. Livest. Sci. 161, 17-27.
Lu, D., et al., 2013. BMC Genet. 14, 80.
Magalhães, A.F. et al., 2016. PloS one 11(6):e0157845.
Stich B., et al., 2008. Genetics 178(3):1745-1754.
Stich, B. & A.E. Melchinger, 2009. BMC Genomics 10(1):94.
Tizioto, P.C., et al., 2013. Physiol Genomics 45(21):1012-1020.

ACKNOWLEDGMENTS AND CONTACT

Financial support provided by Florida Agricultural Experiment Station Hatch FLA-ANS-005548, Florida Beef Council, and Florida Beef Cattle Association – Beef Enhancement Fund Award 022962.

Contact: joelleal@ufl.edu