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A Case-Control Genome-Wide Association Study of Dark-Cutting in 2 Beef Cattle Populations

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Objectives

Dark-cutting beef carcasses are graded Canada B4 in the Canadian Beef Grading System, resulting in economic loss for beef producers. Dark-cutting beef is caused by depletion of muscle glycogen before slaughtering, which may also be affected by animal genetics. This study aimed to identify possible single nucleotide polymorphisms (SNPs) associated with dark-cutting through a case-control genome-wide association study (GWAS) and explore the biological relevance of these SNPs to the formation of dark cutting beef.

Materials and Methods

Two cattle populations were used in this study, population I had 64 beef cattle, of which 40 were graded Canada B4 (dark-cutters, treated as cases), and population II had 837 beef cattle, of which 30 were graded Canada B4. The 2 populations were genotyped using GeneSeek Genomic Profiler for Beef Cattle-HD (GGP-HD) of 76,783 SNPs and Illumina BovineSNP50v2 BeadChip of 54,609 SNPs, respectively. All SNPs with a call rate lower than 90% or a minor allele frequency (MAF) lower than 5% were removed in quality control. Association analyses were conducted using Plink 1.9 and dark-cutting beef was analyzed as a binary trait (cases versus controls) through a logistic regression model under an additive model. UCSC Genome Browser RefSeq genes harboring (1 Mb window) the top 50 SNPs with lowest raw *P* values in each population were used for GO (Gene Ontology) analysis through DAVID (Database for Annotation, Visualization and Integrated Discovery).

Results

In total, 418 SNPs were detected in population I, 383 SNPs in population II and 267 SNPs in the combined data with a less stringent significance level ($P < 0.01$); 12 SNPs in population I, 30 SNPs in population II and 22 SNPs in the combined data with a significance level ($P < 0.001$); 2 SNPs in population II and 2 SNPs in the combined data with a relatively stringent significance level ($P < 0.0001$). These detected SNPs showed suggestive association with dark-cutting beef. GO analysis revealed that genes (717 in total) harboring top-scoring variants (150 SNPs in total) were involved in molecular functions like poly (A) RNA binding, and calcium ion and GTP binding which are related to energy metabolism.

Conclusion

Based on our association study with a relatively small sample size, no evidence was found for a large genetic effect for beef dark-cutting, the trait may therefore be polygenic. Significant SNPs showed suggestive association with dark-cutting beef. Although the detected SNP associations require validation in a larger dataset, the results suggested the possibility in the future for marker-assisted selection or genomic selection in beef cattle to reduce dark cutting.