Identification of Genetic Markers and QTL for Carcass Quality Traits within the American Simmental Association Carcass Merit Program

J. K. Hieber, R. L. Endecott[†], and J. M. Thomson[*]

Department of Animal and Range Sciences, Montana State University, Bozeman, MT 59717

IMPACT STATEMENT

Beef quality is the driving force behind consumer decisions to consume beef. When quality is poor or inconsistent, genetic improvement can be one strategy to improve meat quality. The American Simmental Association's Carcass Merit Program has allowed us to identify genetic markers that impact carcass traits in Simmental and Simmental-influenced cattle, which could be used to improve the accuracy of breeding value estimations and increase the value of genetic evaluations to Simmental producers

SUMMARY

Genetic improvement of beef product quality benefits both producers and consumers. Beef quality is a leading influence in consumer decisions to consume beef. Insufficient marbling and subsequent lower quality grades, lack of a uniform product, reduced or insufficient tenderness, high carcass weight, or high yield grade can negatively impact beef quality. Improvements can be achieved by making selection decisions based on the results of genetic evaluations in the form of EPDs, real-time ultrasound imaging, and physical evaluation of candidate breeding animals. In an effort to improve their ability to accurately predict the breeding value of potential sires for carcass traits, the American Simmental Association (**ASA**) launched the Carcass Merit Program (**CMP**) back in 1997 as a means to collect progeny sire-group carcass information. This program has allowed the ASA to accumulate significant genetic performance information that can reliably be conveyed to producers who utilize Simmental genetics. The objective of this study was to determine genetic markers and QTL in carcass traits from the CMP data collected by the ASA in order to further increase the accuracy of EPD predictions. Data were extracted from the ASA database. Eight chromosomes were found to have genome-wide significance and this conservative approach yielded putative QTL in regions of these chromosomes.

INTRODUCTION

In 1997, the American Simmental Association (**ASA**) launched the Carcass Merit Project (**CMP**), the top sires of the Simmental and Simbrah breeds were randomly mated to commercial females with the plan to collect difficult-to-get progeny sire-group carcass information and sometimes tenderness data. Additionally, information about carcass traits in this program contributed well over 1,000 birth, weaning, and yearling weights and calving ease scores each year, and to date nearly 4,000 shear force records have been collected.

These data have allowed the ASA to amass substantial information necessary for benchmarking, so that performance and value expectations can be conveyed to current and potential customers of ASA's members.

In the last 25 yr, a shift has occurred in the U.S. beef industry from a commodity-based market to one that is based on quality or value added. This has been facilitated by the ability of cattlemen to identify and select animals with superior carcass merit. In an effort to retain market share and increase overall consumer acceptance, many producers have placed at least some importance on selection for marbling development or carcass quality. This means that

a large number of our current cattle herds have females that possess merit in the area of marbling or carcass quality. As a result, there is much interest in how carcass-based selection impacts the maternal performance of these animals. In addition, there is a desire to continue to improve genetic merit for carcass and product consistency. Genomic or marker-based selection is a tool that can be used to improve these traits. With that, our hypothesis is that we can identify genetic markers and QTL for carcass traits from the 30 yrs of CMP data collected by the ASA.

PROCEDURES

Data were generated by the ASA CMP. All records containing calf birth weights, calving ease scores, weaning weights, back fat, ribeye area, marbling, HCW, KPH were extracted from the ASA database. Sire EPD, performance, and genotype data were also extracted.

Progeny data were organized into sire families for all traits, and progeny performance phenotypes were constructed. Sires that had either SNP50K or imputed 50K data were used in the overall analyses. Quality control of samples, markers, and SNP data was done through a series of filters (Golden Helix, 2017).

Principal component analysis (**PCA**) was used to determine relatedness between individuals. The relatedness was used as a covariate in the association analyses.

A single-locus, mixed linear model (EMMAX; Kang et al., 2010) in SVS software (Golden Helix, version 8.7.2-2017-08-11) was used to analyze the data. Manhattan plots were created to visualize the association analyses. On the Manhattan plots, the genome-wide significance level for the Benjamini-Hochberg correlation with -log10(*p*-value) is 5 x 10^{-8} (Ehret, 2010) and markers that were above the level of significance were considered to be associated with the trait in question. Regions with clusters of significantly associated markers were then labeled as putative QTL and used to identify potential positional candidate genes within each.

RESULTS AND DISCUSSION

The data contained samples from 3,849 individuals. We were able to group individuals by sire, in which 2,745 individuals had known sires, producing 395 sire families. Sire families ranged in size from 1 progeny up to 150 progeny; however, not all of the progeny had reported information for their carcass traits. For those who had reported carcass trait information, progeny average performance phenotypes were constructed.

To identify potential candidate genes and pathways related to each carcass trait, Manhattan plots were created for each trait and were used to identify regions of the genome that associated with the traits. In the Manhattan plots, each new color represents a new chromosome, beginning with chromosome 1 on the left and continuing in ascending order to chromosome 29, and each dot represents a marker.

We found 8 out of 261 total chromosomes to have genome-wide association significant markers. For HCW, chromosomes 6, 7, 14, and 20 had 5, 1, 2, and 1 significant markers, respectively (Figure 1). For KPH, chromosomes 11 and 16 each had one significant marker (Figure 2). Chromosome 20 for average HCW, chromosome 16 for average carcass marbling, and chromosome 17 for average carcass fat each had one significant marker.

In order to identify candidate genes, we used a 100,000 bp window around regions or markers that were significantly associated with the trait of
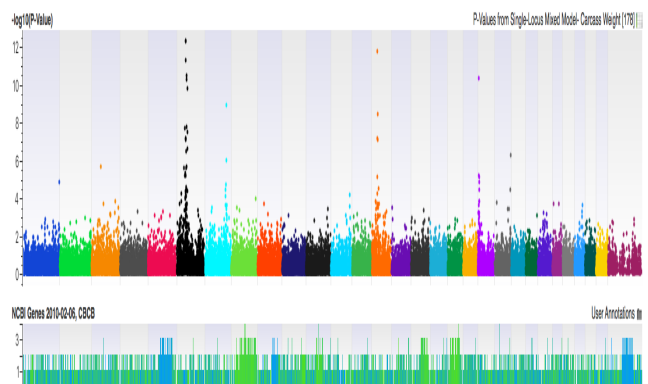

Figure 1. Manhattan plot for hot carcass weight (HCW). Markers above –log10(*p*-value) of 5 x 10^{-8} are genome-wide association significant markers. Vertical clusters of markers are of interest as they indicate putative QTL in those regions.

interest. Regions harboring significant associations were cross-referenced with the University of California-Santa Cruz Genome Browser to determine if known bovine genes were within the regions. Not all significant genomic regions had previously reported positional candidate genes indicating that there are carcass traits that are being impacted by genes not yet identified.

This study demonstrates the value of the ASA CMP for identifying and characterizing genomic variants that impact carcass traits in Simmental and Simmental-influenced cattle, and, can be used to improve the accuracy of breeding value estimations and increase the value of genomic data to Simmental producers. Further research is needed before these results are immediately applicable to the ASA and producers. Additional research needed includes determining the amount of variation in the traits of interest the markers and QTL explain.

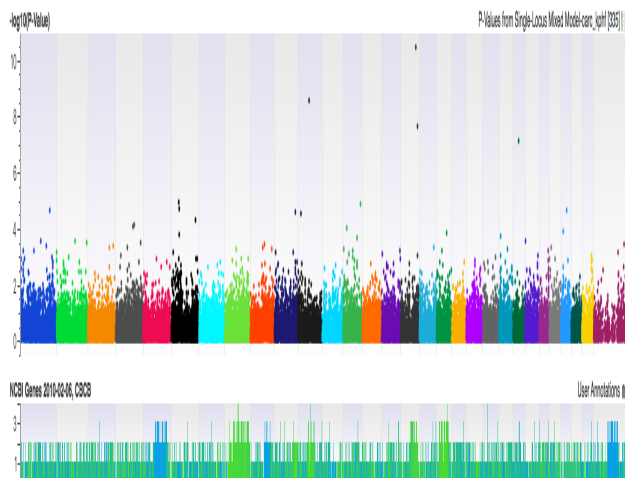Lastly, genetic and phenotypic correlations to other economically important traits, specifically

Figure 2. Manhattan plot for kidney, pelvic, heart fat (KPH). Markers above –log10(p-value) of 5 x 10^{-8} are genome-wide association significant markers. Vertical clusters of markers are of interest as they indicate putative QTL in those regions.

maternal traits, will be calculated. This will allow for the ASA to advise breeding recommendations to maximize producer profitability by determining the best balance of selective pressure to continue to improve carcass traits while minimizing the negative impacts on other traits.

REFERENCES

Ehret, G. B. 2010. Genome-wide association studies: contribution of genomics to understanding blood pressure and essential hypertension. Curr. Hypertens. Reps. 12:17-25. doi:10.1007/s11906-009-0086-6.

Golden Helix. 2017. Bovine GWAS with mixed linear model tools. Golden Helix SNP and Variation Suite User Guide. 8.7.0 rev. ed. Golden Helix, Inc., Bozeman, MT.

Kang, H. M., J. H. Sul, N. A. Zaitlen, S. Y. Kong, N. B. Freimer, C. Sabatti, and E. Eskin. 2010. Variance component model to account for sample structure in genome-wide association studies. Nat. Genet. 42:348-354. doi:10.1038/ng.548.

Segura, V., B. J. Vilhjálmsson, A. Platt, A. Korte, Ü. Seren, Q. Long, and M. Nordborg. 2012. An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. Nat. Genet. 44:825-830. doi:10.1038/ng.2314.

[†]Present address: American Simmental Association, Bozeman, MT 59715

*Corresponding author email: jennifer.thomson@montana.edu