



“Whole-genome positional candidate gene association analysis for fat deposition and carcass merit in beef cattle using a high-density SNP marker set”

DNA MARKERS FOR CARCASS TRAITS

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RESEARCH INSTITUTION: Agriculture and Agri-Food Canada and University of Alberta

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Background: New technologies are helping researchers to discover and characterize the genes that underlie production traits in beef cattle. Cattle have 3.1 billion DNA nucleotides that make up over 30,000 genes. Small changes in the DNA nucleotide sequence (called Single Nucleotide Polymorphisms or SNPs) occur naturally, and are passed on to the offspring. So far, 2.2 million different SNPs have been found in cattle. Some SNPs have absolutely no effect on gene function, but some SNPs have important effects. For example, a mutation can prevent a gene from being expressed (e.g. the polled mutation prevents horn development). Some SNPs cause a gene to be over-expressed (e.g. mutations in the leptin gene can increase carcass fatness). Most important cattle traits (e.g. growth rate, feed efficiency, fertility, carcass traits, etc.) are controlled by many genes.

To increase the odds of finding a SNP located within a gene that is involved in these traits, some researchers look for SNPs in areas of the chromosome that are known to influence the particular trait. These are called *positional candidate genes*. Another approach is to look for SNPs in *functional candidate genes* that are known to code for a structural protein (e.g. collagen or gristle influences toughness), an enzyme (e.g. calpain and calpastatin are believed to influence muscle aging after slaughter) or

controls gene expression (e.g. a section of DNA that switches genes on or off).

Objectives: These researchers identified positional candidate genes that may be involved in beef carcass weight, fat depth, ribeye muscle area, lean meat yield and marbling score. This project was completed in 2009.

“Effective DNA markers would help identify breeding stock that can produce replacement females that maintain body condition, or feeder cattle with more predictable carcass grades.”

What they did: These researchers examined 1,536 individual SNP markers in 454 separate genes. Of these, 149 new SNP markers in 35 different positional candidate genes were discovered during this project. The other markers (over 1,300 SNPs in more than 400 genes) had been discovered in earlier studies. Over 1,000 Charolais, Angus, and crossbred steers were then genotyped to see which version of each SNP marker they carried. Five live (ultrasound fat deposition rate and end-of-test ultrasound fat depth, ultrasound ribeye area growth rate and end-of test ultrasound ribeye area, and end-of test live weight) and five carcass (weight, fat depth, ribeye muscle area, lean meat yield and marbling score) measurements were

collected on each animal. Statistical analyses were conducted to identify SNP markers that were associated with each weight, muscle, fat or marbling measurement.

What they learned: A total of 1146 SNP markers were significantly associated with at least one of the ten traits in Angus (411 SNPs), Charolais (317 SNPs), and crossbred steers (418 SNPs).

SNP markers for all live and carcass traits were found for Angus (203 SNPs for live traits, 208 for carcass traits), Charolais (174 live and 143 carcass trait SNPs) and crossbred (178 live and 240 carcass trait SNPs).

Between 25 and 53 SNP markers were significantly associated with each trait in the Angus steers. Similar results were found for the Charolais (23 to 48 SNP markers per trait) and crossbred steers (26 to 52 markers per trait). A smaller number of these SNP markers worked in two breeds. Across all traits, 29 SNP markers had significant associations in both Angus and crossbred steers, 24 SNPs had significant associations in both Angus and Charolais steers, and 23 SNPs had significant associations in both Charolais and crossbred steers.

Three SNP markers were associated with ultrasound ribeye area growth rate in all three breeds, one marker was associated with end-of-test ultrasound ribeye area in all three breeds, and one SNP was associated with carcass marbling score in all three breeds.

Some markers worked for more than one trait in all three breeds. For example, one particular marker was significantly associated with ultrasound ribeye area growth rate as well as end-of-test ultrasound ribeye area size in all three breeds. However, the marker did not behave the same way in all three breeds. The SNP genotype that was associated with the greatest ribeye area size and growth rate in Angus steers was associated with the lowest ribeye area size and growth rate in the Charolais and crossbred steers. This suggests that this SNP marker may not be located in a causative gene that actually influences ribeye muscle development, but may be located very close by. More work using “fine mapping” techniques may help to identify the actual genes involved in these traits.

What it means: Finding markers (or groups of markers) that can accurately identify differences

in weight, yield grade and quality will help seedstock breeders and commercial bull buyers select breeding stock that will produce feeder cattle with more predictable performance and carcass grades, or replacement females that are genetically predisposed to maintain body condition at preferred mature sizes. Sorting feeder cattle according to expected finishing date and carcass weight, yield and quality grade would also benefit feedlot operators and packers.



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