

QUANTITATIVE TRAIT LOCI MAPPING AND CANDIDATE GENE ANALYSIS
FOR GROWTH AND CARCASS TRAITS ON TWO BOVINE CHROMOSOMES

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ABSTRACT

The first objective of this study was to identify genomic regions on BTA4 and BTA14 which harbor QTL affecting weight and carcass traits in a commercial Angus population. The mapping population consisted of 1,510 purebred commercial Angus steers grouped into 36 half-sib families with not less than 30 progeny per sire. Forty-seven genetic markers were used to scan two bovine chromosomes for QTL using QTL Express. There is strong evidence for a pleiotropic QTL affecting hot carcass weight and ribeye area, a QTL influencing yield grade and back fat and two marbling QTL on BTA14. On BTA4 there were four birth weight, four marbling, four weaning weight, two hot carcass weight, two ribeye and one yield grade QTL. The second objective of this study was to test published SNPs within Leptin, thyroglobulin and diacylglycerol O-acyltransferase 1 for their effects on growth and carcass traits in the commercial Angus population. The ANOVA analysis results indicate that these SNPs were associated with several of the carcass traits, however, linkage analysis revealed that none of these genes underlie bovine growth and carcass QTL in Angus cattle.