

Public Abstract

First Name: Ping

Middle Name:

Last Name: YAO

Degree: M.S.

Degree Program: Animal Science

Advisor's First Name: Jerry

Advisor's Last Name: Taylor

Co-Advisor's First Name:

Co-Advisor's Last Name:

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

The first objective of this study was to identify genomic regions on BTA4 and BTA14 which harbor QTL affecting weight and carcass traits in the commercial Angus population. Many QTL were identified for most of the analyzed phenotypes of the 36 half-sib families using QTL Express. BTA14 appears to harbor three QTL affecting marbling score at 46, 90 and 106-cM, three QTL affecting hot carcass weight at 61, 75 and 87-cM, three ribeye area QTL at 65, 75 and 90-cM, two QTL influencing yield grade at 66 and 79-cM, two weaning weight QTL at 79 and 107-cM and one birth weight QTL at 82-cM. Since *DGATI* was located at 0-cM and *TG* at 12-cM on BTA14, none of the detected QTL would lead us to consider either of these genes as candidates for the detected QTL. There were also several QTL detected on BTA4; four birth weight QTL, four marbling QTL, four weaning weight QTL, two hot carcass weight QTL, two ribeye QTL and one yield grade QTL. The QTL mapping interval is not fine enough so that more high density markers are needed to find the positional candidate genes. Leptin is a candidate gene for the carcass fat QTL since there was a CFAT QTL at 90-cM. *UASMS2* and *UASMS3* were located 13-cM from the marbling QTL at 103-cM which explains their association with marbling.