

Public Abstract

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Department:Genetics Area Program

Degree:PhD

Title:Whole Genome Scan in Commercial Angus Cattle for Quantitative Trait Loci Influencing Growth, Carcass, and Reproductive Traits.

Most genome scans in beef cattle have found only a small number of quantitative trait loci (QTL) to influence any one trait and genetic improvement in cattle by livestock producers using marker-assisted selection (MAS) has been hindered by this limited information. By genotyping a twenty-nine generation mapping population (N=1,769) that represents the major commercial bloodlines within American Angus with 402 genetic markers we have captured the majority of the chromosomes represented within the breed. We have tested for quantitative trait loci influencing 14 economically important traits and have identified multiple carcass, growth and reproductive related QTL on every autosome. In total 439 QTL were identified, averaging 31 QTL per trait, with of which 366 appear to be novel. On average these identified QTL explained 60% of a trait's genetic variation. By itself this study provides solid support for Fisher's infinitesimal model, where variation in a quantitative trait is the result of a large number of genes, each with a small effect on the phenotype.