

GENOME SCAN IN COMMERCIAL ANGUS CATTLE FOR QUANTITATIVE TRAIT LOCI INFLUENCING GROWTH, CARCASS, AND REPRODUCTIVE TRAITS

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ABSTRACT

Experimental designs historically used for quantitative trait loci (QTL) mapping in cattle have captured a limited number of parental chromosomes and therefore have only detected the few heterozygous QTL within these parents. Consequently, most genome scans have found only a small number of QTL to influence any one trait and genetic improvement in cattle by marker-assisted selection (MAS) has been hindered by this limited information. By using a twenty-nine generation mapping population (N=1,769) that represents the major commercial bloodlines within American Angus, we have captured the majority of the chromosomes represented within the breed. Our experimental design allows the flexibility of using several different analytical approaches which exploit both the full pedigree information and within family variation. This design maximizes the potential for identifying all of the QTL of large effect that segregate within Angus cattle.

Our analyses revealed that a large number of QTL of moderate to large effect influence all of the economically important growth and carcass traits, even for traits under strong selection. Despite considerable selection pressure by Angus producers on economically important traits over the past 30 years there remains a wide range in the allele frequency of trait-enhancing QTL. Thus genetic improvement programs that use information at only one, or a few QTL will have little value in beef cattle. Strategies must quickly be devised to simultaneously test for multiple QTL for MAS to be economically viable. The identification of multiple QTL underlying variation in carcass, growth and reproductive traits in this study will assist in the development of QTL tests. Ideally, QTL information will be integrated with available phenotypic data for the estimation of EPDs in cattle to allow producers to select for genetically superior animals.