

Genome-wide Association Study of Birth and Weaning Weights in Brangus Beef Cattle

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Summary and Implications

The objective of this study was to map quantitative trait loci (QTL) associated with birth weight and weaning weight in Brangus beef cattle. A total of 6 significant QTL over 4 chromosomes were identified. Two QTL were common to both traits. The genome-wide association study (GWAS) results could help us understand the biological process of growth in Brangus. Further analyses are needed to find and validate the casual mutations responsible for these QTL.

Introduction

Regions that are responsible for genetic variation can be identified by undertaking GWAS. The precision by which genomic regions are identified could be improved by increasing the number of animals in the GWAS (i.e. sample size), increasing marker density, and including markers with stronger linkage disequilibrium with causal mutations responsible for QTL. Bayesian regression methods are useful for GWAS because the posterior distributions used for inference take full account of uncertainty in all unknown parameters. Recently, several QTL associated with growth traits in *Bos taurus* have been published. One QTL is on *Bos taurus* autosome (BTA) 6, in a region which harbors the candidate genes *NCAPG*, and *LCORL*. The objective of this study was to identify QTL associated with birth weight and weaning weight in Brangus beef cattle using real or imputed 770K SNP genotypes and determine if the QTL present in Brangus were concordant with those found in other breeds.

Materials and Methods

Brangus is a composite crossbred among Brahman (*Bos indicus*) and Angus (*Bos taurus*) breeds. Estimated breeding values (EBV) of birth weight and weaning weight in 1,495

Brangus cattle were obtained from the American Brangus Breeders Association. The cattle were genotyped using one or other of Bovine50K, GGPHD77K, or BovineHD770K panels; then all animals were imputed to BovineHD770K using FImpute. Deregressed estimated breeding values were calculated, and fitted in a weighted BayesB analysis to estimate SNP effects using GENSEL. The non-overlapping 1 Mb windows that explained at least 1.0% of genetic variance (GV%) were considered to harbor QTL. The posterior probabilities of association (WPPA) of candidate windows were used for significance testing. The most strongly associated SNP which had the highest posterior probability of inclusion (PPI) within a candidate window, was identified as the lead SNP for that window. The GV% explained by each lead SNP was assessed, and candidate genes included in these QTL windows were obtained from NCBI or Ensembl databases.

Results and Discussion

A total of 6 significant QTL over 4 chromosomes were identified (Table 1). Two QTL exhibited pleiotropy by influencing both traits. Saatchi et al. (2014) used 50k genotypes and reported large effect QTL located in the same regions on BTA6 at 37-42Mb, on BTA7 at 93Mb, and on BTA20 at 4Mb across ten US cattle breeds including Brangus. The identified QTL windows harbor promising candidate genes. For example, BTA6 at 38Mb is near to *LCORL* and *NCAPG*, while BTA7 at 93Mb is near to *ARRDC3*. A candidate gene identified on BTA20 at 4Mb is *ERGIC1*. No positional candidate genes associated with growth were found on BTA5 at 47Mb.

The GWAS results could lead us to better understand the biological processes accounting for variation in growth in cattle. Further analyses are needed to find and validate the casual mutations.

Acknowledgments

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Table 1. The significant 1-Mb genome windows and lead SNPs associated with growth traits in Brangus beef cattle.

Trait	BTA_Mb	No. SNP	GV%	WPPA	Lead SNP	PPI	GV% SNP
BW	6_38	276	6.94	1.0	rs133837477	1.0	6.90
BW	5_47	341	4.38	0.90	rs134538017	0.13	0.04
BW	7_93	232	1.68	0.91	rs110253449	0.11	0.33
WW	7_93	232	2.10	0.94	rs136675904	0.10	0.12
WW	6_38	276	1.58	0.68	rs133837477	0.37	1.16
WW	20_4	308	1.22	0.70	rs42661321	0.14	0.27