**INTRODUCTION & OBJECTIVES**

bGHR gene underlies QTL for milk and body fat traits on chromosome 20. Hale et al. (2000) described a microsatellite in the 5' UTR of this gene. *Bos indicus* cattle typically contained a TG tandem repeat of 11 bp while *Bos taurus* cattle typically possessed a 16-20 bp repeat. The short allele was associated with lower weaning weight, carcass weight, and marbling score in Angus steers. Since most commercial genotyping platforms involve SNPs, the initial objective was to identify SNP variation among breeds in 1000 bp of DNA sequence flanking the GHR TG microsatellite. A second objective was to associate SNP genotype and (or) haplotype data with growth and ultrasound carcass trait measures in composite populations of *Bos indicus* (3/8 Brahman) x *Bos taurus* (5/8 Angus) Brangus bulls.

**MATERIALS AND METHODS**

**Resequencing:** DNA was obtained from familial-unrelated bulls from dairy breeds Brown Swiss, Holstein, and Jersey and beef breeds Simmental, Angus, Brahman, and Brangus. Sequencing 1,000 bp was completed at SeqWright (Houston Texas). Sequences were assembled and SNPs detected with CodonCode© (Figure 1 and Table 1).

**SNP Genotyping, Haplotype Visualization, and Association:**

- Two populations of Brangus bulls provided data and DNA: 1) Chihuahuan Desert Rangeland Research Center Expanded (CDRRC; n = 552 growing bulls from 96 sires).
- 2) International Brangus Breeders Association (IBBA) semen/DNA repository (n = 65 AI sires with ≥100 progeny, 48,623 total progeny).
- Genotyping of three SNPs 3' and 5' to the microsatellite was performed using Taqman® and BioRad iCyqer iQ™ Real-Time PCR Detection System.
- Haplotypes and LD were visualized with Haploview® (Figure 2).
- Association of genotype/haplotype to growth and ultrasound carcass phenotypes were completed with mixed model analyses in SAS® (Table 2).

**RESULTS**

Figure 1. Schematic of the bGHR gene. Exons are denoted with an E followed by the exon number. Introns are denoted with an I following the intron number. SNP detected through resequencing are denoted as SNP followed by the bp number.

**Additional Results**

Frequencies of alleles, genotypes, and haplotypes appeared parallel between the CDRRC Expanded population and AI sires of IBBA. Minor allele frequency for the tag SNP 125634 > 10%. Bulls possessing an Angus-derived haplotype (CCG or CCTG) had 7.4% more (P < 0.06) rib fat than bulls possessing a Brahman-derived haplotype (TCCA).

**CONCLUSION**

In a 1000 bp region flanking a microsatellite in the 5' UTR in bGHR, SNP variation exist. An A/G tag SNP from this region may offer an alternative method of genotyping to the TG microsatellite in association studies involving measures of corporal fat in *Bos taurus* x *Bos indicus* composite cattle.

**Acknowledgements**

USDA-NRI (2006-35205-16651), USDA-CSREES-NM-AES (#180674), and California Dairy Board Project XXXX.