

Bovine Growth Hormone Receptor (bGHR) Gene: 5' UTR Re-sequencing, SNP Detection, and Association With Performance in Brangus Bulls.

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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 iCycler 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

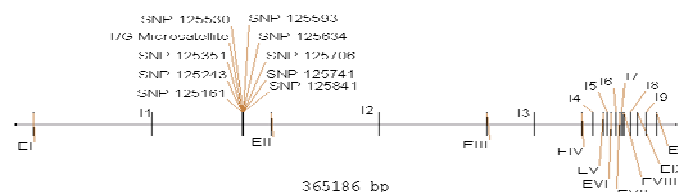


Figure 1. Schematic of the bGHR gene. Exons are denoted with an E followed by the exon number. Introns are denoted with an I following the intron number. SNP detected through resequencing are denoted as SNP followed by the bp number.

Table 1. SNPs detected among breeds in the 5' UTR bGHR flanking a TG microsatellite. Nucleotides of the SNP are in columns identified by SNP location (125,XXX). Sequence variations genotyped and used in an association study of genotype/haplotype with phenotype are bold.

Breed	n ¹	SNP									
		161*	243*	351	TG	530	593	634*	706	741	841
Brown Swiss	8	C	C	A/G	.	G	C	G	C	T	C
Holstein	8	C	C	A/G	.	G	C	G	C	T	C
Jersey	8	C	C	A	.	G	C	G	C	T	C
Simmental	6	C	C	A	.	G	C	G	C	T	C
Angus	6	C	C	A/G	.	G	C/T	G	C	T	C
Brahman	6	T	T	.	.	A/G	C	A	A	A	G
Brangus	6	C	C	A/G	.	G	C	C	C	T	C

* SNPs Previously reported by Hale et al. 2000.

¹ Number of unrelated individuals based on three generation pedigrees used for SNP detection.

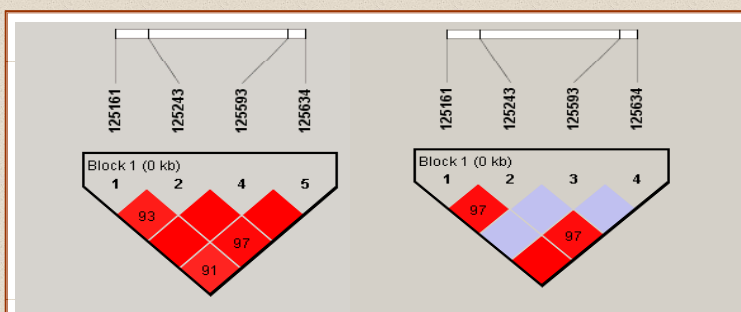


Figure 2. Pattern of LD among SNPs detected in the 5' UTR-bGHR gene. Left: CDRRC Expanded population and right: IBBA population. **SNP 125634 = Tag SNP.**

Table 4. Least squares means ± SE for growth and ultrasound carcass traits among genotypes of SNP 125634 in the growth hormone receptor (GHR) gene in Brangus bulls.

	Genotypes			Pooled SE
	AA	AG	GG	
CDRRC Expanded				
n	87	283	180	
Birth weight, kg	36.60	36.51	36.84	0.51
205-d weight, kg	271.85	267.44	273.39	0.37
365-d weight, kg	510.34	500.00	499.14	6.07
205-d to 365-d ADG, kg/d	1.46	1.44	1.43	0.03
Test ADG, kg/d	1.57	1.52	1.51	0.04
Scrotal circumference, cm	35.42	35.14	35.08	0.35
Intramuscular fat, %	3.56	3.55	3.64	0.06
LM area/body weight, cm ² /kg	0.17	0.17	0.17	0.002
LM area, cm ²	81.81	81.27	82.01	1.18
Rib fat, cm	0.63 ^{ab}	0.62 ^a	0.66 ^b	0.02
IBBA				
n	15	33	15	
Birth weight, kg	40.21	40.91	40.18	1.64
205-d weight, kg	301.45	304.93	305.20	9.04
365-d weight, kg	579.63	655.67	609.59	27.38
205-d to 365-d ADG, kg/d	1.47	1.42	1.41	0.08
Scrotal circumference, cm	37.09	36.68	36.30	0.67
Intramuscular fat, %	3.30	3.58	3.38	0.24
LM area/body weight, cm ² /kg	0.17	0.15	0.16	0.009
LM area, cm ²	90.59	89.77	86.73	4.63
Rib Fat, cm	0.64	0.62	0.57	0.08

^{ab} Within a row, means without a common superscript differ ($P < 0.05$).

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 was > 10%. Bulls possessing an Angus-derived haplotype (CCCG or CCTG) had 7.4% more ($P < 0.06$) rib fat than bulls possessing a Brahman-derived haplotype (TTCA).

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

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Hale, C.S., W.O. Herring, H. Shibuya, M.C. Lucy, D.B. Lubahn, D.H. Keisler, and G.S. Johnson. 2000. Decreased growth in Angus steers with a short TG-microsatellite allele in the P1 promoter of the growth hormone receptor gene. *J. Anim. Sci.* 78:2099-2104.