# An SNP association study evaluating Brahman and Brahman-influenced steers for growth and carcass traits



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#### Introduction

- ➤ Tendon and ligament injuries in performance horses are common, serious, and costly (Ely 2009).
- > A significant risk factor appears to be genetic (Welsh 2014).
- ➤ Many genetic variants affecting athletic performance and susceptibility to injury have been described in humans (Maffulli 2013) and horses (Tully 2014)

## **Materials and Methods**

- ➤ A population 42 Brahman and F1 Brahman steers born between 2009-2014.
- Six candidate genes TG, CAST, CAPN3, ADPIOQ, GH1 and IGF-1) were selected for SNP genotyping.
- ➤ Growth, performance and carcass traits were fit as dependent variables and breed, breed\*snp, and SNP marker as independent variables.
- ➤ Sire was fit in the model as a random variable

# **Objective**

The objective of the current study was to evaluate SNP's located on six candidate genes and their potential associations with growth, performance and carcass traits in a population of Brahman and F-1 Brahman steers.

Table 1. SNP significantly associated with growth traits and genotypic frequencies

				Minor	Het	Major	SNP	Breed
Traits	Gene	SNP ID	Allele	Genotype	Genotype	Genotype	P-value	P-value
1				Frequency	Frequency	Frequency	0.004	0.040
$BW^1$	ADIPOQ	rs210865525	C/T	0	1	40	0.0247	0.9135
$\mathbf{BW}$	TG	rs110553649	A/C	2	20	19	0.0162	0.4128
$\mathbf{BW}$	TG	rs378900777	T/C	0	2	39	0.0458	0.9770
$WW^2$	IGF-1	rs109022910	A/G	4	9	26	0.0009	0.0001
WW	IGF-1	rs109227434	T/C	0	16	25	0.0238	0.0032
WW	CAPN3	rs109050259	G/A	2	23	16	0.0118	<0.0001
WW	CAPN3	rs109122904	A/G	0	5	36	0.0001	<0.0001
WW	CAPN3	rs109337751	T/C	0	14	27	0.0159	<0.0001
WW	CAPN3	rs109372443	G/A	11	13	16	0.0316	0.0224
WW	CAPN3	rs110822150	T/G	0	14	27	0.0159	<0.0001
WW	CAPN3	rs109806627	G/C	0	14	25	0.0192	<0.0001
WW	CAST	rs110496242	G/A	2	10	29	0.0060	0.1202
WW	CAST	rs137140434	G/T	0	5	13	0.0308	0.0838
WW	GH-1	rs137651874	T/C	0	6	29	0.0134	0.0742
WW	ADIPOQ	rs383535987	G/A	0	3	38	0.0287	0.0361
WW	TG	rs110553649	A/C	2	20	19	0.0083	<0.0001
WW	TG	rs378567477	T/C	8	16	9	0.0452	0.0228
WW	TG	rs386026054	G/C	3	24	12	0.0092	<0.0001
$HH^3$	CAPN3	rs109337751	T/C	0	14	27	0.0476	0.5599
НН	CAPN3	rs110822150	T/G	0	14	27	0.0476	0.5599
НН	CAPN3	rs109372443	G/A	11	13	16	0.0028	0.9220
НН	CAPN3	rs109806627	G/C	0	14	25	0.0531	0.5522
нн	CAST	rs110496242	G/A	2	10	29	0.0362	0.7902
нн	CAST	rs134030456	C/T	0	15	26	0.0552	0.7172
НН	ADIPOQ	rs209050698	G/A	1	14	26	0.0217	0.0954
нн	ADIPOQ	rs210258853	A/G	1	14	26	0.0213	0.0954
НН	ADIPOQ	rs210607551	C/T	0	5	36	0.0037	0.4730
НН	ADIPOQ	rs210865525	C/T	0	1	40	0.0004	0.6798

Table 2. SNP significantly associated with feedlot performance traits and genotypic frequencies

Traits	Gene	SNP ID	Allele		Het Genotype Frequency		SNP P-value	Breed P-value
INWT <sup>1</sup>	IGF-1	rs109022910	A/G	4	9	26	0.0420	0.1068
INWT	IGF-1	rs109227434	T/C	0	16	25	0.0223	0.0070
INWT	CAPN3	rs109122904	A/G	0	5	36	0.0120	0.0643
INWT	CAST	rs110496242	G/A	2	10	29	0.0065	0.0651
INWT	CAST	rs137265200	C/T	0	5	28	0.0051	0.0438
INWT	GH-1	rs133403174	G/A	1	12	28	0.0139	0.0070
INWT	GH-1	rs133438805	G/C	1	12	28	0.0175	0.0070
INWT	GH-1	rs134389836	C/T	1	12	28	0.0158	0.0070
INWT	GH-1	rs136132855	T/C	1	12	28	0.0139	0.0070
INWT	GH-1	rs137252133	A/G	1	12	28	0.0139	0.0070
INWT	TG	rs378567477	T/C	8	16	9	0.0123	0.0168
INWT	TG	rs133980693	G/A	9	22	10	0.0058	0.0078
INWT	TG	rs110501231	C/T	9	22	10	0.0065	0.0078
INWT	TG	rs135059985	C/T	9	22	10	0.0064	0.0078
INWT	TG	rs110553649	A/C	2	20	19	0.0425	0.0737
INWT	TG	rs132813094	A/C	1	7	33	0.0432	0.0670
INWT	TG	rs386026054	G/C	3	24	12	0.0022	0.0053
HRVWT	CAST	rs109702795	G/T	0	10	29	0.0291	0.2385
HRVWT	CAST	rs110136749	G/A	0	16	24	0.0509	0.1410
HRVWT	CAST	rs110374623	T/C	0	10	28	0.0415	0.1796
HRVWT	CAST	rs133120980	C/A	0	10	31	0.0376	0.1721
HRVWT	CAST	rs133891017	A/T	0	10	30	0.0376	0.1721
HRVWT	CAST	rs134030456	C/T	0	15	26	0.0413	0.1563
HRVWT	CAST	rs136875549	T/C	0	15	24	0.0472	0.1229
HRVWT	CAST	rs137371179	T/C	0	12	29	0.0310	0.1967
HRVWT	CAST	rs137601357	C/T	0	17	24	0.0533	0.1377
HRVWT	CAST	rs137726884	A/G	0	8	29	0.0330	0.1643
DOF <sup>3</sup>	CAST	rs110496242	G/A	2	10	29	0.0362	0.1574
ADG <sup>4</sup>	TG	rs136849694	G/A	3	0	5	0.0054	0.0229
ADG	ADIPOQ	rs210607551	C/T	0	5	36	0.0430	0.7253

Table 3. SNP significantly associated with carcass traits and genotypinc frequencies

				Minor	Het	Major	SNP	Breed
Traits	Gene	SNP ID	Allele <sup>4</sup>	Genotype	Genotype	Genotype	P-value	P-value
				Frequency <sup>5</sup>	Frequency <sup>5</sup>	Frequency <sup>5</sup>		
HCW <sup>1</sup>	CAST	rs109702795	G/T	0	10	29	0.0303	0.2473
HCW	CAST	rs134030456	C/T	0	15	26	0.0544	0.1792
HCW	CAST	rs137371179	T/C	0	12	29	0.0324	0.2117
REA <sup>2</sup>	CAST	rs109020860	A/G	0	5	36	0.0425	0.1612
REA	CAST	rs110386026	C/T	0	6	35	0.0425	0.1612
REA	CAST	rs136873074	C/T	0	6	34	0.0425	0.1753
REA	CAST	rs136882857	C/T	0	6	35	0.0425	0.1612
REA	CAST	rs136982429	C/T	0	11	28	0.0032	0.2548
REA	CAST	rs137561617	T/A	0	6	31	0.0139	0.1775
REA	IGF-1	rs109022910	A/G	4	9	26	0.0459	0.1891
REA	CAPN3	rs109122904	A/G	0	5	36	0.0354	0.1713
REA	CAPN3	rs110452450	G/A	10	13	13	0.0367	0.0025
REA	TG	rs110553649	A/C	2	20	19	0.0333	0.1136
REA	TG	rs110946911	T/G	2	17	22	0.0113	0.2394
REA	TG	rs132813094	A/C	1	7	33	0.0400	0.1784
REA	TG	rs134743669	G/A	0	39	2	0.0076	0.1787
REA	TG	rs386026054	G/C	3	24	12	0.0221	0.4712
REA	GH-1	rs137651874	T/C	0	6	29	0.0401	0.3600
$YG^3$	CAST	rs134030456	C/T	0	15	26	0.0443	0.1951

### Results

- ➤ Multiple SNP from all six candidate genes were associated with growth traits, feedlot performance and carcass traits
- ➤ Multiple SNP from all six candidate genes were associated with more than one trait in the current study

# Conclusions

- >SNPs identified in the current study must be validated in larger, more diverse populations prior to implementation into selection strategies.
- ➤ More SNPs and candidate genes must be evaluated to account for as much variation as possible due to the complex nature of the currently evaluated traits.
- ➤ Utilizing proper selection strategies extracted from current analyses has the potential to benefit the Brahman breed through the early identification of fast growing, efficient individuals that are genetically predisposed to yield high quality carcasses.

#### **Literature Cited**

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