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## Associations of Beef Production Traits with Polymorphisms in the Growth Hormone Gene and Insulin-Like Growth Factor-1 Gene

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**CATTLE 00-11**

### Summary

The effects of cow and (or) calf genotype for two candidate gene markers [growth hormone (GH) and insulin-like growth factor-1 (IGF-1) genes] on production traits were evaluated in a beef cattle herd. The GH polymorphism is located in exon V of the GH gene and is associated with a leucine/valine amino acid substitution. The IGF-1 polymorphism is located in the 5' flanking region of the IGF-1 gene. Cow GH genotype was not significantly associated with cow production traits (milk yield, average weight, hip height, and condition score) or progeny weight at birth or weaning. The regression of weaning weight on number of valine (versus leucine) alleles in the calf GH genotype indicated a possible association with calf weaning weight, although genotype least-squares means were not significantly different. Calf GH genotype tended to be associated with carcass cutability, but not with birth weight, carcass weight, or marbling score. Cow IGF-1 genotype was significantly associated with estimated milk yield and progeny weaning weight, but not with cow size traits or cow body condition score. Calf IGF-1 genotype was not significantly associated with any of the calf growth or carcass traits evaluated.

### Introduction

Developments in genetic technology have created much interest in the possible use of DNA-based diagnostic tests to enhance strategies for genetic evaluation and improvement of livestock. Molecular marker-assisted selection could be especially beneficial for improvement of traits that are difficult to measure (e.g., feed efficiency) and to evaluate genetic potential of animals that do not express a trait (e.g., meat quality of breeding stock or

maternal traits of bulls). Other potential advantages of DNA-based evaluation include a reduction in generation interval (animals can be evaluated at any age) and an increase in accuracy in cases when marker information can be combined with conventional performance records.

Gene mapping research has led to the discovery of many polymorphic sites throughout the cattle genome that can serve as genetic markers. However, relatively little is known regarding relationships between specific markers and production traits. Polymorphic sites in genes involved in the mediation of growth factors are logical candidates to study for possible associations with livestock production traits. The objective of this study was to determine if polymorphisms within the growth hormone (GH) gene and insulin-like growth factor-1 (IGF-1) gene were associated with economically important production traits in beef cattle.

### Experimental Procedures

The cowherd used in the study consisted of two-breed rotations of Angus x Hereford, Simmental x Hereford, and Tarentaise x Hereford. Calves were sired by purebred bulls in conventional rotational backcrosses or by Charolais in terminal crosses. Calves were born primarily in March and April, and weaned in October at an average age of about seven months. Milk yield was estimated periodically throughout lactation by the calf nursing method. Calves were placed in a feedlot immediately after weaning and slaughtered in one or two groups per year at an average age of 427 days.

The GH polymorphism is located in exon V of the bovine GH gene and is responsible for an amino acid substitution (leucine versus valine) at

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position 127 of the GH polypeptide. The IGF-1 polymorphism is located in the 5' flanking region of the IGF-1 gene.

DNA samples of individual cows and their progeny were extracted from blood and amplified by polymerase chain reaction (PCR). Primer sequences used in PCR were 5'-CCG-TGT-CTA-TGA-GAA-GC-3' and 5'-GTT-CTT-GAG-CAG-CGC-GT-3' for GH and 5'-ATT-ACA-AAG-CTG-CCT-GCC-CC-3' and 5'-ACC-TTA-CCC-GTA-TGA-AAG-GAA-TAT-ACG-T-3' for IGF-1.

Allelic makeup of a given animal for GH was determined following Alu-I restriction enzyme digestion of a 427-bp amplified PCR product (L allele: 264, 96, 51, and 16 bp; V allele: 264, 147, and 16 bp) and gel electrophoresis. Allelic makeup for IGF-1 was determined following digestion of a 249-bp amplified PCR product with SnaB-I ( $A_1$  allele: 223 and 26 bp;  $A_2$  allele: 249 bp). Each animal was assigned a GH genotype of LL, LV, or VV and an IGF-1 genotype of  $A_1A_1$ ,  $A_1A_2$ , or  $A_2A_2$ .

Data were analyzed separately for the two marker systems by mixed linear models, accounting for fixed effects of marker genotype (of either cow or calf), year-management, cow breed-type, calf sire breed, cow age, and calf sex. Random effects included calf sire within sire breed and (or) cow sire within cow breed-type. The linear effect of calf weaning age, slaughter age, or carcass weight was included as a covariate when appropriate. Additional analyses were conducted in which the discrete effect of genotype was replaced with the linear and quadratic effects of the number (i.e., 0, 1, or 2) of V alleles in the GH genotype or  $A_2$  alleles in the IGF-1 genotype.

### Results and Discussion

Cow GH genotype was not significantly associated with estimated milk yield, cow body weight, cow body condition score, or progeny weight at birth or weaning (Table 1). Least-squares means did not differ significantly between calf GH genotypes for calf birth weight or age-adjusted weaning weight (Table 2). However, there was a slight linear trend toward increased weaning weight for each additional L allele in the genotype.

When calf carcass traits were adjusted to a constant final age of 427 days (Table 3), calf GH

genotype tended to be associated with external carcass fat thickness, estimated KPH fat percentage, and estimated retail cutability, but not with carcass weight, rib-eye area or marbling score. Allele V was associated with slightly decreased external fatness and higher cutability than allele L. Animals with the LV genotype tended to have the most KPH fat, whereas VV animals had the least. When carcass traits were adjusted to a constant carcass weight (Table 4), the tendency toward leanness for allele V was similar to that noted above for age-constant analyses. There was a linear tendency toward larger ribeye area (relative to carcass weight) with increasing number of V alleles in the GH genotype, although least-squares means did not differ significantly across genotypes.

Cow IGF-I genotype was not significant for cow size traits or cow body condition score (Table 5). Cows with genotype  $A_1A_1$  produced more milk and heavier progeny weaning weights than cows with  $A_1A_2$  or  $A_2A_2$  genotype ( $A_1A_2$  and  $A_2A_2$  cows did not differ significantly). Calf IGF-I genotype was generally not significantly associated with calf weights (Table 6) or carcass composition (Tables 7-8).

### Implications

There was evidence that polymorphisms in the GH and IGF-1 genes were associated with several production traits, although the magnitude of effects tended to be modest in most cases. The GH allele that displayed possible association with increased calf weaning weight could be antagonistic with respect to carcass cutability. It should be noted that an association detected between marker and trait does not necessarily indicate a direct effect of this polymorphism on the trait, but could to some degree reflect the effect of a linked polymorphism.

Table 1. Effect of Cow GH Genotype (LL, LV, or VV) on Cow-Calf Production Traits.

Trait	LL		LV		VV		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Cow mature weight, lb	190	1208 ± 13	155	1217 ± 13	28	1213 ± 26	0.84	NS	NS
Cow hip height, in	189	52.5 ± 0.17	154	52.4 ± 0.16	28	52.3 ± 0.33	0.86	NS	NS
Cow condition score <sup>b</sup>	190	4.4 ± 0.08	155	4.5 ± 0.08	28	4.7 ± 0.16	0.24	NS	NS
Estimated milk yield, lb/day <sup>c</sup>	186	16.3 ± 0.31	150	16.3 ± 0.31	26	16.7 ± 0.62	0.83	NS	NS
Progeny birth weight, lb	186	104.1 ± 1.5	150	103.4 ± 1.5	26	103.0 ± 2.8	0.86	NS	NS
Progeny weaning weight, lb	186	518 ± 6.6	149	517 ± 6.8	26	525 ± 12.3	0.76	NS	NS

<sup>a</sup>Trait value regressed on number of V alleles in genotype.

<sup>b</sup>Scale of 1=extremely emaciated to 9=extremely obese.

<sup>c</sup>Calf nursing method.

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Table 2. Effect of Calf GH Genotype (LL, LV, or VV) on Calf Birth Weight and Weaning Weight.

Trait	LL		LV		VV		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Calf birth weight, lb	208	103.6 ± 1.5	129	103 ± 1.7	18	101 ± 3.3	0.55	NS	NS
Calf weaning weight, lb	205	522 ± 6.6	126	514 ± 7.3	18	505 ± 13.9	0.19	-9.5 ± 5.1 <sup>*</sup>	NS

<sup>a</sup>Trait value regressed on number of V alleles in genotype.

<sup>\*</sup>P < .10

Table 3. Effect of Calf GH Genotype (LL, LV, or VV) on Carcass Traits, Adjusted to Constant Final Age (427 Days).

Trait	LL		LV		VV		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Carcass Weight, lb	204	734 ± 6	122	725 ± 7	18	719 ± 16.0	0.45	NS	NS
Rib eye area, in <sup>2</sup>	204	12.7 ± 0.1	122	12.8 ± .2	18	12.9 ± 0.34	0.69	NS	NS
External fat, in	204	.45 ± .02	122	.41 ± .02	18	0.39 ± 0.04	0.07	-.035 ± .015 <sup>*</sup>	NS
Marbling score <sup>b</sup>	204	393 ± 5.8	122	401 ± 6.3	18	405.0 ± 14.0	0.43	NS	NS
Choice grade, %	204	52.3 ± 4.6	122	55.3 ± 5.2	18	48.6 ± 11.6	0.79	NS	NS
KPH, %	204	2.21 ± 0.04	122	2.30 ± 0.05	18	1.97 ± 0.13	0.04	0.30 ± 0.13 <sup>*</sup>	-0.21 ± .083 <sup>*</sup>
Retail cut, %	204	51.3 ± 0.16	122	51.6 ± 0.17	18	52.0 ± 0.38	0.05	0.35 ± 0.14 <sup>*</sup>	NS

<sup>a</sup>Trait value regressed on number of V alleles in genotype

<sup>b</sup>slight = 300 to 399, small = 400 to 499, etc.

<sup>\*</sup>P < .05

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Table 4. Effect of Calf GH Genotype (LL, LV, or VV) on Carcass Traits, Adjusted to Constant Carcass Weight (739 lb).

Trait	LL		LV		VV		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Rib eye area, in <sup>2</sup>	204	12.8 ± .1	122	13.0 ± .1	18	13.3 ± .31	0.20	.21 ± .12 <sup>*</sup>	NS
External fat, in	204	.45 ± .02	122	.43 ± .02	18	.39 ± .04	0.18	-.028 ± .015 <sup>*</sup>	NS
Marbling score <sup>b</sup>	204	396 ± 5.5	122	407 ± 6.1	18	405 ± 4.1	0.20		NS
Choice grade, %	204	53.0 ± 4.5	122	56.0 ± 5.0	18	52.0 ± 11.0	0.83	NS	NS
KPH, %	204	2.22 ± 0.04	122	2.32 ± 0.05	18	2.03 ± 0.13	0.06	0.29 ± 0.13 <sup>*</sup>	-0.19 ± 0.08 <sup>*</sup>
Retail cut, %	204	51.2 ± 0.17	122	51.5 ± 0.18	18	51.8 ± 0.38	0.10	0.31 ± 0.14 <sup>*</sup>	NS

<sup>a</sup>Trait value regressed on number of V alleles in genotype

<sup>b</sup>slight = 300 to 399, small = 400 to 499, etc.

<sup>\*</sup>P < .10, <sup>\*</sup>P < .05

Table 5. Effect of Cow IGF-1 Genotype (A<sub>1</sub>A<sub>1</sub>, A<sub>1</sub>A<sub>2</sub>, OR A<sub>2</sub>A<sub>2</sub>) ON Cow-Calf Beef Production Traits.

Trait	A <sub>1</sub> A <sub>1</sub>		A <sub>1</sub> A <sub>2</sub>		A <sub>2</sub> A <sub>2</sub>		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Cow mature weight, lb	90	1224 ± 16	186	1208 ± 13	97	1210 ± 15	0.62	NS	NS
Cow hip height, in	90	52.4 ± .2	184	52.4 ± .2	97	52.4 ± .2	0.98	NS	NS
Cow condition score	90	4.6 ± 0.10	186	4.5 ± 0.08	97	4.5 ± 0.09	0.64	NS	NS
Estimated milk yield, lb/day <sup>b</sup>	86	17.0 ± .4	183	16.1 ± .3	93	16.3 ± .3	0.04	-1.39 ± .62 <sup>†</sup>	.51 ± .29 <sup>†</sup>
Progeny birth weight, lb	86	106.0 ± 1.9	183	103.4 ± 1.5	93	102.7 ± 1.7	0.17	-1.72 ± .95 <sup>†</sup>	NS
Progeny weaning weight, lb	85	533 ± 7.7	183	512 ± 6.4	93	519 ± 7.3	0.01	-35.1 ± 2.1 <sup>**</sup>	13.8 ± 5.6 <sup>†</sup>

<sup>a</sup> Trait value regressed on number of A<sub>2</sub> alleles in genotype.

<sup>b</sup> Calf nursing method.

<sup>†</sup>P<.10, <sup>\*</sup>P<.05, <sup>\*\*</sup>P<.01

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Table 6. Effect of Calf IGF-1 Genotype (A<sub>1</sub>A<sub>1</sub>, A<sub>1</sub>A<sub>2</sub>, OR A<sub>2</sub>A<sub>2</sub>) on Calf Birth Weight and Weaning Weight.

Trait	A <sub>1</sub> A <sub>1</sub>		A <sub>1</sub> A <sub>2</sub>		A <sub>2</sub> A <sub>2</sub>		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Birth weight, lb	101	103.2 ± 1.8	190	103.4 ± 1.5	65	101.9 ± 1.9	0.72	NS	NS
Weaning weight, lb	100	520 ± 8.2	187	518 ± 6.6	63	518 ± 8.6	0.99	NS	NS

<sup>a</sup>Trait value regressed on number of A<sub>2</sub> alleles in genotype

Table 7. Effect OF Calf IGF-1 Genotype ( $A_1A_1$ ,  $A_1A_2$ , OR  $A_2A_2$ ) on Carcass Traits, Adjusted to Constant Final Age (427 DAYS).

Trait	$A_1A_1$		$A_1A_2$		$A_2A_2$		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Carcass Weight, lb	98	736 ± 8	185	730 ± 6	62	728 ± 9	0.75	NS	NS
Rib eye area, in <sup>2</sup>	98	13.0 ± .18	185	12.9 ± .14	62	12.6 ± .20	0.20	NS	NS
External fat, in	98	.41 ± .02	185	.43 ± .02	62	.44 ± .02	0.52	NS	NS
Marbling score <sup>b</sup>	98	404 ± 7.1	185	400 ± 5.6	62	395 ± 8.0	0.61	NS	NS
Choice grade, %	98	48.0 ± 6.0	185	54.4 ± 4.6	62	53.5 ± 6.6	0.54	NS	NS
KPH, %	98	2.29 ± 0.06	185	2.22 ± 0.04	62	2.15 ± 0.07	0.26	-0.07 ± 0.04 <sup>+</sup>	NS
Retail cut, %	98	51.6 ± 0.20	185	51.5 ± 0.16	62	51.2 ± 0.22	0.25	NS	NS

<sup>a</sup>Trait value regressed on number of  $A_2$  alleles in genotype

<sup>b</sup>light = 300 to 399, small = 400 to 499, etc.

<sup>+</sup>P < .10

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Table 8. Effect of Calf IGF-1 Genotype ( $A_1A_1$ ,  $A_1A_2$ , or  $A_2A_2$ ) on Carcass Traits, Adjusted to Constant Carcass Weight (739 lb).

Trait	$A_1A_1$		$A_1A_2$		$A_2A_2$		F-test P-value	Gene action <sup>a</sup>	
	N	LSMean ± SE	N	LSMean ± SE	N	LSMean ± SE		Linear	Quadratic
Rib eye area, in <sup>2</sup>	98	13.0 ± .16	185	13.0 ± .13	62	12.7 ± .18	0.18	NS	NS
External fat, in	98	.42 ± .02	185	.44 ± .02	62	.46 ± .02	0.39	NS	NS
Marbling score <sup>b</sup>	98	400 ± 7.1	185	400 ± 5.7	62	406 ± 8.0	0.78	NS	NS
Choice grade, %	98	48.0 ± 5.9	185	55.0 ± 4.5	62	45.0 ± 6.5	0.47	NS	NS
KPH, %	98	2.28 ± 0.06	185	2.23 ± 0.05	62	2.17 ± 0.07	0.43	NS	NS
Retail cut, %	98	51.6 ± 0.21	185	51.5 ± 0.17	62	51.1 ± 0.22	0.15	-0.22 ± 0.12 <sup>+</sup>	NS

<sup>a</sup>Trait value regressed on number of  $A_2$  alleles in genotype

<sup>b</sup>slight = 300 to 399, small = 400 to 499, etc.

<sup>+</sup>P < .10