CANDIDATE GENES FOR GROWTH TRAITS IN BEEF CATTLE CROSSES *Bos taurus* X *Bos indicus*

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INTRODUCTION

Animal improvement has been achieved by selection based either on phenotype or on predicted additive genetic merit of the animals for production traits. Molecular biology techniques allow the identification of genetic variation at specific loci and the association between variation at quantitative trait loci (QTL) and production traits. The final goal is to use marker assisted selection to improve the genetic gain achieved by selection as a result of higher accuracy. Candidate gene strategy has been proposed to direct the search for QTLs, assuming that the genetic variation at genes affecting the physiological pathways related to a phenotype would be more likely to affect the quantitative variation at that phenotype. Polymorphisms at growth hormone gene have been associated with several production traits in bovine such as milk production and quality (Lagziel *et al*., 1996), growth (Rocha *et al*., 1992) and carcass composition and quality (Taylor *et al*., 1998). Genes coding for milk proteins have been associated with milk quality and yield (Ron *et al*., 1994) and also with growth traits (Lin *et al*., 1987 ; Moody *et al*., 1996). The objective of the present work was to investigate the effects of growth hormone (*GH*), κ-casein (*CSN3*) and β-lactoglobulin (*LGB*) polymorphism in growth traits of three beef cattle crosses (Aberdeen Angus X Nellore, Canchim X Nellore and Simmental X Nellore).

MATERIAL AND METHODS

A total of 211 animals resulting from crosses between Nellore females with sires from either Aberdeen Angus, Canchim and Simmental breeds were analyzed. The restriction fragment lenghth polymorphisms κ-casein – *Hinf*I (*CSN3*), β-lactoglobulin – *Hae*III (*LGB*) and growth hormone – *Alu*I (*GH*) were determined by digestion of polymerase chain reaction (PCR) products. DNA samples were obtained from white blood cells according to Olerup and Zetterquist (1992) with modifications (Regitano, 2001).

PCR reactions. PCR reactions were conducted in a Perkin-Elmer model 2400 termocycler. Each reaction consisted of 200 ng genomic DNA in PCR buffer (20 mM Tris-HCl, pH8.4; 50 mM KCl), 1.5 mM $MgCl_2$, 200 nM of each dNTP, 0.4 μM of each primer and 0.5 units *Taq* DNA polimerase in 25 μl reactions. Restriction fragments were resolved in 3% low melting point agarosis gels containing 0.67 μg/ml ethidium bromide. Electrophoresis were carried out in Tris-borate-EDTA at 5 V/cm.

Statistical Analysis. Average daily gain from birth to weaning (ADGbw) and from weaning to yearling (ADGwy) were analyzed by the statistical computational program SAS (1999) using the following statistical model :

$$Y_{ijklm} = \mu + + B(GG)_i + CG_j + GH_k + LGB_l + GHLGB_{kl} + e_{ijklm}$$

where :
Y_{ijklm} = trait measured (ADGbw and ADGwy) on the ijklmth animal,
μ = population mean for the trait measured,
$S(GG)_i$ = effect associated to the ith sire nested within genetic group,
CG_j = effect associated with the jth contemporary group,
GH_k = effect associated with the kth *GH* genotype ,
LGB_l = effect associated with the lth *LGB* genotype ,
$GHLGB_{kl}$ = interaction effect between kth *GH* genotype and lth *LGB* genotype,
e_{ijklm} = random error effect associated with ijklmth observation.

RESULTS AND DISCUSSION

All three loci were polymorphic for the three genetic groups. *CSN3* genotype did not affect the traits studied so it was excluded from the statistical model. Significant effects on ADGbw were observed for GG, CG, sire (GG) and *GH*. Significant differences ($p < 0.01$) were found for ADGbw means between Canchim and Aberdeen Angus and between Canchim and Simmental progenies (data not shown). For the latest period of growth (ADGwy) CG, *GH* and the interaction *LGB*GH* contributed significantly to the variation (Table 1).

Table 1. Summary of the analyses of variance for ADGbw and ADGwy

Source[a]	DF	Type III SS	Mean Square	F Value	Pr>F
			ADGbw		
GG	2	0.160	0.080	8.69	0.0002**
CG	10	0.615	0.061	6.66	<0.0001**
Sire (GG)	10	0.263	0.026	2.85	0.0025**
GH	1	0.051	0.051	5.48	0.0203*
LGB	2	0.006	0.003	0.33	0.7201
*GH*LGB*	2	0.054	0.027	2.92	0.0567
			ADGwy		
GG	2	0.023	0.011	0.87	0.4223
CG	10	4.565	0.456	34.77	<0.0001**
Sire (GG)	10	0.247	0.025	1.88	0.0506
GH	1	0.139	0.139	10.58	0.0014**
LGB	2	0.019	0.009	0.70	0.4963
*GH*LGB*	2	0.083	0.041	3.15	0.0455*

** $P \leq 0.01$; * $P \leq 0.05$, a GG, CG = genetic group, contemporary group, respectively.

LGB alone did not influence ADGbw and ADGwy but there was a significant interaction of this locus with *GH* ($p < 0.05$) for ADGwy and an approximation of significance for ADGbw (Table 1). Animals with LL genotypes for *GH* had higher ADGbw ($p < 0.05$) than LV animals

but lower ADGwy (Table 2). Since all Nelore females were homozygotes for the L allele no homozygote for the V allele were observed in the progenies of these crosses so that it was not possible to determine the type of gene action. Differences in ADGwy means of AA and AB animals were only significant when *GH* genotype was LV. The interaction between *GH* and *LGB* may be more clearly seen in Figure 1.

Table 2. ADGbw and ADGwy means and standard error (SE) according to *GH* genotype and *GH*LGB* combinations

GH	*LGB*	ADGbw	ADGwy
		Mean ± SE	Mean ± SE
LL	-	0.8345 ± 0.0144 kg	0.6505 ± 0.0159 kg
LV	-	0.7836 ± 0.0203 kg	0.7349 ± 0.0242 kg
LL	AA	0.8322 ± 0.0167 kg	0.6309 ± 0.0351 kg
LL	AB	0.8092 ± 0.0166 kg	0.6712 ± 0.0195 kg
LL	BB	0.8622 ± 0.0144 kg	0.6494 ± 0.0174 kg
LV	AA	0.7642 ± 0.0427 kg	0.7923 ± 0.0510 kg
LV	AB	0.8095 ± 0.0236 kg	0.6778 ± 0.0294 kg
LV	BB	0.7772 ± 0.0251 kg	0.7348 ± 0.0304 kg

ADGbw, ADGwy =average daily gain from birth to weaning and from weaning to yearling, respectively.

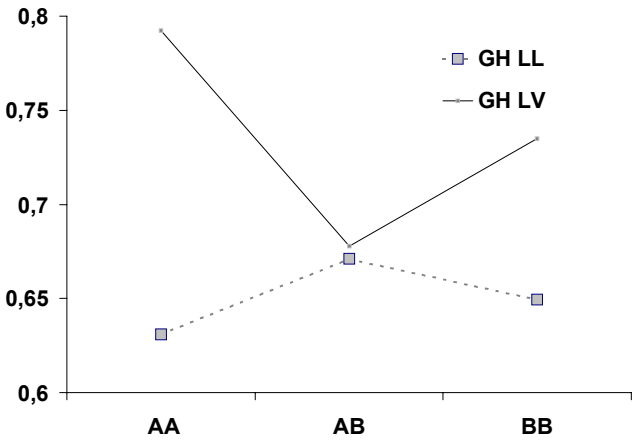

Figure 1. Interaction of *LGB* and *GH* genotypes for ADGwy

CONCLUSION

In most QTL studies statistical analysis have routinely considered each locus separately. Thus, they do not account for interaction between different loci. Recently, Casas *et al.* (2000) demonstrated that interaction may play an important role in QTL analysis. The present study reinforces that interactions between marker loci should be more carefully investigated since such interactions may account for differences on genotype responses across populations and genetic backgrounds.

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