Detection Of Quantitative Trait Loci For Growth Traits On Bovine Chromosome 2

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Introduction

Classical quantitative genetic approach is applied successfully to improve livestock production using phenotype and pedigree information to estimate population genetic parameters such as heritabilities, genetics variances and genetic correlations. However, this process is slow and there is no knowledge of the genetic architecture of the quantitative traits. Molecular genetics techniques can be used to identify genes or chromosomal regions (Quantitative Trait Loci - QTL) that affect traits of importance in livestock production. Genetic response can be improved by direct selection on genes or genomic regions that affect economic traits through marker-assisted selection (MAS) or gene introgression (Dekkers and Hospital, 2002). The objective of this study was to detect QTL affecting growth traits in BTA 2 using F2 Holstein x Gyr population and microsatellite markers.

Material and methods

A F2 crossbred population of 375 animals was produced mating between Holstein and Gyr. Base population was composed for 28 Gyr females artificially inseminated with four Holstein bulls, resulting on 150 F1 animals. Five F1 males were chosen to be the parents of the F2 generation and were crossed with 59 F1 females, giving five families and a total of 375 F2 animals. Growth traits analyzed were birth weight (BW), adjusted early weaning weight (WW), adjusted weight at 205 day (W205), adjusted yearling weight (YW), adjusted weight at 720 day (W720) and average daily gain (ADG).

Six microsatellite markers were selected from bovine chromosome 2 (*TGLA44, MNB-83, BM4440, TGLA226, BMS2519 and IDVGA-2*). According to the latest MARC map reported at http://www.marc.usda.gov (published Jan. 20, 2005; Ihara *et al*., 2004), the six markers covered 117.5 cM; average interval length was about 23.5 cM. Markers were chosen based on map position, number of alleles and heterozygosity, according to information available at Animal Biotechnology laboratory of Embrapa Southeast Cattle (São Carlos-SP, Brazil). Genotyping and Linkage map were described in Miyata *et al*. (2007).

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Statistical analysis. All traits were analyzed by mixed linear model using QXPAK software version 3.1 (Pérez-Enciso and Misztal 2004). The general model in matrix form was as follows:

$$\mathbf{y = Xb + Zu + Qg + e},$$

where y represents the vector of phenotype data, b represents a vector of fixed effects included in the model, X represents an incidence matrix for fixed effects, u represents a vector of individual polygenic effects, Z and Q represent the incidence matrix for the polygenic effects and the QTL respectively, g represents a vector of QTL effects and e represents a vector of random residuals. Identity-by-descent probabilities were calculated as Pérez-Enciso *et al*. (2000).

Significance Thresholds and confidence interval the phenotypic variance explained by QTL. The experiment-wise threshold value was calculated according to Lander and Kruglyak (1995). A likelihood ratio test (LRT) statistic was considered suggestive of linkage (statistical evidence that would be expected to occur one time at random in a genome scan) if it exceeded a value of LRT = 8.3, and significant of linkage (statistical evidence that would be expected to occur at random with $P< 0.05$) if it exceeded a value of LRT = 13.9. These results correspond to a nominal P-value of P= 0.0038 and P = 0.00019, respectively. The LOD drop-off method of Lander and Botstein (1989) was used to obtain 95% confidence intervals. The phenotypic variance explained by QTL was estimated according to Sorensen *et al*. (2003) as follow: $VP_{QTL} = 2P_Q (1- P_Q)a^2$, where VP_{QTL} is phenotypic variance explained QTL, P_Q is the frequency of allele Q of QTL and a is the additive of effect of the QTL.

Table 1: Position, heterozygosity, allelic diversity, polymorphism information content (PIC) and number of alleles for markers used.

Marker	Position	heterozygosity	Allelic diversity	PIC	Alleles
TGLA44	0	0.92	0.84	0.82	8
MNB-83	21.5	0.67	0.65	0.57	3
BM4440	56.3	0.91	0.87	0.85	10
TGLA226	75.9	0.86	0.79	0.75	7
BMS2519	102.5	0.83	0.81	0.79	10
IDVGA-2	117.5	0.89	0.82	0.80	8
Mean	-	0.85	0.80	0.76	7.67

Results and discussion

Position, heterozygosity, allelic diversity, number of alleles, and polymorphism information content (PIC) values for markers are presented in Table 1. Analysis of the six BTA2 microsatellite markers produced a total of 46 alleles, with an average of 7.67 alleles per locus. Most of markers in this study can be considered highly polymorphic, once the average of heterozygosity, allelic diversity, and polymorphism information content (PIC) values for markers were 0.85, 0.80 and 0.76, respectively.

There was evidence indicating the presence of two suggestive QTL affecting W720 and ADG (P < 0.1). The highest likelihood ratio test values were found at 30 cM and 32 cM with an associated *P*-value of 0.0006 and 0.0008, flanked by markers *MNB-83* and *BM4440* for W720 and ADG, respectively (figure 1). The 95% confidence intervals for W720 and ADG were the fragment from 4 cM to 49 cM and 3 cM to 53 cM, respectively. The additive effects indicate that the animals inheriting the Holstein allele were 15.08 kg heavier at W720, and grow faster by 0.0206 kg/day compared with animals inheriting the Gyr allele. The phenotypic variances explained by the QTL are 6.02% and 6.06% for W720 and ADG, respectively. Because QTL identified for W720 close to the QTL identified for ADG, a test for pleiotropy versus linkage was performed. But not reveal evidence for pleiotropy. No other significant QTL effects were detected for BW, WW, W205 and YW (data not shown).

The BTA 2 is a harbor for QTL affecting the growth traits. The locus causing double muscling in cattle has been mapped to the centromeric end of bovine chromosome 2 (Charlier *et al*., 1995; Dunner *et al*., 1997; Casas *et al*. 1998). Kim *et al*. (2003), identified multiple QTL for postnatal growth traits on BTA 2. One group of QTL for yearling weight and slaughter weight were positioned in the proximal region (18 and 8 cM) of the chromosome with highly suggestive evidence for linkage. Another QTL for slaughter weight was detected in the interstitial region (72 cM) of the chromosome with suggestive evidence for linkage. Kneeland *et al*. (2004), described two QTL affecting birth weight spanned two chromosomal regions located at 9.1 to 22.5 cM and 95.0 to 100.3 cM in the chromosomal region of 9.1 to 22.5 cM, which affected birth weight, also had a significant effect on postweaning average daily gain on feed.

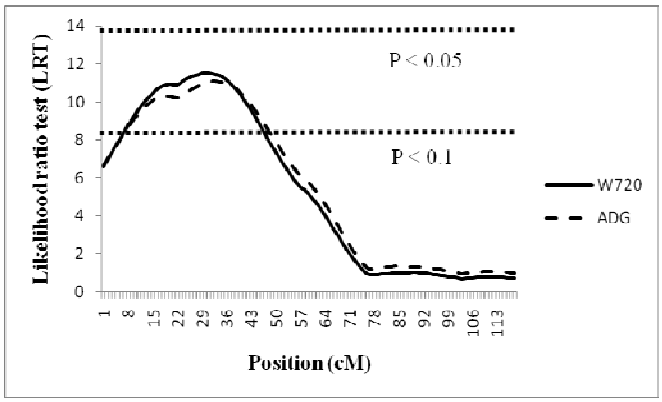

Figure1: Likelihood ratio test statistic (LRT) profile for weight at 720 day (W720) and average daily gain (ADG) on BTA 2. The upper horizontal line represent the significance linkage (LRT = 13.9), the lower horizontal line represent the suggestive linkage (LRT = 8.3).

Conclusion

The results of current study showed evidence for two suggestive QTL for W720 and ADG (P<0.10) on BTA 2. Identification of quantitative trait loci affecting post-natal growth but not the birth weight and contrariwise will help to break up the genetic correlation between birth weight and post-natal growth.

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