Identification Of Quantitative Trait Loci For Growth Curve In Crossbred Dairy Cattle Population

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Introduction

Detection of quantitative trait loci for growth traits have been described in previous study (e.g. Kim *et al*. 2003, Kneeland *et al*. 2004). These QTLs were estimated at certain time or stage of animal growth by single-trait QTL mapping, where the growth traits treated as different traits and analyzed separately. This approach does not take into account the correlated structure of phenotypes measured at different time points and the statistical powers of hypothesis tests tend to be lower and the sampling variances of parameter estimation tend to be higher for separate analyses (Jiang and Zengt 1995). The other approach which can used is multi-trait mapping which can take into account the correlation between measurements, but their applications are suitable for few traits. As the number of traits increases, computational time will be a prohibitive factor (Yang *et al*. 2006). Wu *et al*. (2002) showed that fit the growth curve for every individual and mapping the QTLs for the growth parameters can reduce the amount of phenotypic data for QTL analysis, efficiently analyze unbalanced phenotype data, and help us to better understand the genetic basis of quantitative trait development. The objective of the present study was to identify quantitative trait loci (QTL) for growth curve on BTA 2 using F2 Holstein x Gyr population and microsatellite markers.

Material and methods

Animals. An experimental F2 population was produced by the Brazilian agricultural company Empresa Brasileira de Pesquisa Agropecuária (Embrapa) on the Santa Monica Experimental Station, in the Brazilian state of Rio de Janeiro. The population was started from 28 Gyr females artificially inseminated with semen from four Holstein bulls that produced 150 F1 individuals. Five F1 males were chosen to be the parents of the F2 generation and were crossed with 59 F1 females that produced five families and a total of 375 F2 individuals.

Marker data. 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 6 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

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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).

Statistical analysis. Data consisted of 8021 weight performances recorded from birth weight to approximately 2 years of age for 375 F2 offspring was used to estimate the growth curve by random coefficient model (fig. 1). There were on average 21 weight records per animal, and weights of animals were recorded monthly. The random coefficient model involves a random intercept and slope for each animal can be written as

$$\mathbf{y= X\beta+ Z}\nu \mathbf{+ e,}$$

where y = vector of measurements, β = vector of fixed effects (sex and year-season of birth), ν = vector of random effects of age, e = vector of random errors, and X and Z were the incidence matrix for fixed and random effects, respectively.

Mixed linear model, allowing for the estimation of QTL effects was fitted 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 growth curve, **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).

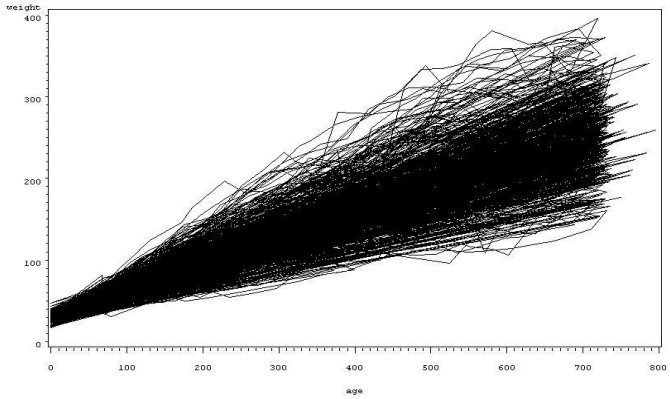

Figure 1: Growth curve for individuals of F2 Holstein x Gyr.

Significance thresholds, confidence interval and 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

The position, heterozygosity, allelic diversity, number of alleles, and polymorphism information content (PIC) values for markers are presented in Table 1, and indicate that most markers in this study considered as highly polymorphic.

The suggestive QTL was found for growth curve (P< 0.1). The additive effect is 0.0195 kg and the phenotypic variance explained by the QTL is 6.15%. The highest likelihood ratio test value was found at 34 cM with an associated *P*-value of 0.00086, flanked by markers *MNB-83* and *BM4440* (figure 2). The most likely position (95% confidence interval) of the QTL identified, estimated by the LOD drop-off method was the fragment from 10 cM to 55 cM.

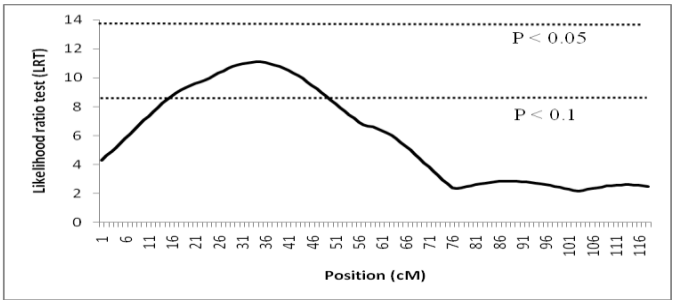

Figure2: Likelihood ratio test statistic (LRT) profile for growth curve on BTA 2. The upper horizontal line represent the significance linkage (LRT = 13.9), the lower horizontal line represent the suggestive linkage (LRT = 8.3).

To our knowledge, no literature reviews are available about estimation of QTL for growth curve in livestock and this area need more attention. However, the BTA 2 is a harbor for QTL affecting the growth traits for example 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).

Conclusion

This study revealed that a suggestive QTL affecting growth curve on BTA 2 at 34 cM in F2 Holstein x Gyr population, which can help in understanding the genetic basis of development of growth traits, and reduce the amount of phenotypic data required to mapping the QTL for growth traits. Detection of QTL for growth curve in livestock needs more attention.

ACKNOWLEDGMENT

This project was supported by the Brazilian agencies Embrapa – Prodetab. I would like to thank TWAS-CNPq for the PhD fellowship for M. M. I. Salem.

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