Application of Computer Software in Mapping Quantitative Trait Loci

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1 Introduction

The process of locating quantitative trait loci (QTLs) using genetic linkage maps, an ordered array of genetic markers placed along the chromosome, could be facilitated by applying efficient computer software packages. Construction of linkage maps requires that the rate of recombination be converted to distance in cM using appropriate mapping functions. However, computer software packages differ with respect to methods of computing relative distance between markers, for example, while Map Manager QT [3] does not include a mapping function and instead computes recombination frequencies in genetic linkage map, Mapmaker/QTL [2] includes a mapping function. Furthermore, Mapmaker/QTL computes the LOD score directly, whereas in Map Manager QT it has to be computed from the Likelihood ratio statistic (LRS). The purpose of this paper is to investigate the effectiveness of Map Manager QT in comparison to Mapmaker/QTL in mapping quantitative trait loci.

2 Material and Methods

F-2 mouse data from Horvat and Medrano [1] was used to examine the effectiveness of Mapmanager QT in mapping quantitative trait loci. Details regarding experimental design and data structure are given by Horvat and Medrano. Briefly the data consists of 403 F-2 progeny, (213 females and 190 males), scored at 9 genetic markers (microsatellites), with an average density of 3.83 cM. The measured trait was weight gain from 14 to 63 days. The goal is to locate the high growth (hg) locus (QTL), a region in the mouse genome that increases body weigh and body size. The data was checked for any missing information. One marker was not informative and hence was removed from the data, this may cause slight difference in relative distance between makers in this study and that reported by Horvat and Medrano. However, the effect is assumed to be negligible. It was assumed that there is a single QTL segregating, thus no control for other QTL is envisaged in this study. The data was not transformed, thus the distribution worked with here is an approximation of normal distribution and interpretation of the results may therefore be conservative. Two genetic linkage maps one for the females and the other for males were constructed and subsequently used for locating QTL using Map Manager QT. In either case, interval mapping was used on chromosome 10 assuming a free regression model. The LOD score was computed from the LRS. The results were compared to those reported by Horvat and Medrano computed using Mapmaker/QTL under the unrestricted model and are discussed in the context of comparison of computer software packages, with respect to QTL mapping.

3 Results and Conclusion

Results showing the position of the QTL of the high growth hg locus computed using Map Manager QT are presented in Fig. 1. and Fig. 2. for F-2 females and males, respectively. The maximum likelihood position of the hg locus for F-2 females was found between MIT10 and MIT41, with a LOD Score of 27.6, accounting for 44% of the variance. The same locus was found between MIT10 and MIT41, with a LOD score of 24.81, accounting for 41.5% using Mapmaker/QTL. In F-2 males the hg locus was found at MIT41 with a LOD Score of 10.1, accounting for 21% of the variance (Fig. 2.). The same locus was found at MIT41 with a LOD score of 9.56, accounting for 22.2 of the variance [1]. From these results, we can conclude that Map Manager QT and Mapmaker/QTL produce identical results. Thus either of the two softwares can be used in QTL mapping, provided other conditions for mapping QTL are met.

Acknowledgements

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References

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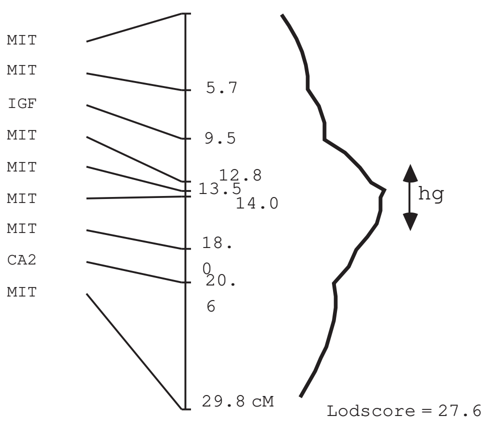

Figure 1: Interval mapping of the high growth locus (hg) in mouse for weight gain from 14 to 63 days of age for females using free regression model.

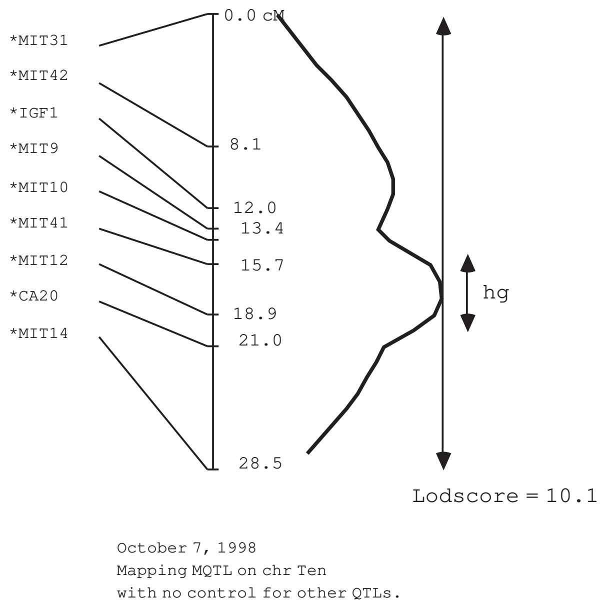

Figure 2: Interval mapping of the high growth locus (hg) in mouse for weight gain from 14 to 63 days of age for males using free regression model.