

A REVIEW OF METHODS FOR IDENTIFYING QTLS IN EXPERIMENTAL CROSSES

BY KARL W. BROMAN¹ AND T. P. SPEED

Marshfield Medical Research Foundation and University of California, Berkeley

Identifying the genetic loci contributing to variation in traits which are quantitative in nature (such as the yield from an agricultural crop or the number of abdominal bristles on a fruit fly) is a problem of great importance to biologists. The number and effects of such loci (called quantitative trait loci or QTLs) help us to understand the biochemical basis of these traits, and of their evolution in populations over time. Moreover, knowledge of these loci can aid in designing selection experiments to improve the traits.

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1. Introduction. Identifying the genetic loci contributing to variation in traits which are quantitative in nature (such as the yield from an agricultural crop or the number of abdominal bristles on a fruit fly) is a problem of great importance to biologists. The number and effects of such loci (called quantitative trait loci or QTLs) help us to understand the biochemical basis of these traits, and of their evolution in populations over time. Moreover, knowledge of these loci can aid in designing selection experiments to improve the traits.

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There are three major points which we would like to make in this paper: first, identifying QTLs is best seen as a model selection problem; most current methods do not view the problem in this way. Second, it is important to critically compare the different approaches to any problem; more refined analyses and more complicated algorithms do not necessarily lead to improved results. Finally, different situations may require different methods; with each new experiment, one must reconsider the available approaches, as each new problem may require a new method.

We will focus on a backcross experiment, and will assume that the QTLs

¹This work was part of the author's Ph.D. dissertation at the University of California, Berkeley.
AMS 1991 subject classifications. Primary 92D10; secondary 62J05.
Key words and phrases. QTL, interval mapping, model selection.