

# nature REVIEWS

## NATURE REVIEWS GENETICS

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Original design by Jane Walker

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Printed in Wales by Cambrian Printers on acid-free paper

Most would agree that complex trait genetics remains a challenge. Its ultimate goal is to understand the genetic architecture of complex traits. The journey towards this goal begins with mapping quantitative trait loci (QTLs) to broad genomic regions, and ends with the molecular identification of alleles that underlie the trait of interest. The logic of QTL mapping is far from new — today's strategies are not vastly different from those that were used in the 1920s to map traits associated with seed size in the bean *Phaseolus vulgaris*. Since then, the fruitfly has led the way in QTL mapping, and the first rodent QTLs were mapped only in the 1990s. Rodent QTLs are of particular interest owing to their biomedical relevance in the modelling of human disease.

As Jonathan Flint and colleagues point out in their Review on page 271, we have accumulated more than 2,000 mapped QTLs; disappointingly, however, only 1% of them have been identified at the molecular level. Although the field has been frustrated by this apparent crisis, help is at hand. Recent development of several new resources and analytical tools promise to make the mapping of QTLs more efficient. In their Review, Flint and colleagues rigorously evaluate and compare the newly available approaches. What is their true potential? Will they deliver on their promise and allow the community to identify the underlying genes or will they merely finely map more QTLs?

Although some fare better than others in this comparison, one important conclusion is that any one of these methods is unlikely to hold all the answers. Using them in combination will be the key to success.



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