

## Preface

The approach taken for locating the genes that underlie human diseases has shifted from pedigree-based linkage studies to population-based association studies. In both cases the proximity of a genetic marker to a susceptibility locus is inferred from statistical measures that reflect the number of recombination events between them: in a disease pedigree there are no more than a few hundred opportunities for recombination so that recombination rates less than about one percent cannot be estimated and genes can be located only coarsely on a genetic map with that approach. The linkage disequilibrium detected in an association study, however, reflects the actions of many thousands of recombination events since the initial disease mutation and the expectation is that susceptibility genes can then be mapped more accurately.

The editors of this volume have recognized the need for parallel activity in plant species. For the past 20 years, the genes that affect plant economic traits have usually been mapped with data collected from "pedigrees" of populations formed by crossing inbred lines. These Quantitative Trait Loci have been mapped on a coarse scale, and a QTL is likely to refer to several genes in a region. The move to population-based association studies was therefore as necessary in plants as it was in humans, and readers will find this book to be a useful review of the marker technology, statistical methodology, and progress to date. Although one of the authors fears that "plant genetics can be considered as less advanced than human genetics" the chapters suggest that if that is the case it will not be so for long.

The recent increased activity in association mapping in humans has rested on the development of efficient and affordable methods for discovering and employing Single Nucleotide Polymorphism markers. Plant geneticists cannot command the resources available to their human geneticist colleagues, but they can anticipate benefiting from the success of the International HapMap Project. The improvement in marker technology from such large projects will inevitably be imported to plant studies. The editors have provided helpful guides to the use of SNPs in association studies.

Along with the substantial increase in the volume of data when large numbers of individuals are typed at millions of SNPs there are substantial challenges in the statistical interpretation of the data. This book contains a valuable account of the issues of multiple testing and an accessible account of False Discovery Rates. The more basic concepts of linkage disequilibrium and case-control versus family-based association tests are also discussed. It is often the case that geneticists do not receive extensive statistical training and the coverage of the theory of estimation and testing is therefore welcome. Readers will notice a greater use of Bayesian methods than is usually found in statistical genetics books. Such methods are appearing more frequently in scientific papers.

I congratulate the editors and all the authors on this timely and comprehensive treatment of association mapping in plants. The importance of food and fiber for human welfare cannot be overstated, and progress in plant improvement will rest in no small part on the work described in these pages. On a personal level, I am delighted by the leadership shown by my fellow antipodeans.

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