

## MODERN TREATISE OF QUANTITATIVE GENETICS

**Michael Lynch & Bruce Walsh: Genetics and analysis of quantitative traits.** Sinauer Assoc. Sunderland, Mass. 1998, 980 pp.

Quantitative genetics has undergone a rejuvenation in the last ten or twenty years, due to several independent developments. Evolutionary quantitative genetics of natural populations has attracted increasing attention following Russell Lande's contributions in the 1970s. The development of genetic markers and marker maps has allowed the search for genomic areas responsible for quantitative trait variation. High speed computing has allowed implementation of computationally intensive estimation methods.

We now have available the first of the two intended volume. This part deals with the genetics and analysis, the second volume will cover evolution and selection of quantitative traits. The current volume aims at integrating three divergent research cultures. The traditional domain of quantitative genetics has been plant and animal breeding. The authors combine these approaches with materials relating to evolutionary quantitative genetics and to the special aspects of human quantitative genetics. This is a unique attempt, no previous books that I know of have covered such a wide area.

The authors carefully and thoroughly develop the theory so that it is accessible to a wide audience. The necessary basics of statistics, matrix algebra and linear models and estimation techniques are provided in initial chapters and nearly 100 pages of appendices. The actual text starts with a thorough introduction to very basic quantitative genetics: partitioning variances, additive effects and resemblance between relatives. The effects of linkage, gametic phase disequilibrium, assortative mating, and polyploidy on resemblance between relatives are all covered.

Chapter 10 gives a thorough coverage of inbreeding depression. The most recent methods for estimating inbreeding depression and for studying the gene action of responsible loci in natural populations are described. The evidence for different modes of gene action is discussed. Forest trees are part of the empirical data described here, understandably mainly papers that are published in general evolutionary literature.

The second part of the book, nearly 200 pages gives an up-to-date description of different QTL mapping methods. This is especially valuable as the genetic basis of quantitative variation is still so poorly known. I found that these chapters provided a very useful discussion from basics to advanced topics. The many differences between mapping in inbred lines and outcrossed pedigrees were elaborated, which should be appreciated by forest geneticists. Many specialised techniques for human pedigrees were described. Since the publishing of this book, the association mapping techniques based on single nucleotide polymorphisms have become a focus of research especially in human genetics, but this emerging area is not yet dealt with.

The breadth of this volume is remarkable. The book abounds with well chosen biological examples to illustrate various issues. Given the authors' background, it is not surprising that many of the examples are from the evolutionary biology literature. The forest genetics finding could well have been more broadly represented. It seems to me that forest geneticists often have results that would be of significance to a much wider audience that can be addressed through forest genetics journals.

There are several other good quantitative genetics texts, for the field in general and for forest genetics in particular. This one is a very valuable reference for graduate students and scientists. One role of this text is to put the theory and methods known to forest geneticists into a wider perspective. This book might be too much for most forest genetics courses. Reading the whole book is for real devotees. Many parts of it can be read as reasonably independent introductions to individual topics, such as the QTL discussion, or the chapter on inbreeding depression. It is valuable reading to anybody wants to get an inside look at the excitement in this field. The advantages gained by adding molecular genetics to advanced quantitative genetics are evident in many areas.

*Outi Savolainen (Oulu, Finland)*