

## BOOK REVIEW

### The Genetical Analysis of Quantitative Traits

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Chapman and Hall, London; 1996; pages xiii + 381; paperback £ 27.50

Quantitative genetics, as anyone who has tried to teach it will testify, is one of the most difficult areas within genetics to teach successfully. It is a highly conceptual field in which algebraic and statistical models are used to explain the phenotypic consequences of the cumulative action of many genes that individually have relatively small effects on the phenotype in question. Until now, the modes of action of these genes are not really understood very well, and thus there is very little concrete biological reality for the student of this field to latch on to. Till now, there have been only two major textbooks of basic quantitative genetics available: *An Introduction to Quantitative Genetics* by D. S. Falconer, and *Biometrical Genetics* by K. Mather and J. L. Jinks. Given this state of affairs, the arrival of a new textbook of quantitative genetics is bound to interest teachers and students alike. Unfortunately, though, the book by Kearsey and Pooni, although better packaged than its predecessors, does not, to my mind, offer any great improvement over the two aforementioned texts. Many of the most significant biases, shortcomings and lacunae of the previous two books are still perpetuated in *The Genetical Analysis of Quantitative Traits*.

The main drawbacks with both earlier books, in my opinion, were (i) a strong bias toward the agricultural application of quantitative genetics, with a concomitant neglect of the very important role of quantitative genetics in evolutionary theory; (ii) a tendency to jump directly into the statistical models of the components of phenotypic variation, or the algebraic models of modes of gene action at individual quantitative trait loci, without giving the reader any intuitive feel for the biological basis of these models; and (iii) the completely different notational schemes used by the authors of the two books which ended up confusing many readers who were interested enough to try and read both the books. Of these three major drawbacks, only the last has been rectified by Kearsey and Pooni in their new book. To their credit, the authors, despite being the intellectual heirs to the Mather and Jinks legacy, have decided to adopt more conventional notation used by Falconer and many others: this is indeed a good development and one hopes that it will lead to a stabilization of quantitative-genetic nomenclature and notation.

The introductory chapter, though a little terse, is well written and offers a balanced overview of the domain of quantitative genetics. Unlike previous texts, there is also a brief discussion of the historical development of quantitative genetics, a feature that I really liked. In the next couple of chapters, the authors introduce the basic models of gene action underlying quantitative variation. Here, their treatment resembles that of Mather and Jinks in that they develop the models in the somewhat artificial framework of an initial cross between two inbred strains, and then trace the means and variances of

the  $F_1$  and  $F_2$  generations, and of their respective backcrosses. I really did not like this part of the book very much even though the explanations given are quite lucid. I think that it is far easier for students to approach the quantitative-genetic models from a general consideration of phenotypic variation in an outbreeding population which is, incidentally, the approach followed by Falconer. Moreover, by dealing with an outbreeding population first, one can easily extend the concepts to evolutionary issues, as well as to more specific breeding designs used in agriculture, which can then be presented more logically as special cases of the panmictic-population models.

Chapters 4 and 5 deal with the estimation of genetic components of phenotypic variation using various full-sib and half-sib designs. The treatment here is fairly clear, with a welcome emphasis on some of the practicalities of estimating parameters of quantitative-genetic models that was sometimes lacking in previous books, especially Falconer's. Chapters 6, 7 and 8 are, in my opinion, the real strength of this book. Here the authors have dealt with some of the emerging techniques in the chromosomal and molecular approaches to quantitative genetics, and the treatment of these topics is definitely superior to that found in the latest edition of Falconer's book. The authors have provided a fairly comprehensive introduction to the recent techniques of quantitative trait loci (QTL) mapping that are becoming increasingly more important. Once again, the authors have not only provided a good discussion of some of the required background information, but have also stressed some practical issues which are often glossed over in textbooks. This makes the book valuable for researchers as well.

The treatment of panmictic populations (chapter 9) is somewhat brief and introductory in nature, but whatever is explained has been explained clearly and well. For this particular topic, though, readers would be better off consulting the chapter on quantitative genetics in the population genetics text of Hartl and Clark. More impressive is the fact that the authors have addressed in some detail the consequences of linkage, sex linkage and epistasis for the behaviour of the panmictic-population models; this is also an area neglected in previous texts. Equally impressive, and for the same reason, is the authors' treatment of models involving maternal effects and non-diploid organisms in chapter 13. The treatment of threshold characters is fairly standard, as are many of the issues covered in the final two chapters which are a sort of smorgasbord of topics in experimental design, breeding and the quantitative genetics of natural populations.

The one major disappointment I had with the book was the rather poor treatment of correlated characters and of genotype  $\times$  environment interaction. These are areas of quantitative genetics that are of great importance to evolutionary biologists and ecologists. Moreover, the past fifteen years or so have seen a tremendous amount of theoretical and empirical research done on these issues, most of which is not reflected in the very rudimentary treatment of these major topics. The problem set given at the end of the book is small and not very representative of the range of questions one may have to deal with in quantitative genetics. In this regard, I think the accompanying problem set to Falconer's book (which is published separately) is far more comprehensive.

All in all, the book is not bad at all. Its formatting suggests that the publishers are aiming it at the American textbook market (I myself prefer the old-fashioned British style, bereft of numbered subsections and end-of-chapter summaries). In many cases, the exposition of basic issues is clearer and more detailed than in either of the earlier texts by Falconer or Mather and Jinks. At the same time, though, the book will not satisfy those who are interested in quantitative genetics because of evolution rather

than its applications to plant and animal breeding. I still think that Falconer's exposition of the partitioning of variance in panmictic populations is superior to the treatment by Kearsey and Pooni. So it seems that, after all, the best teaching strategy would still be to rely upon different books for different aspects of quantitative genetics. As this is a first edition, however, I hope that the authors will try to redress the imbalance in subsequent editions, and provide a more comprehensive treatment of panmictic populations and evolutionary-genetic issues. If they could combine that with an easily understandable common-sense explanation of the components of phenotypic variation, they could have a real winner.

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