

Book reviews

Quantitative and Ecological Aspects of Plant Breeding. John Hill, Heiko C. Becker and Peter M. A. Tigerstedt. Chapman and Hall, London. 1998. Pp.376. Price £65.00, hardback. ISBN 0 412 75390 1.

The achievements of the so called 'Birmingham School of Biometrical Genetics' founded and developed by Kenneth Mather and John Jinks were described in their classical textbook *Biometrical Genetics* (1982). This is now out of print. It is therefore good to see that two books have recently been published which update the subject and are likely to prove worthy successors to the earlier textbook. The first of these is Kearsey and Pooni's *The Genetical Analysis of Quantitative Variation* (1996) and the second is this one by J. Hill, H.C. Becker and P.M.A. Tigerstedt. This is the fourth book of a series devoted to plant breeding published by Chapman and Hall so that, as might be expected, the emphasis of the Hill *et al.* book is more towards application. Both books have taken the very worthwhile step of changing the rather unfortunate symbolisation adopted by Mather and Jinks, where *d* and *h* referred somewhat confusingly to additive and dominance effects, to *a* and *d*, the symbolisation commonly used elsewhere in biometrical genetics.

The book is divided into two parts. The first deals with the various methodologies for detecting and analysing the genetic and environmental components of quantitative variation and how these may be used in breeding; the second, the interrelationships between the genotype and the environment. The latter includes extensive descriptions of the methods for evaluating genotype/environment interactions using linear as well as multivariate approaches. These lead on to chapters on stability and adaptation and the breeding for abiotic and biotic stress, followed by a final chapter on the increasingly important problems of how best to maintain and utilise genetic resources.

In the first part of the book, the description of the methodologies for analysing components of means and of variation and covariation follow closely the treatment of the subject by Mather and Jinks and by Kearsey and Pooni. There then follow important new sections on the analysis of doubled haploids and lines derived by single seed descent and the ways of using estimates of genetical variation, obtained from early generations, to predict the outcome of crosses. These chapters are well written although marred by a rather minimal treatment of linkage and its consequences for estimation and a lack of any definitions concerning linkage equilibrium/disequilibrium. Two chapters are then devoted to experimental designs, the three North Carolina designs and the complete and partial diallels. There is a fairly full treatment of the

diallel cross introduced somewhat quizzically as 'the ultimate mating design?'. This is one of the most widely used designs, and it is a plus to have its weaknesses and strengths discussed in detail, particularly as there is a great deal of controversy about its usefulness. By contrast, the Kearsey and Pooni book emphasises the weaknesses and downgrades the analysis accordingly. The final chapter of this part of the book is devoted to the principles of selection theory. This encompasses the usual topics, heritabilities, realised and expected responses to selection, and correlated responses and so on. The final few pages of the chapter introduce the subject of the application of markers in breeding and the identification of QTLs. This is a rather disappointing part of the book. This is a rapidly expanding area of interest which should have received greater exposure both theoretically and practically. The treatment of these aspects is much better in the Kearsey and Pooni book.

Throughout the present book, examples using data from arable crops, particularly oil seed rape and wheat, are used extensively. This is a good and valuable feature. The book is therefore a very useful addition to the literature on plant breeding and deserves to be read widely, both at the undergraduate and graduate levels. One wonders, however, whether in 10 years time the subject will have changed out of all recognition with the continuing onslaught of molecular analytical techniques and gene transfer technology. In this respect the authors could have done their cause a great deal of good by expanding these growth areas and speculating a little about future developments.

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Evolutionary Quantitative Genetics. Derek A. Roff. Chapman and Hall, London. 1997. Pp. 258. Price £39.00, paperback. ISBN 0 412 12971 X.

An interest in life-history evolution leads inevitably to curiosity about the genetic mechanisms that underpin it — how many genes underlie each life-history trait? do

they interact? do they affect more than one trait? how much genetic variation is there in the trait? what maintains genetic variation in natural populations? These are not such simple questions to answer, and we are lucky indeed that Derek Roff, who in 1992 gave us his classic *The Evolution of Life Histories*, has now expanded his interest in quantitative genetics into the present volume, aimed primarily at postgraduates and above. Roff's great strengths are the breadth of his scholarship, the lucidity of his writing, and his gift for simple exposition of needed mathematics. His reviews are up-to-date, as near comprehensive as is sensible and on the whole balanced, a remarkable achievement in this difficult and fast-moving field. As in his earlier book the text is illuminated by tables and graphs summarizing the main findings.

The book is logically laid out, starting with chapters on heritability and genetic correlation, what they mean and how to measure them, and going on to consider the theory and practice of selection experiments in chapters on directional selection and correlated responses. There is then a topical chapter on phenotypic plasticity and reaction norms. After two chapters on questions of effects that are sex-related or due to population size, he concludes with a major chapter on the maintenance of genetic variation.

Most chapters begin with a description of the underlying theory, although the harder parts are bridged by reference to earlier authoritative works, such as Bulmer (1985), Becker (1985) and Crow & Kimura (1970). Falconer's (1989) text, which many of us have found invaluable and used perhaps too uncritically, is found in some areas to be wanting. Perhaps a little too much space is given to the exposition of methods for estimating heritability and genetic correlation which are known to be biased.

Roff is notably optimistic about the future contribution of quantitative genetics to field studies, but here more caution is surely advisable. His confidence is partly based on his conclusion that genetic parameters are as well estimated by midparent-offspring regression as by full-sib/half-sib experiments, but he does not discuss sufficiently the problems with the regression method. Midparent-offspring regressions can be biased by nongenetic mechanisms such as maternal effects — mothers in good condition because of lucky developmental conditions may produce good quality offspring. In addition, since it is not possible to control for it by experimental design, it is assumed that parental and offspring environments are equivalent. But is this a safe assumption? The difficulty of controlling environmental effects in laboratories equipped with temperature and humidity controls makes me doubt it. Also controversial is the conclusion based on a paper just published that 'contrary to conventional wisdom' laboratory estimates of heritability will reliably indicate field heritabilities. This conclusion is based on 22 estimates from eight studies, and the evidence is clearly and fully presented. The 'conventional wisdom' is that since heritability is known to be highly dependent on environ-

ment, and since laboratory environments are generally poor mimics of field conditions, it is *a priori* unlikely that laboratory estimates can give useful guidance to what obtains in the field.

Despite these reservations and some typographical errors this is a powerful book. Its strengths can be appreciated from the last chapter, which presents an overview, and also indicates where appropriate what further research is needed. The overview summarizes the best available answers to some of the core questions used to structure the book. How many loci underlie life history traits? The answer is probably much more than 10, although whether hundreds are involved is not yet clear. However, the number is sufficient to justify the statistical modelling that is quantitative genetics. Are life-history loci independent, and is dominance important? Dominance is important but the jury is still out on epistasis, and better analytical tools are needed. How far into the future can quantitative genetics predict the outcome of directional selection? Answer, 10 to 20 generations. What maintains genetic variation in life-history traits in natural populations? Ah, the big question. Roff concludes that although mutation-selection balance models have been extremely popular, this is unlikely to be an important mechanism because fitness traits are under strong selection. He argues that antagonistic pleiotropy has been prematurely discounted, because the data show, which is needed, that dominance variance contributes significantly to the total genetic variance.

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Plant Variation and Evolution (3rd edn). D. Briggs and S. M. Walters. Cambridge University Press, Cambridge. 1997. Pp. 512. Price £22.95, paperback. ISBN 0 521 45918 4.

An earlier edition of this work has long resided on my shelf and is regarded as an old friend. It does not collect dust because it is a book I frequently dip into to refresh half-remembered examples with which to flesh-out lectures. This new version is a substantial rewrite with one hundred extra pages, but with one fewer chapters, than the previous edition. Logically, a further chapter could

also have been lost if the two short sections entitled 'Species and Speciation' and 'The Species Concept' had been merged. The first third of the book remains mostly unaltered as a wonderfully presented history of the development of our understanding of the nature of intra-specific variation. This approach is not only fascinating, but it also sets in context what is to come. The bulk of the new material is to be found in the expanded chapters on 'Recent Advances in Genecology', 'Gradual Speciation and Hybridisation', 'Abrupt Speciation' and 'Conservation: Confronting the Extinction of Species'. While these sections are certainly improved, I felt they could be a little more up-to-date and accommodate fuller explanations of recent advances in molecular, cytological and computer-based methods. Perhaps the historical perspective gives the authors scope to open the chapter on recent advances, with a statement that 'isozymes are being increasingly used'. However, as someone who spends much time crying in the wilderness 'do not forget isozymes', this came as rather a shock.

Although I have never had the pleasure of being lectured to by either Briggs or Walters, reading this book gives an impression of a verbal discourse because the text is littered with personal opinions. For example, after discussing the 1980s fashion for the study of the evolution of life-history strategies in terms of cost-benefit trade-offs, they suggest that this may not be unlinked to the 'monetarist' language which was prevalent at the time. Comments of this type and the stylish manner in which the work is crafted, result in a thought provoking and readable volume.

For all my fondness for this book I remain unsure of its intended readership. The preface suggests a target audience of sixth form and undergraduate students. However, the text frequently demands an advanced level of understanding of the subject while offering little new for the career scientist. A fine example is to be found in the three sentences we are offered in the section on late-acting self-incompatibility systems. The language is exact, the ideas perfectly correct, but if you can gasp the point you are probably already familiar with it. Consequently I am able to continue to use this new edition as an aide memoir, but wonder how easy it will be for a student to profitably dip into.

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Molecular Tools for Screening Biodiversity. Angela Karp, Peter G. Isaac and David S. Ingram (eds). Chapman and Hall, London. 1998. Pp. 498. £75.00, hardback. ISBN 0 412 63830 4.

The torrent of molecular data in evolution and ecology studies has been difficult to keep up with for anyone

familiar with the field. Several well-established and long-standing organismal-oriented journals, such as *Evolution*, *Heredity*, *Journal of Heredity* and *Genetics*, routinely carry articles on the subject and to my knowledge at least five new journals have been initiated during the past decade or so to accommodate the onslaught of molecular data in ecology and evolution — *Molecular Biology and Evolution*, *Molecular Phylogenetics and Evolution*, *Molecular Ecology*, *Molecular Marine Biology and Biotechnology* and *Ancient Biomolecules*. In addition, many edited volumes have appeared this decade that attempt to summarize and synthesize the technology (Miyamoto & Cracraft, 1991; Burke *et al.*, 1992; Zimmer *et al.*, 1993; Avise 1994; Schierwater *et al.*, 1994; Avise & Hamrick, 1995; Ferraris & Palumbi, 1996; Hillis *et al.*, 1997; Smith & Wayne, 1997). Why would we need yet another volume and set of papers on the subject such as Karp *et al.*, have produced?

I would argue the more the merrier, as the subject matter and technology involved in understanding ecology and evolution from a molecular perspective is a relatively complex and incredibly broad subject. But I would also suggest that as the number of volumes offered to students and scientists in this area increase, we need to be more focused and rigorous in our descriptions of the techniques and analyses used. So how does Karp *et al.*, fare with respect to this 'stepping up' of rigour and focus?

The authors have done an admirable job of utilizing and reining in 103 contributors from over 13 countries for this volume — a truly international effort. The book is very logically and tightly organized with five major sections describing DNA extraction, basic screening methods, probes and primers, data analysis and case studies. Twenty-four 'boxes' are scattered throughout the volume that focus the chapters in the five sections and elaborate upon many of the main topics in the book. The only section in the volume that shows a lack of focus is the final one where 16 case studies are offered to the reader to demonstrate the application of the techniques. But any volume that attempts to cover as broad a range of case study topics as the editors have, would also face this problem. The only section of the book that shows a lack of rigour is the one on data analysis, but even in failing to address some topics, such as philosophical issues in systematic analysis, the section is admirable for its even-handedness in presentation. At the very least the analysis section will tell students and researchers where to begin more detailed excursions into the difficult problems that face systematists and population biologists in analysing DNA sequence data.

Mark Chase writes in his foreword to the book 'No other recent book has devoted so much time to problems with extracting DNA.' This devotion to detail about DNA (and RNA) extractions is an example of the rigour the editors have attempted to impart to the first four sections of the book. The protocols here are amazingly detailed and helpful. Even old-pros at DNA isolation could learn something new from reading the protocols that offer safety tips and coherent reasons for safety tips, tips for

beginners, equipment needed, times required for protocols, and several boxes that elaborate on detailed protocols for nucleic acid isolation. Equally detailed, with protocols and trouble shooting tips, are the chapters that address the 'bread and butter' of modern nucleic acid technology — the Polymerase Chain Reaction (PCR).

Rigour and focus are indeed inherent in this volume. My review copy has already been in my lab and handled by several students and postdocs and has rapidly gathered many tears and chemical stains from use on the lab bench. Too bad, because the cover is kind of interesting too.

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Selection in Natural Populations. Jeffry B. Mitton. Oxford University Press, Oxford. 1997. Pp. 240. Price £50.00, hardback. ISBN 0 19 506352 X.

Jeffry Mitton has performed a valuable service in bringing together the information in this book. Despite its title, the

subject is not selection in all its guises. Rather, it reviews the data collected during the recent intense round of research on proteins, usually carried out through the agency of electrophoresis. Most of the examples concern enzymes and, as the author points out, most of these are involved in some way with respiration. *Pace* Lewontin and Hubby, the sample is not a random one from which to assess average behaviours or levels of variability. In fact, random is not a word in the index, although neutral theory does get three mentions, compared with 33 for natural selection. This reflects not only the subject matter but also the favoured hypotheses when there may be a choice. 'It is curious to me that evolutionary biologists embrace the notion that natural selection acts on the sickle cell hemoglobin polymorphism in humans — but that they usually regard as sloppy or uncritical science the notion that natural selection acts on other proteins, such as enzymes' (p. 171). Enzyme polymorphisms. 'are not trivial side-effects of randomly assembled neutral mutations but adaptations orchestrated by natural selection.' (p. 167).

The evidence for abundant genetic variation, positively correlated with environmental variability, is reviewed. Much of it can be understood in terms of enzyme kinetics, and an impressive array of data now supports the association of heterozygosity with developmental stability, high growth rate and low fluctuating asymmetry. Routine metabolic costs decline with heterozygosity. Yes, there are exceptions, but the evidence is strong enough to favour the notion of widespread balancing selection. A chapter on female choice and a final review chapter propose some coordinating genetic system models.

The author also has a sense of being at the end of an era. Evolutionary biology has turned to techniques measuring variation in DNA, opening up exciting vistas, often much more neutralist in character and some seeming to imply the existence a sort of stochastic Sargasso. Here we have a fine view of results from the enzyme period. Much has been learnt and many advances have been made, some of which extend the observations and conclusions from the study of visible characters in the pre-electrophoresis age. This book should be kept to hand by today's researchers. We need an approach which considers all levels, from the gene through the genotype to the genome, from field observation to sequencing. Only then can there be a proper perspective on evolutionary genetics. At £50 for 240 pages this book is not cheap, but it is a useful review. Roll on the paperback.

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Influential Passengers: Inherited Microorganisms and Arthropod Reproduction. Scott L. O'Neill. Ary A. Hoffmann and John H. Werren (eds). Oxford University Press, Oxford. 1997. Pp. 214. Price £22.95, paperback. ISBN 0 19 850173 0.

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