

Book reviews

Biotechnology and the Improvement of Forage Legumes (Biotechnology in Agriculture Series 17). B. D. McKersie and D. C. W. Brown (eds). CAB International, Oxford. 1997. Pp. 444. Price £75.00, hardback. ISBN 0 85199 109 2.

McKersie, in the final chapter to this volume, concludes that biotechnology offers attractive solutions to the problems of forage production in legumes; forage quantity and quality, hardiness and sustainability. This volume reviews the state of knowledge of forage legume biochemistry and molecular biology and ends with a plea for a concerted effort towards coupling biotechnology and agronomy for the improvement of forage production systems.

As one of the largest, most diverse and economically important plant families the value of legumes as forage is amply illustrated, although most of the papers concentrate on herbaceous species (e.g. *Medicago* and *Trifolium*), rather than woody species (e.g. *Leucaena* and *Calliandra*) which have great importance in many tropical production systems. The recurrent theme of the volume is the potential role of biotechnology in resolving the classical problems of forage legume production. The editors have brought together an eclectic mixture of papers that deal with topics as varied as using alfalfa as an industrial enzyme bioreactor (Austin & Bingham) to legume breeding methods (Bowley). Biotechnology in breeding method improvement is reviewed in chapters dealing with germplasm conservation (Yamada & Okumura), somatic hybridisation and embryo rescue (Arcioni *et al.*), somatic embryogenesis (McKersie & Brown) and the use of molecular markers in alfalfa (Osbourne *et al.*). Forage quality and stress tolerance biotechnology are reviewed in chapters concerned with condensed tannin manipulation (Morris & Robbins), temperature and drought stress (Castonguay *et al.*) and salinity and aluminium stress (Bouton & Parrott). The role of biotechnology in resistance to insects (Burgess & Gatehouse), fungi (Manners & Dickman) and viruses (Forster *et al.*) is also reviewed. The final section of the book contains reviews of nitrogen metabolism (Barran & Blomfield; Vance) and signalling (Phillips & Streit), whilst Austin and Bingham raise the possibility of industrial enzymes being manufactured by fields of alfalfa and it is in this paper that an omission from the book is evident. Given that the aim of the *Biotechnology in Agriculture Series* is to review advances and current knowledge in key areas of biotechnology, a paper concerned with issues related to the release of genetically engineered organisms would have been valuable and timely given the current media interest in another legume, transgenic soy bean.

The papers in this volume are likely to appeal to post-graduate students as starting material for wider exploration

of the subject area. However, it is uncertain how far this volume will stimulate the collaboration that the editors have aspired to.

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New Uses for New Phylogenies. Paul H. Harvey, Andrew J. Leigh Brown, John Maynard Smith and Sean Nee (eds). Oxford University Press, Oxford. 1996. Pp.349. Price £19.95, paperback. ISBN 0 19 854984 9.

In the past 40 years there has been a series of fads which have swept through Evolutionary Biology leaving their signatures on the fields like the sweeps of advantageous alleles: caryotypes/ banding, morphometrics, electrophoresis, molecular evolution, and now the conjunction of molecular sequences and phylogenetic reconstruction. In each case there has been a period of hard sell where the proponents pretend (or perhaps even believe) that their new methods will solve all of the major questions (Harding's chapter has equivalents in the earlier fads), then a mindless period of frantic data gathering, then a phase in which questions are finally addressed (or even asked), and finally a phase in which the strengths and weaknesses of the formerly new techniques are realistically assessed. Some of the chapters suggest that we may finally be getting to phase III of the shifting intellectual balance process. We can still hope that this will result in a greater increment in evolutionary understanding than the previous ones because we are now integrating many disparate fields with Evolution (e.g. Palaeontology, Systematics, Developmental Biology), and as a result have completely new sources of data, and this allows us to ask questions that we couldn't even have dreamt of asking before.

The book provides a snapshot of many of the new approaches. Examples include taking advantage of the dependence of gene tree growth and pruning rates upon N_e (Barton & Wilson, Nee *et al.*), individuals containing deleterious haplotypes or traits leave few descendants and therefore should be at the tips of haplotype networks (Crandall & Templeton), selected traits should yield different patterns than those more affected by history (Malhoutra *et al.*, Losos). Differences in evolutionary lability and changes in population structure, colonization and speciation may yield characteristic tree patterns (several authors). Host-parasite systems have been especially illuminated by the new approaches, for example we now have information on between-species transmission and recombinational events of diseases such as AIDS

(Sharp *et al.*), information on where strains have originated, whether and when new strains are entering populations as epidemics continue (Holmes *et al.*), whether colonisation of new hosts is opportunistic or are parasites tracking a particular resource (Page & Hafner), and whether parasite population structure affects relative rates of evolution of hosts and parasites (Page & Hafner). It may be possible to distinguish between areas which contain rapidly speciating lineages vs. those with predominantly old lineages, which is particularly useful in vulnerability studies for conservation, but the same principles could also suggest environmental conditions favourable for speciation (Moritz). These methods also allow the study of the origin and spread of evolutionary innovations, rates of evolution, speciation and extinction, cospeciation, and the effects of the environment on these processes (several authors). Among the most interesting and exciting applications are the search for general evolutionary mechanisms driven by environmental (Losos) or by morphogenetic processes (Meyer). The gems of the book were the chapters by Barton & Wilson, Otto *et al.*, Malhoutra *et al.*, Moritz, and Losos; they provided the broadest and most thorough discussions of what could and could not be done with the data, and provided the best indications of directions for future work. Oddly, the editors provided neither overview nor suggestions for future work, not the least being the evolution of sex.

My reaction to the book was unexpected: for the first time in my career I sympathized with the criticism levelled at evolutionary biologists for our lack of use of strong inference. Most chapters mention that the inferences are only as good as the phylogenies, yet nobody bothered to place confidence limits on tree structure even though methods have been available for a decade. Only Losos used a randomization test to compare the structure of two trees. There are two historical factors operating here. First, the originators of cladistics regarded tree estimates as exercises in pure reason rather than statistical inference. Second, most trees are based upon parsimony rather than maximum likelihood. As a result there are no data on uncertainty of each phylogeny reconstruction so we do not know the reliability of the topology, node lengths, or node values. Yet these are treated as given. Worse, the phylogenies are often constructed by people different from those who use them to test evolutionary hypotheses, so the users of the trees often have no idea of the data quality which went into the reconstruction, or what the uncertainty values are. Yet a good third of the chapters purported to be estimating evolutionary rates, which depend completely on tree structure. We teach our students to report standard errors as well as means and not to assume means are different without doing a test which requires using the variances, yet we are committing precisely that error in phylogenetic reconstruction and the application of reconstructed trees.

This is a very serious deficiency because there is a cascade of variances associated with these techniques. There are large variances associated with estimates from

single loci (such as mtDNA; Barton & Wilson). It is unknown how rapidly the variance declines with increasing sample loci, or the additional effects of linkage, linkage disequilibrium, or pleiotropy between apparently independent loci, but thousands of base pairs may be necessary to reduce the unknown variance to an acceptable level (Otto *et al.*). In addition, there are large amounts of intraspecific variation (Malhoutra *et al.*) making studies with one or two individuals per species suspect. There is a remarkable lack of calibration in most studies of rates, branching points, etc, yielding additional unknown variance components. There is circular reasoning about rates and spread of traits (or diseases), particularly when the constant rate assumption is used. There are additional problems in rate and other estimates because it is assumed that each trait is evolutionarily independent; even for different classes of traits this has not been tested. The statistical independence problem also applies to contiguous base pairs (Otto *et al.*). Even in studies with attempts at time or rate or character change order calibration it is still unknown, even theoretically, whether outgroups or fossils give the lower error rate in tree reconstruction and character evolution, how much the error is reduced by the addition of each fossil or an outgroup of a particular distance, and how the reduced error is propagated through the rest of the tree after the addition of the calibrating taxon. There are still arguments on how to combine different kinds of data (Benton). One of the worst problems is that sporadic events cannot be placed in a quantitative model, making theory difficult. These problems affect the quality of the reconstruction as well as what is done with the trees. Even if the reconstruction is perfect there are additional sources of variance associated with the tree-based inference. For example, there are huge errors in population structure reconstruction, genealogies from multiple loci or traits are only informative if affected in the same way by history, and the variance contribution to differing histories of loci within a species has not been examined. Coalescent methods are more sensitive to large scale ancient events than recent ones, and contractions of range and N_e will only leave a signature if N_e is small enough for long enough to induce coalescence. The critical values have not been worked out and this time inhomogeneity will bias the estimates. Rate estimates also have an error even if the phylogeny is perfectly known, and part of the error may be hidden by constant rate assumptions. Any model fitted to a tree will have an associated error and this must be combined with the error in estimating the tree itself. There are additional unknown variances contributed by the assumption that trees are branched with no hybridisation events (note the absence of botanical chapters in the book), and that current conditions are the same as those under which the species evolved. For example Moritz points out that most species in need of conservation have undergone recent dramatic changes in N_e , structure and connectivity, yet the methods cannot yet handle this.

All of these problems contribute to the variance and uncertainty of our estimates and hypotheses tests, yet no one is making any attempt to estimate their combined magnitude. Because both the underlying phylogenies and the tests of the theory have unknown error distributions and rates, it is difficult to take most of the conclusions seriously, even though the theory is clever and interesting. Hopefully this will change in time. In summary, the book is a summary of what could be done, but readers must remember the unknown levels of confidence one can place on the inferences. The best estimate is not equivalent to minimum uncertainty; just as knowing the mean tells us nothing about the standard error.

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Concepts of Genetics (5th edn). William S. Klug and Michael R. Cummings. Prentice Hall International, Inc., New Jersey. 1997. Price £29.95, paperback. ISBN 0 13 724410 X.

A glance in any university library might lead a casual observer to wonder why anyone would choose to write yet another book on Genetics. There already appears to be a staggering array of titles covering the subject from every conceivable angle. In truth, though, the competition is not as fierce as it first seems. Not to put too fine a point on it, most books on genetics are either painfully dry or else hopelessly out of date - not the type of book one would naturally choose to browse through in a spare moment and sadly, not the sort that would instill enthusiasm into the average undergraduate. In consequence, most of us who teach genetics are still seeking a standard text which covers the subject logically and accurately but without curing the reader of chronic insomnia.

Thankfully, dull is not a word which springs to mind when referring to this book. The writing style is simple but fluent, whilst the illustrations are both attractive and informative. Furthermore, each chapter closes with a short but fascinating essay which serves to illustrate key concepts. These little gems are highly topical, can be read in minutes and help to stimulate enthusiasm for the subject. There are, for example, essays on the dilemmas of genetic testing, the importance of preserving plant germ-plasm and one entitled 'Prions, mad cows and heresies'.

To my mind, however, the greatest strength of this book lies in the fact that it does not attempt to be both a work of reference and a tool for teaching. Effort is focused entirely on the latter. The layout and the text are aimed specifically at conveying a basic understanding of the subject to first/second year undergraduates. Topics covered in the book are ordered logically although the same is also true of many similar works. The difference in this book lies in the fact that the sections and chapters are designed 'to be used interchangeably, providing the

instructor with increased flexibility'. This is achieved partly through the liberal use of headings and subheadings but largely through the skilfully written explanations, most of which can be read in isolation. Specialized vocabulary is carefully defined where it is introduced and is highlighted in bold font. I found this an extremely thoughtful addition. There is also an extensive glossary containing simple definitions. At the end of each chapter is a series of simple and advanced problems which aim to test the full extent of the student's understanding. Thankfully, answers are provided. I found these of enormous value as teaching aids both in their own right and as inspiration for setting test/exam questions of my own.

Overall then, this book is an attractive buy, particularly since this edition is in paperback form and is appropriately priced for students. My only minor gripe is that the coverage of botanical genetics is perhaps a little superficial in places. For example, allopolyploidy and autopolyploidy, the behaviour of multivalents during meiosis, the importance of plant breeding systems, tetrasomic inheritance and self-incompatibility mechanisms are either not, or else poorly, covered. That said, the book still contains much of value for agricultural or botanical genetics courses. For the more general genetics courses, it is a must.

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The Molecular Biology of Insect Disease Vectors — A Methods Manual. J. M. Crampton, C. B. Beard and C. Louis (eds). Chapman and Hall, London. 1997. Price £60.00, hardback. ISBN 0 412 73660 8.

This publication claims to be 'the first detailed and comprehensive handbook of laboratory methods covering all aspects of molecular entomology'. The three editors had the unenviable task of arranging contributions from over 70 authors into 46 chapters, grouped into eight parts. In common with other works of this type, an attempt has been made to give some semblance of unity with similar section headings for each chapter. Most users of this book will not read it from cover to cover, but will instead dip into chapters relevant for their own research, so the endless repetitions of certain basic techniques will not be as noticeable. I am sure this book will be a useful addition to the shelves of many laboratories, and would make an excellent introduction for students and for more experienced researchers new to the field.

The first 6 chapters (Part One) describing the maintenance of insect colonies in the laboratory are excellent. I particularly liked the list of sandfly species and where they were being maintained; it would have been useful if