

blau and Amasino. The authors describe some of the 'triggers' that influence the onset of senescence and the characterized senescence-associated genes (SAGs) which regulate or participate in the senescence syndrome. A detailed description is given of many of the SAG products and a useful list of characterized SAGs is provided. The authors also discuss the prospects for genetic engineering to enhance or diminish senescence through manipulation of phytohormone levels and to help understand the molecular basis of induction and progress of senescence.

One of the most important applications of plant genetic engineering is the manipulation of oilseed crops as renewable sources of lipids for industrial processes. This is the topic of the review by Anthony Kinney in which he describes the objectives and strategies underway to understand the multiple steps in lipid biosynthesis and to enable manipulation of the end products. Recent progress in this field has been rapid; many genes encoding enzymes associated with the various metabolic steps in lipid synthesis have been isolated and the first commercial examples of manipulated oilcrops - rape and soybeans, are already in the market place. The author also discusses the prospects for the synthesis of biopharmaceuticals, biopolymers and multiple lipid-derived products in transgenic oilcrops.

Four contributions cover topics associated with prokaryotic molecular biology. The stable maintenance of plasmid cloning vectors in host bacteria is of great importance for many aspects of genetic engineering. Gerdes *et al.* review the recent theoretical and practical aspects of plasmid stabilization by post-segregational killing of progeny cells devoid of plasmid. The review concentrates on the anti-sense RNA regulated *hok/sok* system as found in plasmid R1, its mechanism of action and practical use as an efficient plasmid stabilization system for use in protein expression systems. The authors also describe the construction of their *hok/sok* plasmid vector which is offered to potential users.

Bastia, Manna and Sahoo provide up-to-date information on the processes involved in the termination and completion of replication in circular chromosomes of prokaryotes. The review describes the identification and structure of replication termination sites and associated proteins, particularly the replication termination protein (RTP). This is a detailed review with some good quality diagrams and colour graphics illustrating the molecular structures and interactions involved. Salyers and Shoemaker provide a short but informative description of the structure and functions of conjugative transposons, a widespread group of bacterial self-transmissible elements. The mechanisms of integration, excision and transfer of the elements and co-resident plasmids are described and the implications for the horizontal transfer of antibiotic resistance genes between different bacterial species discussed.

Polycyclic aromatic hydrocarbons (PAHs) such as naphthalene and phenanthrene, are extremely harmful and possibly carcinogenic compounds found as pollutants in the environment. Zylstra, Kim and Goyal review the

state of knowledge concerning the biochemistry and molecular biology of microbial systems capable of the modification and degradation of these compounds. Sequence comparison of the genes encoding the modifying enzymes in different organisms has indicated potentially valuable diversity in these systems for degradation of different PAHs.

Two items are concerned with aspects of animal genes and genetic engineering. Li and Perrimon discuss recent research in the rapidly expanding field of tyrosine receptor kinases (RTK) and the complexes formed with associated proteins known as the 'RTK signalling cassette'. This is a concise and interesting review with some good clear explanatory diagrams. It is based largely on data from *Drosophila* mutant experimental systems and discusses the mechanisms and specificity of signal transduction by the RTK cassette following ligand binding at the cell surface.

In another interesting contribution Kenneth Peterson reviews the use of yeast artificial chromosomes (YACs) to generate transgenic mice. The methodology of handling and manipulating YACs, the generation of transgenic mice and the subsequent identification and genomic analysis of the transgenics are described. The advantageous use of YACs to investigate transgene expression from inserted genes or gene loci is discussed.

All in all this is an excellent collection of reviews by experts in their respective fields, several of which are of particular interest for plant molecular biologists. As in other issues in the *Genetic Engineering* series, these reviews present current information but do not assume the reader has expert knowledge in any of the topics. At \$85 the book is not cheap, although considering this works out at less than \$6 per review and they are largely up-to-date and comprehensive, this is a worthwhile purchase and should be available in all science libraries and biology departments.

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Plant Breeding Systems (2nd edn). A. J. Richards. Chapman and Hall, London. 1997. Pp. 529. Price £29.99, paperback. ISBN 0 412 574500.

It is just over a decade since John Richards' massive work *Plant Breeding Systems* appeared. The first edition was an ambitious review of the vast literature on the biology of mating in seed plants from an ecological and evolutionary viewpoint. Not surprisingly given the author's interest in natural history and systematics, the first edition was crammed full of personal observations and an extensive literature on the pollination biology and mating systems of plant species. No other text on plant reproduction was as comprehensive and the volume has served as a valuable resource for students interested in the complex but fascinating world of plant sexuality. Now a second edition has

appeared providing an opportunity to review recent progress in the field and to assess the extent to which the author has responded to reviews of the first edition. Unfortunately, on both counts the discerning reader may be disappointed.

Over the past decade research on plant mating has largely focused on three general approaches: the development of theoretical models, microevolutionary studies on the ecology and genetics of populations and the application of phylogenetic methods for reconstructing the history of reproductive adaptations. The last two approaches have worked best when specific predictions arising from theory have been tested. Unfortunately, as pointed out in reviews of the first edition (e.g. Ennos, 1987; Barrett, 1988) Richards' distrust of mathematical models meant that he was frequently forced to develop complex verbal arguments to explain particular evolutionary scenarios. These often lacked rigour, appeared *post-hoc*, and in most cases were virtually untestable. This problem is again evident in the second edition. Dismissive comments about theoretical models are sprinkled throughout the book; instead Richards provides a mass of undigested observations and speculations from which it is hard to draw any general principles. The new edition, like the first, cries out for a sound conceptual framework accompanied by a careful winnowing of relevant empirical data. A recent review by Morgan & Schoen (1997) pointed out that most problems in plant reproductive biology can be addressed by considering four general theoretical principles. Readers of the second edition of *Plant Breeding Systems* would likely find the text a lot easier to digest if the many observations and experiments covered in this book were related to these principles.

Not only is much theory development over the past decade absent from this work, but also research using phylogenetic analyses to investigate the evolution of plant reproductive traits has been largely ignored. This is unfortunate because in many places the author constructs evolutionary stories involving trait evolution among related taxa that could best be examined within an historical framework. This is particularly evident in chapter 7 where all manner of evolutionary transitions are hypothesized to explain the patterns of variation in his favourite genus, *Primula*. Elsewhere in this chapter the claim is made that floral monomorphism in *Amsinckia* is ancestral to dimorphism (p.283), but without any evidence. A recent molecular phylogenetic study of this genus by Schoen *et al.* (1997) indicates the reverse polarity.

Aside from the limited use of theory and the lack of consideration of phylogenetic issues, important topics such as modes of self-pollination, pollen discounting, cryptic incompatibility, *S*-allele genealogies, developmental analysis and QTL mapping of reproductive traits, and the measurement of selection on floral variation are either not mentioned or are given cursory treatment. Literature citations are idiosyncratic, with many influential papers by leaders in the field missing. For example, there are no references to Marcy Uyenoyama's important work

on self-incompatibility and no references to the many papers that have been published on the floral biology and mating systems of *Mimulus* spp. over the past decade by Kermit Ritland, Mark Macnair, Doug Schemske and others. David Lloyd and Dan Schoen's important articles on the ecology of self- and cross-fertilization are missing, as are Tom de Jong and Peter Klinkhammer's slew of papers on floral display and geitonogamy. Illustrations and photographs are much improved over the first edition, but several should never have been included (e.g. figs 5–14, 7–7, 9–2).

What are the major differences between the first and second editions of *Plant Breeding Systems*? In the preface it is stated that 'nearly all of the book is completely rewritten', but a careful read indicates that this is a rather exaggerated claim. True, there is an impressive number of new figures and 500 additional references, with many as recent as 1996, but the basic structure of the book and most of the section headings are the same in the two editions. The chapter on vegetative reproduction has been dropped from the second edition, as has any mention of ferns and gymnosperms. Chapters 1–5 are concerned primarily with the basic features of sexual reproduction in flowering plants and various aspects of floral biology with the next five chapters covering self-incompatibility, heterostyly, gender strategies, selfing and apomixis. A rather unsatisfying five page final chapter lists six main conclusions of the work and then goes off on a tangent by summarizing Jim Hamrick's surveys of the associations between various ecological and life history traits and allozyme variability. A peculiar finish to the book.

As is evident from this review, I have serious reservations about the content and style of Richards' book. However, my major criticism concerns the lack of scholarship evident in almost every chapter. While differences of interpretation and some speculation are to be expected, the occurrence of many factually inaccurate statements is not. Earlier reviewers drew attention to this problem following publication of the first edition, but unfortunately Richards' carelessness with facts is also a feature of the second. Authors cited in the book would do well to check the details of how their work is presented. My own discovery that *Narcissus* has five distylous species (p.245) and that *Eichhornia paniculata* is 'mostly clonal' (p.375), pollinated by 'sphingids' and that its populations experience bottlenecks due to 'cold spells' (p.295) came as a bit of a surprise. In fact our papers said nothing of the sort. *Narcissus* has no distylous species and *Eichhornia paniculata* is a bee-pollinated annual native to the tropics!

As a general entrée into plant reproductive biology there is probably no better buy than *Plant Breeding Systems*. The book has hundreds of examples of floral adaptations and is full of potentially interesting research problems that would benefit from in-depth study. My only suggestion would be that researchers consider placing a clear warning on their copy of this book that states: *students beware — check all facts carefully before proceeding further!*

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Molecular Evolution. Wen-Hsiung Li. Sinauer Associates, Inc., Publishers, Sunderland, MA. 1997. Pp. 487. Price £32.95, hardback. ISBN 0 87893 463 4.

Most people are aware that one of the most employable areas in biology is currently 'bioinformatics'. The reason is simple. Having spent the last decade pouring money into genome mapping projects and developing ever more efficient methods for gathering DNA sequence data, we are now waking up to the fact that data are being collected rather faster than they can be analysed. Despite the fact that the world's burgeoning DNA databases probably already contain important clues that would help solve many key questions about genome function and molecular evolution, these resources remain largely untapped. Li's book has the potential to ameliorate this sad imbalance by reviewing both what we know about molecular evolution and the methods by which we can analyse and interpret patterns in DNA sequences.

The book is aimed at advanced students and young researchers, and overall I found it a very enjoyable read. The style is light and clear, particularly in view of some of the more technical areas covered. In structure, the book falls somewhat into two halves. The first half comprises

chapters which deal with processes acting at the level of the nucleotide base itself, covering mutational biases, rates of change, the molecular clock and phylogenetic analysis. This section includes a thorough review of methods by which one can estimate the rate and nature of evolutionary change, and leans perhaps predictably towards mathematical rather than empirical approaches. The second half contains a number of rather more descriptive chapters, many of which are pleasantly laced with well-selected and well-presented examples. Complex and challenging concepts such as concerted evolution are explained particularly lucidly.

My main concern is that the book's great strength is also one of its weaknesses. For the reasons outlined above, mathematics and statistics are likely to play an ever greater role in leading-edge biology and, as time goes by, niches available for the numerically challenged will become fewer and fewer. Consequently, books like *Molecular Evolution* can only become more important. Unfortunately, most of the students I deal with are still a long way from feeling comfortable with the sorts of equation which they will meet when they open this book, and I fear that many will be scared away. It is an understandable shame that wherever there is a chance to ameliorate the problem by expressing a concept in words rather than symbols, Greek letters invariably seem to win the day. Similarly, I was mildly peeved to find the same predilection colouring subjects such as microsatellite evolution, where key empirical evidence is passed over in favour of, rather than complemented by, a host of interesting but rather inconclusive theoretical studies.

In summary, this is a enjoyable book which reminds me somewhat of cough medicine. Although initially unpalatable to those who suffer from long-equationophobia, it slips down surprisingly easily and will certainly go a long way towards preparing the recipient for an increasingly quantitative future.

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