

## Book reviews

**The Production and Uses of Genetically Transformed Plants.** M. W. Bevan, B. D. Harrison and C. J. Leaver, (eds). Chapman and Hall (London) in association with The Royal Society. 1994. Pp. 111. Price £40.00, hardback. ISBN 0 412 60060 9.

In the Spring of 1993, 10 years after the discovery of a technique for introducing foreign genes into the plant genome via *Agrobacterium tumefaciens*, a discussion meeting on plant genetic engineering was held at the Royal Society. Speakers at the meeting were asked to contribute short review papers dealing with different aspects of plant transformation technology, and this volume contains those papers collected together, in the form in which they originally appeared in the Transactions of the Royal Society. There are 14 papers in total, with an average length of 7 printed pages (more than it might seem, since the book is in A4 format, with 2 columns to a page), plus introductory and closing remarks by the editors. The book is handsomely produced, and has a reasonably comprehensive if rather quirky index.

This publication is very different from most volumes of conference proceedings, which are of little interest to anyone except specialists well-advanced in their research careers. Here we have a collection of articles which are written in an approachable style, which individually provide clear summaries of their sub-topics, and which taken as a whole provide a wide-ranging survey of plant genetic engineering as of 1993. It is remarkable how far this technology has advanced in 10 years, from the first experiments which suggested what might be possible, into something like maturity. Contributors to the volume include some well-known names in the field, from the international scientific community both inside and outside academic institutions.

The subjects covered in this volume are all the favourite and fashionable ones in plant genetic engineering. Possibly, a reader familiar with the field might complain that the contents are rather predictable; thus we have chapters by Caroline Dean on *Arabidopsis* as a model system for cloning genes, Mark Stitt on using transgenic plants to investigate metabolic regulation, control of ripening by Grierson and Schuch, and so on. However, on reading these chapters, one is struck by the fact that these people have become well-known names for good reason, namely that they are experts in their subjects, and are able to convey the essence of their expertise in a succinct and comprehensible manner. Of course, not all the chapters are written at quite the same level, but the volume does not suffer from the marked variability in content from chapter to chapter that is normal in conference proceedings. Further subjects covered include genetic engineering of plants for resistance to viruses, fungi and insects, manipulation of defence and stress responses,

plastid engineering, the more academic areas of transcriptional control and RNA splicing, and the more technological areas of rice transformation, production of industrial materials, and commercialisation of genetically engineered crops. There are one or two areas that are not covered which could well have been included; production of antibodies (and other proteins), manipulation of fertility, and new transformation methods (biolistics is hardly mentioned) are several that spring to mind.

The one major criticism that could be made of this volume is that many of the chapters are just a little too short, and a number bear the signs of having been given the Procrustean treatment to reduce them to a rigidly applied size limit. This is a pity, as the extra space required to allow the authors to express themselves fully would not have been that great. As it is, the chapters tend not to contain quite enough information to make the topic fully comprehensible to undergraduate students. Several chapters would also have benefitted greatly from the addition of a diagram or two. Despite this caveat, the reviewer has found that chapters from this volume have been well received by second- and third-year undergraduates as topics for essays and tutorial discussions. Possibly first-year postgraduates would also find the book a useful survey of this rapidly widening area of research.

In summary, perhaps not a volume for the specialist's bookshelf, but one that can be warmly recommended to University, College and Departmental libraries. If it were only half the price (in paperback?), it could also be recommended to anyone who wants to inform themselves or others about how far plant genetic engineering has progressed in 10 years.

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**Crossover: Concepts and Applications in Genetics, Evolution and Breeding — An Interactive Computer-Based Laboratory Manual.** Jack E. Staub. The University of Wisconsin Press, Madison. 1994. Pp. 359 (+3.5" DS DD Macintosh formatted floppy disk). Price £27.00, comb-bound. ISBN 0 299 13564 0.

'Crossover', is a combination of a ring-bound laboratory manual and Macintosh software (built with and requiring HyperCard) which is designed to teach some of the principles of genetics (heavily biased towards plant genetics and

plant breeding). It runs the gamut from chromosomes and meiosis, through Mendelian genetics and genetic linkage, natural and artificial selection and quantitative genetics, to plant breeding, mating designs, molecular markers and patents. Many of these areas (although not patents) are accompanied by computer exercises which are designed to illustrate the main concepts.

So how well does the combination work? Not very well in this instance, in my opinion. This is largely because the software is not very exciting (visually or in action) and 'Crossover' does not make use of the computer's ability to generate and sample populations. Hence, the programs add little to the message that is conveyed in the text. Variation is at the heart of genetics and yet all of the computer illustrations are entirely deterministic! The computer has great potential to get across the concept of stochastic processes, from the sampling of alleles or gametes within a family, through genetic drift at neutral or selected loci in populations to variation in the outcome of breeding programmes. Yet nothing in 'Crossover' exploits this potential.

So what do the computer programs demonstrate? They are often simple demonstrations which require the user to supply an answer to a simple question. For example, in an exercise at the beginning of the course, simple diagrams of the stages of meiosis are given and these have to be identified. Later, one has to provide the genotype frequencies in a population undergoing selfing, or one can follow (deterministic) changes in a population undergoing selection. Towards the end of the course, there are computer modules allowing the calculation of parent-offspring regression on small sets of data (supplied by the computer or by the user) or to predict genetic gain in a number of alternative breeding schemes. The computer programs are of more value in the later part of the course, where there are too many alternative sets of parameters for pen-and-paper exercises, but they are not as useful as they might have been.

The computer programs are also misleading at times and not very robust to user error. In one example the user is asked to enter 'Probability of including all alleles or % alleles retained in sample'. Supplying the probability works, supplying the percentage does not. In this, as in other programs, there is no warning if the value you supply is out of range.

Is the book itself of great utility? No, I do not think so. In sampling genetics from Mendelian inheritance to patenting it touches lightly on each subject and omits many. Hence, many of the ideas are explained in insufficient detail to make them comprehensible and others are simplified to the extent that they become misleading. (In defence, it has to be said that the foreword emphasizes that 'Crossover' is designed to complement, rather than replace, formal texts).

Although computer demonstrations and simulations are of great value in the teaching of genetics and breeding, I do not think that this package of book and software makes the grade. There are some great packages out there simply waiting to be lifted from anonymous ftp sites around the world (try, for example, GENU and PEDIGREE from metz.une.edu.au/pub/genup — great fun for animal breeders or those wanting to plot their pedigree and calculate their

breeding value for body weight), so why pay for something less exciting?

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**Handbook of Human Genetic Linkage.** J. D. Terwilliger and J. Ott. The Johns Hopkins Press Limited, London. 1994. Pp. 307. Price £49.50, paperback. ISBN 0 8018 4803 2.

Genetic linkage analysis has revolutionized human genetics in the last ten years. Genes responsible for cystic fibrosis and other important Mendelian disorders have been isolated and, recently, more complex disorders such as familial forms of cancer have also succumbed — as a direct result of their initial localization by linkage analysis. By the standards of mouse or *Drosophila* genetics, human pedigrees are pitifully small and the phenotypes increasingly complex as interest turns to more common diseases. Yet linkage still looks set to remain the cornerstone of human genetics. This year also marks the tenth anniversary of the most widely used human linkage analysis programme, LINKAGE, published by Marc Lathrop and co-workers including Jurg Ott, one of the authors of this book. The book is a practical handbook for human linkage analysts which will be warmly welcomed by the gene mapping community. A book of this sort is also long overdue. It is sad that it has taken 10 years to obtain reasonable documentation and descriptions of the programmes. This title is misleading — it should be 'Handbook to the LINKAGE Program Package' — since it confines itself largely to explanations and worked examples for these programmes. It is also ironic that the book should appear at a time when many have moved on to using or developing a variety of other programmes, capable of tackling knottier problems such as homozygosity mapping or extended sib pair analysis more efficiently. Some people will therefore be disappointed that alternative programmes and approaches are not covered in much detail. However, this is not an ideal world and probably no-one is sufficiently familiar with the variety of software that is currently available to provide a *vade-mecum* for the complete mapper.

First, the book's strong points. It has a short but succinct introduction to the theory followed by an 88 page section covering all aspects of two-point linkage analysis using LINKAGE software. It leads the reader step-by-step through the various files and shows how to enter the data as well as providing worked examples. This is followed by a similar section on multipoint analysis. It covers the bread-and-butter topics of human genetic mapping and includes brief sections on exclusion mapping, sex differences in recombination, and interference. The final section deals with 'advanced topics' — mutation rates, estimating allele frequencies, linkage disequilibrium, parametric and nonparametric analyses of complex disorders, heterogeneity and simulations. This section is especially interesting to those already familiar with the