

dition of relationships between Hawaiian *Drosophila* species, and Marvin Wasserman does the same for the *repleta* species group. John Sourdis and Krimbas describe how the traditional methods of inversion phylogeny can be combined with modern methods of phylogeny reconstruction.

This book provides an invaluable resource for *Drosophila* evolutionists, with extensive bibliographies which cover both the classical and modern literature. With the advent of the *Drosophila* genome project, it should soon be possible to establish the ages of origin of many of the inversions which have been the objects of study for so long by sequencing of genes close to the breakpoints; this will probably mean another burst of activity in this venerable area of research, for which the information summarized here forms an essential background.

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*Experimental Design and Analysis for Use in Tree Improvement.* By E. R. WILLIAMS and A. C. MATHESON. CSIRO. 1994. 174 pages. Paperback. Price US\$45.00 plus US\$6.00 postage. ISBN 0 643 05555 X.

This book started life as a series of two-week courses given by E. R. Williams in China (along with A. C. Matheson), Thailand and Kenya on behalf of the Australian Centre for International Agricultural Research (ACIAR). Experience gained whilst delivering those courses caused the authors to generate a book aimed particularly at experiments involved in the design and analysis of forestry field trials.

It is a relatively short book divided into eight chapters. Each chapter covers a different aspect of design and analysis so that gradually the experimenter understands what sort of experiment he should be planting, how to organize himself so that he collects data most efficiently, how to analyse the data at a single site and how to bring data together for across sites analysis. There is a complete chapter on calculation of variance components and heritability before finishing up with a further two chapters on the theory and analysis of more complicated incomplete block designs. Mixed model analysis is being used increasingly in connexion with genetic tests in tree improvement circles. The book makes a good attempt at introducing Residual Maximum Likelihood (REML) and illustrating its use in analysis of progeny tests.

The book is concentrated reading. GENSTAT 5 is the recommended statistical package and throughout the book every step of analysis is accompanied by a sample set of data, GENSTAT 5 programme to analyse the data, and likely output from GENSTAT. This means that any experimenter could just follow

the supplied 'recipe' when it comes to data analysis and should be sure of getting results.

It is also nice to see a GENSTAT orientated book whilst so many others prefer SAS. I did, however, get the feeling that too many pages are occupied with GENSTAT programs and output as opposed to a more thorough breakdown of how to calculate variance components and heritabilities from calculated mean squares. And really it is not necessary to supply two or more pages of sample data when space is so scarce. There are often so many tables in each chapter that the text becomes far removed from the table it may be referring to.

Two other software packages are heavily recommended – DATACHAIN to help collect data in a logical manner and in a form readily understood by GENSTAT, and ALPHA+ which provides a convenient means of constructing alpha (incomplete block) designs. If a tree improvement team decides to use any other form of computer software, it really does devalue the relevance of the book.

When it comes to planting a large number of varieties in genetic tests the use of multi-tree plots in incomplete blocks is suggested rather than Single Tree Plots (STPs) with many replications. This book is quite clear that the former is best despite use of the latter by large numbers of organizations across the USA, Europe and New Zealand. It takes advantage of a few opportunities to relate the problems of missing trees and less effective ways of calculating error components in ANOVAs when using STPs.

Despite these minor criticisms it has to be recommended as a good 'how to do it' book. Following the directions of this book will result in properly collected and analysed data (if you use the illustrated software), but it will probably be better to refer to some of the other texts in order to interpret what the numbers mean in terms of genetic gain.

I suggest that if you are in the business of experimental design and analysis of forest trees, or a student of tree improvement, you buy this book. But make sure you keep it next to Falconer (*Introduction to Quantitative Genetics*) or Fins, Friedman and Brotschol (*Handbook of Quantitative Forest Genetics*).

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*Molecular Mechanisms of the Immune Response. Cancer Surveys Volume 22.* Edited by W. F. BODMER and M. J. OWEN. Cold Spring Harbor Laboratory Press. 1994. 117 pages. Price \$75.00. ISBN 0 87969 442 4.

This slim volume represents the proceedings of a symposium held in late 1993 to celebrate the career of

Dr Mike Crumpton, formerly Director of Research at the Imperial Cancer Research Fund (ICRF). The symposium focused on the role of cell surface molecules in presentation of antigenic peptides by antigen presenting cells, specific recognition of these peptides by T lymphocytes, transduction of antigen-specific and accessory signals from the cell surface to the interior of the cell and initiation of immune responses such as cell division and cytokine production.

The first chapter (Bodmer) reviews the evolution of major histocompatibility complex (MHC) molecules from primitive histoglobulins, the functional significance of MHC polymorphisms and the down regulation of MHC expression in placental and neoplastic tissues as a mechanism for immune avoidance. Chapters 2 and 3 (Young *et al.* and Grey *et al.*) summarize the mass of data regarding interactions between antigenic peptides and the peptide-binding groove of Class I MHC molecules. The wealth of detail in these two contributions highlights the relative paucity of information regarding the equivalent reaction between antigenic peptides and the T cell receptor (TcR).

Chapter 4 (McMichael *et al.*) puts the preceding chapters into a functional context, detailing the peptide specific cytotoxic T lymphocyte (CTL) response to polymorphic antigens of the human immunodeficiency virus (HIV). Meuer *et al.* (Chapter 5) discuss the role of accessory signals in regulating the response to TcR triggering. In particular they have examined the mitogenic consequences of the physical interaction between the TcR and CD2 and the differential requirement for accessory signals in the induction of IL-2 receptor and IFN $\gamma$  synthesis on the one hand and of IL-1, IL-2 and IL-6 synthesis on the other.

In the last three chapters, the intracellular signalling events downstream from the TcR are reviewed. Izquierdo Pastor and colleagues have dissected the molecular pathway from the TcR/antigen complex, via p21<sup>ras</sup> to expression of the IL-2 gene. Perlmutter describes the role of the SRC protein tyrosine kinase family in controlling thymocyte differentiation and Jackson *et al.* attempt to unravel the sequence of tyrosine phosphorylation events and the formation of signal transducing multimolecular complexes.

This is not a book for beginners: the editors assume a fairly detailed working knowledge of the immune system. However, although not as all-embracing as the title might suggest (B cells and antibodies scarcely get a mention), this book is a concise, comprehensive and extremely readable review of current understanding of the molecular mechanisms of T cell activation.

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*The Families of Flowering Plants, Interactive Identification and Information Retrieval.* By L. WATSON and M. J. DALLWITZ. CSIRO. 1993. Booklet 40 pages and CDROM. Available from CSIRO Information Services, P.O. Box 89, East Melbourne, Vic 3002 Australia. Price US\$180 for customers outside Australia & New Zealand (+10% for postage + handling). ISBN 0 643 05507 X.

This publication provides detailed descriptions of the characters of all the world's families of flowering plants, together with computer programs for identification and retrieval.

The information available includes the traditional kind of plant taxonomic morphology, such as details of the flowers and fruits, but also a great deal of other data, such as the photosynthetic pathways, germination type, stigma type, anther ontogeny and pollen morphology, wood anatomy, sieve tube plastids and phytochemistry, making about 470 characters in all for 563 families. In addition, the families are assigned to various different classifications and there is an outline of their world geographical distribution. Lastly, there are 690 colour images.

Watson has been working on the project for 20 years or more, and has been at great pains to make his data both comparable and complete. His personal interest in plant anatomy is reflected in the choice of characters. Dallwitz was the creator of the DELTA (Description Language for Taxonomy) format, now an international data standard, upon which this and other major projects are based e.g. the Grass Genera of the World (1988). He is also the author of the INTKEY program for identification and retrieval.

ANGIOFAM is not a database in the relational sense, but rather a data file with accompanying programs. These are intended for the DOS operating system on the IBM PC only. The programs are user friendly and provided with numerous help screens, but users who are accustomed to use only software under Microsoft Windows 3 will need to make a little more effort than they are accustomed to do. The INTKEY program has a wealth of different commands, and a beginner will not need all of these.

Are there any alternatives? You might try the MEKA program by Duncan & Meacham (1986), based on the punched card key published by Hansen & Rahn (1969). That is a good deal simpler, but does not include nearly so much information. It is expected to become available on the Internet at the University of California at Berkeley quite soon.

## References

- Duncan, T. & Meacham, C. A. (1986). Multiple-entry keys for the identification of angiosperm families using a microcomputer. *Taxon* 35, 492-494.