*Heredity* **75** (1995) 547–548


# Book reviews

**DNA Fingerprinting.** M. Krawczak and J. Schmidtke. BIOS Scientific Publishers, Oxford. 1994. Pp. 107. Price £16.00, paperback. ISBN 1 872748 43 0.

This book provides a commendably brief, and more than commendably comprehensive, up-to-date account of the topic of DNA fingerprinting. There is good coverage of all aspects of the subject, from the basic physical and chemical structure of DNA and the organization of genomes through to the statistical analyses of the genetics of populations. Thus, a sound overall account of this important and rapidly developing area is provided.

The book begins by covering the molecular structure of DNA and genome organization, and this provides some useful background information, although the coverage of certain topics is rather sketchy and incomplete (for example, section 1.2.3 on Gene expression). However, in those areas most relevant to the subject of DNA fingerprinting, the information provided is sound and comprehensive; section 1.3 on the molecular organization of the human genome is especially good.

Chapter 2 gives a valuable account of the many different techniques relevant to this field and is greatly strengthened by the inclusion of illustrated examples. However, I was a little surprised to find no mention of the techniques of DAF (DNA amplification fingerprinting) or RAPD (random amplified polymorphic DNA) analysis. A final section on the applicability of DNA fingerprinting to human genome research and clinical medicine makes a very worthwhile addition.

Chapter 3 deals with the origins and maintenance of DNA polymorphisms. This is a particularly valuable part of the book as it draws together, in a succinct and unifying way, the many different mechanisms involved in these processes. The inclusion of brief accounts of both the selectionist and neutralist theories of molecular evolution should stimulate critical consideration of these complex and relevant issues.

Chapters 4 and 5 are devoted to the application of DNA fingerprinting to the specific cases of suspect identification and the establishment of familial relationships, respectively. In both chapters, the coverage of the different techniques available and the relevant statistical analyses is very good indeed and there is a frank and valuable discussion of some of the problems encountered in the statistical analysis of DNA fingerprinting data.

The book concludes with a brief, but important, examination of some of the ethical matters pertinent to the uses and possible abuses of DNA fingerprinting. These are matters of which those working in this field should be keenly aware.

The book is well and generously illustrated and the inclusion of a glossary, as well as references and titles for suggested further reading, are additional strengths.

There are two specific matters that require attention. First, the alignment of the terms '2N' and '4N' on the right hand side of Figure 1.4 is imprecise; secondly, on the top line of page 22 (section 2.1.6.) the word 'virus' should be replaced by the word 'vector'.

Overall, this is an excellent short text on a complex and rapidly expanding field that spans many different disciplines. It should prove very valuable to anyone with any interest in this area and I would commend it heartily.

SIMON HETTLE
*Department of Biological Sciences*
*University of Paisley*
*High Street*
*Paisley PA1 2BE*
*U.K.*

**Environmental Gene Release: Models, Experiments and Risk Assessment.** M. J. Bazin and J. M. Lynch (eds). Chapman and Hall, London. 1994. Pp. 166. Price £24.99, hardback. ISBN 0 412 54630 2.

The ability of recombinant DNA techniques to allow the genetic manipulation of plants and microorganisms towards improved or novel abilities has opened widespread possibilities for both deliberate and accidental release of engineered organisms. Most public and scientific attention in recent years has been focused on the deliberate release of organisms, primarily for agricultural benefit, but also for such specialist tasks as the removal and detoxification of pollutants. It is probably true to say that the issue of releasing such genetically-manipulated organisms (GMOs) into the open environment has spawned more multi-authored books than it has refereed papers. This volume is, however, novel in that it deals with the subject from the standpoint of mathematical modelling of plant and microbial populations and gene flow. The ultimate aim of such studies is presumably to provide measurable parameters for risk assessment within the context of international regulatory legislation.

The book contains chapters on modelling plant growth, models for microbial population dynamics and interactions, gene exchange in soil and the phytosphere, sampling difficulties, risk assessment and a round table paper on mobile genetic elements as risk factors in the dissemination of released genes. These diverse topics are embraced by a mixture of theoretical papers, reviews and semi-experimental communications written by an international panel of authorities in this field. As is always the case in such books, the experimental/methodological contributions suffer from the occasional poor quality gel photograph or autoradiograph, because the authors would understandably wish to

publish their best quality primary results in refereed journals. However, the statistical analyses are clearly set out and explained in the context of the ecology of the plant, bacterial and fungal systems examined.

A number of minor and not so minor irritations were encountered on reading the book. For example, although it is relatively trivial, the specific names of some microorganisms such as *Thermomonospora chromogenum* and *Cladosporium* are incorrectly spelled. More importantly, statisticians and modellers should not forget the ultimate sources of their primary data — I was surprised to find experimental results in one chapter that had been extensively processed, but whose primary experimental source had not been acknowledged.

Apart from the chapters on genetic exchange and the appendix on mobile genetic elements, the book will be of passing interest only to most card-carrying geneticists. There is more here for modellers, soil microbiologists and ecologists, who will find some of the statistical treatments useful. This is probably a book of most use in the library of the specialist in this area, or of those interested in agricultural sciences as opposed to mainstream genetics.

JON SAUNDERS
*Department of Genetics and Microbiology*
*Life Sciences Building*
*The University of Liverpool*
*PO Box 147*
*Liverpool L69 3BX*
*U.K.*

**DNA Sequencing: The Basics.** T. A. Brown. IRL Press at Oxford University Press, Oxford. 1994. Pp. 101. Price £9.99, paperback. ISBN 0 19 963421 1.

To the novice, DNA sequencing gels that yield more than three hundred base-pairs of unambiguous sequence are a cause for celebration. Too often such experiments are blighted by technical shortcomings, and provide only one or two hundred base pairs of information. Yet with experience, one can consistently obtain beautiful sequence data.

The transition from novice to experienced sequencer is rapidly achieved if the investigator understands how DNA sequencing works, and learns to diagnose problems causing sub-optimal results. *DNA Sequencing: The Basics* is expressly written to facilitate this transition. It explains DNA sequencing from first principles, and guides the beginner through the standard sequencing protocols, explaining the significance of each step along the way.

The book has five chapters. The first chapter outlines current methods used to sequence DNA. The next three chapters, the heart of the book, focus on Sanger's dideoxy mediated chain termination method. They explain how template DNA is prepared, how the strand synthesis reactions are carried out, and how sequencing gels are run and the sequence read from autoradiographs. The chapter on strand synthesis is particularly informative. It details how the properties of different DNA polymerases affect sequencing reactions, and describes various methods used to label terminated chains. It also explains clearly how nucleotide concentrations and reaction incubation periods can be manipulated to obtain sequence from regions of the template which are at different distances from the primer binding site. The final chapter describes Maxam–Gilbert chemical degradation sequencing, and lists some advantages of chemical degradation sequencing over the more commonly employed chain termination method.

*DNA Sequencing: the basics* is well written: it is short and easy to read. The author makes abundant and fruitful use of simple figures to outline procedures and to describe graphically what is happening at the molecular level at each step of the protocol. Primary data are provided to show the results of successful experiments, and to illustrate problems frequently encountered in sequencing. The book also has a comprehensive glossary, an index, and short lists of references at the end of each chapter. Readers expecting protocols will be disappointed: *DNA Sequencing* does not provide sequencing protocols.

Inevitably, the contents of this book overlap significantly with information found in standard molecular biology laboratory manuals. The principal advantage of *DNA Sequencing* over these manuals is that it is far more lucidly written. Because of its simplicity, *DNA Sequencing* will appeal more to scientists about to begin sequencing that to 'old hands'. However, even experienced sequencers will benefit from an afternoon spent reading it. In short, this book is likely to be a useful reference in laboratories that carry out sequencing.

MARIO DE BONO
*MRC Laboratory of Molecular Biology*
*Hills Road*
*Cambridge CB2 2QH*
*U.K.*