question! So much for the fly; what about the Lords?

Morgan was a tenured Professor of Zoology at Columbia. As the only Faculty member in the fly group, he alone could take students. But he was casual about this, generally passing them to Sturtevant and Bridges who taught them techniques and, to some degree, organized their work. Morgan himself mucked-in (and that is the right phrase for the Fly Room was an overcrowded tip), taking his share of scoring other people's flies, continually informing the group about what was going on, to the extent of reading out his mail as he opened it. There is much to be learnt from this uninhibited and cooperative laboratory set-up which Morgan led; but I am afraid the Health and Safety Executive would ban any place like it today! We have lost a lot of human spontaneity the more we have become managed by society. Kohler's text illustrates this very well.

While Morgan was 'the Boss', Sturtevant and Bridges were 'his boys', and he kept them in the subordinate position through his manipulation and control of the Carnegie funds. Sturtevant was the intellectual of the pair and Bridges the brilliant, and complementary, technician. Sturtevant obviously understood the significance of the work being done and kept abreast of researches on plants, especially the experiments of plant breeders, but the handsome Bridges concentrated on the immediate work in hand and on fulfilling his belief in free love and communism – in that order. So there is plenty of interesting anecdotal information about the relationships between these three key players. There's nothing new about lab. gossip or its, apparently eternal, interest: Kohler illustrates its role in keeping the lab. together.

It could not last since organizations, like individuals, have a life cycle (little studied by historians) and while his boys remained almost subservient to the Boss, newcomers like Muller and Metz found the 'moral economy' restrictive and moved away. Still, 'no trade secrets, no monopolies, no poaching, no ambushes' remained the practical rules for establishing trust and harmony among the fly people! And this was consolidated on the publication by Demerec and Bridges of the *Drosophila* Informative Service (1934) which became the public means for transmission of craft procedures, of stock lists and of news of new mutants; as it does to this day. Before that *Drosophila* work had survived the disruptive move of Morgan *et al.* to Cal Tech (1929); but it had also received a great boost from Painter's (1933) discovery of the polytene salivary gland chromosomes. Recombinant maps could now be related to chromosome structures: Bridges formulated the programme which was to be his last contribution to *Drosophila* genetics as relating one cross band to one locus. Thus recombination, mapping and chromosome studies were given a new lease of life.

Since the stocks were designed for mapping, they proved unsuitable for Sturtevant's and Schultz's early attempts to use the fly to study development (gynanders, gene dosage effects, eye colour, gene interactions etc.). Surprisingly, Kohler does not note that the group's exclusive attention to adult features precluded them from looking at embryonic and larval lethals which, a generation later, were to make *Drosophila* the organism of choice for development studies. But he is very instructive, and accurate, in his discussion of the quandary with which the synthesized fly confronted those who questioned the thesis that maps equalled genetics. The break-through which Beadle and Ephrussi made by using the embyologist's transplantation technique (of different eye colour imaginal discs) proved to be a false steer since they were studying the biochemical syntheses of eye pigments, not development. But it did bring biochemistry into *Drosophila* studies; and with the 'bitch the other guy if you can' attitude of the biochemists!

Initial attempts to relate genes to evolution using species crosses generally failed as a result of inviability, and ended with the usual, laborious mapping of these species. *D. melanogaster* chosen for its physiological adaptability was also useless, and it was only when Sturtevant and Dobzhansky found the undomesticated *D. pseudoobscura* and used its natural genetic diversity to adapt to geographical and climatic difference that it became possible to trace the spread of adaptive mutations through populations, using salivary gland chromosome analyses. This work was summarized in Dobzhansky's '*Genetics and the Origin of Species*', and marked the second break in the 30 yr mapping tradition.

Kohler's careful history covers almost precisely the same material as Sturtevant and Beadle's *An Introduction of Genetics* (1939) but it provides the inside story of what was really going on. So not only should Drosophilists read it for its intrinsic interest, but so should those who sit on grant giving committees for here they will learn how science really functions at the level of individuals (Lords, do you think; or just historically lucky?). I hope the success of this book will encourage the author to sort out the post-war activities of *D. melanogaster*, in a very different cultural environment.

JAMES H. SANG
Biology School, Sussex University

Molecular Ecology and Evolution: Approaches and Applications. Edited by B. SCHIERWATER, B. STREIT, G. P. WAGNER and R. DESALLE. Birkhäuser Verlag, Basel. 1994. 640 pages. Hard cover. Price £98. US$ 165.00. ISBN 3 7643 2942 4 (Basel). ISBN 0 8176 2942 4 (Boston).

Studies in ecology and evolution have gained great impetus from the new techniques of molecular biology, so that many previously intractable problems are

https://doi.org/10.1017/S001667230003319X Published online by Cambridge University Press

being tackled with interest and unexpected results. The volume under review gives us a very good idea of recent progress and the variety of topics now under study, and also includes helpful advice on the different techniques available. The 36 articles are grouped broadly under the four headings: Part I: 'DNA Fingerprinting and behavioural ecology' (seven articles); Part II: 'Population biology' (nine articles); Part III: 'Molecular systematics' (nine articles); Part IV: 'Speciation, development and genome organisation' (11 articles). Each article has an extensive list of references, but the subject index is rather thin, with only one page reference for most items, some of which turn up again and again in the text.

Before discussing the articles I want to comment on the numerous acronyms in the form of groups of capital latters. We probably all know RFLP, PCR and even RAPD, but the book offers us AP-PCR (arbitrarily primed polymerase chain reaction), DAF (DNA amplification fingerprinting – I would never have guessed that one), AFLP, DGGE, SCAR, NILs (near-isogenic lines – which may be the same as 'consomics' recently defined in Mouse News Letter), BSA, EDV (essentially derived variety), MAAP, SRFA (defined in the index but not in the text, where you also need the definition), SSR, tecMAAP (not in the index, but it appears on pp. 25 and 28, without an explanation I could understand), EPY (extra pair young, in birds of course). Again in birds we have EPC, EPF and ISBP (which the reader may know stand for 'extra pair copulation', 'extra pair fertilization' and 'intraspecific brood parasitism'). I looked for a number of these abbreviations in a very recent dictionary, *Biotechnology from A to Z*, by William Bains published by IRL Press in 1993, and could not find most of them though I was pleased to find SCBU, Special Care Baby Unit.

This impressive list of terms, which can be found with some labour in the index, points to the ever increasing use of acronyms, and I think book editors should help the reader by listing them with suitable definitions at the beginning of their books (some do). They would then get more easily into new dictionaries.

Part I opens with J. S. G. Smith and J. G. K. Williams on 'Arbitrary primer mediated fingerprinting in plants: case studies in plant breeding, taxonomy and phylogeny'. This method can promote more effective management of genetic resources and can describe varieties in order to obtain Plant Breeders' Rights, and examples of its application, with references, are given. Among these, 'recently the ability of DNA data to identify plants received international attention when RAPD profiles of Palo Verde trees provided evidence at a criminal trial (Yoon, 1193, Botanical witness for the prosecution. *Science* 260: 894)'.

Applications of DAF as a general tool in plant breeding are next discussed by Caetano-Annollés and Greshoff. This method uses very short arbitrary oligonucleotide primers and its advantages are described. Next, T. Lubjuhn, F.-W. Schwaiger and J. T. Epplen examine 'The analysis of simple repeat loci as applied to evolutionary and behavioral sciences', and K. Weising *et al.* discuss 'Multilocus DNA fingerprint and genetic relatedness in plants: a case study with banana and tomato'. Two papers on insects follow: M. P. Scott and S. M. Williams on 'Measuring reproductive success in insects', focusing particularly on the strengths and weaknesses of RAPD analysis, which they believe is an excellent option for behavioural ecologists who wish to determine parentage; and H. Hadrys and M. T. Diva-Jothy on 'Unravelling the components that underlie insect reproductive traits using a simple molecular approach', also concentrate on RAPD technology. Part I ends with an excellent discussion by D. F. Westneat and M. S. Webster on 'Molecular analysis of kinship in birds: Interesting questions and useful techniques', which has a very long list of references, as one would expect from its subject, and an appendix listing 92 quantitative or unique studies on kinship in birds using molecular techniques, each with a brief summary of the major result and any interesting auxiliary results.

Part II, on Population Biology, includes a brief history of molecular techniques in population genetics by J. R. Powell, which many readers will find interesting. M. Kreitman and M. L. Wayne discuss the 'Organisation of genetic variation at the molecular level: Lessons from *Drosophila*'. They briefly describe Kimura's standard neutral theory of molecular evolution with key evidence in support of it, and then the nearly neutral (variant) model. A table summarizes 36 studies of polymorphism in *D. melanogaster*, and the authors provide an overview of theories about neutral variation when there is selection at linked sites with, respectively, balancing selection, directional positive selection, and directional selection against deleterious mutations. They remark that the propensity to study individual loci in great detail sacrifices the generality that was possible with allozymes, and that the validity of the assumption that protein polymorphism is neutral remains an open question.

The next two articles (by M. V. Ashley and B. D. Dow, and by C. Schlötterer and J. Pemberton) concentrate on the use of microsatellites. The first gives a detailed discussion of the method and its applications, while the second presents two interesting examples of its application. Both sexes of Soay sheep on the island of St Kilda are extremely promiscuous. Field censuses showed that each female has many partners per oestrus but often none of the males seen consorting with her was the father of the subsequent lamb. In the second example, on pilot whales, the whales swim in groups ('pods') of 50–200 individuals of both sexes, but the hypothesis that a dominant male was the father of most of the young (tested as foetuses) could be excluded because there were too many paternal

alleles which did not come from any of the males in the group.

The remaining articles in this part include: G. Amato and J. Gatesy on 'PCR assays of variable nucleotide sites for identification of conservation units', who apply the method to the *Cayman crocodilus* complex; D. M. Rand on 'Concerted evolution and RAPping in mitochondrial VNTRs and the molecular geography of cricket populations'; B. Streit *et al.* on 'Molecular markers and evolutionary processes in hermaphrodite snails'; A. P. Vogler on 'Extinction and the formation of phylogenetic lineages': Diagnosing units of conservation management in the tiger beetle *Cicidela dorsalis*; and S. J. O'Brien on '*Perspectives on conservation genetics*', which includes a discussion of the controversial status as an endangered species of the African cheetah.

Part III begins with F. H. Sheldon on 'Advances in the theory and practice of DNA-hybridization as a systematic method'; and G. B. Hartl, R. Willing and K. Nadlinger on 'Allozymes in mammalian population genetics and systematics: Indicative function of a marker system reconsidered'. The latter ask a number of questions about allozyme diversity: (1) Is average heterozygosity the most appropriate estimator? (2) Is it accurately assessed by any set of enzymes chosen? (3) Is allozymic diversity indicative of morphological variation within populations? (4) Is it indicative of developmental homeostasis? (5) How sensible is it in revolving patterns of geographic differentiation and migration? (6) What are the limitations and further potentials of allozymic analyses?

R. H. Thomas on 'Analysis of DNA from natural history museums' makes an excellent case for PCR-based extraction of DNA from museum specimens, which in the Natural History Museum of London alone include some 27 million zoological, 30 million entomological and 6 million botanical specimens. Only the Museum National d'Histoire Naturelle, Paris substantially betters these numbers with 60 million entomological specimens. Thomas describes methods of avoiding contamination, and as an example of the success of this approach the Lyme disease bacterium, *Borrelia burgdorferi*, was found in museum specimens of the deer tick, *Ixodes dammini*, which is responsible for passing the bacteria on to humans. A number of other examples are listed with references, including mammals, birds, arthropods and plants, and the reader can also consult the *Ancient DNA Newsletter*. W. C. Wheeler on 'Sources of ambiguity in nucleic acid sequence alignment', R. DeSalle, C. Wray and R. Absher on 'Computational problems in molecular systematics', A. Larson on 'The comparison of morphological and molecular data in phylogenetic systematics', U.-R. Böhle *et al.* on 'Non-coding chloroplast DNA for plant systematics at the infrageneric level', C. W. Cunningham and T. M. Collins on 'Developing model systems for molecular biogeography: vicariance and interchange in marine invertebrates', and J. Hey on 'Bridging phylogenetics and population genetics with gene tree models' complete the Part.

Part IV, subtitled 'Speciation, development and genome organisation', contains a mixture of topics among its 11 articles. Templeman describes the role of molecular genetics in speciation studies; Ochman and Groisman illuminate the origin and evolution of the differences between *Escherichia coli* and *Salmonella typhimurium*, two coliform bacteria which are very closely related, with the order, orientation and spacing of their mapped loci highly conserved, but have rather different life styles. This is a particularly interesting comparison of two species which probably diverged 100–150 million years ago, whose gene maps have been developing side by side in *Bacteriological* (later *Microbial*) *Reviews* for 40 years or so. 'The evolutionary ecology of Daphnia' (B. Schierwater *et al.*), with species widely distributed in large lakes and small ponds and some species forming hybrids, is excellent material for allozyme, PCR-based and RAPD analyses. M. D. Kane and N. E. Pierce on 'Diversity within diversity: molecular approaches to studying microbial interactions with insects' discuss the effects of cytoplasmically inherited bacterial endosymbionts present in testes or ovaries of a number of insects, and causing, respectively, cytoplasmic incompatibility or parthenogenesis. Strains of the bacterial genus *Wolbachia* are responsible for these interactions in various beetles, mosquitos, fruit flies, a plant-hopper and a number of wasps and moths, Mycetocyte bacteria are another group found in specialized cells of at least six insect orders, which benefit their hosts.

The next three chapters discuss evolutionary studies that focus on development: D. Tautz on genes involved in early embryonic pattern formation in *Drosophila*, D. K. Jacobs on developmental genes and the origin and evolution of the metazoa, and G. P. Wagner on evolution and multi-functionality of the chitin system. Finally, D. L. Hartl and E. R. Lozovskaya discuss 'Genome evolution: between the nucleosome and the chromosome', E. Routman and J. M. Cheverud on 'Individual genes underlying quantitative traits: molecular and analytical methods' survey the present status of methods designed to identify QTLs and take perhaps an over-optimistic view of the problems these involve; and E. A. Zimmer rounds up the book discussing 'Perspectives on future applications of experimental biology to evolution'.

The editors of this book (assuming that they wrote the publisher's blurb) tell us that it 'describes, from a molecular perspective, several methological and technical approaches used in the fields of ecology, evolution, population biology, molecular systematics, conservation genetics, and development'. This seems to me like an attempt to pull wool over the unwary reader's eyes by proclaiming that the grand new discipline of Molecular Ecology (with Evolution

thrown in to plug the gaps) covers almost every branch of biology which uses PCR and similar new tricks. An alternative view was expressed by a colleague who said to me 'molecular ecology is surely a contradiction in terms'. Many of the topics in the book have little or nothing to do with ecology, e.g. molecular systematics, development and genome organization, but almost every topic can be squeezed under the umbrella of Evolution. The book contains many excellent articles, but the price is very high for our fund-starved academic libraries and could have been substantially reduced by deleting those articles whose inclusion could be questioned. Nevertheless, I hope the book will find a home in many of these libraries, as its 'ecological' slant should have considerable appeal.

ERIC REEVE
Institute of Cell, Animal and Population Biology, University of Edinburgh

DNA–Protein Interactions: Principles and Protocols, Methods in Molecular Biology, vol. 30. Edited by G. G. KNEALE. Humana Press, NJ, USA. 1994. 427 pages. Price £49. ISBN 0 89603 256 6.

Breakthroughs in our understanding of the molecular basis of the control of gene expression, nucleic acid replication and recombination have been made possible by the continuing development of sophisticated techniques for the analysis of protein–nucleic acid interactions. In this complex area of investigation, clear resolution of these interactions can be difficult to achieve and results may vary depending on the methods employed. Very often, complementary experimental techniques need to be used before a clear picture emerges.

DNA–Protein Interactions: Principles and Protocols is a welcome addition to the highly successful *Methods in Molecular Biology* series, with each of its 32 chapters achieving the required aim of providing complete experimental protocols that can be readily understood and used by relative newcomes to the field. The early chapters describe a variety of related methods which are used to investigate 'protection' of DNA sites and 'interference' with DNA–protein interactions. Analyses of both DNA base contact and contact with the phosphate groups of the DNA backbone are described. A series of chapters devoted to studies of the protein component of a complex includes the use of site-directed mutagenesis as a prerequisite for determining the functional requirements for particular amino acid residues. This is followed by protocols for cross-linking DNA to protein molecules, and for determining DNA-binding affinities. A number of spectroscopic techniques are then described, with the final chapters including functional assays for protein activities (such as the assay of restriction enzyme and transcriptional factor activities).

Inevitably, there is a degree of overlap between the introductory sections of related chapters, but the book is none the worse for this. As in all the volumes of this series, the protocols are clearly laid out, are complemented by clear diagrams, and there are many tips and hints to guide the uninitiated and to help when things go wrong. In conclusion I found this to be a welcome addition to the series, and would recommend it to those currently working in this rapidly growing area of research.

ARTHUR C. ROBINSON
Department of Biological Sciences, Napier University, Edinburgh, UK

Protocols for Gene Analysis, Methods in Molecular Biology, vol. 31. Edited by A. J. HARWOOD. Humana Press, NJ, USA. 1994. 411 pages. Price $59.50. ISBN 0 89603 258 2.

Now that methods for gene cloning, DNA sequencing and DNA amplification (including that by the polymerase chain reaction, PCR) are well-established and relatively straightforward, attention has shifted to the development of procedures for the analysis of genes starting at the DNA level.

Protocols for Gene Analysis is divided into seven parts. The first part describes a set of basic recombinant techniques and is intended as an addition to techniques covered in earlier volumes of this well-established series. Part 2 is devoted to the *in vitro* mutagenesis technology which enables studies to be made of gene expression or gene product function. Part 3 covers a number of electrophoresis and labelling techniques for the elucidation of genomic structure, while Part 4 describes technical innovations which allow for the rapid detection of DNA sequence variations within a population. The latter part includes a protocol for the direct sequencing of PCR products. Methods for the study of gene expression in general, and for the quantification of transcription rates and identification of transcription start-sites are among the topics covered in Part 5. Part 6 describes the identification of protein-binding DNA sequences and how the genes of DNA-binding proteins may be identified and isolated, while the final part describes novel methods for recombinant protein expression and purification from cloned DNA, and the identification of proteins through their association with this DNA.

Each chapter is clearly and succinctly written and begins with a short introduction. Extensive descriptions of the materials required and the methods employed are followed by detailed notes which cover everything from the safe handling of reagents to technique variation and suggestions for trouble-shooting. Clear diagrams are to be found throughout.

Overall, this book is a valuable addition to any

https://doi.org/10.1017/S001667230003319X Published online by Cambridge University Press