role that selection plays. Selection is not irrelevant, but is one-sided: deleterious mutations are eliminated but favourable ones of sufficient selective advantage occur so rarely as to comprise only a small fraction of the observed substitutions. This view conforms with the higher rate of substitution in non-coding sequences or redundant bases, but it is strange that most of the changes we observe at the molecular level have not aided adaptation at all.

There remain some problems with the neutral theory, but these are not ignored by Kimura. Perhaps the single most elegant result of the neutral theory is that the rate of fixation of new neutral mutants is equal to their rate of mutation, which accords with the observed molecular clock of species differences. Unfortunately one rate is in generations, the other in years, so the neutral theory predicts the steady progress of the clock among species with wide differences in generation interval only if mutation rates are proportional to generation intervals. The neutralists have to wriggle to get round this problem: a nice but somewhat unconvincing balance between population size and fixation rates of slightly deleterious mutants is required. Whilst Kimura shows that the level of heterozygosity does not span as narrow a range as Lewontin had originally argued, it is still a little too narrow a range of effective population size for comfort. It will be interesting to see what light new sequence polymorphism data will shed on this. Nevertheless I think Kimura tries too hard to dispose of quite good selective evidence, e.g. on Drosophila ADH he has no need to: there must obviously have been some positive selection in evolution, and presumably there must be some in our current populations.

Overall, this is a most impressive piece of work. It presents the formal theory, but Kimura's powerful mathematics are summarized or removed so as to make it understandable to a wide audience, and it contains an extensive review of the relevant data. It is almost free of unnecessary polemics. The book should be required reading for all geneticists, both those concerned with molecular structure (who are wont to construct elaborate hypotheses on the basis of a few kb sequences on two or three species) and those who deal with ecological genetics (who are wont to construct elaborate hypotheses on the basis of some electrophoretic or structural polymorphism). It is undoubtedly the most important book on evolution to come out for many years. My only regret is that its price puts it beyond the range of students, for it can serve not only as a reference but as a text for courses on molecular aspects of evolution.

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Recombinant DNA Techniques: An Introduction. By RAYMOND L. RODRIGUEZ and ROBERT C. TAIT. London: Addison-Wesley. 1983. xviii + 236 pages. £16.95. ISBN 0 201 10870 4.

Many geneticists may have reached a stage in their work where studies at the DNA level would be the next logical step. However, they may be so intimidated by the prospect of recombinant DNA technology that this next phase never takes place unless an able and willing molecular biologist is nearby. There is no need to fear recombinant DNA when such books as the well known Cold Spring Harbor manual and *Recombinant DNA Techniques* are available. The latter is based on a laboratory course and is written in the form of a teaching manual with specific, detailed practical exercises. This book by Rodriguez and Tait contains sections on vectors and cloning strategies, microbiological technique, DNA isolation, restriction endonucleases, gel electrophoresis, ligation of DNA, bacterial transformation, identification and characterization of recombinant transformants and cloning regulatory DNA sequences. These are all the procedures necessary to obtain a cloned DNA segment of interest from a mixture of genomic sequences. In

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addition there are very useful appendices which include detailed recipes, protocols and up-to-date restriction maps and nucleotide sequences of plasmid and phage vectors. Of course it is impossible to keep up to date completely in this rapidly changing field. However, the authors have done an admirable job. It is worth while to compare this book with the Cold Spring Harbor manual. The latter is much more comprehensive and deals more with strategies for cloning and characterizing eukaryotic genes. For example, in *Recombinant DNA Techniques* there is no description of methodology for mRNA isolation and cDNA cloning. Also, if one wanted to relate a eukaryotic gene to its corresponding polypeptide, hybrid selection of mRNA plus translation or hybrid arrest of translation would be the techniques of choice. The book by Rodriguez and Tait does not describe these techniques but describes the use of mini and maxi cells and coupled transcription–translation systems, which of course are only appropriate for the study of prokaryotic genes at present. The authors, however, state clearly that this book is designed for cloning prokaryotic genes and regulatory sequences. However, these techniques are, in the main, directly relevant for work on eukaryotic genes. The strength of the book is that there is much more emphasis on the rationale and background for the approaches taken than there is in the Cold Spring Harbor manual. This is a very useful book which complements the Cold Spring Harbor manual. I believe there is room for both on the shelves of scientists either carrying out or contemplating recombinant DNA technology.

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The Contribution of Genetics to the Study of Parasitic Protozoa. By DAVID WALLIKER. Published by Research Studies Press Ltd, Letchworth, Hertfordshire, England, and marketed and distributed by John Wiley, 1983. ix + 218 pages. £29.50 ISBN 0 863 80005 X

This is a clearly written and timely little book on a vital but very difficult area of applied genetics, and it deserves to be widely read. Academic geneticists by and large select problems and organisms for study which will give rapid returns on their labours, and most of them crowd into the fashionable areas of research. So the difficulties involved in advancing our knowledge of the genetics of the parasitic protozoa have been tackled by very few research workers, in spite of the great medical and ecological importance of malaria, trypanosomiasis and coccidial diseases in the tropical and subtropical lands of the world.

The need for such knowledge to help in the effective design of control measures is obvious, and Walliker describes both the difficulties and the successes that have been achieved. In the case of malaria, genetic variations have been identified in the form of naturally occurring enzyme variants detected by electrophoresis, mutational resistance to different drugs, and level of virulence. Population studies on enzyme variation have enabled the four rodent *Plasmodium* species of Africa to be distinguished (i.e. *P. berghei*, *P. yoelii*, *P. chabaudi* and *P. vinckei*), even in a multiply-infected host, and have shown regional differentiation of each of these species into subspecies which may not be reproductively isolated. The human malaria parasite, *P. falciparum*, on the other hand, probably consists of a potentially interbreeding population world-wide.

Experimental laboratory systems based on mice, a rodent malaria parasite and the corresponding vector mosquito have made strain crossing and progeny analysis possible, and have led to convincing evidence that the blood forms of the parasite are haploid, that enzyme variants and drug resistance are inherited in a Mendelian manner, and that free recombination between genes occurs. No linkage between any of the genes tested

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