in a unique overview of the field of vaccine design and development.

There are enough subject specialities covered in this book to keep most people happy. As a molecular parasitologist acutely aware of the lack of any recombinant vaccine to date against any parasite, it is particularly encouraging to see how far the virologists have progressed and to keep in touch with new developments in basic immunology. The section on AIDS is of use to non-specialist and specialist alike, documenting the latest developments in this rapidly expanding field. In addition to specific articles such as the mapping of protective epitopes and the recognition of a role for T-cell immunity in AIDS patients, there are also good general articles on the molecular biology of HIV including an excellent account of transcriptional regulation of HIV I by Peterlin *et al.*

If there is a dominant theme within this book, it is perhaps that of the T helper cell epitope. Such epitopes are reuired to stimulate the T helper cells which are responsible for the boosting of antibody production upon subsequent exposure of the immune system to an appropriate antigen. The importance of these epitopes is well illustrated by the tortuous progress being made towards developing a vaccine against the sporozoite stage of malarial parasite, *P. falciparum*. Synthetic peptides known to represent B-cell epitopes of the circumsporozoite protein have proved ineffective as a vaccine. This has subsequently led to the immunological dissection of circumsporozoite protein so that T–cell epitopes may be identified. The latest twist in this story is described in this volume by Michael Good and his colleagues. They find that although the circumsporozoite protein is highly conserved between different strains of the malarial parasite *P. falciparum*, the few areas of variability that exist appear to coincide with T-cell epitopes.

Another aspect of T-cell epitopes of relevance to vaccines is the host-based phenomenon of genetic restriction, where individuals differ in their ability to recognize given T-cell epitopes. This phenomenon is illustrated by Francis *et al.* in the opening article. These authors were able to overcome genetic restriction in mice to a Foot and Mouth Disease Virus nonadecapeptide by coupling T-cell epitopes from foreign heterologous proteins such as ovalbumin and sperm whale myoglobin to the peptide. Interestingly, different T-cell epitopes resulted in antibodies being raised to different regions of the FMDV peptide.

Studies of these types show how subtle our understanding of the immune response must become in order to design subunit vaccines utilizing peptides or recombinant proteins representing only a small portion of an important antigen. To overcome this one must put efforts into obtaining bacterial expression of full-length, protective recombinant immunogens, which is not a simple task. Even when these are available, a problem exists for human diseases in that there is a severe lack of safe, suitable adjuvants. This area of adjuvant research is a severely neglected area of vaccine development. Other approaches to this problem are described, however. Immunologists have tried to overcome the adjuvant problem by using 'natural' immunological stimulators such as the Interleukins and Interferons. Molecular biologists have tried to overcome the problem by inserting cloned DNA into surface protein genes of infective viruses, e.g. vaccinia, or bacteria. An interesting development related to this area is the work of Clarke *et al.* on the formation of chimeric proteins based on the Hepatitis-B Core Antigen. These proteins automatically self-assemble into virus-like core particles that are highly immunogenic. The trouble with these examples, once again, is that often only a limited size of recombinant protein can be expressed.

The most successful vaccines to date are undoubtedly those of the 'Jennerian' approach where 'attenuated' viruses or organisms are used to induce a protective immune response. Interestingly, molecular biology techniques are now being used to identify the mutations giving rise to these 'attenuated' forms with a view to developing new vaccines and modifying old ones. In many ways this work has brought us full circle in our approach to vaccine design.

Our increased understanding of the immune system and the immunological properties of antigens, and the availability of new chemical and genetic tools, is allowing us to develop rational approaches to vaccine design. Vaccines '88 must be recommended reading for anybody wishing to keep abreast of the latest developments in this exciting field of study.

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Genome Analysis: A Practical Approach. Edited by K. E. Davies. Oxford: IRL Press Ltd. 1988. 192 pages. $27·00/US$54·00. ISBN 1 85221 109 1.

Another winner for the 'Practical Approach' series! We have been fans and avid users of several earlier volumes of these technical tracts in our laboratories and the magpies are ready to swoop on my reviewer's copy should I leave it lying around. Luckily it is the more expensive spiral version which is very easy to xer...–oops, too many of life's pleasures are illegal.

Having said how keenly we espouse the latest technology, I will compound the conceit by suggesting that this volume in particular is aimed at the *cognoscenti* in the field of genome analysis. There are excellent chapters on genome transfer (which I loosely call somatic cell genetics), contig mapping, pulsed field gel electrophoresis (with a lovely trouble-shooting appendix of gel photographs which never get published), chromosome jumping, detection of single base changes in DNA, polymerase chain reaction (almost better known as PCR), fingerprinting and linkage

analysis – without exception written by giants in the field. Each chapter gives detailed instructions on how to carry out the specialized procedures but you would need to be an experienced cell biologist, molecular biologist and geneticist to supply the background knowledge which obviously has to be taken for granted when preparing such an advanced text. Alternatively, if you have a few years to spare (a laughable idea in this rat race), you could work your way through some of the earlier volumes in the series that has grown apace with this fast moving subject.

The problem that is not addressed at all in most of the chapters and only scantily in the others (e.g. chromosome jumping and linkage analysis) is why and under what circumstances you would want to use the technologies described. What is genome analysis? How do the techniques described dovetail together? For example the PCR technique has been enthusiastically hailed by the clinical geneticists who analyse genomes at a most practical level. There is no discussion of how PCR will be used in this area, nor of the possible pitfalls that must be avoided when life and death decisions depend on the outcome of the procedure. Moving to the wider arena of human genome mapping, it would be interesting to find out whether the contig mapping fraternity believe that their technoloy can be scaled up from the 2000 cell, $< 10^7$ bp nematode to the 3×10^9 bp man. Perhaps the easiest way to put these excellently presented methodologies into context would be to include a fairly brief chapter with a carefully selected reference list on how the techniques have been used and what future adaptations are on the horizon.

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The Biology of Paramecium. (2nd Edition). By R. Wichterman. New York: Plenum Publishing Corp. 1986. 599 pages. US$89·50. ISBN 0 306 420279 9.

Paramecium. Edited by H.-D. Görtz. Berlin: Springer-Verlag. 1988. 444 pages. DM 248 ISBN 3 540 18476 7.

In former times, most university courses in zoology started with the protozoa. First came *Amoeba* and then *Paramecium*. Nowadays, however, protozoa enter the curriculum, if at all, much later, and are usually considered to be important, and worthy of the award of research grants, only in so far as they cause disease in man or agricultural animals. Some certainly do, and cause malaria, sleeping sickness and so on.

However, free-living protozoa are also of enormous interest and research potentiality from a biological point of view. These two books on *Paramecium* make available most of the information which a student or research worker would require. They are written from very different angles: Wichterman's book is in the classical tradition, and deals extensively with taxonomy, morphology and general biology, but also finds space for some more specialized topics. As the author points out in his preface, the book celebrates his half-century 'love-affair' with *Paramecium*. Perhaps its most valuable part is the magnificent bibliography of 4400 titles, starting with Leeuwenhoek's original description of *Paramecium* in 1674 and ending with a considerable number of papers written in the early 1980s.

The other book, edited by H.-D. Görtz, is a collection of thirty chapters dealing with current work on *Paramecium*, prefaced by a succinct foreward by J. R. Preer, who has himself done some of the most important work on the molecular biology of antigen variation, as well as on numerous other aspects of *P. aurelia*.

Probably the peak of interest in *Paramecium* was reached in the 1940s and 1950s as a result of the discovery by T. M. Sonneborn of the 'killer' paramecia and their determinant kappa particles. The latter were at that time thought to be caused by novel genetic units called 'plasmagenes', which aroused much controversy amongst geneticists. Now all this has died down and kappa is seen to be a bacterium with a respectable Linnaean name – *Caedibacter* – living in the *Paramecium* cytoplasm. However we now know that there is a whole world of myriads of endosymbionts (or endocytobionts or endonucleobionts, as they are called by Görtz), living in the cytoplasm or nuclei of *Paramecium*; and there are astonishingly complicated interactions between the genes and gene products of the ciliate host, the endosymbionts and in some cases viruses or plasmids within the latter.

A topic which is of fundamental importance as a model for understanding cellular differentiation in eukaryotes, and one which has *not* died down, is that of the surface or immobilization antigens, here reviewed by H. J. Schmidt. Although the basic genetics of this system was unravelled more than thirty years ago (by Sonneborn and Beale), that was before the era of molecular biology. Recently much has been elucidated but the basic mechanism of switching from one cellular state (controlling antigenic type) to another is still not clear. It seems to be different from the somewhat analagous situations in *Trypanosoma* and yeast. *Paramecium* provides us with exceptionally favourable material for further study of these phenomena. Incidentally, in the course of the recent work on the immobilization antigens, it was discovered that *Paramecium* does not abide by the rules of the 'universal' genetic code. The codons TAA and TAG, which are elsewhere used as stop signals, in *Paramecium* code for the amino acid glutamine and the same occurs in two other ciliates – *Tetrahymena* and *Stylonychia*, but amazingly not in yet another one –