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Book reviews

Exploring Genetic Mechanisms. Maxine Singer and Paul Berg (eds). University Science Books, Sausalito, CA. Pp. 674. Price £60.00, hardback. ISBN 0935702 70 9.

I am writing this review (already late) during the bouncing excitement and expectation of the Soujourner landing on Mars. This foray to the Red Planet is destined to animate our assumptions on the totality of the molecular basis of life here on Earth and elsewhere. So exciting, it doesn't get any better than this!

A measure of a good text book is that it conveys a sense of excitement and achievement (after the fact) of those discoveries that changed our view of biology and led to our present mixture of prejudice and understanding. In their preface Singer and Berg stress the unity of genetic processes among different organisms in relation to the structure, organisation and expression of genes and genomes. This book has the highly laudable aim of introducing how genetic complexity is analysed by focusing on an eclectic collection of experimental systems. If there is a message, it is that genetic strategies are limitless and anything goes (so there must be hope for discovering life on Mars). However, the level of excitement in this book is low. This trend begins by anticipating that in future biology will be represented by a bland continuum which ranges from the properties of a gene to the hierarchical interactions of systems. This, the editors avow, will make arguments over the reductionist vs. the holistic view of biology irrelevant. It sounds really boring and really wrong? Genes are not the sole explanation for complex etiologies and syndromes.

Initially the book concentrates on the analysis of viral life cycles (papo-, RNA- and retro-viruses) in relation to their gene expression programs and effect on host cells. This is followed by an excellent chapter on viruses and cancer which comes closest to the ideal set out in the preface because it at least gives the reader a slight frisson with the analysis of oncogenes, taking as its starting point the discovery of the *Src* gene by Varmus and Bishop. Then there are chapters on human gene mapping (resulting in a very low LOD score), haemoglobin gene expression, antigen receptor diversity, intracellular signalling peptides, *Drosophila* development, manipulating protein structure and two excellent chapters on the genetic modification of animals and plants. In choosing this format there are going to be omissions such as chromatin analysis, epigenetics and the uses of frogs, worms and yeasts. It just makes you wonder why some topics were included and others omitted. By way of compensation the layout is superb and all the diagrams are built up from a set of key figure symbols which are consistently used in different chapters. In addition the book contains examples of real data; many textbooks try to get by with unreal graphic representations instead of the raw blobs and blots of experiments.

Ultimately the book does not live up its lofty aims, in part because although the different topics demonstrate genetic and cellular complexity, there is no overall view as to what theories and ideas are being tested. Thus there is no sense of thrill, pace or achievement. Why not delve into how scientists came to comprehend what makes normal cells cancerous and the persistent role of the tumour viruses in that story, from the first filtrate that caused sarcomas in chickens to the pioneering work of Little and Gross with mice in the 30s and 40s? The powerful insights of Dulbecco (influenced by his work on bacterial viruses), Baltimore, Temin, Bishop and Varmus should be used as a vehicle of explanation and excitement especially in relation to the ingenious oncogene hypothesis of Huebner and Todaro. This story also serves as a good example of a scientific advance that was challenged by the scepticism of peers whose beliefs are bounded by, and finally convinced by, experimental evidence. It also illustrates the pluralism of science which tolerates a wide set of beliefs built on the assumption of the unity of the molecular basis of life wherever we find it. This reminds me of a story from Ray Bradbury's *Martian Chronicles*. Two Martians are looking up at Earth hanging in their night sky. One says to the other 'Do you think there is life on that planet?' The other replies 'Nahhhh, too much poisonous oxygen there!'

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Understanding DNA and Gene Cloning: A Guide for the Curious (3rd edn). Karl Drlica. John Wiley and Sons, Inc., New York. 1997. Pp. 329. Price £19.99, paperback. ISBN 0 471 13774 X.

The book has 14 chapters, that start with DNA structure, replication and gene expression, followed by a discussion of bacteria, plasmids, phages and enzymes, as used for

DNA cloning. All of this is put together by describing the cloning of haemoglobin genes. In a logical progression, the remaining chapters deal with the use of cloned genes to understand their structure, function and regulation of expression as well as disease. In these chapters the reader is introduced to introns, transposons, retroviruses, oncogenes and finally testing for genetic diseases, DNA fingerprinting and gene therapy. This is an impressive journey into the methodology and principles of biotechnology, for any 'curious' reader. The book ends with a list of additional reading and an extensive glossary that explains the molecular jargon.

The author should be congratulated for steering a clear path through many difficult concepts and intricate experimental protocols. He achieves this by the clever use of analogies and flow diagrams which aid in explaining the various techniques and the underlying principles upon which they are based. My favourites are on pages 16 and 261 where the appearance of DNA is described as a 'featureless piece of string' and a metaphase chromosome as 'a hot dog with a constriction'.

With regard to the level at which is pitched, the book will not teach anybody to carry out gene cloning and in this respect is no challenge to Sambrook *et al.* (1989) nor does it pretend to be. In the Preface the author states that it was written for science and non-science college students as well as a general public without prior knowledge of chemistry. I believe that the latter (general public) is a specially valuable niche in an era in which biotechnology, and the explosion of knowledge it brings, has the potential to touch all our lives. It could also be useful to some school teachers or pupils who are preparing to enrol on a university course, families struggling with genetic diseases, or any member of the legal and medical profession who may need to recommend or explain some forms of treatment and testing or to learn about genetic cloning and fingerprinting.

The reservations I have concern aspects of the book that might deter the casual reader, namely too many details, the price and the use of colour. Some details are not crucial for the understanding of DNA or cloning but are included, I suspect, for scientific completeness. For example, explaining the differences in translation between Prokaryotes and Eukaryotes (page 65) or the function of aminoacyl-tRNA synthetase (pages 66 and 67), etc. At this price (£19.99), the use of coloured diagrams may have made the book more attractive to the uninitiated reader.

Only a very brief mention is made of the economic, ethical and political aspects of the technology described. Some of these would have been worthy of greater consideration, as they are of great interest to the general public. The impact on society of gene therapy, transgenic organisms and genetic diagnosis, not least in predicting susceptibility to the late onset of acquired diseases, carries with it implications and responsibilities that cannot and should not be left entirely to the scientific community.

Yes, I think that this book should be read widely as a primer for some of the many promises and problems biotechnology will raise and, hopefully, in due course answer.

Reference

SAMBROOK, J., FRITSCH, E.F. AND MANIATIS, T. (1989) *Molecular Cloning - A Laboratory Manual*. Cold Spring Harbor Laboratory Press.

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Fingerprint Methods Based on Arbitrarily Primed PCR. Maria R. Micheli and Rodolfo Bova (eds). Springer-Verlag, Heidelberg. 1997. Pp. 441. Price DM 128.00, paperback. ISBN 3 540 61229 7.

Confused by RAPD, AP-PCR, DAF, ASAP, tecMAAP, AFLP, RAHM, RAMPO, DS-PCR, AS-PCR, SCAR, SRFA? You will learn from this book that they are all variants of MAAP, which presumably stands for Multiple Arbitrary Acronym Production. The first three are alternative brands of the same basic idea, and are covered exhaustively in this book. ASAP and tecMAAP are given a few pages each, but the rest get little more than a cursory nod. This is a pity in the case of AFLP, as this is a method whose fortunes seem to be rising.

The aim of these methods is to use the polymerase chain reaction (PCR) to amplify multiple DNA sequences of unknown origin from each of a large number of organisms, and hence reveal genetic differences that can be used for genetic mapping or diversity studies. Compared to the conventional use of PCR to target known genes, this approach is quick and dirty, and the macho acronyms seem somehow to reflect this. Perhaps the best known, and potentially the quickest and dirtiest, is RAPD. Hundreds of researchers saw it as a quick way to generate diversity data, but often found that the results were ambiguous and poorly reproducible. As Majerus *et al.* (1996) remarked 'Any scientist who understands the basis of RAPDs, and so potentially could use them in an informative way, would almost certainly know enough to avoid them like the plague!'

Micheli and Bova go a long way towards rehabilitating the reputation of these methods. The need to standardise DNA template preparation is repeatedly emphasized, and detailed protocols are given for a variety of organisms. With this attention to detail the methods need not be so dirty, but they are not so temptingly quick either. Nevertheless, they have been invaluable in generating useful genetic maps for many organisms, and have enjoyed some more limited success in analyses of natural genetic diversity. Detailed protocols and authoritative discussion of the important considerations, often written by the developers of the methods themselves, are an excellent feature of this

