important need: it also makes stimulating reading, and it should be on the library shelves of all genetics and microbiology departments/laboratories. The paperback edition is also cheap enough to find its way into many pockets, haversacks or briefcases.

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A Genetic Switch: Gene Control and Phage. By MARK PTASHNE. Oxford: Blackwell Scientific Publications. 1986. 128 pages. £12.95. ISBN 0 86542 3156.

Phage lambda has been the subject of intense interest since the early 1950's, after its happy discovery as a resident of *E. coli* K 12. A flood of papers followed, culminating in the famous 1971 book *The Bacteriophage Lambda*, which left many of us floundering in the complexities and mysteries of its terminology and dual life-style; until an equally important book, *Lambda II*, appeared in 1983, cleared up most of these mysteries, and added the complete DNA sequence (48,514 b.p.) and much associated information for us to brood upon. Since then, research on lambda has eased off a little, though the phage has meanwhile acquired a vivid new life-style as a cloning vehicle. One may hope that Lambda III will appear in 5–10 years with solutions of all the remaining mysteries; but in the mean time one of the leading contributors to lambda biology, Mark Ptashne, has produced the book under review.

Lambda possesses a complex and subtle switch mechanism to determine its choice of path towards lysis or lysogeny after infection, and the author thinks that an understanding of this biochemical apparatus may be relevant to the problems of cell differentiation in higher organisms, where genetic switch mechanisms must also be operative. His book, then, concentrates on the present view of the lambda switch mechanism, and describes this system in a novel way that makes it comparatively easy to understand for the newcomer to this branch of biology (and for dippers into the area like myself). After introducing some basic facts about genes and how they work, the book's first three chapters describe lambda's development 'from three perspectives: from a distance, showing the overall pattern of events involved in the interaction between virus and host; more closely, describing in coarse molecular terms a key event in the process; and very closely, showing precise molecular interactions'. These chapters give no experimental justification for the processes as described, but chapter 4 explains the principles of some of the key experiments leading to the present view, and gives a number of references to both research articles and reviews. Three appendices then discuss 'Designing an efficient DNA-binding protein', 'Strong and weak interactions', and 'Control of transcription in eukaryotes and prokaryotes – a common mechanism'.

This book is a welcome addition to the lambda literature. It is very lucidly written and extremely well illustrated, so that the essentials of the switch mechanism become very clear; and it is both a pleasure to read and a most helpful introduction to the complexities of the complete lambda biology described and speculated on in *Lambda II* (edited by Hendrix, Roberts, Stahl and Weisberg, Cold Spring Harbor Laboratory, 1983). The Lambda switch mechanism is very complicated, involving not only the DNA-protein interactions of the cI and Cro proteins and the tripartite operator site separating the *cI* and *cro* genes and overlapped by their promoters, but a number of other genes and their products – *N*, *Q*, *cII* and *cIII* – and a confusion of promoters and terminator sites which can be overridden when convenient by the N or Q proteins. The choice of switch setting seems to depend on the concentration of the unstable cII protein and the backup it gets from cIII (if I understand it correctly).

Some of the difficulty in grasping the details of this system come from the terminology, which evolved not with the organism but with its students. This terminology is even more firmly built into the subject than QUERTYUIOP... is built into the English typewriter and computer keyboard. The latter was, I believe, designed to make it impossible for early typists to type fast and so snarl up the crude mechanism, but attempts to replace it by an easier symbol order have never got anywhere. Likewise, we shall just have to get used to lambda terminology, as have those who use it: it is needlessly confusing, but not impenetrable.

In conclusion, I should like to suggest that lambda may not need such a complex system to maintain its place in *E. coli*. So I challenge Mark Ptashne – or others in the field – to design a better/simpler switch mechanism and associated circuitry for lambda, on the assumption that evolution does not always produce the best solution. Addressing this question might help in understanding lambda.

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Molecular Biology and Crop Improvement. A case study of wheat, oilseed rape and faba beans. R. B. AUSTIN, R. B. FLAVELL, I. E. HENSON AND H. J. B. LOWE. Cambridge University Press for the Commission of the European Communities. 1986. 114 pages. £17.50. ISBN 0521 32725 3.

This book deals with the ways in which the techniques of molecular biology could be applied to crop improvement, especially of wheat, oilseed rape and faba beans. It comprises a report to the Commission of the European Communities by the Cambridge Plant Breeding Institute. While the attention to wheat requires no comment, oilseed rape and faba beans are of increasing economic significance as substitutes for imported vegetable oils and meals for animal feed.

The breeding objectives for each crop are discussed, practical difficulties are noted and the ways in which molecular biological methods could supplement or replace traditional methods are outlined succinctly. Although three crops attract most of the comment, there is sufficient generality in the discussion to make this text a useful summary of the kinds of practical problem likely to engage the attention of plant breeders for the next two decades.

At first glance, the shining new instruments of molecular biology promise a revolution in working methods, an extra dimension of genetic manipulation. There is the prospect of isolating genes by one means or another, identifying their products by polyclonal and monoclonal antibodies, transferring genes from one species to another, with or without tailoring to produce desirable effects, increasing the copy number of particular genes, locating specific alleles by exploiting restriction fragment length polymorphism, to mention some of the thrills in store. Transference of genes between species which do not hybridize beckons entrancingly as a route to novel genotypes, while the confident identification of the carriers of particular genes at an early stage of development will make selection faster, more precise and cheaper.

All these and other possibilities are discussed in relation to the three crops. But it is also made clear that, although some problems could and should be tackled by molecular biological methods right away, many of the exciting and potentially far-reaching applications hinge on a better understanding of the genetics, biochemistry and physiology of plant growth, differentiation and reaction to different kinds of environmental stress, both physical and biotic. Before they can be manipulated the right genes have to be identified. When successfully transferred, to be useful, they have to be de-repressed at the right time and in the right tissue or organ and they must be compatible with the genetic background.

The authors list four main areas which are particularly suitable for analysis by the new methods. Taking them in turn, photosynthesis, in spite of all that is known about it, remains a problem area because limiting components cannot be identified with certainty. It is suggested that molecular biological methods can make a unique contribution here by making it possible to change particular components of a complex system. Plant water relations, especially in relation to drought resistance, pose an economically important challenge which directs research attention to the properties of osmoregulation. There may be genes in wild species which confer drought resistance and would therefore be candidates for transference to crop species, if such genes could be identified. Seed composition has evoked a great deal of interest and much is already known about the seed proteins and other compounds in some species. But for oilseed rape and faba beans less is known and there is a need to alter the composition of the seed to make it more suitable for animal feeds. Finally there is pest and disease resistance, where there may also be a case for looking in other species for genes which confer general resistance. Progress in this area requires a better understanding of recognition systems and the molecular and cellular basis of defence reactions.

In all these, and other areas we have not space to notice, there is ongoing need for basic research on several fronts if the potentially great economic advantages of applying the methods of molecular biology are to be realized. At present there are very few short cuts; in future there may be many more. Traditional methods of analysis must be fully integrated with the molecular approach in a new operational synthesis. It is also worth remembering that, at the end of the day, the performance of any new cultivar will have to be evaluated in large scale field trials, which take account of variation in both soil and climate.

This very readable book can be recommended to anyone interested in the practical applications of genetics. It should also prove attractive to plant breeders, who would like to consider an imaginative but hard-headed assessment of the scope for molecular biology in plant breeding.

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Papillomaviruses. Ciba Foundation Symposium 120. John Wiley. 1986. £27.50. 259 pages.
ISBN 0 471998370.

Anyone reading the popular press or viewing the television in current times cannot fail to be reminded that screening for cervical precancerous cells in the UK as a whole is not a prodigious success. This trend is not, however, universal for all of the UK; several areas including Aberdeen do show significantly decreased statistics for deaths from cervical carcinoma as a result of early detection of precancerous cells. In addition, several countries, notably Canada, have highly significant figures to show that screening of women for precancerous cells (smear tests) leads to significantly reduced mortality from the cancer.

Since cervical cancer is a venereal disease interest has always centred on detecting the virus (presumably) responsible. At present the most likely candidate is the human papilloma virus (HPV). In the West of Scotland and North East of England 83% of all genital cancers are associated with the detection of the genome of one specific type of the virus, HPV type 16, whose DNA can be detected in tumour tissues.

The human papilloma group of viruses consist of about 40 different types and new types are added to the current list frequently. To be considered a new type requires that the isolate share less than 50% DNA homology under stringent conditions with any previous isolate. Whether HPV actually causes genital cancer is not clear since the genome can also be found