

A Universal Primer for Prokaryotic Molecular Genetics

Bacterial and Bacteriophage Genetics: An Introduction. Second Edition.

By E. A. Birge.

New York: Springer-Verlag. (1988). 414 pp. \$44.50.

After reading this concise summary of prokaryotic molecular genetics, I felt as though I had completed the ultimate in Cliff Notes, those much-maligned synopses of classic literature used by some college undergraduates in the United States to avoid reading the original works of art. Packed within the 414 pages of *Bacterial and Bacteriophage Genetics* (BBG, for short) is a compendium of facts discovered over the past forty years covering most of the basic areas of prokaryotic molecular genetics.

Focusing primarily on *Escherichia coli* and its phages and plasmids (the primary tools for research in this area), Birge has impressively condensed into a coherent whole an incredible amount of information on a large number of topics. These include replication, recombination, gene regulation, mutagenesis, transcription, translation, plasmid biology, suppression, single- and double-stranded DNA phages, restriction and modification, RNA phages, elements of lysogeny, DNA repair, conjugation, transduction, transformation, transposition, heat shock, and much more. Selected techniques ranging from DNA sequencing and molecular cloning to replica plating as well as some commonly employed statistical methods are also outlined. Furthermore, there are descriptions of classic studies, and some of the folklore of microbial genetics is included. The reader learns, for example, about the use of T4rII mutants in fine-structure genetic analyses and the humor behind the derivation of the name *amber* for the UAG translation termination codon.

In spite of what might appear to be information overload, the uninitiated reader should be able to use BBG because of the clear writing and judicious selection of illustrations, tables, and charts. Moreover, when appropriate there are references to chapters where topics are discussed in more detail or from other perspectives, and at the end of each chapter there are lists of general review articles and specialized research papers dealing with some of the topics covered in that chapter. Although the choice of articles cited in some cases can be questioned, they should prove useful to the reader who wants additional information.

BBG, by giving a broad overview of the field, is a good introduction to prokaryotic molecular genetics, and I think that it could be a useful adjunct to the teaching of introductory molecular genetics courses. There are problems with the book's all-encompassing approach, however, stemming from the sheer volume of information that must be summarized. The enormity of this task becomes apparent

when one considers the sizes of two recent multiauthor, double-volume treatises reviewing the same topics. *Escherichia coli and Salmonella typhimurium: Cellular and Molecular Biology*, edited by Frederick Neidhardt (American Society for Microbiology, 1987), contains some 1650 pages, and *The Bacteriophages*, edited by Richard Calendar (Plenum Press, 1988), contains about 1350 pages.

First, covering such a mass of information obviously makes it possible to present detailed consideration of only a few, if any, of the experimental approaches; and there can't be any significant attempt to raise questions about the work. For many in the field, the beauty of bacterial and phage genetics is found not just in the facts deduced from the experiments, but in the elegance of the experimental approaches per se. In this regard it is only necessary to read Mark Ptashne's monograph *A Genetic Switch* (Cell Press and Blackwell Scientific Publications, 1986) to see the heuristic value of covering one topic in depth. Perhaps the most successful book summarizing the breadth and depth of the field is William Hayes's *The Genetics of Bacteria and Their Viruses* (John Wiley & Sons, 1968). But this classic was written when the field was in its infancy and the volume of information to be reviewed was more manageable.

Second, by necessity information will be left out. For example, it can be questioned whether a presentation of the work on T4rII is complete without a discussion of that most famous of deletion mutations, *r1589* (Champe and Benzer, *JMB* 4, 288–292, 1962). Particularly questionable is the failure to discuss the use of *r1589* in two classic studies: In one, Crick and co-workers (*Nature* 192, 1227–1232, 1961) demonstrated the three-letter nature of the genetic code and in particular that "... the sequence is read in groups from a fixed starting point." In the second, Benzer and Champe (*PNAS* 48, 1114–1121, 1962) elucidated the nature of nonsense mutations.

Third, inaccuracies will inevitably creep in owing to the inability of a single author to be an expert in all areas. Here, I mention only a few of a number of such inaccuracies I found, and my list is probably far from complete because of my own limited knowledge of many of the subjects covered by Birge. First, as an aficionado of the λ N transcription antitermination protein, I was surprised to learn that "... appropriate *nusB* mutant proteins can substitute for N and *nusA* function" (p. 160). To my knowledge, such *nusB* mutations do not exist. There are, however, *nusB* mutations that suppress the N-defective phenotypes of *nusA* and *nusE* mutations (Ward et al., *JMB* 168, 73–85, 1983). Second, the product of the *lit* gene is not required for late T4 mRNA synthesis (p. 115). In fact, T4 grows normally on an *E. coli* host missing E14, the cryptic genetic element encoding the *lit* gene (Kao and Snyder, *J. Bacteriol.* 170, 2056–2062, 1988). Third, study of recombination in the *rII* region did not yield a lower limit that defines the nucleotide as the unit of recombination (p. 105 and p. 122). Although this was initially concluded, later studies by I. Tessman (*Genetics* 51, 63–75, 1965) showed that the

T4 recombination frequency is too high to permit such a calculation. Finally, to my knowledge there is no evidence that RNAase II is involved in the retroregulation controlling λ *int* gene expression (p. 319).

It can reasonably be argued that having a few errors in a work of such breadth is tolerable. However, it can also be debated whether such a volume is useful when more complete reviews, such as the two mentioned above, are available. Rather than being required to read through a book such as *BBG*, even the beginning student might benefit more by studying a limited number of topics so that more complete and accurate reviews, and in some cases the original literature, can be used. However, whether one teaches by emphasizing breadth or depth is fundamentally a matter of personal taste, and those interested in giving the student a wide-ranging view of prokaryotic molecular genetics will surely find use for *BBG*.

David I. Friedman

Department of Microbiology and Immunology
University of Michigan
Ann Arbor, Michigan 48109-0620