

## Microbial Genomes

CLAIRE M. FRASER,  
TIMOTHY D. READ,  
KAREN E. NELSON

2004. Humana Press,  
Totowa, NJ, USA  
536 pp, 26 × 18,2 cm  
Price: US\$ 149.50  
ISBN 1-58829-189-8

The human oral cavity shelters more than 600 species of bacteria, of which only about 150 can be currently grown in the laboratory. Most of these bacteria are not harmful, but a few species tend to aggregate and form dental plaques. There, oral pathogens interact and cause gum disease. The complete genome of one of those pathogens, the spirochete *Treponema denticola*, was published in April 2004 [4]. Antonie van Leeuwenhoek (1632–1723) must have been the first to see *Treponema* spp. in scrapings from the back of his own teeth. In a letter he sent to the Royal Society in 1683, he described a kind of animalcules “a swimming more nimbly than any I had ever seen” and that “bent their body in going forwards” [1]. Up to now, the biology of *T. denticola*, like that of most spirochetes, has been poorly understood. Things may change soon, however. Analysis and comparison of the complete genomes of the four spirochetes (*T. denticola*, *T. pallidum*, *Borrelia burgdorferi* and *Leptospira interrogans*) sequenced thus far have provided new insights into their evolutionary pathways and will surely enable researchers to determine the ultimate mechanisms for their pathogenicity. The genome of *L. interrogans* was sequenced at the Chinese National Human Genome Center, whereas the other three were sequenced at The Institute for Genomic Research (TIGR) in Rockville, Maryland. TIGR conducts research and comparative analyses on the structure and function of genomes and gene products in viruses, bacteria, archaea, and eukaryotes. Of the more than 150 microbial genome sequences currently available (see the list at [www.tigr.org/tigr-scripts/CMR2/](http://www.tigr.org/tigr-scripts/CMR2/)

CMRGenomes.spl), around 40 have been contributed by TIGR. It was at the TIGR that the first complete genome of a free-living organism—*Haemophilus influenzae*—was sequenced, in 1995.

The editors of *Microbial Genomes* are researchers from TIGR, and they have focused their efforts on the analysis of microbial genome sequences. Claire Fraser is TIGR President and Director, and Timothy Read and Karen E. Nelson are Assistant Researchers. Fraser is a pioneer in comparative genomics and has led the teams that have sequenced several microorganisms. Read has participated in the sequencing of both the *Chlamydia* group of intracellular pathogens and *Bacillus anthracis*, the causative agent of anthrax. Nelson led the whole-genome sequencing of both *Thermotoga maritima* and *Pseudomonas putida*.

‘Genomics’, ‘proteomics’ and ‘functional genomics’ are biological terms that currently pervade the life sciences literature. Thomas Roderick coined the term ‘genomics’ in 1997 to describe the study of genomes by using molecular techniques that differed from those of traditional genetics [2]. Genomics refers to the modern field of biology that maps, sequences, analyzes and compares the complete genome sequences of organisms. While the development of such a discipline over the last decade has been dramatic, it did not arise out of the blue. In fact, the foundations for the building of genomics date back to 1977, when Frederick Sanger and his collaborators sequenced the first complete genome. Nevertheless, it was not the genome of an organism, but that of bacteriophage  $\phi$ X174. The DNA of that phage has 5375 bp, and the sequence was determined by using the “plus and minus” method [3]. In *Microbial Genomes*, an introductory chapter (History of microbial genomics) describes the pathway that has led from those first labor-intensive, time-consuming sequencing methods, which were a kind of craft, to the discovery of the whole-genome shotgun method. The latter uses automated sequencers and allows sequencing even of previously unknown and unstudied organisms from the environment.

Finding genes in prokaryotic genomes has become routine thanks to the development of a computational method that scans the genome and analyzes statistical characteristics of the sequences. The section “Bioinformatics as a tool in genomics” discusses the automated annotation methods to analyze completed genome sequences, focusing on the stan-

dard operational procedures currently used by TIGR. It provides URLs for a dozen microbial genome resources on the World Wide Web and data for complete bacterial genomes. Although most bioinformatic approaches can be applied to the study of microbial pathogens, the book contains a chapter that focuses especially on methods to study pathogens and pathogenicity. Several factors have contributed to the enormous growth of pathogen bioinformatics, including the increase in antibiotic resistance among pathogenic bacteria, the need to develop drugs to fight possible biological weapons, and the threat from emerging and reemerging infectious diseases. Related to pathogens bioinformatics is bacteriophage bioinformatics. Bacteriophages act as messengers for the exchange of genes among bacteria and can be carriers of virulence. However, most of the information available in public databases pertains not to bacteriophages that carry factors of virulence but to those from bacteria used in dairy industries to make yogurt and cheese.

The “Core Functions” section describes how genomic sequencing has enabled a better understanding of the biology, biochemistry and physiology of microorganisms. It also discusses how data generated from genome sequencing, along with those of microarray experiments and high-throughput functional genomics, can help to analyze membrane transport and to set up computational models of microbial transport and metabolism. A chapter focuses on the molecular mechanisms of cell cycle control, an issue that has been extensively studied in several eukaryotic systems, but is poorly understood in prokaryotes. “The evolution of microbial genomics” discusses the use of genomics as a tool to reconstruct the tree of life in its early stages and to decipher the dependences and interactions in microbial-host associations. It also deals with the general principles of bacterial-genome dynamics, and the contribution of genomics to a better understanding of microbial diversity. “A survey of microbial genomes” provides some examples of the biological information that can be extracted from genomic studies. The microbial genomes discussed in this section are from very different physiological or ecological groups, including plant pathogens, anoxygenic phototrophic bacteria, extremophiles (thermophilic and halophilic bacteria), and pathogenic enterobacteria.

Finally, “Applications of genomic data” describes practical applications deriving from knowledge of genomes sequences. The parallel development of genomics and microarray technology has offered a wide range of possibilities for new kinds of studies or for dramatically improving classical ones. RNA expression analysis, comparative genome hybridization, RNA-decay studies, as well as the development of new drugs and diagnostic tools have all benefited from that combination. ‘Environmental genomics’ or

‘metagenomics’ are terms that refer to the analysis of microbial communities independent of cultures. The term ‘metagenomics’ derives from the combination of meta-analysis (the process of statistically combining analyses that had been carried out separately) and genomics. Metagenomics allows the study of unculturable prokaryotes, which in some environments can comprise more than 90% of the microorganisms. The last chapter is devoted to the emerging field of proteomics, which is the study of the total protein contents of cells—the proteome. The proteomic approach is suitable to studying prokaryotes because of their relatively small genomes and short life cycles.

*Microbial Genomes* is a major reference book that discusses not only the goals achieved, but also the challenges that researchers will have to face in this field, such as the need to use identical data types and identical criteria for comparing genomes successfully. As J. Craig Venter states in the Foreword, the book “represents not only the most comprehensive attempt to date to bring together in one volume many of the major contributors to modern microbial genomics, but also a broad view of the contributions that sequencing genomes has had on our understanding of microbial metabolism and evolution.”

---

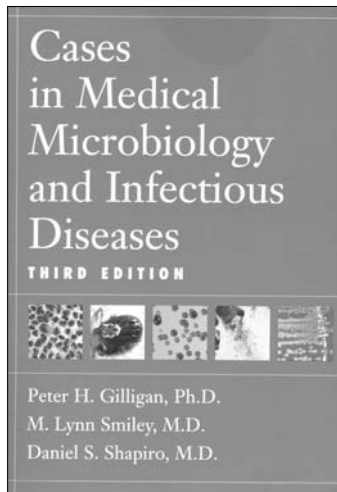
## References

1. Dobell C (1958) Antony van Leeuwenhoek and his “little animals”. Russel & Russell, NY, 435 pp
2. Durick K, Mendlein J, Xanthopoulos KG (1999) Hunting with traps: Genome-wide strategies for gene discovery and functional analysis. *Genome Research* 9:1019–1025
3. Sanger F, Air GM, Barrell BG, Brown NL, Coulson AR, Fiddes CA, Hutchison CA, Slocombe PM, Smith M (1977) Nucleotide sequence of bacteriophage  $\phi$ X174 DNA. *Nature* 265:687–695
4. Seshadri R et al. (2004) Comparison of the genome of the oral pathogen *Treponema denticola* with other spirochete genomes. *Proc Natl Acad Sci USA* 101:5646–5651

**MERCÈ PIQUERAS**

INTERNATIONAL MICROBIOLOGY  
mercepiqueras@wanadoo.es

---



## Cases in Medical Microbiology and Infectious Diseases (3rd ed)

PETER H. GILLIGAN,  
M. LYNN SMILEY,  
DANIEL S. SHAPIRO  
(EDS)

2003. ASM Press,  
Washington DC, USA  
354 pp, 25.5 × 17.5 cm  
Price: US\$ 49.95  
ISBN 1-55581-207-4

Infectious diseases are caused by microbial pathogens transmitted from one individual to another within a population. These pathogens can be viruses, bacteria, fungi, protozoa and, in some cases, parasitic metazoa, but this book focuses on pathogenic bacteria. Infectious diseases have coevolved with humans for millennia, especially after the appearance of the first great civilizations and the first big cities. During the development of our civilization, infections have played an important role as a population control factor; two examples are the so-called Black Death (bubonic plague caused by *Yersinia pestis*), in the Middle Ages, and the Spanish influenza epidemic of 1917–1919. Infectious diseases affect us in our daily life and, due to the work of physicians and microbiologists specialized in isolating and identifying infectious agents, we are accustomed to living with most of them. While, nowadays, fast and powerful technologies exist to identify important pathogens, the brunt of the work continues to depend on skilled clinicians and researchers. *Cases in Medical Microbiology and Infectious Diseases* is particularly recommended for future microbe hunters, but both medical and life-science students, it will also be of interest to anyone interested in infectious diseases. The book is clearly written and contains a large glossary for those readers needing explanations of technical terms.

In a very descriptive and didactic way, the authors present a variety of cases of infectious diseases. A series of questions related to each case leads the reader to identify the microorganism originating the disease, to consider diagnostic techniques, and to recognize the course of the illness. At the end of each case, the reader can find the answers to the questions.

Following an interesting general introduction and presentation, there is a useful description of basic laboratory techniques of clinical analysis that serves as a good review and

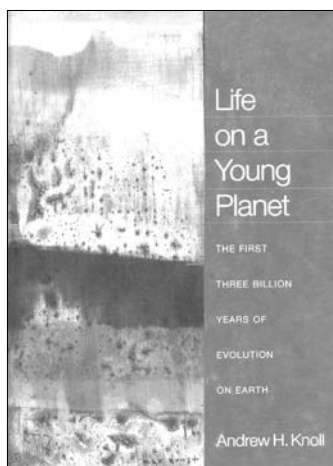
which allows the reader to approach the case-related questions with greater confidence and without fear of having forgotten or ignored specific techniques. Both classical methods and the most recent molecular tools to identify pathogens and the diseases they cause are explained. The case descriptions that form the body of the book are distributed in seven chapters corresponding to diseases of the different systems of the body—genitourinary tract infections, respiratory tract infections, gastrointestinal tract infections, skin and soft tissues infections, central nervous system infections—and systemic infections. Chapter 7 (“Emerging and reemerging infectious diseases”) is the most interesting. Whereas the previous chapters present cases of diseases well known to most health professionals, Chapter 7 deals with the unexpected: new pathogens and old, nearly forgotten ones that have reappeared because of the excessive use of antibiotic drugs; the acquisition of resistance to antibiotics by microorganisms; HIV-related infections; and the current fear of the world’s population, microorganisms, such as *Bacillus anthracis*, that can be used as terrorist weapons.

*Cases in Medical Microbiology and Infectious Diseases* is well edited and contains easy-to-understand explanations as well as high-quality graphical material. These features makes it simple to follow every case and helps the reader to draw conclusions even without the guidance of the tutorial questions. The book is of great interest to both students and professionals, which is not very common in most textbooks.

Human beings have long considered microorganisms as mortal enemies—since the early studies by Louis Pasteur and Robert Koch, who “discovered” these invisible killers and initiated the development of methods to fight them. Indeed, microbes are responsible for the worse plagues that have affected humanity throughout history, causing death and pain, transmitting illness and misfortune. The third edition of this book will help to train future microbe hunters in identifying and destroying these troublesome and sometimes deadly pathogens.

**JAVIER DEL CAMPO**

University of Barcelona, Spain  
jcampo@porthos.bio.ub.es



## Life on a Young Planet

ANDREW H. KNOLL

2003. Princeton University Press, Princeton, NJ, USA  
277 pp, 24 × 16.5 cm  
Price: US\$ 29.95  
ISBN 0-691-00978-3

Knoll explains in this book, in his accessible prose and serious science, an unusual mixture, how different places worldwide have a dose of “tectonic grace”, by which ancient rocks are protected from metamorphic destruction. By this he refers to both heat and pressure from the interior of the Earth that together tend to obliterate the evidence for past life in sedimentary rocks. Indeed, in this wonderfully readable tome, the protected oases that, all over the world avoided the metamorphic fate, become our cherished destinations.

The main sites of tectonic grace we visit include Knoll’s big six (here ordered from ancient toward modern). They are: the Gunflint Iron Formation of the Lake Superior region (especially in Ontario), the Great Wall of China, the Bil’yakh formation (Siberia), Akademikerbreen (Spitsbergen, a desolate Arctic island in the Svalberg Archipelago that belongs to Norway), the Doushantuo (China), and the Nama (of the southwest African Namibian desert). All of these sites are Proterozoic, which means the rocks were laid down as sediments between 2500 and 540 million years ago. To this we add the Kotuikan rocks of Siberia that are the youngest of our sites. They extend from the latest Proterozoic until well into the modern Eon. Modern means the Phanerozoic, which begins with the shelly animal fossils of the Cambrian Era, fewer than 540 million years ago, and extends through the age of dinosaurs to the present. Therefore, Kotuikan rocks straddle the period of most interest to Knoll: the stretch of time when sediments underlain by a relative paucity of fossil predecessors gave rise to those replete with abundant and diverse animal remains. Knoll’s extensive field experience and eagerness to share data and ideas with his colleagues enable him to responsibly reconstruct the broad evolutionary scenario yet remain very close to the evidence.

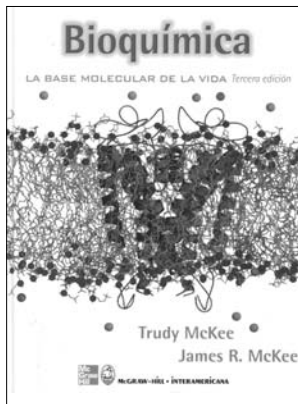
Readers unfamiliar with the revolution in evolution still divide the living world into animals and plants. They may at first be confused when paleontologist Knoll explains that the ancient fossiliferous rocks contain neither animals nor plants.

Indeed, many of the large fossils illustrated here, some beautifully in color, are neither animal nor plant. Then what are they? Knoll successfully answers: he describes this great domain of aquatic life that includes the plasmodial slime molds, ciliates, red seaweeds, labyrinthine slime nets, green algae, diatoms, shelled foraminifera, and their naked relatives the reticulomyxids. They comprise over 50 inclusive groups (phyla). He approaches their evolution from prehistory and raises our consciousness of the extraordinary diversity of non-animal and non-plant life. And here we do not mean “Kingdom Monera” (archaeobacteria and eubacteria) or “Kingdom Fungi” (molds, yeast, mushrooms) either. Unless they are pathogens or commercially important sea weeds, these 250,000 extant species, all members of the “Kingdom Protoctista”, tend to be ignored. Extrapolation from general paleontological principles reveals that most, whether or not they formed hard parts, are extinct. Among them lived the earliest cellular ancestors of all animals, plants, and fungi. Modern and ancient protoctista are composed of cells with nuclei whose descendants include ourselves. Fossil counterparts of live ones (now amenable to molecular and other investigation in the field and the laboratory) are surprisingly abundant. Knoll’s book provides a fascinating entry into the first world appearance of these unruly beings on the stage of planet Earth.

An outstanding, new item in Knoll’s account concerns the marine environment of early life. His proterozoic rock and fossil experience coupled with his vast knowledge of the scientific literature and lively communication with geochemists and geophysicists lead him to conclude that the proterozoic oceans were far less oxygenated and far more sulfide-rich at depth than previously realized. The earliest nucleated organisms probably coped with fluctuating concentrations of hydrogen sulfide and free oxygen. Knoll describes research by Don Canfield, an imaginative and industrious isotope geochemist now at the University of Odense in Denmark. Canfield and Knoll posit that, until the Late Proterozoic, deep ocean basins resembled today’s Black Sea. An “intermediate ocean” separated the Archean Eon anoxia (no oxygen) from the modern Phanerozoic Eon oxygen-rich oceans. Knoll argues that the early Proterozoic oxygen revolution did not directly usher in the fully oxygenated modern world but “rather an alien intermediate marked by moderate oxygen in the atmosphere and surface sea and hydrogen sulfide in deep water” (p. 157). Certainly *Life on a Young Earth* must be slated for a long-lasting paperback student edition.

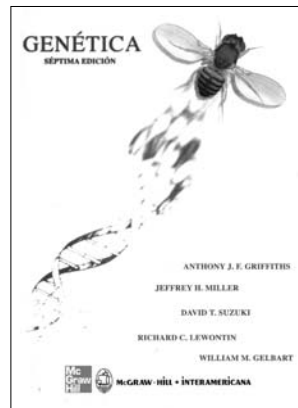
LYNN MARGULIS

Univ. of Massachusetts-Amherst, USA  
pbi@bio.umass.edu



## Bioquímica. La base molecular de la vida (3ª edición)<sup>1</sup>

TRUDY MCKEE,  
JAMES R. MCKEE  
2003. McGraw-Hill ·  
Interamericana de España,  
Madrid, Spain  
773 pp, 28.2 × 22 cm  
Price: 74.00 €  
ISBN 84-486-0524-1



## Genética (7ª edición)<sup>2</sup>

ANTHONY J.F. GRIFFITHS,  
JEFFREY H. MILLER,  
DAVID T. SUZUKI,  
RICHARD C. LEWONTIN,  
WILLIAM M. GELBART  
2002. McGraw-Hill ·  
Interamericana de España,  
Madrid, Spain  
845 pp, plus Glossary and Indexes.  
28.7 × 22 cm. Price: 90.00 €  
ISBN 84-486-0368-0

<sup>1</sup> Translation of the book *Biochemistry: The Molecular Basis of Life*, 3rd ed. McGraw-Hill, New York, NY, USA. 2003. ISBN 0-07-231592-X

<sup>2</sup> Translation of the book *An Introduction to Genetic Analysis*, 7th ed. McGraw-Hill, New York, NY, USA. 2000. ISBN 0-7167-3520-2

Biochemistry and genetics now comprise two of the main fields of science, similar to the more traditional fields of biology, chemistry, medicine and health sciences in general. The study of those sciences is easier and more accessible to students thanks to publications such as those reviewed here. Both books contain high-quality graphics and well-structured chapters that allow them to be readily used by students. These two features and some others discussed below make these books very good alternatives to their previous editions.

*Bioquímica. La base molecular de la vida* is the Spanish translation of *Biochemistry: The molecular basis of life* (3rd ed.). The translation has appeared in the same year than the original (!). The book has 19 chapters, distributed in three sections. The first section (Chapters 1–4), which introduces the main themes discussed in the book, provides information regarding types of biomolecules, cellular structure (both prokaryotic and eukaryotic), the structure and properties of water, and several basic concepts of thermodynamics. The second section (Chapters 5–16) describes biomolecules,

including amino acids, peptides, proteins and enzymes, as well as carbohydrates, lipids and their respective metabolisms. Chapter 13 reviews basic concepts of photosynthesis, and Chapters 14 and 15 are concerned with nitrogen metabolism. Chapter 16 covers general metabolism, showing how the different parts of the body are involved in metabolic functions. The third and last section (Chapters 17–19) discusses genetics concepts, such as the structure of genetic material and the different processes that take place to yield its expression.

This 3rd edition also has new material, such as the ‘Special Interest’ sections. One section of particular interest is “The origin of life” (pp. 58–59), in which a hypothetical scenario for abiogenesis (the process in which non-living matter from the early Earth was converted to the first living organism) is proposed. A series of highlighted boxes called ‘Biochemical Method’, which focus on the major classic and current laboratory techniques for the study of living beings, can be found throughout the book. Like the figures, the illustrations, photographs and other graphics are excellent. A Summary at the end of each chapter reviews the main concepts pertaining to each subject. A series of “Review Questions” and “Key Questions” helps students to determine their comprehension of the presented material.

The English version has a series of supplementary learning and teaching aids, including an Online Learning Centre ([www.mhhe.com/mckee](http://www.mhhe.com/mckee)), where answers to questions that might have arisen while reading and studying the different chapters or subjects can be found, and also help for biochemistry teachers. Information about the authors can also be found on that web page.

*Genética* (7ª edición) is the Spanish translation of the seventh edition of *An introduction to genetic analysis*, by Anthony J.F. Griffiths, Jeffrey H. Miller, David T. Suzuki, Richard C. Lewontin, William M. Gelbart. Its 26 chapters are distributed over six sections. Section 1 (Chapters 1–4) deals with some of the general aspects of genetic inheritance. Section 2, “Genetic cartography” (Chapters 5–7), presents the basic ideas on genetic mapping. Chapter 7 is devoted entirely to “Genetic transfer in bacteria and their viruses”. Section 3, “Molecular genetics”, comprises Chapters 8–14. Chapter 8, “Structure and replication of DNA”, introduces the foundations of molecular genetics, which are more deeply explored in the following chapters. Current issues, such as the “Technology of recombinant DNA” and its applications, are discussed in Chapters 12 and 13. Chapter 14 is devoted exclusively to Genomics, both structural (physical mapping and new technologies) and functional. Section 4, “Genetic variation generation”, (Chapters 15–20) in which mutations are the main subject, focuses on the mechanisms

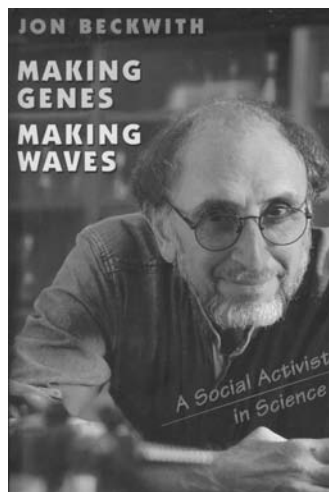
of mutation and the changes both in chromosomes structure and number. Chapters 19 and 20 deal with “Recombination” and “Genetic transposable elements”, respectively. Section 5 (Chapters 21–23) is about “Development”, and includes a chapter on Cancer (Chapter 22). Section 6 (Chapters 24–26) discusses the “Genetic analysis of populations”, The respective chapters include basic “Quantitative genetics”, which revises important concepts such as inheritability, and a discussion of interesting issues relating to “Evolutionary genetics”. Both Chapters 22 and 26 are new in this edition.

Some chapters have been rearranged and others have been reorganized in order to provide a better presentation of the matter; new material has been added to most chapters. The book has also been extensively updated to include topics such as “Lod punctuation” (Chapter 5), “Functional genomics”, which includes material on “Yeast double-hybrid analysis”, “DNA microchips” and “Global regulation” (Chapter 14) and “Mitochondrial DNA, ageing and certain illnesses” (Chapter 21).

Consistent with its pedagogical and didactical approach, this book starts with a discussion of the basic ideas of classic genetics, so that students can assimilate concepts easily during further reading of the book. As one advances in the book, concepts of molecular genetics—more common nowadays—are also introduced. As an aid to students, sections of problems are included, the solutions to some of which are described step by step at the end of the book. The “Fundamental Ideas” and the “Summary” sections enumerate the main ideas explained in the chapter. The English edition has additional material, such as a Manual of Solutions and a CD-ROM containing animations of the figures. The book’s website also contains useful images and is updated regularly ([www.whfreeman.com/iga/](http://www.whfreeman.com/iga/)).

Both websites of *Bioquímica. La base molecular de la vida* and *Genética* are of great interest for students and visiting them is highly recommended, since they help non-English-speaking students to become familiar with the terminology of English scientific literature.

MARTA LEÓN MONTAGUT  
INTERNATIONAL MICROBIOLOGY  
[martaleon@yahoo.com](mailto:martaleon@yahoo.com)



## Making Genes, Making Waves. A social activist in science

JON BECKWITH

2002 Harvard University Press,  
Cambridge, London, UK  
242 pp. 14.5 × 22 cm  
Price: £ 18.50  
ISBN 0-674-00928-2

In his autobiography *Making Genes, Making Waves*, Jonathan B. Beckwith, Professor of Microbiology and Genetics at Harvard Medical School, calls himself a social activist in science. This is a role he has played since the beginning of his scientific career. To identify a starting point, we must look at the press conference that followed a major scientific goal achieved by Beckwith’s group in 1969: the isolation of the lac gene, which encodes  $\beta$ -galactosidase, from a chromosome of a living organism. The technology used in that procedure meant the success of genetic manipulation. At the time the research was done, it was unusual for scientists to publicly express concern about the social implications of scientific discoveries. However, while the applications of gene manipulation for the treatment of genetic diseases were expected to bring real progress to the field of gene therapy, the specter of uncontrolled human genetic manipulation emerged, together with the fear that the nightmare scenarios of science fiction would become reality. Currently, such fears largely have to do with threats to privacy resulting from the misuse of genetic information and the subsequent possibility of public and private control of individuals with respect to their health insurance, employment, etc. Real or potential, this is a danger that needs to be considered in order to avoid irreversible errors. It also adds new elements to the controversy about the neutrality of science.

While developing a career spanning most of the post-war developments in genetics and molecular biology, Jon Beckwith frequently pointed out the social responsibility of scientists. In his book, he also describes the changes in thought and attitudes that took place during the 1960s and the 1970s on university campuses, where a wide range of ideas created a vital atmosphere among students and professors. This was a highly productive period that agitated the so-called “establishment” in western countries, affecting almost

all aspects of society. Beckwith writes about how his “enchantment with science grew and how that enchantment was paralleled by a growing concern about the consequences of science”. And “about a period when social activism was almost the norm in science”. Along with a discussion of the development of molecular biology and genetics, the author provides a picture of the parallel changes in the social and political atmosphere, then and now, including anarchism, socialism, and other political “isms” and their roles in history.

In pursuing the normal career of a young scientist, Beckwith carried out postdoctoral research in prestigious laboratories in London and Paris where past and future Nobel Prize winners had worked. It was a time characterized not only by the exchange of ideas among young and senior scientists, but also by the presence of harsh critique, rivalry and envy, feelings that erupt in all environments where competition and pressures act—as evidenced by the contentious history of numerous scientific discoveries.

At the Pasteur Institute, Beckwith participated in the development of a successful method to remove genes from their chromosomal locations and insert them into small pieces of viral DNA, which were easier to manipulate. It was the antecedent of cloning. Beckwith offers an historical perspective of this scientific field in a clear style, recounting the halting steps toward success, such as the discovery of the genetic element that turns genes on. He also discusses his conversion into a social activist of science, which occurred during this time. Consequently, *Making Genes, Making Waves* is a compelling history of the controversies in genetics over the last half century. The book, which is well written and uses easily understandable terms, may thus be considered as “popular science”. Beckwith describes the dramatic changes that biology has undergone since the late 1950s and the personalities involved throughout. Most of them are surely well known to the reader; for example, François Jacob and André Lwoff, who worked at the Institute Pasteur in Paris, where the author worked in 1964 during his last postdoctoral years. In fact, the most prominent names of molecular genetics appear in the book, but also other scientists that for different reasons remained ignored or did not reach the same

recognition. Having experienced the attitudes and environments of other laboratories outside the USA, mainly in Europe, the different styles of scientists are brought to light as well as the different ways in which science is presented within the scientific community and to the public at large. Ranging from the travails of Robert Oppenheimer and the atomic bomb to the Human Genome Project, under the direction (at the beginning) of James Watson, Beckwith’s book provides a view of science and its social context and the growth of the radical science movement in the 1970s. The search for a scientifically based “genetic determinism” was directly helped by the development of genetic engineering and its techniques enabling manipulation of the genetic heritage. It also served to those that looked for a scientific basis to relate abnormal behavior (i.e. criminal acts) to genetics, avoiding any consideration to environment or circumstantial factors. The tragic abuses of the eugenics movement in United Kingdom, USA and Canada in the early decades of the 20th century, derived from or were justified by attempts at social applications of Darwinian concepts. They had an active revival during nazism period under Hitler in Germany. Very well known names including Galton and Davenport played a role in the diffusion of this doctrine. Complete reports and sad histories sleep at the Eugenics Record Office at Cold Spring Harbor, the center of American Eugenics research throughout 1910–1940.

Jon Beckwith has been active in front-line science through his contributions to research on bacterial cell division, the role of disulfide bonds in protein folding, membrane protein structure and assembly, protein secretion, genetics and society. He has also actively participated in a wide range of other activities related to art, philosophy and the history of science, and in publishing articles and book chapters on the social application of science and its social implications.

We live in times where image is essential, and, consequently, where the borders between reality and marketing have become obscured. Thus, it is always gratifying to find scientists with a critical attitude, and who are able, and willing, to share their worries and concerns about the potential misuse of science.

**CARMEN CHICA**  
INTERNATIONAL MICROBIOLOGY  
carmen.chica@fcr.es