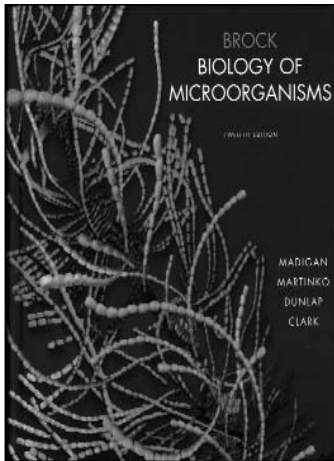


# BOOK REVIEWS

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## Brock Biology of microorganisms 12th edn.

MICHAEL T. MADIGAN,  
JOHN M. MARTINKO,  
PAUL V. DUNLAP,  
DAVID P. CLARK

2009,  
Pearson Benjamin Cummings,  
San Francisco, CA  
1061 pp, 22 × 28 cm  
Price: US\$ 165.20  
ISBN 0-13-232460-1

Microorganisms are present in every habitat on Earth and are crucial to the sustainability of life. Anton van Leeuwenhoek's observations, 325 years ago, were among the first of many startling insights that have elucidated the biology of microorganisms. In the 1960s, progress made in the fields of basic and applied microbiology resulted in the insights that ushered in the current era of molecular microbiology. Today, microbial research is close to defining the minimal genome (the minimum complement of genes necessary for a living cell) and thus, at least in biochemical terms, all of the prerequisites for life. Clearly, the study of microorganisms is essential for an understanding of all life on our planet. The careful reader of *Brock Biology of microorganisms* (BBOM) will be prepared to understand the microbial world, what microorganisms are, what they do. For professionals as well as students, the BBOM is an essential source of information about the latest discoveries in microbiology. The continuing success of this textbook, and evidence of the rapid advances in our understanding of microorganisms, is reflected in the new editions published every three years. Indeed, the history of this book goes back nearly 40 years! Thomas D. Brock authored the first edition in 1970; shortly thereafter, the book was translated into several languages, including the Spanish translation by Ricardo Guerrero, prepared as soon as in 1971. As a tribute to Brock, the book has incorporated his name into the title since the 8th edition.

The teaching function of this book begins with the cover photo, which shows the filamentous bacterium *Crenothrix*, and the information about this microorganism provided on the back cover. The text includes important pedagogical tools, such as sidebars, reviews of key terms, mini-reviews, review questions, and application questions, all of which are

aimed at reinforcing the topics discussed in each chapter. Additional information can be obtained from the book's website [[www.microbiologyplace.com](http://www.microbiologyplace.com)].

The textbook is organized into 37 chapters comprising nine units, with the four first constituting the body of the book. In this 12th edition, two co-authors (PV Dunlap and DP Clark) make their debut, and their contributions have greatly strengthened the chapters on molecular biology/genetics and evolution/systematics. The book's visual presentation is excellent: A fabulous photograph introduces each chapter. Illustrations and photomicrographs give readers a clear and fascinating view of the microbial world. Tables and figures have been completely redesigned to make the information easier to understand. Chapters included in a Unit are color-coded at the upper right-hand corner. Considerable improvements in the text have been made as well. Of note is the fact that this is the only general microbiology book that describes extensively the unique biology of *Archaea* (anatomy, flagella, molecular biology, replication, transcription and protein synthesis, regulation of gene expression, genetic exchange, and diversity).

Unit 1, "Principles of microbiology" (Chaps. 1–6), provides the student with a basic background in microbiology, including historical perspectives, microbial structure, structure and function of prokaryotic and eukaryotic cells, and the growth and nutritional requirements of microorganisms. One of the most significant advances in microbial biology in recent years has been the discovery of broadly conserved cytoskeletal elements in bacteria. Although the absence of a cytoskeleton was one of the features originally used to distinguish prokaryotes from eukaryotes, bacteria in fact contain many of the cytoskeletal elements that are found in eukaryotic cells, such as microtubules, actin, and intermediate-filament homologs (i.e., MreB, FtsZ, and crescentin), which have significant functions in diverse cellular processes. The book's discussion of cell division is supported by spectacular color photos.

Unit 2, "Molecular biology of microorganisms" (Chaps. 7–13), describes essential and current topics of microbial genetics and molecular biology in *Bacteria*, *Archaea*, and *Eukarya* and provides an overview of viruses and prions. It also underlines the revolution in molecular biology that has resulted from the development of modern in vitro molecular methods, such as cloning and genetic engineering. BBOM has also expanded its coverage of the regulation of gene expression, with special emphasis on *Bacillus* sporulation and the life cycle of *Caulobacter*.

Unit 3, "Microbial diversity" (Chaps. 13–19), provides an evolutionary and systematic foundation for the diversity of

microbial life, from the earliest cells to eukaryotes. The discussion encompasses the major bacterial groups (phyla), such as proteobacteria, gram-positive bacteria, and cyanobacteria, as well as *Archaea*, *Eukarya* (protists, fungi and unicellular algae), and viral diversity, from bacteriophages to animal and plant viruses.

Unit 4, “Metabolic diversity and microbial ecology” (Chaps. 20–24), strongly emphasizes the idea that, in prokaryotes, diversity is expressed in terms of metabolism rather than structure, as evidenced by the ability of microorganisms to make use of a wide range of energy sources and electron acceptors. The long-standing inability to enrich or detect organisms capable of anaerobic growth on methane and ammonium compounds led to the idea that ammonium and methane were inert under anoxic conditions; however, it is now apparent that this is not true. Recent studies using molecular techniques have shown that the syntrophic consortium of an archaeon and a sulfate-reducing bacterium is involved in anaerobic methane oxidation, and that anaerobic ammonium oxidation (“anammox”) contributes significantly to biological nitrogen cycling in the world’s oceans—up to 50% of marine  $N_2$  production. BBOM outlines the basic principles of microbial ecology and examines the types of habitats where microorganisms are found, along with nutrient cycles, bioremediation, and symbioses. Also included are reviews of current methods to study the diversity and activities of microorganisms.

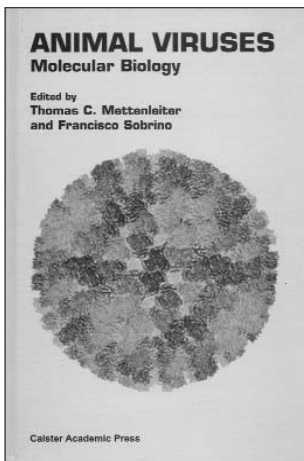
Unit 5, “Putting microorganisms to work” (Chaps. 25 and 26), describes applications of microbial activities (fermentations) to food and industrial production, and the use of biotechnology for industrial or commercial processes, such as the production of hormones, proteins (enzymes), genetically engineered vaccines, and transgenic organisms. Genetic engineering can make plants resistant to certain insects, e.g., through the introduction of genes encoding the protein toxin of *Bacillus thuringiensis*, Bt-toxin. This same technique can yield improvements in product quality (i.e., enrichment of vitamins or some amino acids).

Unit 6, “Antimicrobial agents and pathogenicity” (Chaps. 27 and 28), shifts the focus to the relationships between humans and microorganisms. First, the major methods of microbial control, i.e., the use of physical treatments (heat, radiation and filtration) and chemical biocides (alcohols, aldehydes, antimicrobial metals, and halogens), to achieve microbial disinfection and sterilization of surfaces or materials are discussed. Antimicrobial agents (antibiotics) used for treating infectious diseases and the challenges posed by antibiotic resistance are described. In addition, the unit offers overviews of the microorganisms that inhabit the healthy human body, the harmful interactions that cause disease, and the mechanisms of pathogenesis.

Units 7–9 (Chaps. 29–37) start off with the subject of immunology—specifically, with the immune response that has evolved in humans to recognize and destroy dangerous pathogens. Both innate and adaptive (acquired) immunity are described. Unit 8, “Diagnosing and tracking infectious diseases”, discusses a major objective of the clinical microbiologist, to identify the microorganisms that cause illness, and the culture, immunologic, and molecular methods used to achieve this goal. In Unit 9, “Microbial diseases,” microbial infectious diseases are grouped within each chapter according to their mode of transmission.

The BBOM not only contains fundamental knowledge essential to an introductory course on general microbiology, but also information for students seeking to expand or update their knowledge of the current state of microbiology. As the evolutionary biologist Stephen J. Gould put it, we are living on “Planet Bacteria”. It is an exciting time to be a part of the science of microbiology—as BBOM once again well reminds us.

**MERCEDES BERLANGA**  
University of Barcelona  
mberlanga@ub.edu



## Animal viruses: molecular biology

THOMAS C. METTENLEITER,  
FRANCISCO SOBRINO (EDS.)

2008, Caister Academic Press,  
Norfolk, UK  
532 pp, 23.6 × 16 cm  
Price: £ 150  
ISBN: 978-1-904455-22-6

In 1796, Edward Jenner developed what became a widely adopted vaccine against smallpox. This was followed by vaccination against other viral diseases—including the successful post-exposure rabies vaccine designed by Louis Pasteur in 1886. Nonetheless, the nature of viruses remained unclear to those researchers and to their colleagues. In 1898, Friedrich Loeffler and Paul Frosch reported their results on the filterability and replicative capacity of the infectious agent responsible for foot-and-mouth disease (FMD) in cattle. That same year, Martinus Willem Beijerinck published his finding that tobacco mosaic disease was caused by something smaller than a bacterium, but which was also a “filterable agent which grew in the host, and was thus not a mere toxin” (the article was indeed written in German, but the title explained the new concept with three words in Latin: *contagium vivum fluidum*). These pioneering studies laid the foundation for the new scientific discipline of virology.

Virology studies biological viruses and virus-like agents: their structure, classification and evolution, the ways in which they infect and exploit cells for reproduction, the diseases they cause, the techniques to isolate and culture them, and their potential uses in research and therapy. There are many ways in which viruses can be classified, one of them being according to the host cell they infect. In fact, an infectious agent of veterinary importance (FMD) led to the development of the specialized field of “animal virology,” which includes viruses that infect humans.

In *Animal Viruses: Molecular Biology*, the book’s editors, Thomas C. Mettenleiter and Francisco Sobrino, have entrusted an international panel of leading virologists with providing a state-of-the-art overview of the field of animal virology. The book’s focus on “veterinary” viruses serves to highlight how this group of infectious agents has contributed to our current understanding of the molecular basis of viral

infections, especially those that have had a transcending impact on our understanding of viruses as a whole and of their mechanisms of action.

The study of animal viruses is obviously important from a veterinary viewpoint since the diseases they cause are often economically devastating. But one of the main motivations for their study is that many of these viruses are also important from a human medical perspective, being responsible for infectious diseases, such as the common cold, many forms of diarrhea, hepatitis, and AIDS, and contributing to certain forms of cancer. The emergence of zoonotic diseases provides additional compelling evidence. According to Julie Gerberding, director general of the US Centers for Disease Control and Prevention (CDC; in Atlanta, Georgia), “eleven out of twelve emerging human infectious diseases in the world have arisen from animal sources.”

Overall, working with animal viruses has one important advantage over the study of viruses that only infect humans: natural virus-host systems are experimentally accessible, and multiple animal models are available to analyze infections *in vivo*. Advances in this field have helped us in understanding how viruses cause disease and have revealed the molecular basis of many types of viral infections by elucidating pathways that may be used by related viruses, including those that are pathogenic to humans. This information has provided the basis for developing prevention and intervention strategies.

*Animal Viruses: Molecular Biology* consists of ten review articles that offer a detailed discussion of key virus groups and their impact on the veterinary environment. The field of animal virology has benefited greatly from the methodological and conceptual advances that have emerged in several related disciplines during the past few decades. Thus, the authors have paid special attention to emphasize the role of these parallel developments in current research and to provide the reader with key references.

Chapter 1 discusses how the molecular biology of FMD has been relevant to our understanding of the viral infectious cycle, and includes an in-depth discussion of what is needed to control viral pathogenesis and disease spread. Chapter 2 deals with pestiviruses, which are responsible for diseases such as swine fever and bovine viral diarrhea, and which share many similarities at a molecular level with human hepatitis C virus. Chapter 3 is devoted to arteriviruses. No human pathogens have so far emerged from this family, but it contains important animal ones. Besides the uncertainty surrounding their “out-of-nowhere” origin, the nearly simultaneous appearance of two distantly related porcine respiratory and reproductive syndrome viruses (PRRSV) in North America and Europe continues to puzzle researchers. Chapter 4 focuses on coronavirus (CoV) replication and its

host interactions. The recent advent of the severe acute respiratory syndrome (SARS) brought worldwide attention to this viral group and highlighted the importance of animals harboring infectious agents that can be potentially transferred into human populations. At the same time, CoV-based vectors have emerged with high potential for vaccine development and, possibly, for use in gene therapy. Chapter 5 covers the Hendra and Nipah viruses, part of the diverse family of paramoxiviruses, which encompasses many important human pathogens and is considered to have one of the most extensive, but still largely unknown, natural reservoirs. The Hendra and Nipah viruses are highly virulent and contagious; they have been designated as biosafety level 4 and are the source of concern regarding their potential use as bioterrorism or biological warfare agents. Chapter 6 analyzes the avian influenza virus (AIV), its host range and the molecular mechanisms of its pathogenicity. It is well-known that certain strains of AIV are occasionally transmitted from their normal reservoir, thereby causing devastating outbreaks in domestic poultry and, in a few cases, fatal disease in humans. Chapter 7 is a molecular dissection of Bluetongue virus, responsible for serious disease in livestock (sheep, goat, cattle) and, both molecularly and structurally, one of the best understood viruses. Chapters 8 and 9 describe the molecular biology of porcine circoviruses—the smallest viruses to replicate autonomously in eukaryotic cells—and of animal herpesviruses, respectively. The latter are highly successful pathogens, infecting animals and humans. Moreover, they remain in their host for its lifetime, and are reactivated from the latent state at irregular intervals, which allows them to infect other hosts. The study of these viruses has led to a new concept in animal disease control: the use of blanket vaccination to reduce the circulation of an infectious agent. Finally,

Chapter 10 provides an overview of the African swine fever virus, which is responsible for hemorrhagic fever and is associated with high mortality in pigs.

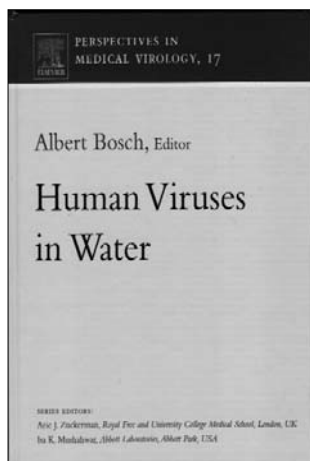
Lethal viruses present a paradox: killing its host is obviously of no benefit to the virus, so how and why did it evolve to do so? In the book's epilogue, "Animal virology: a showcase of evolution," Esteban Domingo and Marian C. Horzineck discuss some of the considerations regarding the evolution and long-term survival of viruses as pathogens in animal populations. Since most viruses are relatively benign in their natural hosts, lethal viral diseases may arise from an "accidental" jump of the virus from a species in which it is benign to a new one that has not been previously exposed to it.

So far, despite all the available tools of modern molecular biology, it has not been possible to create effective vaccines against several of the viruses discussed. However, the more detailed our understanding of them, the higher the chances of success in the design of novel approaches towards stimulating protective immunity. Evolution is at the roots of the difficulties we encounter when trying to keep viruses at bay, but it may also unlock possibilities to design virus variants, which can be used to prevent infection and disease. Infections of animals by their authentic pathogens can provide us with detailed insight into viral invasion and its effects on host functions. A better understanding of the evolutionary mechanisms behind the viral response to host defenses should help in the design of preventive and therapeutic strategies.

**NICOLE SKINNER**

INTERNATIONAL MICROBIOLOGY  
nskinner@microbios.org

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## Human viruses in water (Perspectives in medical virology, vol. 17)

ALBERT BOSCH (ED.)

2007, Elsevier, Amsterdam, Netherlands  
299 pp, 17 × 24.5 cm  
Price: €78.95  
ISBN: 978-0-444-52157-6

Around 1.1 billion people currently do not have access to an adequate water supply, and 2.4 billion people lack any type of access to decent sanitation facilities. About 2 million people die every year due to diarrheal diseases; most of these victims are children less than 5 years of age. The most affected are the populations of developing countries. Globally, the impact of waterborne viruses that cause gastroenteritis is difficult to assess because of the paucity of epidemiological data and the difficulty in detecting these viruses. *Human viruses in water* is an evaluation of the impact of viruses on water quality and, as such, offers information on new tools for the detection of viruses and risk assessment, the utility of water-quality indicators, environmental monitoring (virus occurrence and survival), and the regulations and guidelines that must be established to control water quality.

Viruses predominantly associated with waterborne transmission infect primarily the gastrointestinal tract; they cause gastroenteritis and are excreted through the feces. However, there are also viruses that cause other illnesses, such as hepatitis and polio. Gastroenteritis is a communicable disease characterized by fever, abdominal cramps, nausea, vomiting, diarrhea, and headache. After providing an overview of health-related water virology, the book goes on to discuss the numerous viruses found in the human intestinal tract (e.g., astrovirus; rotavirus; enteric adenoviruses; and the two genera of enteric caliciviruses, norovirus and sapporovirus; hepatitis A virus and hepatitis E virus; enterovirus) and the nature of the diseases they cause.

Developed countries normally have properly treated water and efficient sewage systems, such that viral gastroenteritis is predominantly self-limiting, with low mortality. Instead, most outbreaks of viral gastroenteritis are due to the consumption of contaminated vegetables, fruits, and other products, usually imported from regions where the responsible viruses are endemic. Shellfish, especially oysters and

other mollusks, growing and harvested in polluted waters represents a potential threat both in developed and in developing countries. In fact, the food most commonly implicated in infectious outbreaks are oysters. Shellfish are normally consumed raw or undercooked, so there is no inactivation or killing of the enteric pathogens that may be present. While simple depuration processes are usually sufficient to remove bacteria, this is not the case for viruses, which persist in shellfish for extended periods of time (Chap. 10).

Numerous physical, chemical, and biological factors, such as temperature, light, pH, salts, and the presence of organic matter, influence the persistence of viruses in the environment; however, the most significant factor controlling virus survival is temperature. At nearly freezing temperatures, viruses can survive for many months. For example, at 8°C in groundwater and 4°C in surface water, viral inactivation is less than 0.01 log<sub>10</sub> per day. Thus, an important characteristic of enteric viruses is their prolonged survival in the environment, and therefore their ability to continuously find new susceptible (human) hosts (Chap. 5).

Hazard analysis and critical control point (HACCP) programs have been applied to the quality assessment of drinking water in order to develop control measures and reduce risks to acceptable levels. The term “hazard” refers to a biological agent with the potential to cause adverse health effects. To manage water safety risks, it is important to identify the pathogen (viruses) as well as situations that may lead to waterborne illness, and to determine the magnitude of the impact that viruses have on human health. Such information allows rational decisions to be made about the need for increased management or regulation and guides the adoption of interventions to effectively reduce waterborne disease. Risk assessment consists of four steps: (1) Hazard identification (types of pathogens and description of the illnesses they cause, the need for hospitalization, and mortality); (2) exposure assessment or dose-response (quantitative relationship between dose and outcome, e.g., ID<sub>50</sub>, the number of microorganisms required to initiate infection in 50% of the exposed population); (3) hazard characterization (prevalence, concentrations, distribution in time and space in water or food consumed); and (4) risk characterization (the quantitative likelihood of potential adverse health outcome based on the above) (Chaps. 7 and 8).

The era of pathogen discovery is clearly not over, and all of the recent microbiological advances must be employed to improve our understanding of the transmission of diseases through water. Nonetheless, the detection of viruses in water and other environmental samples poses particular challenges and often cannot be achieved by routine screening methods. Viruses in water are usually present in concentrations too low

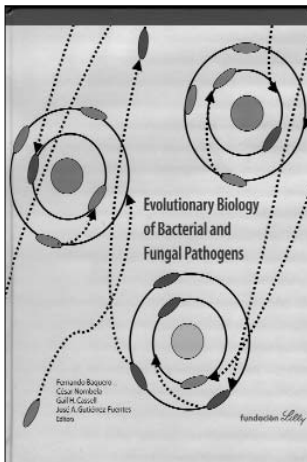
for detection by direct analysis, so a multi-stage process, involving concentration of a potential virus-containing sample, is almost always required. This concentrate is inoculated into cell cultures, which facilitates identification of the virus, or it can be analyzed by molecular biology procedures, such as the polymerase chain reaction (Chaps. 9 and 13). The complexity of these approaches on a large-scale basis underlines the importance of indirect indicators to assess water quality. Bacteriophages of enteric bacteria, such as coliphages or phages infecting *Bacteroides fragilis*, have been proposed as viral indicators. Bacteriophages persist longer than conventional bacterial indicators in aquatic environments and their persistence reflects that of human enteric viruses (Chap. 11).

The regulatory requirements for virus reduction are usually 99.99% reduction from a water source. Removal processes are normally implemented at the beginning of water treatment, whereas disinfection is a follow-up treatment used to inactivate viruses that have "escaped" the removal process. Viruses are normally removed by coagulation, sedimentation, flocculation, and filtration. Inactivation processes render viruses non-infectious to host cells even if they remain present in the treated water. The main inactiva-

tion methods used in water treatment include disinfection with chlorine, chloramines, or chloride dioxide, sometimes preceded by ozonation or UV irradiation (Chap. 6).

As discussed in the book's closing chapters, monitoring of human viruses in water must be done according to internationally accepted standards. It is essential that the methods and techniques undertaken by a laboratory are fit for their intended use and appropriately documented according to standard operating procedures. It is also necessary to adequately validate new methods and to compare them with previously established ones. In addition, monitoring of water quality should be regulated at the national level to insure uniform standards. This approach must mandate regular sampling of water sources. Such data provide the basis of water treatment and can be employed to generate predictive models of the potential risks to public health.

**MERCEDES BERLANGA**  
University of Barcelona  
mberlanga@ub.edu



## Evolutionary biology of bacterial and fungal pathogens

FERNANDO BAQUERO,  
CÉSAR NOMBELA,  
GAIL H. CASSELL,  
JOSÉ A. GUTIÉRREZ-FUENTES  
(EDS.)

2007, ASM Press, Washington, DC  
622 pp, 22 × 29 cm  
Price: US\$ 119.95  
ISBN: 978-1-55581-414-4

Interactions between microorganisms and humans range from a benign, even symbiotic collaboration to a form of competition that may become fatal for the host. Symbiotic indigenous microbiota colonize those regions of the human body that are in contact with the external environment, such as the skin, eyes, oral cavity, and gastrointestinal tract, in addition to some parts of the respiratory, urinary, and reproductive tracts. Despite the fact that humans are fully exposed to a wide variety of microorganisms, only certain populations are able to permanently inhabit the available body sites. In order for a microorganism to become established and thus to colonize a particular site, the environment of that site must satisfy the microorganism's nutritional and physicochemical requirements. In addition, the microorganism must be able to withstand host defenses, including various mechanical removing systems and the innate and acquired immune systems, as well as competition from the resident microbial community. At present, little is known about the mechanisms that enable the survival and long-term host tolerance of indigenous microbial communities or why these microorganisms do not elicit a damaging chronic inflammatory response. The evolutionary dynamics of host-pathogen interactions result in an ongoing process of natural selection in which there is adaptation and counter-adaptation by the two competing species. As pathogens develop new ways to avoid host recognition or elimination, host defenses must evolve in parallel to keep pace with them.

During the course of pathogen-host coevolution, there have been several infectious diseases that have notably shaped human history, especially those marked by the novel entrance into a population of a previously unknown infectious agent. Nonetheless, these opportunities seem to be limited since, among the millions of species of microorganisms

(30 million species have been estimated for prokaryotes), only 1922 species of infectious agents have been recorded, of which 632 are bacteria (no archaea is known to be pathogenic), 499 helminths, 329 fungi, 145 protists, and 317 viruses and prions.

*Evolutionary biology of bacterial and fungal pathogens* is a multi-authored book based on a meeting organized by Fundación Lilly [www.fundacionlilly.com] in El Escorial, Madrid, in November 2004. The editors, Fernando Baquero, César Nombela, Gail H. Cassell, and José A. Gutiérrez-Fuentes (director of Fundación Lilly), have collaborated to produce an excellent textbook, introducing evolutionary biology to clinical microbiologists, infectious disease specialists, and public health professionals. The contributions of the invited authors have resulted in an impressive book of six sections comprising 49 chapters that cover topics fundamental to understanding the evolution of microbial pathogens. The book is preceded by a short Foreword by Julian Davies, who once more corroborates the dictum of the Spanish classical writer Baltasar Gracián: "Good, if it's short, twice as good".

Section I, "Evolutionary biology of microbial-host interactions" (chaps. 1–11). Bacteria gain no advantage by making their hosts ill and illness certainly confers few, if any host benefits. Virulence is a consequence of bacteria being in the wrong host, or at the wrong site in the right host. The strategies employed by bacterial pathogens, the number and nature of the virulence factors required to activate them, and the regulatory systems that control virulence gene expression are the result of coevolution between bacteria and their hosts. The emergence of a new "professional" pathogen (an organism adapted for circulation within the host population as a pathogen) from a non-pathogen is a relatively rare event, because it requires the selection of multiple adaptive changes. Each pathogen has a reservoir habitat and a virulence habitat. The reservoir habitat is defined as an environmental site, host organism or population, or specific body compartment where the pathogen can sustain itself and from where it can be transmitted to other habitats or hosts. The virulence habitat is a disease-susceptible host, or a specific compartment within that host, in which growth of the pathogen causes clinical infection, thereby inducing host damage either directly, by the production of toxic compounds, or indirectly, by provoking self-damaging host responses. Host genetic factors determine differences in host susceptibility to infection and contribute to the pattern of clinical disease. The host's immune response represents an important selective force because it creates indirect compe-

tition between pathogens by limiting the number of non-immune or susceptible hosts. Social changes, such as those arising through “globalization,” and climate change are important determinants of the susceptibility to infections by different human populations.

Section II, “Evolutionary genetics of microbial pathogens” (chaps. 12–20). Evolution occurs through genetic variation and selection and is the fundamental strategy of life, allowing organisms to adapt to new environments and to adverse conditions. Variation in microbial pathogenesis is based on three mechanisms of genetic variability: point mutation, genetic rearrangements, and lateral gene transfer. Genomics and genome sequencing studies have corroborated that the position of genes in the chromosome (or genophore) is not random but is a result of selection. The relative positions of genes may influence their expression, mutational bias, and rearrangement, as well as paralogous gene evolution and the reductive evolutionary process. Besides its “original” set of genes, the genome of a bacterium may contain other elements from other bacteria: genomic islands, plasmids, and bacteriophages.

Some virulence determinants are clustered in pathogenicity islands acquired by horizontal gene transfer from another, unknown bacterial species. Genomic islands are parts of the genomes of many bacteria, pathogenic as well as non-pathogenic, and pathogenicity islands were the first group of genomic islands to be described. In addition, many bacteria harbor extrachromosomal elements in the form of plasmids that carry genes conferring a selectable phenotypic character under specific niche conditions. Finally, bacteriophages (prophages), present in both pathogenic and non-pathogenic strains, shape bacterial evolution in that they are ideal carriers for horizontal DNA transfer. Based on our current understanding, ~12% of the *Escherichia coli* chromosome consists of phages, with 51 different functional prophages identified in 27 *E. coli* strains. Incorporation of external genomic elements gives rise within a population to clones with different pathogenicities. Such pathogenic clones are responsible for disease outbreaks and increases in bacterial infection frequencies. These observations have important implications for our understanding of infectious diseases and the public health measures required to reduce their detrimental and potentially devastating effects on society.

Section III, “Evolutionary biology of drug resistance” (chaps. 21–28). Antibiotic resistance is not only a clinical problem but also a unique opportunity to observe “evolution in real time.” Antibiotic resistance may be regarded as the paradoxical consequence of successful antibiotic therapy.

Antibiotics were initially developed for the treatment of bacterial infections in humans, but their miraculous effects quickly led to their use in other animals and in plants. Antibiotics are used both internally and externally, maintaining the health of people, animals, and agricultural crops, and have vastly changed the relationships between bacteria and humans. Today, we are witnessing another change—in the relationships among bacteria themselves. Almost as soon as it was known that certain substances could kill microorganisms, it was also recognized that some microorganisms could survive normally lethal doses of these same agents. The first clinical report of acquired resistance to an antimicrobial agent was published in 1937, when Crean, a naval genitourinary specialist, reported in *The Lancet* that six of 100 patients with gonorrhea were unresponsive to treatment with sulfonamides. Reports of resistance to penicillin appeared in 1941, and to streptomycin in 1946. The term “antibiotic resistance” soon acquired a notorious meaning. Traditionally, it was thought that exposure of bacteria to antibiotics caused the selection of pre-existing resistant variants, but it seems that, under certain conditions, an antibiotic may also increase the mutation rate of a bacterial population (hypermutable strains or mutators). Mutators increase the probability of favorable mutations and they can accelerate the evolutionary rates of resistant variants that become fixed in the population.

Sections IV–VI, “Evolutionary pathogenicity of gram-negative and gram-positive bacteria and of fungi (chaps. 29–49). Although a wide range of microorganism–host relationships can ultimately lead to disease, the two most general strategies used by pathogenic microorganisms are aggressive “frontal” assaults and “stealth” assaults. Typically, frontal assault strategies require that the infecting microorganism rapidly replicates, induces disease symptoms that overwhelm the innate defenses of the host, and then find a new host before engagement of the latter’s “adaptive” or “acquired” immune system, in which antigen-specific lymphocytes respond to antigen exposure. These microorganisms typically produce toxins or effector proteins that disrupt the normal function of the host cell. Stealth assaults, by contrast, typically involve a slower infection process, in which the microorganism subverts the host’s innate and adaptive immune systems to set up a chronic or persistent infection. This section of the book includes a description of the pathogenic traits characteristic of several species of bacteria and fungi pathogens.

A major goal of *Evolutionary biology of bacterial and fungal pathogens* as a whole is to convey the idea that bac-

teria undertake similar forms of microbial variation in different habitats. The main distinction is that the habitat of a “natural” microorganism is the abiotic environment, while that of a pathogen is another living organism—the (human) host. Pathogens, but also non-pathogenic bacteria, harbor genetic elements that contribute to fitness adaptations in different environments. Microbial infections of humans are a relatively recent interaction, whereas the genetic and biochemical functions necessary for invasion and infection of the “modern host” probably evolved in an ancient environment from cell to cell interactions between microbes and protists or small invertebrates. As such, bacterial virulence factors have not evolved merely to cause disease in humans; rather, they are part of a general mechanism to coexist with, to cover, or to penetrate eukaryotic cells.

A significant and practical aspect of the book is its Glossary, which covers most of the evolutionary microbiology terms used in the book. Not only specialists but also advanced students will quickly find that the book is an essential part of any library of microbiology or related sciences. Moreover, microbiologists, and not only those active in the health sciences or field of infectious disease, will

enjoy the opportunity to learn more about the natural history and evolution of “bad” microorganisms. As noted in the Foreword by Julian Davies, “All microbiology is environmental microbiology and has been for billions of years.” Accordingly, pathogens can only be efficiently fought if we employ the knowledge developed by eco-evo approaches. Although the evolutionary origins of the relationships between prokaryotes and eukaryotes remain to be elucidated, we at least know the context in which they must be understood. As Francis Bacon wrote in *Advancement of Learning*: “If a man will begin with certainties, he shall end in doubts; but if he will be content to begin with doubts, he shall end in certainties.”

**RICARDO GUERRERO**  
University of Barcelona  
rguerrero@iec.cat