

THE GENETICS AND EVOLUTION OF INFECTIOUS DISEASES

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BOOK REVIEW

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The Genetics and Evolution of Infectious Diseases. Second Edition. By M. Tibayrenc (editor). Elsevier, Amsterdam, the Netherlands. 2017. 667 pp. ISBN: 978-0-12-799942-5. US \$190 hardback.

Review by James E. Childs

The Genetics and Evolution of Infectious Diseases, Second Edition, is a good text, with some caveats. I did not read the first edition so I won't comment on how this new edition improves on the old text published in 2010, but I note that the first edition contained 32 chapters vs. 27 in the second edition and was slightly longer (772 vs. 667 pages). The approach taken by the editor and chapter authors is multidisciplinary and topics range from cellular biochemical pathways and detailed genetics to vector biology and theoretical (e.g., pathogen effects on mate selection) and basic ecology. Sprinkled in-between are methods chapters that describe the current technologies available for examining pathogens and hosts such as next generation sequencing, methodologies for conducting multilocus sequence typing, and choosing appropriate methods and models for deriving phylogenies.

No individual can be an expert in all the fields and organisms covered within the volume. However, most of the chapters are clearly written, highly informative, and annotated by detailed examples drawn from the literature. By weaving sufficient history and background for each subject and illustrating core concepts, most chapters are engrossing,

enjoyable to read, and the material is accessible to any motivated reader.

The multidisciplinary approach is extended to individual chapters dealing with specific pathogens, vectors, and hosts where genetics, evolution, and ecology are intermixed. Many of the pathogens and diseases covered are either vector-borne (e.g., malaria, African sleeping sickness, Chagas disease, arboviral diseases) or were initially geographically and epidemiologically limited in the scope of their occurrence—such as human immunodeficiency virus (HIV) arising in Africa from primate simian immunodeficiency virus and severe acute respiratory syndrome coronavirus arising in China from certain lineages of bat coronaviruses with palm civets (*Paradoxurus hermaphroditus*) serving as an intermediate hosts—and would be expected to show natural 'nidality' (Pavlovsky 1966). A central theme in infectious disease study over the last few decades has been how infectious agents emerge from obscurity or rapidly change their spatiotemporal patterning, and that is the focus of many of the specific topics covered within this text. Other topics covered are emerging and previous threats such as tuberculosis and methicillin-resistant *Staphylococcus aureus* in addition to other drug-resistant organisms, the epidemiology and public health importance of which have dramatically changed in many regions of the globe and which have challenged hospital infection control systems. Further evidence of the challenges posed by drug resistance is highlighted in chapters on malaria and in the detailed treatment of the rapid development of insecticide resistance among many vector species. These processes are discussed within

the context of coinfection and natural selection and the challenges they represent to ongoing control or “eradication” programs.

I found the organization of the text to be somewhat idiosyncratic. The first 12 chapters mostly address broad issues such as the theoretic and philosophic issues of defining species of microparasites and the challenges to establishing meaningful phylogenies (Chapters 1 and 2) and how formal application of phylogenetic models take these issues into account (Chapter 8). Chapters 3, 5, and 12 review the population structure, clonal evolution, and development of antimicrobial resistance among bacteria. The coevolution of hosts and pathogens and the evolutionary responses of the host to parasitic infections are covered in Chapters 6 and 9. Two chapters (10 and 11) are largely methodological and focus on genomics and proteomics with examples drawn from applications to vaccine and drug development. Nestled in-between these more conventional topics is a treatise on the epidemiology of fungal parasites (Chapter 4), which I would have expected in the latter half of the volume when specific groups of pathogens are covered in detail. Chapter 7 is a very interesting treatment on the use of pathogens as genetic tracers of human demography and geographic expansion which, in my mind, could have been placed near the end of the text as an integrative treatment and application of the genetics of host-parasite evolution.

The remaining 15 chapters primarily review specific pathogens and hosts based on ecologically or genetically related organisms. Interspersed are chapters on genetic methods and their practical applications. Chapters 13 to 15 review characteristics of arthropod vectors for viral, bacterial, and protozoal pathogens including current morphologic approaches (they are heavy on methods) for discriminating among closely related vector species, the evolution of insecticide resistance, and the genetics of insect vectors. These three organism-focused chapters are followed by two methods chapters (16 and 17) on multilocus sequence typing and next generation sequencing, respectively, and then two chapters on private industry’s use of genetic-proteomic information to design and develop vaccines or

drugs and on how pharmaceutical approaches are utilizing host-parasite genetics to inform treatment options. Three chapters focus on protozoans and their hosts including the genetics of kinetoplasts (Chapters 20 and 22), agents of trypanosomiasis and leishmaniasis and the genetics of *Plasmodium* spp. (Chapter 21), and coevolutionary mechanisms to limit infection and disease by their affected host species. There are two chapters on major bacterial threats to human hosts with dwindling treatment options, multidrug-resistant tuberculosis (Chapter 23), and methicillin-resistant *Staphylococcus aureus* (Chapter 24). The remaining three chapters (25–27) review the origin, history, and current status of three viruses of zoonotic origins causing HIV, severe acute respiratory syndrome, and avian influenza viruses (influenza virus type A) (MERS is briefly discussed and this particular chapter could have addressed other coronaviruses as well).

As there is no forward to this text, I was left confused by why certain topics were not covered. I missed chapters on helminths and their related diseases, most notably schistosomiasis and hookworms. This omission also brought to mind the lack of discussion on the potential impact of coinfections on the course of diseases caused by the individual pathogens described. For example, there is a growing literature on how concurrent infection with helminths impact the frequency and severity of clinical malaria and the rapidity of progression of HIV infection to AIDS (Walson et al. 2009). Although the clinical impact of coinfections on the pathophysiology of ‘agent-specific’ disease progression is notoriously and inherently difficult to study in natural populations, coinfection with multiple pathogens is the rule, not the exception, among human populations, and this deserved more coverage.

In some cases, material in individual chapters is repetitive and covered in detail in other chapters, an example being the issues related to defining microparasite species and developing accurate phylogenies. This repetitiveness could have been reduced by having authors cite other chapters within the same text, which I only rarely noted. The diversity of topics covered necessarily involves the use of scientific jargon. However, only a few

chapters provided glossaries. These proved very helpful to me.

Finally, I would have appreciated reorganizing the individual chapters into sections, such as evolution and coevolution, methods of study, specific examples of pathogens-hosts and disease, and finally the application of genetics-proteomics to drug-vaccine development to the treatment of infectious diseases.

As I mentioned earlier, the text chapters are clearly written, highly informative, and annotated by detailed examples drawn from the literature. This text is geared toward students in advanced undergraduate and graduate programs geared toward wildlife diseases and zoonotic pathogens. I recommend looking at this textbook if your interests include or coincide with the range of topics described

above. Persons wishing a more comprehensive textbook dealing with wildlife diseases might look elsewhere, but probably won't find the chapters on the topics above as comprehensively treated.

LITERATURE CITED

- Pavlovsky EN. 1966. *Natural nidality of transmissible diseases*. University of Illinois Press, Urbana, Illinois, 261 pp.
- Walsh JL, Herrin BR, John-Stewart G. 2009. Deworming helminth co-infected individuals for delaying HIV disease progression. *Cochrane Database Syst Rev* 3:CD006419.

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