

Introduction

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The present multidisciplinary book is at the crossroads between two major scientific fields of the twenty-first century: evolutionary biology on one hand and infectious diseases on the other (Tibayrenc, 2001). Evolutionary biology is taken here in a broad sense and includes genetics, genomics, postgenomics, bioinformatics, and population biology. The genomic revolution has upset modern biology and has revolutionized our approach to ancient disciplines such as evolutionary studies. In particular, this revolution is profoundly changing our view on genetically driven human phenotypic diversity, and this is especially true in disease genetic susceptibility.

On the other hand, infectious diseases are indisputably the major challenge of medicine at the dawn of the twenty-first century. When considering a global view, they are the number one killers of humans, and therefore the main selective pressure exerted on our species. Even in industrial countries, infectious diseases are now far less under control than 20 years ago. In New York City, 25% of the strains of *Mycobacterium tuberculosis* are resistant to the main antituberculosis antibiotics. In France, nosocomial infections kill twice as many people as road accidents. The industrial world is now threatened by bird flu, which has reached West European poultry farms. The threat of a major pandemic is becoming increasingly probable (Ragnar Norrby, 2004; Fedson, 2005).

This book is composed of two parts:

1. A set of generalist chapters exposes the main features and applications of modern technologies in the study of infectious diseases. Rather than limiting itself to technological aspects, this part of the book will insist on the theoretical means needed for interpreting the data. Indeed, the major challenge for modern biology is not the development of even more powerful technologies (even if this is always welcome), but rather the search for new theoretical tools able to sort out and interpret the flood of data generated by mega technologies (automatic sequencing, micro arrays, proteomics, mega computers). In genetics and evolution, we are probably facing a conceptual revolution comparable to the transition between Newtonian physics and particle physics (Tibayrenc, 2001). Today technology is ahead of theory and this gap needs to be filled. This is one of the main goals of this book.
2. More specialized chapters delve into today's major stars of infection (malaria, SARS, avian flu, HIV, tuberculosis, nosocomial infections) and a few other pathogens that will

be taken as examples to illustrate the power of modern technologies and the value of evolutionary approaches.

This book will consider the three links of the epidemiological chain (host, pathogen, and vector in the case of vector-borne diseases), as well as the coevolution phenomena among them. This concept of an integrated approach to infectious diseases is also the basis for the MEEGID (Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases) congresses, successfully held since 1996 (next session: Atlanta, Georgia, USA, 31st October–2nd November 2012; see <http://www.meegidconference.com/>), and of the new journal *Infection, Genetics and Evolution* (<http://www.elsevier.com/locate/meegid>), started in 2001 (2009 official impact factor: 3.223). This shows that the concept is meeting resounding success.

The readers of this book will include not only specialized scientists, but also medical doctors, health professionals, professors, students, and the educated public. The authors will make every attempt to avoid overly specialized jargon, to make their chapters accessible to a broad public, while exposing the most updated science.

The double goal of the book is hopefully clear: (i) to emphasize the value of evolutionary approaches to all professionals working in the field of infectious diseases and (ii) to demonstrate the high potentiality of infectious models to all people interested in genetics and evolution.

References

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