

Preface

Despite great advances in public health worldwide, insect vector-borne infectious diseases remain a leading cause of morbidity and mortality. Diseases that are transmitted by arthropods such as mosquitoes, sand flies, fleas, and ticks affect hundreds of millions of people and account for nearly three million deaths per year globally. Additionally, the impact of insect-transmitted diseases to agriculture exceeds \$100 billion annually. Newly emerging patterns of certain vector-borne diseases such as malaria, West Nile encephalitis, tick-borne diseases, and dengue fever underscore the impact of arthropod-borne illnesses. Rapidly expanding patterns of global travel and commerce, coupled with evolution of pathogen resistance, have fueled deadly epidemics of vector-borne diseases in the past 5 years that have affected millions around the world.

Currently, the best methods for control of many insect-borne diseases involve the use of chemical pesticides. Such campaigns may, in the short term, yield spectacular results. Malaria was nearly eliminated from the Indian subcontinent; Chagas disease is rapidly being vanquished in some sections of Central and South America. However, insecticide campaigns are hampered in several ways. Environmental toxicity and adverse effects on human health limit the use of many chemical pesticides. Emergence of insect resistance to a wide variety of insecticides has greatly undermined their efficacy. The cost of repeated applications of pesticides is often prohibitive. Therefore, the wholesale elimination of insect pests is neither practical nor probable. Control of these scourges requires integrated efforts directed at advanced surveillance and epidemiology, vector control through novel genetic strategies, epidemic modeling, and greater understanding of human susceptibility to disease.

In almost all branches of science, research questions are answered from planned repeated experiments. But for infectious diseases, conducting experiments in communities is not ethical or possible. The retrospect epidemiological data may not help predict the future trends of the disease. Realistic mathematical models of the transmission of infectious diseases add a new dimension of information to assist in public health policy for control of the disease. These models provide a dynamic picture of disease transmission and are useful to predict the future trends of the disease. All models require realistic details and realistic parameter values. For practitioners in

this field to make a real-world difference and influence public health policy, medical experts are to be involved to ensure the realism of model structure and estimation of key parameters. Also, intelligent methods based on IT tools can help study various disease patterns.

In Volume 1 of “Dynamic Models of Infectious Diseases,” we have assembled eight chapters from highly acclaimed international scientists to address several of the major insect vector-borne diseases. A diverse and interdisciplinary group of authors has been selected with expertise in clinical infectious diseases, epidemiology, molecular biology, human genetics, and mathematical modeling. Indeed, we believe this collection of chapters is unique and should provide a valuable perspective to a wide audience. Though diverse in approach, all the authors address critical elements of disease control. Myriad tools, whether in the realm of molecular engineering, genomic analysis, predictive modeling, or information technology to improve surveillance, are presented in this collection to provide the reader with a current understanding of research methods directed at control of vector-borne diseases.

Dengue, a global vector-borne disease with propensity for explosive outbreaks, is the subject of Chap. 1 by V. Sree Hari Rao and M. Naresh Kumar. This chapter focuses on evolving tools of mathematical modeling as strategies for mitigation of dengue epidemics. The authors present new predictive models aimed at better characterization of human susceptibility and disease severity.

In Chap. 2, Maia Martcheva and Olivia Prosper have presented a detailed discussion on the dynamic mathematical modeling activity of the vector-borne diseases. This work demonstrates that models involving time delays are best suited for a more realistic description of different types of dynamical behaviors associated with the transmission of these diseases.

West Nile virus, an emerging vector-borne disease, is the focus of Chap. 3 by Eleanor Deardorff and Gregory Ebel. The spread of West Nile virus by invading species of *Culex* mosquitoes in the USA has brought much attention to the study of vector-borne diseases, by illustrating the potential of these illnesses to impact highly industrialized regions of the world. The authors discuss the current state of the epidemic in the USA and critical aspects of vector and host biology that determines effectiveness of control measures.

Chapters 4 and 5, by Dr. Ravi Durvasula and colleagues, address leishmaniasis and Chagas disease, two vector-borne disease complexes with global impact. Current epidemiology of these diseases and the latest therapeutic approaches are outlined. Evolving paratransgenic strategies from the Durvasula Laboratory aimed at reducing competence of insect vectors to transmit pathogens are presented with a perspective of identifying novel methods for control of disease transmission.

Information technology methodologies for monitoring and control of vector-borne diseases in India provide fresh perspectives on two devastating diseases, filariasis and Japanese encephalitis, in Chaps. 6 and 7 by U. Suryanarayana Murty et al. Particular focus is given to the impact of these conditions on the Indian subcontinent and novel modeling strategies that have resulted in IT-based tools for surveillance and control of both vectors and disease transmission.

Finally, in Chap. 8, the most devastating of insect vector-borne diseases, malaria, is discussed by D.J. Perkins et al. The Perkins Laboratory is widely recognized as a leader in the study of human genetic susceptibility to deadly complications of malaria caused by *Plasmodium falciparum*. In this chapter, current research that dissects the immunological and human genetic underpinnings of malarial infection, with particular emphasis on severe malarial anemia, is reviewed with the aim of better understanding and controlling the impact of this disease in sub-Saharan Africa.

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