# Preface

THIS BOOK FOCUSES ON THE FUNDAMENTAL SCIENTIFIC KNOWLEDGE OF MALARIA BIOLOGY that will inform the worldwide elimination campaign. Malaria remains a major global health problem and, over the past decade, there has been a focus on reducing the burden of the disease. This is a historical inflection point—knowledge about the parasite, the insect vector, and the human host is rapidly expanding and the challenge now is to translate this knowledge into tools that can be used to impact the disease and its transmission. At the same time, exploration of these fundamental systems is generating new and interesting basic biological questions. The human host, insect vector, and parasite are interacting in a complex systems ecology. We can see the evolution of both the parasite and the mosquito vector occurring in real time—the emergence of drug and insecticide resistance are prime examples.

The chapters in this book focus on the last decade of research. This is a period when the focus of malaria research shifted from pathogenesis and disease mechanism to interrupting transmission. This change in emphasis was, in part, the result of a set of high-level decisions led by Bill and Melinda Gates and their foundation to focus on malaria elimination and eradication. During this same period, there have been technological advances that have greatly enhanced fundamental science investigation, advances in genomics, systems biology, cell biology and imaging, and, most recently, advanced genetic engineering, including gene drive approaches to modify mosquito populations.

Perhaps most important from the perspective of the editors are the remaining gaps in our knowledge and the gaps in the translation of that knowledge for public health impact. Rather than reiterating what is covered in the book, we identify here key knowledge gaps that need to be addressed as we begin to translate the basic science discoveries to the problem of elimination and eradication of malaria. First is understanding the course of natural infection as transmission is decreasing, including understanding relevant vector biology, identifying key determinants of immunity, and deciphering the differences in infections of the five *Plasmodium* species that cause human disease. Understanding the biology of the *Plasmodium vivax* liver stage is critical. Second is understanding the emergence and spread of insecticide resistance in mosquitoes and drug resistance in parasite populations. The selective force of interventions generates population bottlenecks and understanding these dynamics is now within technical reach with a renewed emphasis on surveillance and molecular epidemiology. Third is a renewed focus on vector competence, including fundamentals of vector biology and the interaction of the parasite with its mosquito vector. The enabling technology of gene drives now makes intervention at the level of mosquito populations possible and understanding the implications is the next opportunity and challenge.

Regardless of the current successes in reducing transmission and resulting decreases in cases and mortality, there is constant evolution of the parasite, the vector, the human host, and the environment and a fundamental understanding of malaria biology is key to the next generation of interventions. Enabling technologies now make it possible to interrogate parasite and vector biology to understand key liabilities for targeting future interventions. Host–parasite and vector–parasite interactions are the next frontier in our understanding of disease progression and transmission. The microbiomes of the human and the mosquito are likely to play key roles, and we are just beginning to understand their interplay with immunity and nutrition.

We are deeply grateful to our colleagues who have authored chapters in this collection for their thoughtful exploration of these and other critical themes in the biology of malaria eradication. The next decade promises great advances in our understanding of malaria biology and the translation of that knowledge to inform elimination and eradication, surely with significant contributions by the authors of this book. Additionally, we are thankful to Dr. Bronwyn MacInnis for her steadfast efforts on spearheading this project, and to Lucia Ricci for her help and creativity with artwork. We are also indebted to Project Manager Barbara Acosta and her colleagues at Cold Spring Harbor Laboratory Press for their professionalism and patience in seeing this ambitious and important volume through to its impressive completion.

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