

Current Topics in Microbiology and Immunology

Volume 419

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Roles of Host Gene and Non-coding RNA Expression in Virus Infection

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Preface

Viruses are obligate parasites relying on the exploitation of host cell processes and resources for replication. The interplay between host and viruses remains largely unknown. Life cycles for individual viruses have been defined with functions ascribed for many viral proteins. The discovery of RNA interference (RNAi) and the subsequent development of tools to specifically silence individual cellular genes enabled genome-wide studies, interrogating gene function in a spectrum of processes, advancing developmental biology, and infectious disease. The advent of functional genomics allowed for the interrogation of the virus–host cell interactions and probing the genome for a role in the virus replication.

Libraries of arrayed siRNAs against human or mouse genomes have been available for more than a decade. More recently, microRNA (miRNA) mimic and inhibitor libraries have also become available for genome-wide screening, and most recently gene editing, e.g. CRISPR/Cas, has also become available. These approaches combined with transcriptomic and proteomic analyses have enabled the identification of new players in the host–virus interactome. Importantly, advances in recombinant technology, virology, and systems biology have allowed mapping of the interaction between cellular and viral gene products, including viral and cellular non-coding RNAs allowing for a better understanding of novel gene functions and pro- and anti-viral activities. These discoveries have provided an opportunity for the development of novel therapeutics and approaches to improve viral vaccines and vaccine production.

This volume presents a current understanding of the interplay between host cells and viruses during infection and replication. The first chapters present our knowledge of coronavirus, flavivirus, and human immunodeficiency virus (HIV), virus–cell interactions, i.e. three positive-sense RNA viruses (*Coronaviridae*, *Flaviviridae*, and *Retroviridae*), respectively. The volume then moves to address to negative-sense RNA viruses, with chapters on Ebola virus (*Filoviridae*), influenza virus (*Orthomyxoviridae*), and two viruses from the *Paramyxoviridae* family. The respiratory syncytial virus (RSV) chapter discusses the role of miRNAs in infection, while the henipavirus chapter explores diverse aspects of virus–host interactions. The volume finishes with a chapter on non-coding RNAs involved in

herpesvirus infection, a double-stranded DNA virus (*Herpesviridae*). These chapters capture many aspects of viral genomes and life cycles, including segmented, integrating, and latent genomes, acute, chronic, and latent infections, as well as vector-borne viruses. This volume provides a representation of virus–host interactions and a valuable resource for advancing our understanding. We are grateful to the authors for their expertise and contributions to this remarkable volume.

Athens, USA

Ralph A. Tripp
S. Mark Tompkins

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