

# Enteroviruses

Omics, Molecular Biology, and Control

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# Preface

The 12 species of the Enteroviruses – enterovirus A–H, enterovirus J, and rhinovirus A–C – are responsible, by many accounts, for more morbidity than any other viruses. The diversity of diseases caused by these genetically similar viruses is enormous, from the common cold to hand, foot and mouth disease to more serious diseases including cardiac infection, bulbar paralysis, and encephalitis.

Despite, or possibly because of, their success as pathogens, these prevalent and successful viruses function as highly efficient machines. Their entire genomes are usually under 8000 nucleosides, perhaps the size of two human genes, in a single positive-sense RNA molecule. The single open reading frames typically encode a single polyprotein which is produced in the absence of typical 5' cap signals, through use of an internal ribosome entry site. The polyprotein is cleaved, by viral proteases encoded within the polyprotein itself, into the proteins required to facilitate virus replication. A subset of these proteins produce a negative sense copy of the genome, which in turn are used to template more positive sense genomes for further translation and, ultimately, packaging in nascent virions. The typical end of the cycle is cell lysis and virus release, although not all infections are lytic and virus can be shed throughout the life cycle as naked and enveloped virions.

Poliovirus, which remains by far the best-studied member of the genus, is on the verge of eradication in the wild. Yet much more work remains to be done, as improvements in available poliovirus vaccines will be needed to complete the final challenges of eradication. In the meantime, enteroviruses D68 and 71 have emerged as significant public health threats over the last decade, and while the available data from study of other Enteroviruses have jump-started research on these viruses, there are clearly enormous differences between the Enteroviruses, such that nothing can be taken for granted or assumed when studying a new member of the genus.

In this volume, some of the best researchers in the *Enterovirus* field take the reader on a tour of the most exciting frontiers in the study of the genus. From understanding viral entry into cells, translation of the genome, and RNA–RNA replication, to the dynamic genomics of these viruses, to studies of viral avoidance of host cell defenses and lipid-mediated exit from cells, the topics are cutting-edge and the expertise second to none.

We are proud to bring you a collection of chapters representing the best of the field and

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our latest understanding of the genus *Enterovirus*. We hope you enjoy reading it as much as we have enjoyed assembling and editing it.

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