

Preface

To date there have been four types of influenza virus identified: types A, B, C and D. They are segmented, negative-strand (–) RNA viruses that constitute four out of the six genera within the *Orthomyxoviridae* family. Influenza A virus is the most troublesome one for the vast animal reservoir, the many subtypes that have been and are yet to be identified, and the tremendous ability to mutate and reassort. It is responsible for all known pandemics in human history including the three major pandemics in the last century. The most recent ‘Swine flu’ pandemic in 2009–2010 had an estimated global death toll of 284,000 according to US Centers for Disease Control and Prevention (CDC), demonstrating the devastating impacts of influenza A virus on our society even in modern days. Influenza A and B viruses together are responsible for seasonal epidemics each year and both have eight segments of genomic RNA. On the contrary, influenza C and D viruses only have seven segments of RNA. While influenza C virus infects human with mild symptoms, influenza D virus has only been detected in swine and cattle.

Recently, new advances in molecular biology, virology, biochemistry and structural biology have enabled the field to make many exciting discoveries that have, in some cases, conceptually revolutionized our understanding of this virus. For instance, influenza D virus, the newest member of the *Orthomyxoviridae* family, was first reported in swine in the Midwest region of the United States. The three-dimensional double-helical structure of the influenza virus RNP was finally visualized for the first time. The atomic structures of the viral polymerase complexes have now become available, thus greatly facilitating structure-based drug design targeting the viral replication. Our understanding of the host factors in influenza virus replication and antiviral responses has been significantly expanded. In addition, novel antiviral therapies have been designed against a broad array of viral proteins as well as host factors and pathways. Broadly neutralizing monoclonal antibodies against the conserved regions of haemagglutinin are currently in various stages of clinical trials. It is conceivable that these exciting new findings and development will one day translate into effective therapeutics against influenza infection.

In this book, eight chapters are showcased to illustrate some of the most important findings made in the flu field. Topics covered include stem-specific broadly neutralizing antibodies to haemagglutinin; virus replication and transcription; influenza B virus haemagglutinin; influenza A virus ribonucleoprotein complex; regulation of the virus replication machinery by host factors; evolution of receptor specificity of influenza A virus haemagglutinin; PB1-F2, a multi-functional non-structural influenza A virus protein; and avian influenza H7N9 virus. While it is mainly meant to provide a glimpse of what is currently

going on in the field, this collection of work will surely show the readers how fast the field is moving forward in various directions.

We are deeply indebted to all authors for their contributions to this book. To keep up with latest discoveries, many have updated their chapters before this book went to the press. We are confident that their patience and efforts are well justified by the end results and will be appreciated by the readers! We are also grateful to Annette Griffin for her insights and patience that made this book possible.

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