
THE VIRUSES

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The Influenza Viruses



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Edited by

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Preface

Influenza virus is an important human pathogen, frequently causing widespread disease and a significant loss of life. Much has been learned about the structure of the virus, its genetic variation, its mode of gene expression and replication, and its interaction with the host immunologic system. This knowledge has the potential of leading to approaches for the control of influenza virus. In addition, research on influenza virus has led to important advances in eukaryotic molecular and cellular biology and in immunology.

A major focus of this book is the molecular biology of influenza virus. The first chapter, which serves as an introduction, describes the structure of each of the genomic RNA segments and their encoded proteins. The second chapter discusses the molecular mechanisms involved in the expression and replication of the viral genome. In addition to other subjects, this chapter deals with one of the most distinctive features of influenza virus, namely the unique mechanism whereby viral messenger RNA synthesis is initiated by primers cleaved from newly synthesized host-cell RNAs in the nucleus. Among the most significant accomplishments in influenza virus research has been the delineation of the three-dimensional structure of the two surface glycoproteins of the virus, the hemagglutinin and neuraminidase. This has provided a structural basis for mapping both the antigenic sites and the regions involved in the major biological functions of these two molecules. The current state of research on the hemagglutinin and neuraminidase is presented in the third and fourth chapters of this book. Chapter 5 describes the research on the biosynthesis, processing, and transport of these two viral glycoproteins. This research has been important not only for understanding the morphogenesis of influenza virus, but also for providing new information about the biosynthesis and transport of all cell-surface glycoproteins.

Defective-interfering virus particles were first discovered in influenza virus preparations, and the sixth chapter describes what is currently known about the generation and mechanism of action of influenza virus defective-interfering particles. The different evolutionary patterns of ge-

netic variation of influenza A, B, and C viruses in humans, and the roles of different influenza virus genes in pathogenicity, are dealt with in Chapter 7. Influenza virus induces thymus-derived lymphocytes (T lymphocytes), which play an important role in antiviral immunity in humans. As discussed in Chapter 8, studies using influenza A viruses have provided some of the most significant findings on the nature of the antigens recognized by T lymphocytes, on the specificity of T lymphocytes, and on the process by which antigens are presented on the cell surface for recognition by T lymphocytes.

This book was put together with two overlapping objectives in mind: providing a current review of the research on influenza virus for virologists, while highlighting for a wide audience of scientists the impact that influenza virus research has had on eukaryotic molecular and cellular biology, and on immunology.

Robert M. Krug

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CHAPTER 1

Genes and Proteins of the Influenza Viruses

ROBERT A. LAMB

I. INTRODUCTION

This chapter describes the structure of the genes of influenza A, B, and C viruses. Influenza viruses contain a segmented single-stranded RNA genome that has been called negative stranded because the viral messenger RNA (mRNAs) are transcribed from the viral RNA segments. A great deal of new knowledge has been obtained about influenza A, B, and C viruses, since the last major multiauthored reviews of the genetics, molecular biology, and structural biology of influenza viruses (Palese and Kingsbury, 1983). The complete nucleotide sequence of the 8 RNA segments of the influenza A and B viruses has been obtained, and significant progress has been made with the sequencing of the influenza C virus genome. Other major developments include the following:

1. The three-dimensional structure of both major surface antigens, hemagglutinin and neuraminidase, has been determined from X-ray studies of crystallized proteins, and the structure of a neuraminidase-antibody complex has been obtained. In addition, the structure of the influenza virus hemagglutinin complexed with its receptor sialic acid has been elucidated, which may provide a basis for the rational design of antiviral drugs that would block viral attachment to cells.
2. In both influenza A and B viruses, previously unrecognized small integral membrane proteins, M_2 and NB, respectively, have been identified and extensively characterized.

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3. The influenza A virus N9 neuraminidase has also been found to exhibit hemagglutinating activity.
4. Influenza C virus glycoprotein exhibits both hemagglutinating and neuraminate-O-acetyl esterase activity.

The following sections review the structure of each of the RNA segments of influenza viruses and their encoded proteins. Emphasis is placed on topics unique to this chapter, as later chapters in this volume concern influenza virus replication, the hemagglutinin, the neuraminidase and antigenic variation. Inevitably, there is some overlap, but attempts have been made to minimize it and at the same time will make this chapter an overall survey. Little attempt is made to discuss the history of the disease, the response to infection, the ecology and epidemiology of the disease or the control of influenza through vaccination strategies or antiviral compounds. For these topics, the reader is referred to a recent review by Kilbourne (1987).

A. Structure of the Genome

Influenza virus, when cultured in tissue culture cells or embryonated eggs, has a fairly regular appearance, when negatively stained and visualized in the electron microscope, of particles of 80–120 nm in diameter. The virion contains a lipid envelope containing surface projections or spikes radiating outward. These spikes are of two readily distinguishable types: the rod-shaped hemagglutinin and the mushroom shaped neuraminidase (Kilbourne, 1987). Inside the virus, and observable by thin sectioning of virus or by disrupting particles, are the ribonucleoprotein (RNP) structures, which contain the different RNA segments. The genetic information of influenza A and B viruses is contained in eight segments of single-stranded RNA and for influenza C virus is 7 segments of single-stranded RNA (see Lamb, 1983, and Air and Compans, 1983, for references to the early paper describing these findings). The RNA of the virus is not infectious, and the mRNAs are transcribed from the virion RNA (vRNA) by the virion-associated RNA-dependent RNA transcriptase. Thus, as by convention, mRNA is plus-stranded (Baltimore, 1971) and thus the influenza viruses are known as negative-strand RNA viruses.

The early evidence for a segmented genome of influenza viruses has been extensively reviewed (Lamb, 1983; Lamb and Choppin, 1983); a major step forward in understanding the structure of the influenza virus genome came from the electrophoretic separation of the virion RNAs on polyacrylamide gels containing 6 M urea (Bean and Simpson, 1976; Pons, 1976; Palese and Schulman, 1976; Ritchey *et al.*, 1976; McGeoch *et al.*, 1976) (Fig. 1). The critical study showing that the eight RNA segments of influenza A viruses were distinct was done by two-dimensional

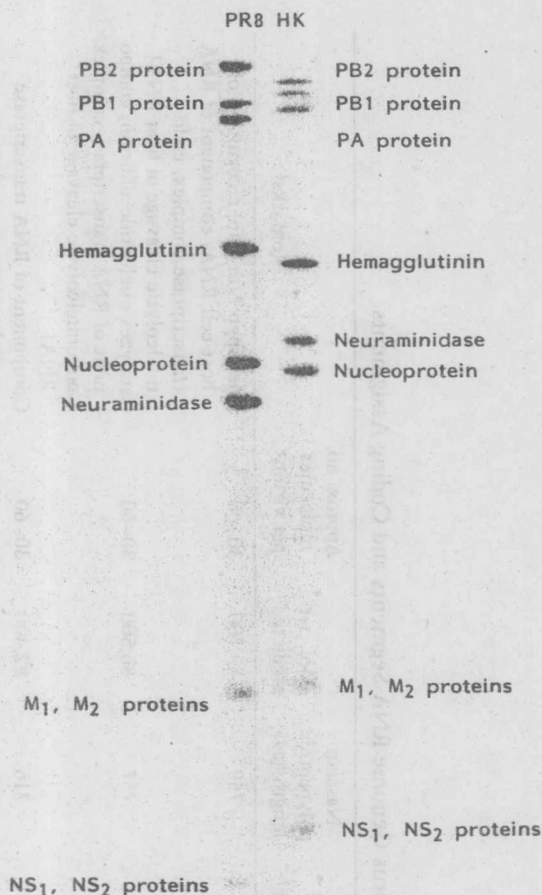


FIGURE 1. The influenza A virus RNA segments indicating their encoded gene products. The RNAs of influenza A/PR/8/34 and A/HK/8/68 viruses (PR8 and HK) were separated on a 2.6% polyacrylamide gel. RNA segments 1–8 are shown from top to bottom of the gel. The gene product assignments are discussed in the text. Under the gel electrophoresis conditions used the migration of the RNAs is dependent on the size as well as the secondary structure of the molecules. From Ritchey *et al.*, (1976) and kindly made available by Dr. Peter Palese, Mount Sinai School of Medicine, New York.

oligonucleotide fingerprinting (McGeoch *et al.*, 1976); this set the stage for a flurry of activity from several laboratories to characterize further the genome RNA segments and to determine their encoded protein products. The assignment of specific RNA segments to virus polypeptides was made in three ways:

1. A method pioneered by Palese, Schulman, and collaborators that depended on the apparent differences between strains in the electrophoretic mobilities of the RNA segments on polyacrylamide gels and the ability to distinguish proteins between strains, either by immunological methods for the hemagglutinin and neuraminidase or by differences in the electrophoretic mobilities of the polypeptides on protein gels [Recombinants were prepared between two parental strains and comparisons made of the mobilities of