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Dengue is caused by infection with one of the four dengue viruses: dengue virus 1 (DENV-1), DENV-2, DENV-3 and DENV-4. Infection with any of these viruses may result in asymptomatic infection, dengue fever (DF), or the more severe forms, dengue hemorrhagic fever (DHF) and dengue shock syndrome (DSS).

The Epidemiology, Virology and Clinical Findings of Dengue ...
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Virology Monographs Die Virusforschung In Einzeldarstellungen
Dengue virus is the cause of dengue fever. It is a mosquito-borne, single positive-stranded RNA virus of the family Flaviviridae; genus Flavivirus. Five serotypes of the virus have been found, all of which can cause the full spectrum of disease. Nevertheless, scientists' understanding of dengue virus may be simplistic, as rather than distinct antigenic groups, a continuum appears to exist. This same study identified 47 strains of dengue virus. Additionally, coinfection with and lack of rapid tes

Dengue virus - Wikipedia
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Part of the Virology Monographs Die Virusforschung in Einzeldarstellungen book series (VIROLOGY, volume 16) Abstract Before proceeding to a review of physical and chemical studies on dengue viruses, it may be helpful to describe briefly the host systems used to obtain virus for experimental work and assay procedures for monitoring virus-specific biological activities.

Biological Systems Used to Study Basic Viral Properties ...
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2. Virological Findings. 90 3. Immunity. 90 C. Secondary Dengue: Dengue Hemorrhagic Fever and the Shock Syndrome 92 1. General Remarks. 92 2. Clinical Course and Clinical Laboratory Findings 93 3. Virological and Serological Findings. 95 4. Immunopathology of Secondary Dengue. 98 XI. Immunization. 104 A. Anamnestic Immune Responses in Sequential Infections With Dengue and Other Group B Togaviruses. 104 1. Results With Members of the Dengue Subgroup 104 2. Results With Dengue and Other Flaviviruses. 107 B. Dengue Vaccines for Use in Man 108 XII. Opportunities for the Future 113 Acknowledgments. 114 References. 114 I. Introduction Dengue fever is a mosquito-transmitted disease of man which has afflicted untold millions of people over the past two centuries. It is caused by viruses classified as a subgroup of the group B togaviruses. Along with other members of that group as well as group A, the dengue viruses have been investigated intensively during recent years. Certain unique aspects of their structure, composition, antigenicity, replication, and antigenic relationships have established the togavirus family as quite distinct from other families of enveloped RNA viruses (see recent review of PFEFFERKORN and SHAPIRO, 1974). The basic studies leading to this conclusion have coincided with epidemiological field investigations which have resulted in a continuing increase in the number of viruses now designated as group A or B togaviruses. This, in turn, has led to a growing appreciation of their immense importance as actual or potential pathogens of man and beast.

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Virus Variability and Impact on Epidemiology and Control of Diseases E. Kurstak and A. Hossain I. INTRODUCTION An important number of virus infections and their epidemic developments demonstrate that ineffec tiveness of prevention measures is often due to the mutation rate and variability of viruses (Kurstak et al., 1984, 1987). The new human immunodeficiency retroviruses and old influenza viruses are only one among several examples of virus variation that prevent, or make very difficult, the production of reliable vaccines. It could be stated that the most important factor limiting the effectiveness of vaccines against virus infections is apparently virus variation. Not much is, how ever, known about the factors influencing and responsible for the dramatically diverse patterns of virus variability. II. MUTATION RATE AND VARIABILITY OF HUMAN AND ANIMAL VIRUSES Mutation is undoubtedly the primary source of variation, and several reports in the literature suggest that extreme variability of some viruses may be a consequence of an unusually high mutation rate (Holland et al., 1982; Domingo et al., 1985; Smith and Inglis, 1987). The mutation rate of a virus is defined as the probability that during a single replication of the virus genome a particular nucleotide position is altered through substitution, deletion, insertion, or recombination. Different techniques have been utilized to measure virus mutation rates, and these have been noted in the extent of application to different viruses.

The time seems ripe for a critical compendium of that segment of the biological universe we call viruses. Virology, as a science, having passed only recently through its descriptive phase of naming and num bering, has probably reached that stage at which relatively few new-truly new viruses will be discovered. Triggered by the intellectual probes and techniques of molecular biology, genetics, bio chemical cytology, and high resolution microscopy and spec troscopy, the field has experienced a genuine information explosion. Few serious attempts have been made to chronicle these events. This comprehensive series, which will comprise some 6000 pages in a total of about 16 volumes, represents a commitment by a large group of active investigators to analyze, digest, and expostulate on the great mass of data relating to viruses, much of which is now amorphous and disjointed, and scattered throughout a wide literature. In this way, we hope to place the entire field in perspective, and to develop an invalua ble reference and sourcebook for researchers and students at all levels. This series is designed as a continuum that can be entered anywhere, but which also provides a logical progression of developing facts and integrated concepts.

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