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CHRISTIAN A. TIDONA GHOLAMREZA DARAI (Eds.)

The Springer Index of **Viruses**

With 434 Figures and 1449 Tables



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Preface

The continuous growth of knowledge in the field of virology makes it very laborious for scientists to retrieve comprehensive data on a specific group of viruses. The desired information is often dispersed in a vast number of books, journals, and online databases. The time had come to create a book that presents the latest facts about all known viruses in the standardized format of an encyclopedic reference. In order to allow for the most up-to-date data possible, the present book was edited entirely via the Internet. For the first time in history many hundred of the world's leading virologists worked together online to create a highly structured and sophisticated source of information on viruses.

Virus taxonomy represents the basic framework that allows an understanding of the complex evolutionary process that continuously takes place among viruses and their hosts. There has always been much controversy and dispute among virologists world-wide about virus taxonomy. The first international effort to find a consensus taxonomic scheme that equally applies to all known viruses was made in 1966 in Moscow at the International Congress of Microbiology. Since then the International Committee on Taxonomy of Viruses (ICTV) has become a central and widely accepted institution that is responsible for the continuous integrity of the universal virus taxonomy.

The structure of the present Springer Index of Viruses is based on the latest virus taxonomy. Each of the 241 chapters treats one of the currently known virus genera, covering a wide range of different aspects including history, virion morphology, electron microscopic images, genome properties, replication strategy, properties of individual transcripts and proteins, biological properties in vitro and in vivo, as well as specific information about individual virus species.

Each chapter of The Springer Index of Viruses was contributed by one of the world's leading experts in that particular field. Although great efforts were made to bring the content of the present encyclopedic reference in line with the latest ICTV Report [van Regenmortel et al. (eds.) *Virus Taxonomy. Seventh Report of the International Committee on Taxonomy of Viruses*. Academic Press, 2001], there are some minor differences. For example additional genera were included that have not yet been approved by the ICTV. Other differences derive from the fact that authors did not always agree with the suggestions of the ICTV. Consequently, the present encyclopedic reference should be regarded as a valuable source of information on viruses, rather than an officially approved derivative of the current ICTV taxonomy rules.

We would like to thank the authors for accepting the Internet as a new editing medium and for their helpful discussions that led to a widely accepted consensus on chapter structure. Our special thanks go to Professor Hans-Wolfgang Ackermann and Dr. Cornelia Büchen-Osmond for their contributions and advice regarding chapter structure and virus taxonomy. Finally, we are especially grateful to Anja Tidona and Sanja Stjepanovic for their administrative help during the editing of this volume.

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Introduction to the Decimal Code for Virus Names

The Springer Index of Viruses is the first major publication to adopt the Decimal Code for unequivocal virus nomenclature. Devised for the universal virus database prepared for the International Committee on Taxonomy of Viruses (ICTV), the Decimal Code was originally introduced because the semantically rich nomenclature used in virology defies direct and systematic interrogation in a database, and because virus taxonomy changes rapidly. The Code was inspired by the recommendations on enzyme nomenclature prepared by the International Union on Biochemistry in 1978. In modern terms, it is analogous to the IP number of personal computers in a computer network. However, at the same time the structure of the Decimal Code simultaneously indicates the taxonomic status of viruses from the order to the isolate.

For example, the taxonomy of two semantically challenging members of the Family *Reoviridae*, the related species *Mal del Rio Cuarto virus* (name includes geographical information) and *Nilaparvata lugens reovirus* (name includes vector/host information), is simply revealed from inspection of their Decimal Codes (00.060.0.07.004 and 00.060.0.07.008, respectively). Moreover, the recent controversial relegation (Pringle, 1999) of such widely used species names as Poliovirus 1, 2 and 3 to serotypes on the basis of pair-wise comparison of genomic data was conveniently accommodated by the Code (Table 1).

Table 1: The Decimal Code applied to taxonomic revisions of *Poliovirus*, and constructed to anticipate the explosion of lower level data (serotypes, strains and isolates).

Taxonomic Level	Decimal Code
Order	00 = (not assigned)
Family	00.052 = <i>Picornaviridae</i>
Subfamily	00.052.0 = (not assigned)
Genus	00.052.0.01 = <i>Enterovirus</i>
Species	00.052.0.01.007 = <i>Poliovirus</i>
Subspecies	00.052.0.01.007.00 = (not assigned)
Serotype	00.052.0.01.007.00.001 = Poliovirus 1 00.052.0.01.007.00.002 = Poliovirus 2 00.052.0.01.007.00.003 = Poliovirus 3
Isolate/Strain	00.052.0.01.007.00.001.001 = Poliovirus 1 Mahoney 00.052.0.01.007.00.001.002 = Poliovirus 1 Brunhilde 00.052.0.01.007.00.002.001 = Poliovirus 2 Lansing 00.052.0.01.007.00.003.001 = Poliovirus 3 Leon/37

The prevalence of zeros in the examples of the Code shown in Table 1 is designed to accommodate the rapid evolution of virus taxonomy in the direction of more conventional Linnean systematics. Thus the ICTV has yet to rule on higher level taxonomy (orders and

Pringle CR (1999) Virus Taxonomy - 1999. The Universal System of Virus Taxonomy, updated to include the new proposals ratified by the International Committee on Taxonomy of Viruses during 1998. *Arch Virol* 144:421-429

families) or on controversial concepts such as subspecies. Increasingly, the most pertinent new data are generated at the level of serotypes, strains and isolates. As taxonomy is revised in the light of new data, the history of the decisions will be tracked from the old to the new Code, both of which are valid for search purposes. Now expanded to 19 digits to accommodate lower level taxonomic information, the Code should cope with even the most ambitious “splitters” in the taxonomic community.

As the universal virus database (ICTVdB) developed, it became clear that the Decimal Code served as more than an unequivocal identifier for taxonomically correct internal linkages. It has been used as a filename for transposing the ICTVdB to the web, and has been adopted as a surrogate accession number by sequence databases such as EMBL and SWISS-PROT that link to the ICTVdB. Similarly The Springer Index of Viruses uses these numbers as a cross reference to the ICTVdB.

If a database is to accept the latest data from all branches of virology, and place these into contemporary taxonomic context, it will most commonly deal with information at the level of isolates. Descriptions at the low end of the taxonomic hierarchy are essential for unambiguous identification of strains and isolates, which is of great importance in medicine and agriculture. These data give insight into evolutionary trends, and precision of identification becomes especially important for new, re-emerging or uncommon viruses.

Thus, the ICTVdB is designed to serve virus taxonomy “from the bottom up”, facilitating the submission of primary data from researchers who use discipline specific semantics that often reflect diverse geographic and linguistic features, as well as internationally accepted terminology at the level of sequence data. At the same time, the database must also accept revisions and consolidations “from the top down” as the consensus in virus taxonomy reflects this new information. These decisions are taken by the ICTV and increasingly rely on sequence data.

The Executive Committee of the ICTV committed itself to the development of a universal database in 1991. The goal of the ICTVdB is to describe all viruses of animals (vertebrates, invertebrates, protozoa), plants (higher plants and algae), bacteria, fungi, and Archaea from the family level down to strains and isolates. Developed at the Australian National University, and now based at Columbia University, ICTVdB owes much to the support of US National Science Foundation and sponsorship by the American Type Culture Collection. These goals have been achieved structurally and conceptually, and the prototype database has been available on the worldwide web since 1993. With much of the information content from printed reports of the ICTV, and linked to genomic and other databases, ICTVdB is currently consulted over 30,000 times daily. Its data and software can be accessed from servers maintained at sites in the NCBI, Bethesda, USA, <http://www.ncbi.nlm.nih.gov/ICTVdb/>, and the IACR, Rothamsted, UK, <http://www.ictvdb.iacr.ac.uk/>. A huge task remains to “populate” the database with isolate data, which is expected to be launched at the 12th International Congress of Virology in Paris in 2002.

Thus the Decimal Code unequivocally identifies a virus and should be routinely cited in publications. It is envisaged that researchers will soon require provisional allocation of a Decimal Code to all newly described viruses, prior to publication. In the future it will be necessary to identify provisionally assigned taxa in the dynamic database, but this can be accommodated without further assignments in the Decimal Code. Although individual virologists are finding the Decimal Code useful, this invention of necessity is by no means universally accepted among virus taxonomists. It is particularly gratifying that the Decimal Code for virus names has been adopted in The Springer Index of Viruses.

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