

Virus Taxonomy at the XIth International Congress of Virology, Sydney, Australia, 1999

C. R. Pringle

ICTV Secretary, Biological Science Department, University of Warwick, Coventry, U.K.

Introduction

The Eleventh International Congress of Virology was held from 9th–13th August at the Convention Centre, Darling Harbour, Sydney, Australia. The Congress included a Workshop on the Taxonomy of Viruses, and was also the occasion of the Eleventh Plenary Meeting of the International Committee on Taxonomy of Viruses (ICTV) and the Twenty-eighth Meeting of the Executive Committee of the ICTV.

Taxonomic proposals

Several taxonomic proposals, that had arrived too late to be incorporated in to the 7th Report of the ICTV, which is now in press, were considered and approved by the Executive Committee at a meeting prior to the Congress. Later in the week all the proposals were ratified at the Plenary Meeting as required by the Statutes of the ICTV. These taxonomic decisions involve plant and vertebrate viruses. There were no taxonomic proposals featuring bacterial or fungal viruses; decisions on several proposals affecting the taxonomy of invertebrate viruses were deferred and referred back to the relevant Study Group for amplification.

The new plant virus proposals and decisions are the following:

1. Downgrading of Petunia flower mottle virus (PetFMV) from independent species to be ranked as a strain of the species *Columbian datura virus* (CDV), because recent sequence data indicates that these two viruses are very similar.
2. Elevation of *Tomato pseudo-curly top virus* (TPCV) from its position as a species in the genus *Curtovirus* to become the type species of a new genus in the family *Geminiviridae* designated the genus *Topocuvirus*.
3. Change of the name Barley yellow dwarf satellite RNA to become Cereal yellow dwarf satellite RNA, since the existing name was inaccurate.

The vertebrate virus decisions affect viruses in the families *Circoviridae* and *Picornaviridae*. The majority of the proposals affecting the family *Picornaviridae* had already been ratified by postal ballot of the ICTV voting constituency and appear in both the 7th Report

and the synopsis previously published in Virology Division News [2]. These decisions entail the abolition of all existing picornavirus species (serotypes) and their replacement by species consisting of groups of related serotypes (previously referred to as “clusters”). Consequently, the family *Picornaviridae* now comprises the genera *Enterovirus* (with eight new species), *Rhinovirus* (with two species), *Cardiovirus* (with two species), *Aphthovirus* (with two species), *Hepatovirus* (with one species) and *Parechovirus* (with one species). The following new proposals were approved by the EC to complete the revision of the taxonomic structure of the family *Picornaviridae*.

1. To designate provisionally “Avian encephalomyelitis-like virus” as a tentative species in the genus *Hepatovirus*.
2. To rename Equine rhinovirus 2 as the species *Equine rhinitis B virus* and to assign it to a new genus *Erbovirus*.
3. To assign *Aichi virus* to a new genus designated *Kobuvirus*, which now becomes the eighth genus in the family. The genus name is derived from a Japanese word meaning hump or knob, reflecting the distinctive icosahedral structure of this group of viruses.
4. To rename Porcine enterovirus 1 as *Porcine teschovirus* and to assign it to a new genus *Teschovirus*, which becomes the ninth genus in the family. The genus name is derived from the name of the disease, teschen disease, associated with the type species.

The remaining taxonomic proposals concerned the family *Circoviridae*.

1. The formation of a second genus, *Gyrovirus*, was approved in order to accommodate the species *Chicken anemia virus* (CAV), which previously had been designated as the type species of the genus *Circovirus*.
2. The genus *Circovirus* now comprises *Porcine circovirus* (PCV) and *Beak and feather disease virus* (BFDV). This was the preferred option of the Study Group, despite the unusual device of reassigning a type species to another genus.

Executive Committee Elections

Other business of the ICTV involved the nomination and election of new officers and committee members to the Executive Committee in accordance with the Statutes of the ICTV (see Arch Virol 143/5, 1035–1040).

- Professor Marc Van Regenmortel (Strasbourg, France) was re-elected as President of the ICTV for a second term of three years.
- Dr. Jack Maniloff (Rochester, USA) was elected Vice-President on the retirement of Professor D. H. L. Bishop.
- Dr. Claude M. Fauquet (St. Louis, USA) was re-appointed as one of the two Secretaries, and Dr. Michael A. Mayo (Invergowrie, UK) was appointed as the other to succeed Professor C. R. Pringle on his retirement.
- Professor Brad Hillman (New Brunswick, USA) succeeds Dr. R. Wickner as Chair of the Fungal Virus Sub-committee.
- Professor Roger W. Hendrix (Pittsburgh, USA) succeeds Dr. J. Maniloff as Chair of the Bacterial Virus Sub-committee.
- Dr. Alan Brunt (Angmering, UK) succeeds Dr. M. A. Mayo as Chair of the Plant Virus Sub-committee.

- Professor Andrew Ball (Birmingham, USA) succeeds Dr. E. Carstens as Chair of the Invertebrate Virus Sub-committee.
- Dr. Anthony Della-Porta (Geelong, Australia) succeeds Professor M. C. Horzinek as Chair of the Virus Data Sub-committee.
- Dr. Mary K. Estes (Houston, USA) was re-appointed Chair of the Vertebrate Virus Sub-committee for a further three years, assisted again by Dr. Duncan J. McGeoch (Glasgow, UK) and Professor Stanley M. Lemon (Galveston, USA) as deputies.

Four of the eight elected members of the ICTV Executive Committee, G. Adam, J.E. Johnson, E. V. Koonin and G. P. Martelli, completed their terms at the Sydney meeting. Lois Blaine (ATCC, USA), Eric Carstens (Kingston, Canada), Anne-Lise Haenni (Paris, France) and Ann C. Palmenberg (Madison, USA), were elected as their replacements. In election of the new Executive Committee geographic spread has been lost to some extent in favour of improving gender balance.

In recognition of their contributions to the development of Virus Taxonomy over many years, Professor D. H. L. Bishop, Dr. G. P. Martelli and Professor C. R. Pringle were elected to Life Membership of the ICTV.

The ICTVdB

The ICTV meetings in Sydney were preceded by a meeting of the Virus Data Sub-committee hosted by Dr. Cornelia Buchen-Osmond at the Australian National University (ANU) in Canberra. Work on the development of the ICTV database (the ICTVdB) is continuing at the ANU with assistance from the American Type Culture Collection and the US National Science Foundation. The Database Subcommittee reviewed the progress of the project and presented an encouraging report at the Executive Committee meeting. The early commitment to the use of Delta software has been fully justified, and since the last Congress several competing systems have withered. The flexibility and general applicability of the ICTVdB system is now more apparent than ever, and it is expected that the database will be functional by the time of the XIIth International Virology Congress in Paris in 2002. Detailed information on the ICTVdB project can be obtained from the following internet addresses: <<http://life.anu.edu.au/viruses/welcome.htm>>, or mirror sites at the NCBI, Bethesda, USA <<http://www.ncbi.nlm.nih.gov/ICTVdB/welcome.htm>> and the IACR, Rothamsted, UK <<http://www.res.bbsrc.ac.uk/mirror/auz/welcome.htm>>.

The Plenary Meeting of the ICTV

At the Plenary Meeting the President of the ICTV reported that the full text of the 7th Report of the ICTV had been submitted to the publisher in January 1999 and the Report is now in press [4]. The 7th Report, under the title *Virus Taxonomy* and illustrated by over 300 figures and diagrams, provides detailed descriptions of 3 Orders, 56 families, 9 subfamilies, 233 genera and 1550 species of viruses. Major changes from the 6th Report [1] include the designation of 1550 species and the adoption of a new orthography [3], and the removal of many redundant names assigned solely on the basis of electron microscopical observations or where no isolates now exist. A significant development has been the allocation of many viral serotypes, previously ranked as different viruses (i.e. species), to a single virus species. This decision was the focus of some adverse comment, voiced both at the Plenary Meeting

and following the recent publication in Virology Division News of a synopsis of the new Universal Taxonomy of Viruses contained in the 7th Report [2]. Some critics considered several radical taxonomic changes had been introduced without adequate consultation and that the Study Groups of the ICTV were failing to consult the virological community widely enough. In the ensuing discussion, the President and others presented a strong defence of ICTV procedures and referred the critics to Workshop presentations on the following day, which illustrated the extent and depth of the analyses supporting taxonomic proposals emanating from Study Groups.

The Virus Taxonomy Workshop

The Virus Taxonomy Workshop, arranged by Colin Ward (Parkville, Australia) and Craig Pringle (Coventry, UK), comprised eight presentations covering a wide range of taxonomic issues. Marc Van Regenmortel (Strasbourg, France) opened the session with a comprehensive review of the concept of virus species and the new rules and conventions applying to the naming of species. The polythetic definition of virus species is now firmly established and the ICTV in 1998 decided that henceforth species names, in conformity with the names of other virus taxa, should be printed in *Italic* type with the initial letter capitalized [3]. He pointed out that this rule only applies when the species name is used to correspond to a taxonomic entity, i.e. as an abstraction corresponding to a taxon in virus classification. However, when used vernacularly in referring to concrete viral objects such as virions, *Italics* and capital initial letters are not required and names can be rendered in lower case Roman type. An advantage of the use of *Italics* when referring to the name of a species as a taxonomic entity is that it signals its status and its recognition as a legitimate species in the 7th Report of the ICTV [4]. The names of tentative species are capitalized but not italicized.

The extensive taxonomic changes included in the 7th ICTV Report [4] that affect the families *Caliciviridae* and the *Picornaviridae* were reviewed by representatives of the respective Study Groups. Nick Knowles (Pirbright, UK) presented a comprehensive survey of the wealth of data now available about the individual members of the family *Picornaviridae*, and described the process of consultation that had taken place. Seen in this context, the decisions of the Study Group were hard to fault despite the disquiet of some at the downgrading of such emotive names as poliovirus 1, 2, and 3 from individual species to serotype status. The Study Group had concluded that related serotypes should be brought together to form species according to the definition that a picornavirus species is a polythetic class of phylogenetically related serotypes or strains, that would normally be expected to share: (i) a limited range of hosts and cell receptors, (ii) a significant degree of compatibility in proteolytic processing, replication, encapsidation, and genetic recombination, and (iii) essentially identical genome maps. The family *Picornaviridae* now comprises nine genera embracing 20 defined species.

Kim Green (Bethesda, USA) similarly described the extensive process of consultation undertaken by the Calicivirus Study Group in reaching their decisions. The family *Caliciviridae* encompasses a diverse group of positive-strand RNA viruses, characterized by the presence of a small protein (VPg) covalently linked to the polyadenylated genome, an icosahedral capsid constructed from a single major structural protein, and phylogenetic evidence of a common ancestor. The family now comprises the genera *Vesivirus*, *Lagovirus*, and two genera with temporary names, the “Norwalk-like viruses” and the “Sapporo-

like viruses". *Hepatitis E virus*, formerly included in the family *Caliciviridae*, has been transferred to an unassigned genus until its taxonomic status can be determined.

There were two presentations on the application of pairwise sequence alignment in virus taxonomy. Robert Flegg (Parkville, Australia) reported that the pairwise comparison of protein sequences had established that this procedure could be used to discriminate strains, species and genera in the family *Potyviridae*. Subsequent analyses had confirmed that this approach is generally applicable and can be extended to the taxonomy of other families. He outlined the methodology of pairwise alignment of protein sequences, and presented the results of analyses of several virus families. The data were generally in agreement with currently accepted taxonomy, but some discordance was observed. Claude Fauquet (La Jolla, USA) described an attempt using similar methodology to devise a quantitative approach to virus taxonomy. He hypothesized that the genetic structure of a family could be visualized by making multiple alignments and plotting distributions of percentages of identities or homologies between pairwise comparisons of complete genomes or specific sequences. He presented a series of such analyses for the families *Geminiviridae*, *Potyviridae*, *Picornaviridae*, *Bunyaviridae* and *Orthomyxoviridae*. Within most families distinct genus, species and strain levels could be distinguished, although the levels differed between families. In specific instances overlaps of taxonomic levels were observed, perhaps revealing recombination events (*Geminiviridae*) or additional taxonomic levels (subspecies of potyviruses).

The remaining three presentations featured specific taxonomic situations. Marielle Van Hulten (Wageningen, the Netherlands) described analysis of a 12 kbp fragment of the 200 kbp genome of White spot syndrome virus of shrimp (WSSV). This virus resembles baculoviruses in morphology and pathology, and is responsible for global economic disease of penaeid shrimp. Eight open reading frames were apparent including genes for the large and small subunits of ribonucleotide reductase. Phylogenetic analysis showed that these genes did not share an immediate common ancestor with the corresponding baculovirus genes. These data suggest that WSSV is either a member of a novel genus in the family *Baculoviridae*, or possibly representative of a new virus family. The name Whispovirus (a siglum for White spot) was proposed.

Fang-Hua Chu (Taichung, Taiwan) reported completion of the sequence of the genome of Watermelon silver mottle virus (WSMV), a member of the genus *Tospovirus* of the family *Bunyaviridae*. Sets of degenerate primers have been designed, which are able to amplify conserved regions of the L genes of tospoviruses belonging to five distinct serogroups. A phylogenetic analysis of the L protein of fifteen members of the family *Bunyaviridae* suggest that the plant virus genus *Tospovirus* is more closely related to the genus *Bunyavirus* than to either of the other two animal virus genera, *Phlebovirus* and *Hantavirus*.

Finally, Dr. Alex Hyatt (Geelong, Australia) presented a review of the genus *Ranavirus* of the family *Iridoviridae*. The viruses belonging to this genus are widely distributed in nature. A collection of suspected ranaviruses, isolated from fish, frogs, toads and a snake, was examined by a battery of molecular techniques. Restriction endonuclease digestion of genomic RNA and sequencing of PCR products established that members of the genus *Ranavirus* could be grouped according to geographic origin and host organism (i.e. amphibian or fish). The one exception to this generalization was that viruses originating from the UK grouped with North American viruses. In the absence of specific neutralizing anti-

bodies, this methodology can be used to confirm the taxonomic identity of isolates and determine their geographic origin. Recognition of the biodiversity of ranaviruses has initiated an assessment of the potential impact of these viruses on commercial fisheries and herpetological wildlife.

Future taxonomic proposals

The Executive Committee of the ICTV is now beginning preparation of its 8th Report, which is intended for publication in mid-2002 in conjunction with the XIIth International Congress of Virology. Virologists wishing to make new taxonomic proposals, or seeking revision of previous decisions, should contact the appropriate Sub-committee or Study Group Chair at an early date so that their taxonomic proposals can be discussed and submitted for approval with the minimum of delay. The addresses of current Sub-committee Chairs and Study Group Chairs can be obtained from the ICTV web-site: <http://www.ncbi.nlm.nih.gov/ICTV/>

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Author's address: Dr. C. R. Pringle, ICTV Secretary, c/o Biological Science Department, University of Warwick, Coventry CV4 7AL, U.K.