

ICTV in San Francisco: a report from the Plenary Session

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At the International Congress of Virology (ICV) in San Francisco in July 2005, the International Committee on Taxonomy of Viruses (ICTV) held a Plenary Session. This note summarizes the reports made to the meeting by the President and the chairs of the ICTV subcommittees acknowledged at the end of this note. It also reports the results of elections to positions on the ICTV Executive Committee (EC) and changes made to the statutes that govern how ICTV operates.

President's report

The composition of the EC will change greatly after the Congress because three of the four officers, 5 of the 6 subcommittee chairs and 5 of the 8 elected members will change. The memberships of the ICTV EC for 2002 to 2005 and for 2005 to 2008 (following the results of the elections at the Plenary Session) are shown in Table 1.

Meetings

Since the International Congress of Virology held in Paris in 2002, the EC met in May 2003 at the Danforth Plant Science Center, St Louis, USA and in July 2004 at Queen's University, Kingston, Ontario, Canada.

Immediately after the Kingston meeting, ICTV organized and, with donated funds, sponsored a 1-day Satellite Symposium on 'Virus Evolution' in association with the annual American Society for Virology (ASV) meeting held at McGill University in Montreal, Canada, on July 10, 2004. Drs. Ann Palmenberg and Andrew Ball co-chaired the Symposium, which featured eight invited speakers. A report of the meeting has been published in Virology Division News [1].

ICTV newsletter

In order to disseminate information related to ICTV activities, in 2003 the EC instituted the electronic distribution of a periodic ICTV newsletter. Drs. Eric Carstens and Andrew Ball co-edited the first three issues of the newsletter, which were distributed in June 2003, February

Table 1. Memberships of outgoing and incoming Executive Committees

	2002–2005	2005–2008
Officers		
President	L. A. Ball	L. A. Ball
Vice-President	J. K. Maniloff	E. Carstens
Secretaries	C. M. Fauquet M. A. Mayo	A.-L. Haenni D. Fargette
Subcommittee Chairs		
Viruses of Vertebrates	D. McGeoch	D. McGeoch
Viruses of Plants	A. Brunt	M. J. Adams
Viruses of Insects	J. M. Vlak	P. Christian
Viruses of Prokaryotes	R. W. Hendrix	I. Molineux
Viruses of Fungi	B. I. Hillman	J. van Etten
Virus Database	A. J. Della-Porta	L. Blaine
Elected members		
	L. Blaine	H. J. Vetter
	H. Brussow	A. M. Q. King
	E. Carstens	J. Mackenzie
	U. Desselberger	A. Davison
	A.-L. Haenni	P. Krell
	A. M. Q. King	C. Suttle
	A. Palmenberg	U. Desselberger
	H. J. Vetter	A. Gorbalenya

2004, and May 2005. The newsletters are available to anyone who subscribes to ICTVnet (http://www.danforthcenter.org/iltab/ictvnet/asp/_MainPage.asp).

Management of taxonomic proposals

A system has been instituted for electronic submission of taxonomic proposals in a standardized format via the ICTV website. To facilitate input from all interested virologists, submitted proposals are now posted on the website before, during, and after review by the EC, with comments from both inside and outside the EC. Dr. Denis Fargette, who from July 2005 is one of the new ICTV Secretaries, is currently engaged in building this into a comprehensive electronic Taxonomic Proposal Management System that will keep track of all taxonomic proposals from their inception, through the several stages of review, to the final decision.

The Eighth ICTV Report

The Eighth Report of the ICTV was published by Elsevier/Academic Press recently [2]. This work, which is the definitive authority on virus taxonomy and nomenclature, lists more than 6000 viruses that are classified into 1950 virus species and distributed among more than 391 different taxa. Under the leadership of Dr. Claude Fauquet, this publication has developed from a list of virus names into a comprehensive and indispensable reference work for all virologists. The Eighth Report comprises 1259 pages that contain succinct and accurate information about all virus species: their taxonomic position, morphology, genome organization, replication, and biological properties.

ICTVdB

Considerable progress has been made with the development of the Universal Virus Database (ICTVdB). This is reported below.

ICTV finances

The ICTV EC acknowledges with gratitude the financial support it receives annually from the Virology Division of the International Union of Microbiological Societies (IUMS). In addition, the work of the EC has been supported in recent years by grants from the American Society for Virology and most recently from the Society for General Microbiology. Despite this welcome support, the annual meetings of the EC, which are essential for the conduct of the EC's business, could not take place without the royalties generated by publication of the periodic ICTV Taxonomic Reports, and the generosity of several EC members in underwriting their own expenses.

Report from the Vertebrate Virus Subcommittee

Dr. D. McGeoch presented the report.

Business of the Vertebrate Virus Subcommittee is co-ordinated by three members of ICTV EC:

- Duncan McGeoch (chair of the subcommittee) liaises with the ten Study Groups for DNA viruses and retroviruses.
- Ulrich Desselberger (elected member of the EC) liaises with the nine Study Groups for negative-stranded RNA viruses and double-stranded RNA viruses.
- Andrew King (elected member of the EC) liaises with the nine Study Groups for positive-stranded RNA viruses and prions.

In the last three years the Study Groups had initiated taxonomic proposals dealing with:

- (1) new species or new species names;
 - (2) new genera or new genus names;
 - (3) new families; and
 - (4) orders.
- (1) Only one species designation was mentioned explicitly, namely that for the SARS agent: *Severe acute respiratory syndrome coronavirus*.
 - (2) New taxonomy at the genus level included:

In the *Herpesviridae*:

 - Designation of the genus *Ictalurivirus* as unassigned within the family (previously temporarily named Ictalurid herpes-like viruses)
 - Designation of the genus *Mardivirus* in the subfamily *Alphaherpesvirinae* (previously temporarily named Marek's disease-like viruses)
 - Designation of the genus *Iltovirus* in the subfamily *Alphaherpesvirinae* (previously temporarily named Infectious laryngotracheitis-like viruses).

In the *Papillomaviridae*, organization of the family into 16 genera:

Alphapapillomavirus, *Betapapillomavirus*, *Gammapapillomavirus*, *Deltapapillomavirus*, *Epsilonpapillomavirus*, *Zetapapillomavirus*, *Etapapillomavirus*, *Thetapapillomavirus*, *Iotapapillomavirus*, *Kappapapillomavirus*, *Lambdapapillomavirus*, *Mupapillomavirus*, *Nupapillomavirus*, *Xipapillomavirus*, *Omikronpapillomavirus* and *Pipapillomavirus*.

In the *Circoviridae*, designation of a new genus, *Gyrovirus*, with type species *Chicken anemia virus*. The *Circoviridae* Study Group also dealt with the beginning of taxonomic arrangements for the viruses known informally as ‘TTV’, with the creation of a new genus (presently unassigned to a family), *Anellovirus*, with type species *Torque Teno virus* (TTV).

In the *Parvoviridae*, creation of two new genera, *Amdovirus*, with type species *Aleutian mink disease virus*, and *Bocavirus*, with type species *Bovine parvovirus V*.

For *Hepatitis E virus*, taxonomic arrangements were established: family *Hepeviridae*, genus *Hepevirus*, with type species *Hepatitis E virus*.

In the *Reoviridae*, a new genus was created, *Bannavirus*, with type species *Banna virus*.

Establishment of the high level taxon Order is being pursued in four cases, and proposals will be posted for comments (proposed names: *Herpesvirales*, *Picornavirales*, *Reovirales*, *Retrovirales*).

In the coming three-year session, a number of topics are expected to be active in addition to the standard business of taxonomic proposals.

- A position on numbers and scopes of Study Groups should be sought, both on account of ever-increasing numbers of groups with the present family-based system and to engage with the trend to higher level taxonomy, specifically involving orders.
- In recent years (or decades) the Vertebrate Virus Subcommittee itself has simplified to one-to-one interactions between the chair (plus deputies) and chairs of Study Groups. It should be valuable at least for some purposes to have broad discussion at the the Subcommittee level.
- Agents of spongiform encephalopathies have traditionally been treated by ICTV. However, there are intractable problems in this field: the Prion Study Group has collapsed because of lack of a common position between ‘prion supporters’ and ‘others’. A way forward must be sought.
- Systems of maintaining a watch for unassigned viruses need to be improved.
- Current developments, primarily in virus structural studies, are hinting at the possibility of higher taxonomy above order (for instance class). Such ideas will need to be examined for their soundness and utility.

D. McGeoch closed with thanking his two co-chairs, the chairs of Study Groups, and the many members of Study Groups for their efforts.

Report from the Invertebrate Virus Subcommittee

Ascoviridae

While there are now at least 30 different isolates of ascoviruses, primarily isolated from larvae of species belonging to the family Noctuidae, there are only five groups of researchers working on these viruses, and in most of these laboratories ascovirus research is a sideline, especially work on taxonomy. Nevertheless, a least two of these groups have applied for funding to work on ascovirus systematics to sort out the relatedness of the various species, tentative species, and isolates. Thus, it is probable that a significant amount of new taxonomic data should be forthcoming in two to three years.

Baculoviridae

Significant effort was given by all committee members to ensure that the *Baculoviridae* taxonomy chapter in the 8th Report was as accurate and current as possible. All GenBank sequences were examined and all viruses that met species criteria were included in the report. The vast majority of all baculoviruses that have sufficient data (biological and molecular) to support a species classification have been included the 8th Report.

Genomics has recently had a significant impact on the baculovirus taxonomy. The recently determined genome sequences of three baculoviruses are fueling a discussion to expand the number of genera currently recognized in the *Baculoviridae*. The genomes are from the mosquito (Diptera) baculovirus, *Culex nigripalpus nucleopolyhedrovirus*, and from two sawfly (Hymenoptera) baculoviruses, Neodipteran sertifer nucleopolyhedrovirus and Neodipteran lecontei nucleopolyhedrovirus. Whole genome phylogenetic analyses indicate that these genomes are distinct lineages that are clearly highly diverged from the previously known genomes that provide the basis for the current genera. The biologies and life cycles of these viruses are also distinct from those of members of both current genera *Granulovirus* and *Nucleopolyhedrovirus*. The mosquito and sawfly virus genomes are also clearly distinct lineages and a proposal is being developed to add two new genera to the family *Baculoviridae*.

Dicistroviridae

The Paris meeting in 2002 saw the establishment of the family *Dicistroviridae* and of the genus *Cripavirus* within the family. At that time, the genus contained 8 species with *Acute bee paralysis virus* (ABPV) being recognized as an unassigned member of the family. In 2003 an additional species (*Aphid lethal paralysis virus*) was added to the genus *Cripavirus*, and *Taura syndrome virus* was removed from the genus and placed alongside ABPV as an unassigned member of the family.

This Study Group also has the responsibility for the other picorna-like viruses of insects that have closer affinity to the picornaviruses, namely the infectious flacherie-like viruses. The unassigned genus *Iflavirus* was created to contain three species (*Infectious flacherie virus*, *Sacbrood virus* and *Perina nuda virus*). The Study Group currently retains the responsibility for this floating genus, although recent discussions have been held with the *Picornaviridae* Study Group to ascertain if there is sufficient evidence to put forward a proposal to include the iflaviruses alongside the picornaviruses.

Iridoviridae

Currently, 5 genera are recognized within the family, including the newly established genus *Megalocytiavirus*. Sequence data support the existence of all genera, with the exception of *Chloriridovirus* for which limited sequence information is available. Current taxonomic research has focused on identifying novel viral isolates and determining where they fit into the current taxonomic scheme.

Tetraviridae

Sequence analyses of members of the *Tetraviridae* indicate that while their capsid proteins have a common origin, their RNA-dependent RNA polymerase genes were derived from two or three different lineages, one of which is shared by some members of the *Birnaviridae*. It is likely that this observation will require some rearrangement of the taxonomy of the *Tetraviridae* in the future.

No new taxa were recognised in the families *Nimaviridae*, *Nodaviridae* and *Polydnaviridae*.

Report from the Plant Virus Subcommittee

Since the last plenary meeting of ICTV at the International Virology Congress in Paris, members of the Plant Virus SC (PVS) have been largely occupied with four major topics:

the creation of new families and genera; preparation of contributions to the 8th Report; a consideration of the possible use of non-latinised virus binomials; and, recently, the submission to the Executive Committee of further taxonomic proposals.

New taxa

Since the publication of the 7th Report, proposals have been approved by ICTV for the creation of three new families of plant viruses and eight new genera, and the replacement of four tentative generic names by more appropriate names. Currently, therefore, there are 89 genera of plant viruses and viroids, of which 72 are included in one of the 20 families; three of these families (*Reoviridae*, *Rhabdoviridae* and *Bunyaviridae*) also include genera of viruses that infect hosts other than plants.

New families

The three new families created were: *Flexiviridae* (genera *Potexvirus*, *Carlavirus*, *Capillovirus*, *Trichovirus*, *Foveavirus*, *Allexivirus*, *Vitivirus* and the newly recognised *Mandarivirus*), *Nanoviridae* (genera *Nanovirus* and the newly recognised *Babuvirus*) and *Tymoviridae* (genera *Tymovirus*, *Marafivirus* and the newly recognised *Maculavirus*).

New genera

The eight new genera created were: *Babuvirus* in the family *Nanoviridae*, *Topocuvirus* in the family *Geminiviridae*, *Ampelovirus* in the family *Closteroviridae*, *Mandarivirus* in the family *Flexiviridae*, *Maculavirus* in the family *Tymoviridae*, *Endornavirus*, *Cheravirus* and *Sadwavirus* (unassigned genera).

Renamed genera

Four genera in the family *Caulimoviridae* were given international names to replace the previous temporary name, namely *Soymovirus* (for “Soybean chlorotic mottle-like viruses”), *Cavemovirus* (for “Cassava vein mosaic-like viruses”), *Petuvirus* (for “Petunia vein clearing-like viruses”) and *Tungrovirus* (for “Rice tungro bacilliform-like viruses”). In the family *Pseudoviridae*, genus *Hemivirus* was renamed as genus *Sirevirus*”).

ICTV 8th report

Study Groups of the Plant Virus Subcommittee have made considerable efforts during the past year or so in finalising their contributions to the 8th Report. These have also included the updating of the criteria used for the demarcation of species within each genus and numerous proposals for the inclusion in genera of newly recognised species. The reports on individual families and genera of plant viruses contribute substantially to the main report.

Possible use of non-latinised virus binomials (NLVB)

After much heated debate and as a result of the ballot held at the ICV in Paris, Study Groups and other members of the PVS were requested to report whether, after further consideration of the matter, they were or were not in favour of using NLVBs. Twelve of the 30 Study Groups failed to express an opinion. As might be expected, there was no unanimity within the majority of the remaining 18 Study Groups. However, overall a clear majority of the

Study Groups supported the use of NLVBs (13 voting in support, 3 against and 2 failing to agree a consensus view). In addition, of the five general members of the subcommittee who responded, four were in favour and one was against the proposal.

Taxonomic proposals

Study Groups and their individual members continue to be active in the preparation of taxonomic proposals. Currently, an additional 15 proposals are posted on the ICTVnet for the scrutiny of the EC prior to possible amendment by the proposers and general consideration by virologists.

Report from the Prokaryote Virus Subcommittee

The responsibilities of the Prokaryote Virus Subcommittee (formerly the Bacterial Virus Subcommittee) include the viruses of bacteria and the viruses of Archaea.

There are very few archaeal viruses known, but a small number of labs have been active in isolating new archaeal viruses over the past few years. Since the last Plenary Session in Paris, one of the four existing families has been renamed to conform to ICTV conventions. Three new genera have been established within the existing families, and one new unassigned Archaea virus genus has been established. More proposals are currently under consideration or contemplated for the near future, and continuing taxonomic activity for this largely unknown group of viruses is expected.

For the bacterial viruses there have been new species established within existing genera of the *Microviridae* and *Tectiviridae* families. In the order *Caudovirales*, two new genera have been added to family *Siphoviridae* and one to family *Podoviridae*. This modest level of taxonomic activity for the bacterial viruses is due in part to a modest level of activity in acquiring new isolates in several of these taxa, though a recent ~10-fold increase in the number of *Microviridae* isolates and a somewhat more modest increase in the number of *Cystoviridae* isolates should translate into taxonomic activity for these groups in the near future.

The tailed phages (*Caudovirales*) are a special case. Here, there are several hundred isolates characterized to at least a moderate degree but still unclassified. The central issue here is that recent genomic studies of this group have made a strong case that the current hierarchical taxonomy in use by ICTV fails to represent adequately the phenotypic relationships among these viruses and in fact, because of the pervasive genetic mosaicism in this group, actually misrepresents most of the relationships. This view is not shared by all members of the subcommittee, and considerable energy has been devoted to discussions of whether a new taxonomic system is needed to describe this group, and if so, what form it might take. Meanwhile, the current (and now outgoing) subcommittee chair has declared a moratorium on establishing additional taxa in the *Caudovirales* until this issue is resolved or until his term expires, whichever comes first.

Report from the Fungus Virus Subcommittee

Two formal sets of proposals were presented by the Fungus Virus Subcommittee.

- 1) The first concerned creating a family to contain genus *Mimivirus* (Mimiviridae) for the virus species *Acanthamoeba polyphaga mimivirus* that had been published under the name *Mimivirus*. The authors will be asked to provide more specific information about the virus and its closest relatives within the body of the proposal template, and to provide a virus number to this species, in accordance with the accepted procedures for naming viruses of fungi and lower eukaryotes.

- 2) The second dealt with higher order taxonomy of reverse-transcribing elements. These proposals concerned virologists represented by several subcommittees but were presented by the Chair of the Fungus Virus Subcommittee. It was proposed to erect two orders, *Retrovirales* and *Retrales*, that would include all such elements. The order *Retrovirales* would contain elements that are known to have the potential for horizontal spread, and would be subdivided into three suborders. One suborder would include the retroviruses in the established family *Retroviridae*, another that would include elements with DNA genomes in the families *Caulimoviridae* and *Hepadnaviridae*, and a third that would include retrotransposons in the families *Pseudoviridae* and *Metaviridae*. The order *Retrales* would contain elements that are not known to spread from one individual to another by horizontal transfer and that do not appear to have potential for such transfer. The idea of grouping the reverse-transcribing elements that have already been accepted by the ICTV as viruses into a higher order taxon has received broad support from those who work with such elements. Potentially more problematic parts of these proposals are: 1) that the ICTV does not at this time recognize "Suborder" as a taxon; and 2) that all elements currently studied by ICTV have been shown to be infectious. A further problem with the Suborder taxa as proposed is that they do not appear to reflect phylogenetic groupings of these elements, as determined from reverse transcriptase alignments. The authors will be asked to remove the suborder taxa, and to remove the proposals concerning the non-transmissible order *Retrales*.

Other recent developments in fungal virus taxonomy include the description and acceptance of the genus *Mycoreovirus* into the family *Reoviridae*, the description of three viruses that appear to fit within the plant virus family *Flexiviridae*, and the description of a new member of the genus *Endornavirus*, previously known only to infect plants, from a fungus-like Stramenopile in the plant-infecting genus *Phytophthora*. The *Phytophthora*-infecting endornavirus was found to contain a UDP-glucosyltransferase gene. Two members of the *Hypoviridae* family of pathogens that infect the ascomycete fungal genus *Cryphonectria* were also found to contain UDP-glucosyltransferase genes that appear to be complete. The description of increasing numbers of viruses of fungi that are closely related to viruses in established families that infect other eukaryotes argues that increasing communication between fungal virus study groups will be required in the future.

Report from the Virus Database Subcommittee

The ICTV Database (ICTVdB) is a copyrighted, interoperable, universal virus database of ICTV-approved taxa that has been in development for more than 10 years. It is available to virologists at <http://www.ncbi.nlm.nih.gov/ICTVdb/index.htm>. The site currently receives many hits, averaging one every 30 seconds (assessed for May 2005). The Chair of the Virus Database Subcommittee, Tony Della-Porta, emphasized the major contributions made by Cornelia Buechen-Osmond, the ICTVdB manager over more than a decade and the work that Lois Blaine (incoming Chair of the Virus Data Subcommittee) has done in raising more than \$10 million to fund the database development over the same period.

Developments and achievements during the last 3 years include:

- Agreement by ICTV that in order to propose recognition of a species, at least one entry of an isolate description should be made into the ICTVdB.
- Data entry into the ICTVdB should be made at the isolate level, but the lowest taxonomic level is that of species. Only the ICTVdB Subcommittee can enter data above the isolate level.
- An isolate is what is described by the data set being entered. Any level above this (i.e. data for a collection of isolates or even a species) represents a taxonomic description and hence a description of an abstraction.

- The Virus Database Subcommittee is working with the National Center for Biotechnology Information (NCBI) to link virus genome descriptions with isolate data entered into the ICTVdB.
- A simple two-page data entry process has been developed and information supplied to NCBI to facilitate the submission of isolate data into the ICTVdB and to facilitate linking these data with GenBank entries.
- Discussions have been held about the long term support of ICTVdB and funding of ICTV EC activities.
- Development of bulk data entry processes for entry from private databases and collections of isolates, resulting in the accessing of information of nearly 10,000 virus isolates, including the World Reference collection of foot-and-mouth disease viruses, major plant virus databases, and data about some substantial collections of arboviruses.
- Agreement that provided that there is sufficient arbovirus information and entry, the next Arbovirus Catalogue will be developed with the assistance of the ICTVdB.
- The movement of the ICTVdB from the Australian National University to Columbia University.
- The copyrighting of the ICTVdB in the name of the ICTV in order to protect it and the data format for the ICTV and virologists.

Elections

1. Executive Committee

The positions that were decided at the Plenary Session were the President, Vice-president, the 2 Secretaries and the 8 elected members. Subcommittee chairs had already been elected by members of the EC. When nominations closed 2 days prior to the plenary session there were single nominations for each officer position and a total of 8 nominations for the 8 elected member vacancies. The nominees were approved unanimously by the voting membership. Table 1 shows the membership of the new EC.

2. Life membership

At the Plenary Session it was proposed that Dr. Charlie Calisher be made a Life Member of ICTV. This was passed unanimously.

Changes to statutes

Two changes have been made to the statutes that govern how ICTV operates. The first change arose because it was felt that it was unreasonable that the ICTV Statutes disqualified Study Group chairs from voting on proposed changes to virus taxonomy, even though they were often the ones making the proposals in the first place and the best informed on the relevant issues. All Study Group chairs are *ex officio* members of one of the five subcommittees of the ICTV (i.e. those for Viruses of Vertebrates, of Invertebrates, of Plants, of Fungi, Algae and Protists, and of Prokaryotes) and they make up most of the members of these subcommittees. The change passed by Virology Division at the Congress gave voting rights to all members of the 6 EC subcommittees (5 types of major host and the Virus Database Subcommittee). Because some subcommittee members would, as a result of these changes, have been qualified to vote more than once, a sentence was added to restrict this entitlement to a single vote on each taxonomic proposal.

The second change that was also passed by the full ICTV membership and by the Virology Division of IUMS concerned the national membership of ICTV. National Members are appointed by member societies of Virology Division independently of the EC of ICTV. The

change will mean that the appointing societies will be required to either renew an appointment or nominate a new National Member shortly after each International Congress of Virology. It is hoped that this mechanism will result in a more active national membership than at present.

Acknowledgements

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