MEETING OF THE STUDY GROUP
CHAIRS AND EXECUTIVE COMMITTEE
OF THE INTERNATIONAL COMMITTEE
ON TAXONOMY OF VIRUSES

1–2 February 2016
Hinxton Hall, Wellcome Trust Genome Campus
Aims of the meeting

Questions
- What are the problems that virus classification is facing?
- What is the ICTV going to do about them?

Aims
- To inform on current plans to develop ICTV resources
- To listen to views on the ICTV
- To see ways forward in the context of wider taxonomy

Threads
- Explanations of the ICTV’s present situation and future plans
- A session devoted to discussion of views on the ICTV
- Discussion of topics of general interest in viral taxonomy
- Plenary lectures that help us look over the battlements
- Opportunities for informal discussions
ICTV resources and organisation

A wide range of members
- Executive Committee (EC)
- Life members
- National representatives
- Subcommittees, including the 83 Study Group (SG) chairs

Involving hundreds of virologists
- 6-12 members in each SG

Representing the top expertise in each field
- ICTV Report publication
- Maintenance of the Master Species List (MSL)
- Rigorous, formalised, democratic procedures for assigning taxa

And yet...
The ICTV thread

1. The current situation
   - History
   - Operations
   - Resources
   - Challenges

2. Redesigning the ICTV Report
   - Change
   - Practicalities
   - Prototype
   - Implications

3. Development of bioinformatic tools
   - Alignments
   - Evolutionary analysis
   - Wikis, etc.
   - Tools

4. The future
   - Metagenomics
   - Taxonomical assignments
   - Nomenclature
   - Databases and tools
THE CURRENT SITUATION

- Development of the ICTV: a historical perspective
  Mike Adams

- Maintaining and updating the ICTV taxonomy
  Andrew King

- ICTV resources: the MSL, the ICTV Database, the 9th Report
  Elliot Lefkowitz

- The challenges ahead
  Andrew Davison
DEVELOPMENT OF THE ICTV: A HISTORICAL PERSPECTIVE

1966  ICTV  2016

Mike Adams
The International Committee on Nomenclature of Viruses (ICNV) was established by the International Association of Microbiological Societies during its 9th Congress in Moscow, July 1966.

Wherever practicable, each country was represented by a member nominated by the national microbiological society (43/46 at the first meetings).

An elected Executive Committee (EC) proposed rules and created subcommittees to propose genera and families for the major virus groups (insect, vertebrate, plant and bacteria). Specialist Study Groups (SGs) were created within each subcommittee.

The aim was to produce an international and universal classification system.
Planned virus taxonomy ‘life-cycle’

- SGs discuss and prepare proposals
- EC discusses proposals and negotiates changes with the SGs
- Proposals finalized at an EC meeting held in association with the triennial International Congress of Virology (ICV)
- Proposals presented to the entire ICTV at a special session of the ICV
- EC prepares and publishes a Report of the latest taxonomy, incorporating the changes
Organisational development

- ICTV is now a standing committee of the Virology Division of IUMS
- ICTV consists of the EC, national representatives, SG chairs and life members (~150 in total)
- Subcommittee remits have expanded and changed
- The EC meets annually; wherever possible, proposals move to acceptance in 6-9 months
- Ratification votes are conducted by email; plenary sessions at ICV are for reports and elections to the EC
- Annual changes to taxonomy are incorporated into the website and announced in Arch Virol (Virology Division News)
The first ICNV votes (26 July 1966)

1. The committee considers that an international nomenclature for viruses is desirable (carried unanimously)

2. An effort should be made towards a latinized binomial nomenclature (carried with 2 against)

3. If and when latinized binomials are introduced, the existing names should be retained whenever feasible (carried with 1 against)
Some of the first ICNV rules (July 1966)

- 6. The law of priority shall not be observed
- 7. New sigla shall not be introduced
- 8. No person's name shall be used
- 10. For pragmatic purposes, the species is considered to be collections of viruses with like characters

Note 2 - Diacritic signs are not used in names or in specific epithets in virology. In names or epithets derived from words with such diacritic signs, the signs must be suppressed and the letters transcribed as follows:

1 – ä, ö and ü become respectively ae, oe, ue (German)
2 – é, è and ê become e (French)
3 – ø (ö), aê (ä) and å become oe, ae, and aa, respectively (Scandinavian)
Virus taxonomy in practice

- Initial work classified viruses (tobacco mosaic virus, rabies virus, etc.) into genera and a few families, based on particle morphology, pathology, transmission and serological properties.

- There was little agreement about the definition of a species and uncertainties about the appropriate taxonomic level for many virus groups; this probably explains why latinized binomials were not adopted.

- Species were only universally adopted (and made the subject of voting) from 1999, often using the existing virus names.
50 years of effort...

First Report (81 pages, published in 1971)

- 2 families
- 43 groups or genera
- 290 viruses listed as members

Latest taxonomy (ratified February 2015)

- 7 orders
- 104 families
- 23 subfamilies
- 505 genera
- 3186 species
MAINTAINING AND UPDATING THE ICTV TAXONOMY

1966

ICTV

2016

Andrew King
Decision-making: approving taxonomic proposals (TPs)

New proposal (usually from SG) -> Executive Committee (SC chair) -> EC approved -> ratification by ICTV members -> Official taxonomy

But taxonomic proposals are

- Posted on ICTV’s discussion pages, where they are open to public comment
- Considered by the EC on a minimum of two occasions, at least 3 months apart, so that any online comments can be taken into account
New proposal (usually from SG) → Executive Committee → EC approved → ratification by ICTV members → Official taxonomy

- New taxonomic proposal discussed for the first time
  - EC gives provisional approval subject to minor changes
    - Provisionally approved (subject to confirmation)
      - Provisionally approved (subject to confirmation)
        - Conditionally provisionally approved
          - Rejected
  - Conditionally approved
    - Action taken by proposer
      - EC approved
        - Further consideration deferred
          - Action taken by proposer
            - EC approved
              - 3 months after EC meeting email vote by EC members to confirm approval
                - Email vote confirms approval subject to minor changes
                  - Conditionally approved
                    - Action taken by proposer
                      - Provisionally approved (subject to confirmation)
                        - Provisionally approved (subject to confirmation)
                          - EC gives provisional approval subject to minor changes
                            - Provisionally approved (subject to confirmation)
                              - Rejected

- Non-controversial, species-only proposal given fast-track approval
In 2015, the EC deferred a decision on only 4 of 131 new proposals.

*In 2015, the EC deferred a decision on only 4 of 131 new proposals*
Mechanics: the TP template

Existing taxonomy  

- Create and name species  
  (Each with designated type virus)
- Create genus
  - Name genus
  - Designate type species of genus
- Create subfamily
  - Name subfamily
  - Assign genera to subfamily
- Create family
  - Name family
  - Assign subfamilies to family
  - Assign genera to family
- Create order
  - Name order
  - Assign families to order
  - Assign unassigned genera to order
- Remove (abolish) taxa
- Reassign taxa
- Rename taxa

New taxonomy
Mechanics: the Secretary steps in

Existing taxonomy  |  taxonomic actions  |  New taxonomy

- Create and name species
  (Each with designated type virus)
- Create genus
  - Name genus
  - Designate type species of genus
- Create subfamily
  - Name subfamily
  - Assign genera to subfamily
- Create family
  - Name family
  - Assign subfamilies to family
  - Assign genera to family
- Create order
  - Name order
  - Assign families to order
  - Assign unassigned genera to order
- Remove (abolish) taxa
- Reassign taxa
- Rename taxa

These are the 18 taxonomic actions provided for in the template

The Proposals Secretary
1. Codes the proposal document
2. Codes each action
3. Posts the document online
4. Extracts taxo-actions into an Excel spreadsheet
5. Curates the proposal docs
6. Keeps all the above updated
Mechanics: the coding convention

description: 2015.009a-gM.N.v2.Sunviridae

- 2015: Year initially submitted
- .009: 9th proposal submitted to this subcommittee
- a-g: Taxonomic actions proposed
  - 2015.009aM: create species
  - 2015.009bM: create genus
  - 2015.009cM: name genus
  - 2015.009dM: assign type species
  - 2015.009eM: create family
  - 2015.009fM: name family
  - 2015.009gM: assign genus to family
- M: Subcommittee (animal ds and RNA–viruses)
- .N: Status code (posted in ‘New’ folder)
- .v2: Version 2 of this proposal
- .Sunviridae: Description (proposed family *Sunviridae*)
Mechanics: the master TP spreadsheet

<table>
<thead>
<tr>
<th>Proposal (filename)</th>
<th>Short Title</th>
<th>Authors (corresponding author’s email in brackets)</th>
<th>action code</th>
<th>proposed taxonomic action</th>
<th>post-EC47 status</th>
<th>pre-E-vote status</th>
<th>post-E-vote status</th>
<th>pre- ratification status</th>
<th>SC</th>
</tr>
</thead>
<tbody>
<tr>
<td>2015.054a-dB.U.v3. Septima3virus</td>
<td>create genus Septima3virus including 5 new species within the family Siphoviridae, order Caudovirales</td>
<td>Kropinski AM (<a href="mailto:Phage.Canada@gmail.com">Phage.Canada@gmail.com</a>)</td>
<td>2015.054aB</td>
<td>create 5 species, (Pseudomonas virus 73, Pseudomonas virus, Kakheti25, Pseudomonas virus Az66 and Burkholderia virus KLI), in genus Septima3virus (new) in the family Siphoviridae</td>
<td>U</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>2015.054bB</td>
<td>create a new genus in the family Siphoviridae, order Caudovirales</td>
<td>U</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>B</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.054cB</td>
<td>name the genus Septima3virus</td>
<td>U</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>B</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.054dB</td>
<td>designate Pseudomonas virus 73 as type species of the new genus</td>
<td>U</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>B</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.001aD.A.v 2. Betabaculovirus_sp</td>
<td>create species Agrotis segetum granulovirus in the genus Betabaculovirus, family Baculoviridae</td>
<td>Alletti GG, Wennmann JT, Carstens EB, Jehle JA (<a href="mailto:Johannes.Jehle@jki.bund.de">Johannes.Jehle@jki.bund.de</a>)</td>
<td>2015.001aD</td>
<td>create species Agrotis segetum granulovirus in the genus Betabaculovirus, family Baculoviridae</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>D</td>
</tr>
<tr>
<td>2015.002a, bD.A.v2. Alphabaculovirus_sp, ren</td>
<td>in genus Alphabaculovirus (family Baculoviridae) create species Agrotis segetum nucleopolyhedrovirus B and change the name of species Agrotis segetum nucleopolyhedrovirus to Agrotis segetum nucleopolyhedrovirus A</td>
<td>Wennmann JT, Alletti GG, Carstens EB, Jehle JA (<a href="mailto:Johannes.Jehle@jki.bund.de">Johannes.Jehle@jki.bund.de</a>)</td>
<td>2015.002aD</td>
<td>create species Agrotis segetum nucleopolyhedrovirus B in genus Alphabaculovirus, family Baculoviridae</td>
<td>Ac</td>
<td>Ac</td>
<td>Ac</td>
<td>A</td>
<td>D</td>
</tr>
<tr>
<td>2015.002bD</td>
<td>in genus Alphabaculovirus change the name of species Agrotis segetum nucleopolyhedrovirus to Agrotis segetum nucleopolyhedrovirus A</td>
<td>Ac</td>
<td>Ac</td>
<td>Ac</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.003a, bD.A.v1. Kappatorquevirus_sp, ren</td>
<td>In genus Kappatorquevirus (family Anelloviridae), create species Torque teno sus virus k2b and change the name of species Torque teno sus virus k2 to Torque teno sus virus k2a</td>
<td>Keikarainen T (<a href="mailto:tuija.keikarainen@irta.cat">tuija.keikarainen@irta.cat</a>)</td>
<td>2015.003aD</td>
<td>in genus Kappatorquevirus (family Anelloviridae), create species Torque teno sus virus k2b</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>D</td>
</tr>
<tr>
<td>2015.003bD</td>
<td>in genus Kappatorquevirus (family Anelloviridae), change the name of species Torque teno sus virus k2 to Torque teno sus virus k2a</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.004a-eD.U.v2. Toursvirus</td>
<td>create genus Toursvirus in the family Ascoviridae and move species Diadromus pulchellus ascovirus 4a from genus Ascovirus to genus Toursvirus</td>
<td>Asgari S (<a href="mailto:s.asgari@uq.edu.au">s.asgari@uq.edu.au</a>), Bideshi D, Bigot Y, Cheng X-W, Federici BA</td>
<td>2015.004aD</td>
<td>create new genus in family Ascoviridae</td>
<td>Uc</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>D</td>
</tr>
<tr>
<td>2015.004bD</td>
<td>name the genus Toursvirus</td>
<td>Uc</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.004cD</td>
<td>designate Diadromus pulchellus ascovirus 4a as type species of the new genus</td>
<td>Uc</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.004dD</td>
<td>remove species Diadromus pulchellus ascovirus 4a from genus Ascovirus</td>
<td>Uc</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.004eD</td>
<td>re-assign the above species to genus Toursvirus</td>
<td>Uc</td>
<td>U</td>
<td>A</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.005aD.A.v1. Aviadenovirus_4sp</td>
<td>create 4 species in the genus Aviadenovirus, family Adenoviridae</td>
<td>Győző Kaján G (<a href="mailto:kajan.gyozo@agrar.mta.hu">kajan.gyozo@agrar.mta.hu</a>), Podgorski I, Harrach B</td>
<td>2015.005aD</td>
<td>create 4 species (Duck aviadenovirus B, Pigeon aviadenovirus A, Turkey aviadenovirus C and Turkey aviadenovirus D) in the genus Aviadenovirus, family Adenoviridae</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>D</td>
</tr>
<tr>
<td>2015.005bD</td>
<td>to genus</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>D</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015.006aD.N.v1. Simplexvirus-sp</td>
<td>create a species in genus Simplexvirus, subfamily Alphaherpesvirinae, family Herpesviridae</td>
<td>Davison A (<a href="mailto:andrew.davison@glasgow.ac.uk">andrew.davison@glasgow.ac.uk</a>), Eberle R</td>
<td>2015.006aD</td>
<td>create a species (name: Panine herpesvirus 3 OR Panine herpesvirus 2, depending on approval of proposal 2015.010aD.N.v1.Herpesvirinae_spren) in genus Simplexvirus, subfamily Alphaherpesvirinae, family Herpesviridae</td>
<td>Ac</td>
<td>Ac</td>
<td>Ac</td>
<td>Ac</td>
<td>D</td>
</tr>
</tbody>
</table>
Keeping taxonomy updated: a wish list

Taxonomic proposals: TP template is complex, prescriptive and demanding

How to – make proposing less of a deterrent?
– give more credit to authors of proposals?
– encourage SGs in other ways to submit TPs?

Document handling: manual, error prone, labour intensive
document transmission almost entirely by email
proposal docs, TP spreadsheet, NOT shared

Need to be able to – submit and update proposals online
– extract, update, share information automatically
– share proposal documents
– update MSL and ICTV Report automatically
### Haemophilus phage HP1

<table>
<thead>
<tr>
<th>Order</th>
<th>Family</th>
<th>Subfamily</th>
<th>Genus</th>
<th>Species</th>
<th>Type Species?</th>
<th>Exemplar RefSeq Accession Number</th>
<th>Exemplar GenBank Accession Number</th>
<th>Exemplar Isolates</th>
<th>Genome Composition</th>
<th>Last Change</th>
<th>MSL of Last Change</th>
<th>Proposal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caecobacteria</td>
<td>Myoviridae</td>
<td>Eucaryophagevirinae</td>
<td>Campylobacter phage CP91</td>
<td>0</td>
<td>HE815464</td>
<td>dssDNA</td>
<td>New</td>
<td>2013.04-04.04.05</td>
<td>E. coli</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
The ICTV Database
The ICTV website
The 9th Report

Virus Taxonomy
Ninth Report of the International Committee on Taxonomy of Viruses
International Union of Microbiological Societies
Virology Division

Edited by
Andrew M. Q. King • Michael J. Adams
Eric B. Carstens • Elliot J. Lefkowitz
THE CHALLENGES AHEAD

1966  ICTV  2016

Andrew Davison
The Wellcome Trust grant

Challenges
- Publishing the next Report
- Linking with other databases
- Involving the community in tackling key questions

Objectives
- Updating resources and making them freely available to all
- Establishing clearer methods for classifying viruses
- Engaging with the community to resolve fundamental issues

Plan
- Making the next Report freely available online in a citable form
- Providing resources: links, methods, alignments, TP submission
- Holding focused meetings
The Wellcome Trust grant

Resources
- Oxford post (1.0): Report, alignments, metagenomic data
- Glasgow post (0.5; Richard Orton): links, alignments, methods, TP submission
- Meetings

Oversight
- Grantholders: Peter Simmonds, Andrew Davison, Stuart Siddell
- Management committee: grantholders plus ICTV officers [Sasha Gorbalevna (Vice-President), Mike Adams (Business Secretary), Andrew King (Proposals Secretary), Elliot Lefkowitz (Data Secretary, Editor-in-Chief)]

Particular recognition of the role of SG chairs
REDESIGNING THE ICTV REPORT

- Limitations of the 9th Report: the need for change
  Stuart Siddell

- The practicalities of publishing online and being cited
  Peter Simmonds

- A prototype of the new Report
  Elliot Lefkowitz

- Implications for Study Groups
  Andrew Davison
LIMITATIONS OF THE 9TH REPORT: THE NEED FOR CHANGE

1966 ICTV 2016

Stuart Siddell
Limitations of the 9th Report

- Infrequent
- No links to databases
- No open access
- Citation of authors

£255, 1344 pages, 3.5 kg
Validated virus and viroid segments

The numbers of validated virus and viroid segments available in INSDC databases are depicted by the black line, and the numbers of RefSeq virus and viroid segments by the gray columns. Brister et al. (2015) NCBI viral genomes resource. Nucleic Acids Research 43: D571-D577. The graphic is used to illustrate the pace of virus discovery, and does not mean that the EC considers sequence alone as the basis of virus classification.
How often is the Report published?

Infrequent

40 years, 9 reports = 4.4 years on average
Why does it take so long?

- Simultaneous updates on 109 chapters for 6 orders, 87 families, 349 genera and 2284 species

- Laborious editing to produce some degree of uniformity with regard to figures, tables and diagrams

- Production and publication

Note that the complete online Report is not for sale. Only individual chapters are available to purchase (at $31.50 each). The complete Report is available as an e-book, but this lacks supplementary material.
How is the Report linked?

No links to databases
How will the Report be linked?

www.ictvonline.org

ViralZone

INSDC
- GenBank
- EMBL-EBI
- DDBJ

Catalogue of Life
- Species 2000

ICTV Master Species List (MSL)

Viral Genome Resource (NCBI)
What about impact?

- The ICTV Reports are not included in the National Library of Medicine catalogue
- Therefore, it is not possible to search authors or chapters in PubMed
- Other searches yield very patchy results
- This makes citation much more difficult, decreasing the impact of the chapters in the Report and failing to acknowledge the contribution of authors

<table>
<thead>
<tr>
<th>Virus Order</th>
<th>Citations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenoviridae</td>
<td>88</td>
</tr>
<tr>
<td>Baculoviridae</td>
<td>49</td>
</tr>
<tr>
<td>Nimaviridae</td>
<td>7</td>
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<tr>
<td>Geminiviridae</td>
<td>122</td>
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<tr>
<td>Paroviridae</td>
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<td>Caulimoviridae</td>
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<td>Paramyxoviridae</td>
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<td>Rhabdoviridae</td>
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<td>Ophioviridae</td>
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<td>Varicosavirus</td>
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<td>Nidovirales</td>
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<td>Arteriviridae</td>
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<td>Coronavirus</td>
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<td>Roniviridae</td>
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<td>Iflaviridae</td>
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<td>Picornaviridae</td>
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<tr>
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<td>Bromoviridae</td>
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<tr>
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<tr>
<td>Flaviviridae</td>
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<tr>
<td>Hepeviridae</td>
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<td>Potyviridae</td>
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<tr>
<td>Umbravirus</td>
<td>5</td>
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<tr>
<td><strong>Mean</strong></td>
<td><strong>48</strong></td>
</tr>
<tr>
<td><strong>Citations of whole book</strong></td>
<td><strong>1097</strong></td>
</tr>
</tbody>
</table>
THE PRACTICALITIES OF PUBLISHING ONLINE AND BEING CITED

1966 ICTV 2016

Peter Simmonds
<table>
<thead>
<tr>
<th>Current</th>
<th>Planned</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>The ICTV Report</strong></td>
<td><strong>On-line publication</strong></td>
</tr>
<tr>
<td>- Last published in 2012</td>
<td>- Electronic format (HTML) and PDF</td>
</tr>
<tr>
<td>- Increasingly divergent from the ICTV classification</td>
<td>- Fully linked to MSL, resources and external databases</td>
</tr>
<tr>
<td>- Restricted availability, especially in developing countries</td>
<td></td>
</tr>
<tr>
<td><strong>Usage by the virology community</strong></td>
<td><strong>Updating</strong></td>
</tr>
<tr>
<td>- Erratic collection of citations</td>
<td>- Updated whenever taxonomy of a chapter (family, order) is changed</td>
</tr>
<tr>
<td>- Not a primary source of taxonomic information for most</td>
<td>- Cannot diverge from the MSL</td>
</tr>
<tr>
<td><strong>Useability</strong></td>
<td><strong>Citation</strong></td>
</tr>
<tr>
<td>- Provides helpful overviews of virus families and orders</td>
<td>- Chapter summaries published in an open access journal</td>
</tr>
<tr>
<td>- Poor or absent linkage to MSL and other databases</td>
<td>- Allows accurate citation metrics to be collected</td>
</tr>
<tr>
<td></td>
<td>- Contains links to online chapter, resources, SG wikis</td>
</tr>
</tbody>
</table>
4. ICTV Report and Master Species List

4a. Do you possess or have access to the 9th ICTV Report (published in 2011)?
- Yes: 196 (44%)
- No: 254 (56%)

4b. Does (or would) access to the 9th (or a previous) ICTV Report provide information that significantly enhances (or would significantly enhance) your research or teaching?
- Yes: 247 (55%)
- No: 87 (19%)
- No opinion: 116 (26%)

4c. On what other sources of information on virus classification do you rely?
- The ICTV Master S...: 214 (48%)
- Published papers or reviews: 377 (84%)
- Other public databases (e.g. the GenBank RefSeq project): 243 (54%)
- Other (specify below): 24 (5%)

4d. Is a 5 year update cycle of the Report sufficient to provide necessary information on current virus classification?
- Yes: 203 (45%)
- No: 167 (37%)
- No opinion: 80 (18%)

4e. From what sources do you cite virus classification information in research papers, books or educational materials?
- ICTV Report chapters: 156 (35%)
- The ICTV Master S...: 127 (28%)
- GenBank or other databases: 204 (45%)
- Reviews or published papers: 319 (71%)
- I never cite information on virus classification (i.e. not needed or irrelevant): 48 (11%)
- Other (specify below): 3 (1%)

Survey of >500 virologists (2014)
The ICTV Report
- Last published in 2012
- Increasingly divergent from the ICTV classification
- Restricted availability, especially in developing countries

Usage by the virology community
- Erratic collection of citations
- Not a primary source of taxonomic information for most

Useability
- Provides helpful overviews of virus families and orders
- Poor or absent linkage to MSL and other databases

On-line publication
- Electronic format (HTML) and PDF
- Fully linked to MSL, resources and external databases

Updating
- Updated whenever taxonomy of a chapter (family, order) is changed
- Cannot diverge from the MSL

Citation
- Chapter summaries published in an open access journal
- Allows accurate citation metrics to be collected
- Contains links to online chapter, resources, SG wikis
Family FLAVIVIRIDAE


The Flaviviridae are a family of small enveloped viruses with RNA genomes of 9600–12,000 bases in length. Most infect mammals and birds, many of which are host-specific and pathogenic, such as hepatitis C virus in the genus, Hepacivirus. The majority of known members in one genus (Flavivirus) are arthropod-borne, many of which are important human and veterinary pathogens (e.g., yellow fever virus, dengue virus).

Table 1. Characteristics of family Flaviviridae.

<table>
<thead>
<tr>
<th>Typical member</th>
<th>Yellow fever virus (YFV), genus Flavivirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome</td>
<td>9–11 kb of positive-sense, non-segmented RNA</td>
</tr>
<tr>
<td>Virus</td>
<td>Enveloped, 40–60 nm virions with a single core protein (except for genus Pegivirus) and 2-3 envelope glycoproteins</td>
</tr>
<tr>
<td>Translation</td>
<td>Directly from genomic RNA containing a type I cap or an internal ribosomal entry site (IRES)</td>
</tr>
<tr>
<td>Host range</td>
<td>Mammals (all genera); most members of genus Flavivirus are arthropod-borne</td>
</tr>
<tr>
<td>Classification</td>
<td>Currently 4 genera containing more than 60 species</td>
</tr>
</tbody>
</table>

Genera.

Flavivirus. This genus consists primarily of >50 species of arthropod-borne virus, with distinct groups infecting mosquitoes or ticks. Mammals and birds are the usual primary hosts, in which infections may be asymptomatic or cause severe or fatal haemorrhagic fever or neurological disease. Important human pathogens include yellow fever virus, dengue virus, Japanese encephalitis virus, West Nile virus and tick-borne encephalitis virus. Other members cause economically important diseases in domestic or wild animals. Additional species infecting only arthropods or only mammals (e.g. Tama bat virus) have been described recently.

Pestivirus. These viruses infect pigs and ruminants, including cattle, sheep, goats and wild ruminants, and are transmitted through contact with infected secretions (respiratory droplets, serum or feces). Infections may be subclinical or cause enteric, haemorrhagic or wasting diseases, including the economically important bovine viral diarrhoea virus and classical swine fever virus.

Hepacivirus. This genus includes HCV, a major human pathogen causing progressive liver disease, and also several other viruses of unknown pathogenicity that infect horses, rodents, bats, cows and primates. Infections are typically persistent and target the liver.

Pegivirus. Members are widely distributed in a range of mammals; species, in which they cause persistent infections. To date they have not been clearly associated with disease.

Virions. These are typically spherical in shape and contain a lipid envelope (Fig. 1). Virions have a single, small, basic capsid (C) protein and two (genus Flavivirus, Hepacivirus and Pegavirus) or three (genus Pestivirus) envelope proteins.

Fig. 1. Cryo EM reconstruction of the mature virion of Dengue fever virus, genus Flavivirus.
Impact

- Authoritative descriptions of virus families and orders
- An accessible and highly visible source of virus taxonomic information and overviews of virus properties
- Through bioinformatic links, the starting point for data compilation, sequence analysis and taxonomical decisions
- Enhanced visibility in the scientific community
A PROTOTYPE OF THE NEW REPORT

1966 ICTV 2016

Elliot Lefkowitz
A prototype of the new Report

Family: Flaviviridae

Introduction

The flaviviruses are a family of small enveloped viruses with RNA genomes of 9000-12,000 bases in length. Most infect mammals and birds, many of which are host-specific and pathogenic, such as hepatitis C virus (HCV) in the genus, Hepacivirus. The majority of known members in one genus (Flavirus) are arthropod borne, many of which are important human and veterinary pathogens (e.g., yellow fever virus, dengue virus).

Table 1. Characteristics of family Flaviviridae.

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</table>
IMPLICATIONS FOR STUDY GROUPS

1966  ICTV  2016

Andrew Davison
Study Group involvement

The Report

- Batches of ~30 chapters and summaries to appear in early 2017, early 2018 and early 2019
- Publication of summaries in an open access journal
- Summaries to be published at about the same time as chapters
- Initial preference for the most highly citable chapters
- Volunteers for the first ~30 chapters for this autumn!

Other things

- Willingness to be consulted on development of other resources

Recognition that all this will be two-way process
DEVELOPMENT OF TOOLS

- Alignment construction and standardisation
  Donald Smith

- Methods for evolutionary analysis
  Richard Orton

- Study Group wikis and other specialised information
  Peter Simmonds

- Bioinformatic tools
  Sasha Gorbalenya
Why provide sequence alignments?

Phylogeny / sequence relatedness required for virus classification
- Proposed taxon assignments have to be consistent with phylogeny
- Assignments can be based on sequence relationships (e.g. *Papillomaviridae*)

Sequence relationships are dependent on
- Sequence type (amino acid or nucleotide)
- Divergence
- Alignment method, exclusion of non-alignable regions

Provision of standardised alignments
- Avoid generating *de novo* for taxonomy proposals
- Ensure appropriate genome region is analysed
- Alignment data ensures objectivity and reproducibility
Alignment issues

HOW?
- Manual/Clustal/Muscle/BLAST

WHAT?
- Nucleotide/amino acid
- Representative/type sequences

WHERE?
- Whole/subgenomic regions
- Concatenated or separate

ACCESSIBLE?
- Provision through ICTV website
- Alignment formats/annotation

Example

Hepeviridae
Positive-sense RNA virus

Orthohepevirus genus, 4 species
- A – hepatitis E virus (HEV; human, pig)
- B – avian HEV (chicken)
- C – rat HEV (rat, ferret)
- D – bat HEV (bat)

Piscihepevirus genus, 1 species
- A – trout HEV (fish)
Choice of alignment method

**HOW?**
- Nucleotide or amino acid
- Manual / Clustal / Muscle / BLAST

**WHAT?**
- Penalty for insertion
- Penalty for size of insertion

**WHERE?**
- Different numbers of sequences in groups?
- Effects of adding new sequences

**ACCESSIBLE?**
Genome scan – *Orthohepevirus A*

**HOW?**

**WHAT?**

**WHERE?**

**ACCESSIBLE?**

- If synonymous saturated – use aa/nonsynonymous
- If nonsynonymous saturated – use protein structure?
Genome aa scan – *Orthohepevirus A*

**HOW?**

**WHAT?**

**WHERE?**

**ACCESSIBLE?**
- Identify conserved regions
- Do they give identical relationships?
# Taxonomy of genus *Orthohepevirus*

<table>
<thead>
<tr>
<th>Species</th>
<th>Host</th>
<th>Accession Numbers</th>
</tr>
</thead>
<tbody>
<tr>
<td>Moose</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Human</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pig, wild boar</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Camel</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Rat</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bat</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chicken</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ferret</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bat</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Amino acid sequence alignment**

**ORF1 aa 28-389**

**Host**

**Species**
Providing alignments

Sequence representation
- Limited to exemplar sequences or examplar sequences clearly identified
- May include provisionally or unclassified sequences from SG

Alignment format
- Importable by standard bioinformatic packages
- Primary labelling by accession numbers, with additional information of taxonomic assignment, strain, host, etc.

Maintained by SGs
- Regularly updated to include newly assigned taxa
- Downloadable for a DOI specified in Report/published summary
The perfect alignment...

**HOW?**
- Method of alignment stated
  - Reproducible

**WHAT?**
- Characters used justified
  - Saturation at synonymous sites?

**WHERE?**
- Choice of regions to compare
  - Variability across genome assessed

**ACCESSIBLE?**
- Alignment available on ICTV website
  - Taxonomic conclusions verifiable
  - Incorporate new variants
Introduction

Richard Orton

- Bioinformatician
- Viral Genomics & Bioinformatics group (Andrew Davison)
- Centre for Virus Research, University of Glasgow

ICTV Wellcome Trust Grant

- A database for the universal classification of viruses
- Peter Simmonds, Andrew Davison, Stuart Siddell

Working on

- Online ICTV Report
- Online standardized alignments and trees
- Online tools for preparing and submitting TPs
- Cross-links with sequence databases such as GenBank, ENA, ATCC, DDBJ, Species 2000, Catalogue of Life

Help SGs

- Report tools
- Proposal tools
- Bioinformatics tools

http://talk.ictvonline.org
Evolutionary analysis (1)

Distance-based
- Create pairwise distance matrix: neighbour-joining: fast and large

Maximum parsimony
- Tree with the smallest number of evolutionary events to explain the observed sequence data

Maximum likelihood
- Model-based (e.g. JC, HKY, GTP ... LG, WAG, JTT)
- Statistically assigns probabilities to possible phylogenetic trees

Bayesian
- Similar to maximum likelihood: model-based
- Bayesian statistics, prior and posterior sampling, MCMC, to produce the most likely tree given the data

Evolutionary analysis (2)

Online
- ICTV website
- Image and tree (e.g. Newick format)

Clear methods
- Type (e.g. NJ, ML ... )
- Substitution model
- Number of bootstraps
- The alignment – protein, nucleotide, gene, genome

Format
- Scale bar
- Bootstrap values
- Standard format/visual

Distance cutoffs
- SGs current criteria for new species definition
- E.g. distance thresholds

Applications

Sequences are playing an increasingly important role in virus classification.

Comparison of new sequences against existing ones can aid virus classification.

PASC
- PAirwise Sequence Comparison
- Bao et al. (2014) Arch Virol

DeMARC
- DivErsity pArtitioning by hieRarchical Clustering

PUmPER
- Phylogenies Updated PERpetually
- Izquierdo-Carrasco et al. (2014) Bioinf

SDT
- Sequence Demarcation Tool
- Muhire et al. (2014) PLoS One

ViCTree
- Virus Classification using phylogenetic Trees
- Modha et al. CVR University of Glasgow
**Parvoviridae Study Group**

Susan Cotmore  
SG Chair

Andrew Davison

Sejal Modha

Joseph Hughes

---

**Parvoviridae family**

- **Parvovirinae** subfamily – viruses that infect vertebrate hosts
- **Densovirinae** subfamily – viruses that infect arthropod hosts

**Tool for use in viral classification**

Automatically produce distance matrices and phylogenetic trees for a set of related sequences derived from GenBank

Update existing alignments and trees in an iterative fashion

---

Cotmore et al. (2014) Arch Virol 159:1239-1247
ViCTree pipeline

Example: *Densovirinae* subfamily
- NS1 protein sequences

Seed Set: a set of sequences that encapsulates the diversity of the family
- E.g. at least 1 for each known species
- Can add novel (non-GenBank) seqs

BLAST parameters
- Optimised for each family

Input
- Taxa ID: txid40120
- Seed Set: 22 NS1 prot seqs: GI in header

Output
- 710 raw *Densovirinae* protein seqs
- Metadata file (GI, accession, species)
- 82 unique NS1 seqs
- Metadata file
- Multiple sequence alignment
- Distance matrix
- Phylogenetic trees

Applicable to other families

Submit Taxa ID

Download all prot sequences

BLAST against Seed Set

Collect sequence info for significant hits

Filtering

Multiple Sequence Alignment – ClustalO

Filter: remove empty sequences

Pre-optimised BLAST parameters
Hit length, coverage

Taxonomy ID, sequence description, lineage

Remove duplicates and subsequences, write to log file

User defined model
Default: PTRGAMMAJTT

RAxML

MrBayes
**Densovirinae ViCTree**

**Phylogenetic tree**
- Cut-offs for within cluster genetic distance and bootstrap support are selected by the user

**Pairwise distance matrix**
- ViCTree integrates the pairwise distance matrix with the maximum likelihood tree to aid species identification
- User defines distance cutoff for family

**Web-based visualisation**
- Sliding window for distance: clusters highlighted dynamically

**Version Control**
- Github
- Pipeline and code
- Alignments and trees

**Tool for helping in new species identification**
Future

Please feel free to contact us with suggestions or ideas for improvements and tools

- Submission tools
- Online format
- Linked databases
- Bioinformatics tools
STUDY GROUP WIKIS AND OTHER SPECIALISED INFORMATION

1966 ICTV 2016

Peter Simmonds
Study Group wikis

A framework for information not contained in the Report chapters
- Other taxonomic levels
- Discussion of classification decisions
- Sequences of currently unclassified (tentative) family members

Accessible and editable by the virology community
- Online discussions of resource or classification issues

Permanence and authority
- A permanent component of the ICTV website
- Actively maintained by the SGs
- Repository for external data requiring visibility in the community
Study Group wikis

A framework for information not contained in the Report chapters

- Other taxonomic levels: *HCV Genotypes, HEV types within species A*
- Discussion of classification decisions
- Sequences of currently unclassified (tentative) family members

Accessible and editable by the virology community

- Online discussions of resource or classification issues

Permanence and authority

- A permanent component of the ICTV website
- Actively maintained by the SGs
- Repository for external data requiring visibility in the community
Adoption by Study Groups

- Repository for sequence data, tentative family members, alignments, programs and literature

- Content variable

- Optional

- Cooperation and cross-linking with other websites and collaborative resources
BIOINFORMATIC TOOLS

1966  ICTV  2016

Sasha Gorbalenya
DEmARC: Software for Virus Taxonomy

Alexander (Sasha) E. Gorbalenya

Department of Medical Microbiology, Leiden University Medical Center; Faculty of Bioengineering & Bioinformatics, Lomonosov Moscow State University
Tree of Life depicts evolution of all life forms but viruses

“scientists consider viruses as NOT living, it is WHY they are not in the tree of life”

Microbe Museum, Amsterdam
Virus Taxonomy is produced by expert virologists

- virus taxa
  - order
  - family
  - sub-family
  - genus
  - species

- institution
  - International Committee on Taxonomy of Viruses

- flexible framework
  - expert-mediated
  - polythetic species demarcation criteria
  - time consuming

ICTV

- Picornavirus Study Group
- Coronavirus Study Group
"A clear distinction is drawn between viruses that are real, concrete objects studied by virologists and virus species that are man-made taxonomic constructions that exist only in the mind."

The basic concepts used in virus classification are analyzed. A clear distinction is drawn between viruses that are real, concrete objects studied by virologists and virus species that are man-made taxonomic constructions that exist only in the mind. Classical views regarding the nature of biological species are reviewed and the concept of species used in virology is explained. The use of pair-wise sequence comparisons between the members of a virus family for delineating species and genera is reviewed.

The difference between the process of virus identification using one or a few diagnostic properties and the process of creating virus taxa using a combination of many properties is emphasized. The names of virus species in current use are discussed as well as a binomial system that may be introduced in the future.
Virus Taxonomy Framework: Benefits & Cost

**Benefits**
- Any virus may be classified

**Cost**
- Across-taxa consistency is lacking;
- Limited biological insight
Knowledge about virus family

Genomes of virus family

ICTV

Most virus families

DEmARC

Coronaviridae
Mesoniviridae
Arteriviridae

Critical factors in decision making:
Quantity & quality of our knowledge (sequences)
Approach to process information

Taxonomy

Classification

ICTV

Taxonomy
Virus Taxonomy: experts define clusters (taxa) in phylogeny

Could clusters be defined in a consistent quantitative manner across the entire family?

Lauber & Gorbalenya (2012) JVI, 86: 3905
DEmARC – DivErsity pArtitioning by hiEarchical Clustering

pair-wise distance matrix

scale

0 ... 2.8

pair-wise distance distribution

distance threshold (T)

D>T, 1
D<T, 0

Lauber & Gorbálenya (2012)
JVI, 86: 3890 & 3905

ICTV SG Meeting, Hinxton, UK
**DEmARC: cost function for defining rank demarcation**

\[ CC(t) = \sum_{e_v} \frac{l(e_v) - t}{t} \]

- \( t \) – threshold
- \( l(e) \) – edge length


“movie” by A. Gulyaeva
DEmARC: cost function for defining rank demarcation


“movie” by A. Gulyaeva
DEmARC: major variables of pipeline

Dataset (April 2014):

Viruses: all full genome sequenced (720)
Proteins: conserved ns and str proteins (20)
Alignment: curated Muscle/Clustal /HMMER

Processing (DEmARC 1.3):

Measure: pairwise ML evolutionary distance
Clustering: Single-linkage
Criterion: minimization of weighted violation of clustering
Thresholds: ranking by cost and “persistence”

Post-processing:

Quality controls: clustering & tree topology violations

Shown is example of devising coronavirus taxonomy; Lauber et al Gorbalenya, in preparation
DEmARC-produced classification closely recovers the ICTV taxonomy of picornaviruses

match
new
difference

27 out of 28 Species
15 out of 16 Genera
are recovered

1) “super-genus” level
2) split of genus Aphthovirus
3) split of species Human rhinovirus C

Lauber & Gorbaleynya (2012) JVI, 86: 3905

April 2010 dataset
DEmARC-based classification facilitates decision making and offers taxonomy with biological insight

Lauber & Gorbalenya (2012) JVI, 86: 3905

Picornaviruses, 2010

Genus- vs Family-based criteria
Man-made construction vs Evolutionary-based structure
Intra-species divergence: limit, host, pathogenicity

Picornaviruses
51 species
23 genera

Coronaviruses
27 species
4 genera

April 2013 datasets

Lauber & Gorbalenya (2012) JVI, 86: 3905
Lauber et al., & Gorbalenya, in preparation
DEmARC package

- Devises hierarchical classification of genomes
- Classifies *all* viruses in group
- Realized in R
- Includes scripts for processing distance matrices and plotting results with biological insight
- Available for download at http://veb.lumc.nl/VEB/tools.cgi
- Being advanced
- WEB-site is under construction

Thank You!
THE FUTURE

- Can viruses be classified by sequence data alone? Andrew Davison
- Taxonomical assignments, procedures and scales Andrew King
- Is it time to consider the adoption of binomial nomenclature? Mike Adams
- Databases and bioinformatic tools Elliot Lefkowitz
CAN VIRUSES BE CLASSIFIED BY SEQUENCE DATA ALONE?

Andrew Davison
Why?

- Not “can” but “should”
- We need to cope with metagenomic data
- We need to remain relevant to the community
- If we don’t do it, someone else will

UTILITARIANISM
Classify much

PURISM
Classify little
Why not?

The species definition

- Previous: “A virus species is defined as a polythetic class of viruses that constitutes a replicating lineage and occupies a particular ecological niche”
- Polythetic: relating to or sharing a number of characteristics which occur commonly in members of a group or class, but none of which is essential for membership of that group or class.
- Present: “A species is a monophyletic group of viruses whose properties can be distinguished from those of other species by multiple criteria”
- “Comment: The criteria by which different species within a genus are distinguished shall be established by the appropriate Study Group. These criteria may include, but are not limited to, natural and experimental host range, cell and tissue tropism, pathogenicity, vector specificity, antigenicity, and the degree of relatedness of their genomes or genes.”

Biology emerges fundamentally from the genome.
The current stance of the ICTV

“The EC has agreed to accept species proposals based only on sequence data with certain safeguards. These include evidence that the sequences are effectively complete, that correct assembly has been verified, and that the sequence is indeed viral in origin. Sequences would have to be analysed to provide evidence of taxonomic placement that did not exclusively rely on a simple measure of genetic difference. Also, the EC encourages Study Groups to submit proposals that would make a convincing case for recognizing taxa of any rank on a genome-only basis.” (2013)

“It was agreed to continue the current policy of considering species proposals based on deep sequencing where there was information on the host and sufficient similarity with well-characterized viruses to be confident that the genome was correctly assembled and coding-complete. No distinctive taxon names would be applied by ICTV. The issues involved would be further explored at a special topic meeting funded as part of the Wellcome Trust Grant.” (2015)
Reaching a clear position

The role of SGs

- ICTV is a grass-roots organisation
- The EC is reluctant to work in a top-down way, recognising that the needs of virus families vary
- This can make clear positions difficult to reach and agree

Meeting on The Impact Of Metagenomic Sequencing On Viral Classification

- Involving ~12 experts and ~12 EC members
- 9-11 June 2016, Boston
- Publication of proceedings

Feeding into the next EC meeting, 22-24 August, Budapest
TAXONOMICAL ASSIGNMENTS,
PROCEDURES AND SCALES

1966 ICTV 2016

Andrew King
What limits the rate of development of virus taxonomy?

generation of new scientific knowledge → submission of taxonomic proposals → low-tech document processing → EC approval of new taxonomy
Rate-limiting steps in taxonomic development

- Generation of new scientific knowledge
- Submission of taxonomic proposals
- Low-tech document processing
- EC approval of new taxonomy
EC decision-making: now

New taxonomic proposal discussed for the first time

EC gives provisional approval subject to minor changes

Decision deferred until next year pending major changes and/or further consultation; to be discussed again at next live EC meeting

Further consideration deferred

3 months after EC meeting email vote by EC members to confirm approval

EC approved

Low-tech document processing

Provisionally approved (subject to confirmation)

Conditionally provisionally approved

Action taken by proposer, approved by SC chair

Provisionally approved

EC approved

Low-tech document processing

Non-controversial, species-only proposals given fast-track approval

Generation of new scientific knowledge

Email vote confirms approval subject to minor changes

Conditionally approved

Action taken by proposer, approved by SC chair
New taxonomic proposal discussed for the first time

EC gives provisional approval subject to minor changes

Conditionally provisionally approved

Action taken by proposer, approved by SC chair

Provisionally approved (subject to confirmation)

Email vote confirms approval subject to minor changes

Conditionally approved

Action taken by proposer, approved by SC chair

Further consideration deferred

Decision deferred until next year pending major changes and/or further consultation; to be discussed again at next live EC meeting

3 months after EC meeting email vote by EC members to confirm approval

EC approves provisionally pending public consultation

Generation of new scientific knowledge

Low-tech document processing

EC approval of new taxonomy

EC decision-making: now

By 2017(?) Non-controversial, species-only proposals will be approved without EC discussion

Non-controversial, species-only proposals will be approved without EC discussion
Rate-limiting steps in taxonomic development

- Generation of new scientific knowledge
- Submission of taxonomic proposals
- Low-tech document processing
- EC approval of new taxonomy

By 2017(?), submission of taxonomic proposals will be web-based
Rate-limiting steps in taxonomic development

generation of new scientific knowledge → submission of taxonomic proposals → low-tech document processing → EC approval of new taxonomy
Rate-liming steps in taxonomic development

Taxonomic proposals: TP template is complex, prescriptive and demanding

- make proposing less of a deterrent?
- give more credit to authors of proposals?
- encourage/help SGs in other ways to submit TPs?
Rate-limiting steps in taxonomic development

- generation of new scientific knowledge
- submission of taxonomic proposals
- low-tech document processing
- EC approval of new taxonomy

Taxonomic proposals: TP template is complex, prescriptive and demanding

- make proposing less of a deterrent?
- give more credit to authors of proposals?
- encourage/help SGs in other ways to submit TPs?

Need for
- more SGs to represent the ICTV in new areas
Rate-limiting steps in taxonomic development

- Generation of new scientific knowledge
- Submission of taxonomic proposals
- Low-tech document processing
- EC approval of new taxonomy

Help for SGs

Online tools:
- Reference sequence alignments
- VicTree for identifying taxonomic cut-offs
- Wikis for sharing information within and between SCs
Rate-limiting steps in taxonomic development

Help for SGs

Online tools:
- Reference sequence alignments
- VicTree for identifying taxonomic cut-offs
- Wikis for sharing information within and between SCs

The human touch:
- Better succession planning and mentoring
Rate-limiting steps in taxonomic development

by 2020?

generation of new scientific knowledge
submission of taxonomic proposals
low-tech document processing
EC approval of new taxonomy

Help for SGs

Online tools:
- Reference sequence alignments
- VicTree for identifying taxonomic cut-offs
- Wikis for sharing information within and between SCs

The human touch:
- Better succession planning and mentoring
IS IT TIME TO CONSIDER THE ADOPTION OF BINOMIAL NOMENCLATURE?

Mike Adams
The confusion in nomenclature (1)

Differences in the styles of virus species names:

- **Mycobacterium** phage **TM4**
- **Human** herpesvirus **1**
- **Bovine** ephemeral fever virus
- **Mammalian** 1 bornavirus
- **Potato** yellow dwarf virus
- **Alphacoronavirus** 1
- **Cardiovirus** A
- **Potato** virus **X**
- **Rhizosolenia setigera** RNA virus **01**
- **Human** mastadenovirus **C**
- **Autographa californica** multiple nucleopolyhedrovirus
- **Drosophila** X virus
- **Sapporo** virus
- **Melolontha melolontha** entomopoxvirus
The virus versus species issue:

**Andes virus**
- Andes virus (ANDV)
- Bermejo virus (BMJV)
- Lechiguanas virus (LECV)
- Maciel virus (MCLV)
- Oran virus (ORNV)
- Pergamino virus (PRGV)

If these are biologically distinct, they are strains or subspecies of *Andes virus*

**Bayou virus**
- Bayou virus (BAYV)

**Black Creek Canal virus**
- etc.
The Latinized binomial (Linnean) system

- Used almost universally in biology and understood by scientists, editors, etc., many of whom have not really understood the current ICTV system.

- Would make integration of virus data with other biological databases much easier.

- Would clearly distinguish the scientific name from the current names, which would become the common (vernacular) names; this distinction is easily understood and easily applied.

- Would clearly be universal, naming viruses of prokaryotes, plants, vertebrates, etc., in exactly the same way.
A possible way forward

_Hantavirus andiensis_

- Andes virus (ANDV)  [ssp. _andiensis_?]
- Bermejo virus (BMJV)  [ssp. _bermejenis_?]

_Bymovirus hordei-luteus_

- barley yellow mosaic virus (English)
- Gerstengelbmosaik-virus (German)
- mosaique jaune de l'orge (French)
- etc.
Of course, there are problems...

These would include:

- Names of genera and above would not be affected, but the names of all species would change
- It could not sensibly be introduced gradually
- As with all changes, it would likely encounter lively opposition
- Current species that are assigned to a family or subfamily but not to a genus would pose a difficulty (but there are not many...)

If there is a reasonable consensus:

- It should be done sooner rather than later
- ICTV could encourage the use of the prefix ‘Candidatus species’ in publications referring to probable new species that had not yet been officially approved
What can the ICTV do to help?

- Discovery
- Annotation
- Classification
- Taxonomic assignment
Classification and taxonomic assignment

Publish unambiguous species demarcation criteria (SDC)

- Demarcation criteria determine approach and tools necessary for classification and taxonomic assignment
- Responsibility of each SG
- Publish on the ICTV website
- Link from the ICTV Report chapter

Provide classification tools and guidance
Requirements: taxon-specific criteria

- Morphological
- Physical
- Structural
- Biological
- Genomic organisation
- Sequence
### TABLE 2  Criteria for taxonomic classification

<table>
<thead>
<tr>
<th>Order: Picornavirales</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virus</td>
</tr>
<tr>
<td>Nonenveloped, icosahedral particles, ~30 nm in diameter</td>
</tr>
<tr>
<td>Capsid proteins composed of three distantly related jelly roll domains forming particles with pseudo-T=3 symmetry</td>
</tr>
<tr>
<td>Genome</td>
</tr>
<tr>
<td>Positive-sense ssRNA</td>
</tr>
<tr>
<td>One or two monocistronic genome segments</td>
</tr>
<tr>
<td>3'-bound VPg protein</td>
</tr>
<tr>
<td>Genome serves as the mRNA</td>
</tr>
<tr>
<td>Genome typically contains a 3' poly(A) tail</td>
</tr>
<tr>
<td>Protein</td>
</tr>
<tr>
<td>Primary polyprotein translation product proteolytically cleaved into mature proteins by one or more virus-encoded proteinases</td>
</tr>
<tr>
<td>Functional domains include a superfamily III helicase (Hel); chymotrypsin-like proteinase (Pro); and superfamily I RNA-dependent RNA polymerase (Pol)</td>
</tr>
<tr>
<td>Nonstructural proteins are arranged as Hel-VPg-Pro-Pol</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Family: Picornaviridae</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome</td>
</tr>
<tr>
<td>Single monocistronic genome segment</td>
</tr>
<tr>
<td>Protein</td>
</tr>
<tr>
<td>Conserved genome organization</td>
</tr>
<tr>
<td>Conserved set of functional mature proteins</td>
</tr>
<tr>
<td>Protein sequence conservation (protease-polymerase region)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Genus: Enterovirus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein</td>
</tr>
<tr>
<td>At least 50% amino acid identity over the length of the polyprotein</td>
</tr>
<tr>
<td>VPg sequence conservation</td>
</tr>
<tr>
<td>Lacks an L protein</td>
</tr>
<tr>
<td>Possesses a type 1 internal ribosomal entry site</td>
</tr>
<tr>
<td>Host</td>
</tr>
<tr>
<td>Virus replication primarily in (but not limited to) the gastrointestinal tract</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Species: Human enterovirus C</th>
</tr>
</thead>
<tbody>
<tr>
<td>Host</td>
</tr>
<tr>
<td>Share a limited range of host cell receptors</td>
</tr>
<tr>
<td>Share a limited natural host range (e.g., human)</td>
</tr>
<tr>
<td>Genome</td>
</tr>
<tr>
<td>Conserved genome map (organization of protein functional domains)</td>
</tr>
<tr>
<td>Common polyprotein proteolytic processing program</td>
</tr>
<tr>
<td>Share a significant degree of compatibility in proteolytic processing, replication, encapsidation, and genetic recombination</td>
</tr>
<tr>
<td>Sequence similarity</td>
</tr>
<tr>
<td>Amino acid identity: 70% in the polyprotein</td>
</tr>
<tr>
<td>Amino acid identity: 60% in the P1 structural proteins</td>
</tr>
<tr>
<td>Amino acid identity: 70% in the 3C + 3CD nonstructural proteins</td>
</tr>
<tr>
<td>Similar base G+C composition (within 2.5%)</td>
</tr>
<tr>
<td>Phylogeny</td>
</tr>
<tr>
<td>Monophyletic</td>
</tr>
</tbody>
</table>
Requirements: sequence similarity

Sequence database

- Comprised of all ICTV species
- Defined genomic region
- Nucleic acid/protein
- Dependent on SDC
Requirements: pairwise comparison

Define a tool and parameters

- PASC
  - PAirwise Sequence Comparison
  - NCBI

- DEmARC
  - DivErsity pArtitioning by hieRarchical Clustering
  - Leiden University Medical Center, Leiden, The Netherlands

- Species Demarcation Tool
  - University of Western Cape, Cape Town, SA

- Other
Requirements: alignments

- Provide existing multiple sequence alignment (MSA) of approved isolate sequences and genomic region
- Provide guidelines for aligning new sequences to the MSA
Requirements: phylogenetic analysis

Algorithm
- e.g. Bayesian

Tool
- e.g. MrBayes

Parameters
- Substitution model

Visualisation
- Rooted phylogram
MEETING SUMMARY

1966 ICTV 2016

Andrew Davison & Peter Simmonds
To take forward

- Diversity within the ranks of the ICTV
- A more significant role for the National Representatives
- Educating the scientific community, especially journal editors, on the importance of taxonomy and the role of the ICTV
- Accept that the ICTV will always be behind the curve
- SGs have the option of using linked wikipages in the new online Report to at least provide listings (and perhaps other data) on nascent information
- Proposing new species needs to be made easier
- 50th anniversary publication incorporating information on the present meeting
- Mentoring of SG chairs
- Classifying viruses from metagenomic data
- Availability of sequence alignments and tools
Meeting summary

Discussion sessions
- Major concern about impact of metagenomic sequences
- Virus classification methods, many differences of opinions
- Are we doing virus classification or are we doing virus evolution?
- Generalism versus pragmatism
- Usability of current ICTV resources, taxonomy proposals

Short-term plans
- Distribution of meeting summary to all SG chairs and EC members
- Request for further opinions about ICTV developments
- Online Report, summaries and publication strategy
- Bioinformatic links and resources

Taking this forward in the medium term
- Templates and requirements for chapter updates and summaries
- Development of wiki pages for SGs, further examples
- Specification for standardised sequence alignments
THANK YOU AND BON VOYAGE!