This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

Part 1: **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2017.005G*** | (to be completed by ICTV officers) |
| **Short title:** Increasing the number of ranks available in virus taxonomy |
| **Modules attached** (Modules 1, 4 and either 2 or 3 are required.  |  **1** **[x]  2 [ ]  3 [x]  4 [x]**  |
| **Author(s):** |
| Alexander E. Gorbalenya, Mart Krupovic, Arcady Mushegian, Andrew M. Kropinski, Stuart Siddell, Arvind Varsani, Jens H. Kuhn |
| **Corresponding authors with e-mail addresses:** |
| Alexander E. Gorbalenya (a.e.gorbalenya@lumc.nl)Jens H. Kuhn (kuhnjens@mail.nih.gov)Stuart Siddell (stuart.siddell@bristol.ac.ak) |
| **List the ICTV study group(s) that have seen this proposal:** |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | The ICTV Executive Committee (EC) has already received an EC-commissioned Report about this matter from the authors of this proposal. During the EC48 meeting, the EC considered two proposals (2016.001aG.N.v1.ICVCN\_new\_ranks & 2016.003G.N.v1.VirusTaxonomyRanks) that had been filed on July 18 and August 4, 2016, respectively, which, along with the Report, form the basis of this unified proposal. |
| **ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV:Date of first revision: | June 8, 2017October 2,2017 |
| Date of this revision (if different to above): | May 28, 2018 |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
| **EC decision** (from the draft EC49 minutes): Decision: Uc. AEG referred to documents circulated recently: (1) a report and (2) a proposal from the working group (AEG (chair), JHK, AK, MK, SGS, AM and AV) on ways to implement the provision of additional taxonomic ranks. Both documents were generally welcomed as having fulfilled their remit, although they had come very late in the day. EJL confirmed that such additions could be accommodated by the website and the ICTV Report and by GenBank.PS and AMQK repeated concerns expressed in documents that they had circulated before the meeting about the feasibility and usefulness of some of the higher-level ranks in particular. After some discussion, it was agreed to postpone any decision until after the taxonomic proposals proposing use of the new ranks had been reviewed.In those later discussions, it was agreed that a modified and shortened proposal to change the Code would be progressed. Names for the topmost ranks had still to be determined.<Updated by AM, Nov 24, 2017: The requested minor updates were made, most notably by voting on the topmost ranks' names and setting them to Realm and Subrealm on Aug. 26, 2017. The proposal status was updated to U on Oct 4, 2017>Although not minuted, the EC expressed a preference for suffixes in the ‘*viri*’ form (e.g. …*viricota* for a phylum).**Authors’ response**: - Names of two top ranks of virus taxonomy were changed from domain and subdomain to realm and subrealm, respectively (in accordance with the e-vote of the EC in August 2017);- A single consensus version of changes to the International Code of Virus Classification and Nomenclature (ICVCN) is presented. This version takes into account the preferences expressed by the EC at EC49, as well as relevant comments made in sections of the emails from Andrew Davison (21/12/2017) and Andrew King (14/12/17).The revised version proposes removal of existing Sections IV to VII (existing Rules 3.23 to 3.31) to be replaced with a new Section IV (Ranks above the level of species), which includes new Rules 3.22 to 3.25. In addition, changes are proposed to other existing Rules, to prevent inconsistency between the new Rules and existing Rules. Specifically, revision of:old and new Rule 3.2. old Rule 3.33, new Rule 3.27. old Rule 3.34, new Rule 3.28. old Rule 3.35, new Rule 3.30, anddeletion of old Rule 3.6- Table 1 was updated with the favoured names of the two top ranks and to include the example of using ranks above the rank of order to accommodate viruses related to the *Picornavirales*;- Table 2 was updated to retain only the version of suffixes that was agreed upon for taxon names of proposed and used ranks;- The text was further edited to remove typographical errors and to improve document accessibility to the reader.In addition, the proposers have extended the Supporting Material section (see below) to address the specific concerns detailed in emails from Andrew King and Andrew Davison (Appendix: Responses to comment)).The proposers have also prepared a draft of the ICVCN, revised according to the changes described in this proposal (Appendix: Draft ICVCN). This draft has been produced to illustrate the changes that would be made to the ICVCN as a result of this proposal, and it includes explanatory notes. It remains the job of the Business Secretary to implement these changes. \*It should be noted that, for the sake of numerical clarity, the current ICVCN has two 3.34 Rules.  |

**Part 3:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

|  |
| --- |
| non-standard proposal |
| **Title of proposal: Increasing the number of available ranks in virus taxonomy** |
| **Text of proposal:** |
| **ICTV EC mandate:**During the ICTV’s EC48 meeting in Budapest, Hungary, in 2016, the EC discussed two taxonomic proposals regarding the need to increase the number of taxonomic ranks in virus taxonomy:* + - * 1. - 2016.001aG.N.v1.ICVCN\_new\_ranks Merge ICVCN sections IV-VII and allow the use of additional taxonomic ranks in virus taxonomy [presented by Jens H. Kuhn]; and
				2. - 2016.003G.N.v1.VirusTaxonomyRanks Increasing the number of available ranks in virus taxonomy from five to ten and adopting the Baltimore classes as taxa at the highest rank [presented by Alexander E. Gorbalenya; see also Gorbalenya AE, 2018, Archives of Virology, in press].

As noted in the EC48 Minutes Draft v2, the two proposals were discussed together. The discussion mostly focused on views of the relative merits of a flexible ‘open’ system with a large but undefined number of possible ranks (proposed in 2016.001aG) as opposed to a ‘closed’ one that specified a limited number of defined new ranks (proposed in 2016.003G). The EC agreed that (1) all EC members were in favor of increasing the number of ranks available; (2) a substantial majority favored the ‘closed’ approach; (3) the adoption of Baltimore classes should be considered separately from considering additional ranks in virus taxonomy; and (4) an EC Working Group should be established under the leadership of Alexander E. Gorbalenya to consider the best way to implement these decisions. According to the EC48 Commitments Draft, the mandate of this Working Group is “to consider the best way to introduce a limited number of additional ranks and report <their recommendations> to the EC within 3 months". They will liaise with Elliot J. Lefkowitz on implications for the database, website and ICTV Report. Further on, the EC48 Minutes Draft v2 states that after preparing the initial report, the group “would seek then to prepare a consensus proposal within the following 3 months to give time for this to be publicized and feedback received before a decision at EC49.” **Working Group**The working group was created, including the three authors of the two proposals and four other EC members who expressed interest in the matter (all are authors of this proposal). The working group represents different expertise, background, and research interests. For brevity, the group will be called the “ART” (for “Additional Ranks in Taxonomy”) group. This proposal is based on the Report submitted to the EC and discussed at EC49, parts of which are reproduced in the original or modified form. **Additional ranks: number and relation to currently known virus diversity**The ART group discussed extensively the number of ranks that could, and should, be permissible. This discussion was conducted with the assumption that virus taxonomy would continue to be developed to reflect the evolutionary relationships/phylogeny of viruses. The group simultaneously acknowledged the considerable complexity and unresolved nature of many questions related to the origin(s) and evolution of viruses, the technical challenges of this field, and the lack of an independent “gold” standard for classification. Given these limitations, the ART group then asked whether the current five-rank system (order, family, subfamily, genus, species) should be extended above the order rank with just one or two ranks, or all four primary ranks of the Linnaean system (as proposed in 2016.003aG), or even a larger number of ranks to classify the largest possible subset of the already known virus diversity.Based on the results of these deliberations (described in the **Annex**, including **Table 1**), the ART group has concluded and now proposes that the extended virus taxonomy structure should permit **15 ranks, including eight primary ranks and seven “sub-“ derivatives**. The specific example chosen to illustrate the logic of this proposal (i.e., order *Picornavirales* and its higher ranks – see Annex) should, in no way, be considered to validate or invalidate certain groupings, or preempt future proposals on virus classification of this group of viruses. It is presnted in this proposal only for illustrative purposes. According to communication with Elliot J. Lefkowitz, the anticipated changes associated with the introduction of additional ranks could be accommodated without harm to the products and activities of the ICTV (for full discussion of this aspect, see Annex).The ART group have also contacted eight leading scientists (see appendix) in the field of viroids and satellites, and they have unanimously replied in favour of including both of these subviral agents in the proposed reorganization.  **Change of the ICVCN to increase the number of ranks in virus taxonomy**The ART group considered changes to the ICVCN that would be required to accommodate additional ranks in taxonomy. Two versions of the changes to the most relevant Sections IV–VII (current Rules 3.23–3.31) of the ICVCN were produced using the text of the 2016.001aG proposal. The first version included the refined suggestions of the original proposal that were modeled after the Draft BioCode 2011 and retained full compatibility with it. The second version is a further derivative of the original suggestions. It was produced by the ART group to fit the needs of virus taxonomy; this version was devised to retain compatibility with the Draft BioCode 2011 wherever it was possible but **allowed deviations either to address ambiguities or accommodate specific attributes of virus taxonomy**. Both versions were considered at the EC49. The second version was approved and was further streamlined and is reproduced below.Additionally, the ART group discussed possible suffixes for the new ranks. They have converged on the suffixes for three ranks, kingdom, subrealm and realm, and outlined possible choices for the five other ranks (those above the order rank) that differ only in the usage of a vowel or lack thereof. The new suffixes of one of the choices were approved by EC49 (**Table 2**). and included in the version of the modified ICVCN rules below.IV – Rules about ranks other than speciesNew Rule 3.22.Every individual virus is a physical entity and treated as belonging to a number of taxa of hierarchical ranks, some taxa of which may remain undefined. New Rule 3.23. Other than species, the ranks currently in use in virus taxonomy, from most to least diverse, are realm, subrealm, kingdom, subkingdom, phylum, subphylum, class, subclass, order, suborder, family, subfamily, genus and subgenus. The names for these ranks shall be single words ending with the suffixes “-*viria*”, “-*vira*”, “-*virae*”, “-*virites*”, “-*viricota*”, “-*viricotina*”, “-*viricetes*”, “-*viricetidae*”, “-*virales*”, “-*virineae*”, “-*viridae*”, “-*virinae*”, “-*virus*" and “-*virus*”, respectively.New Rule 3.24. The classification of a virus at the species and genus ranks is mandatory. Classification may also encompass any further number of taxa at higher hierarchical ranks.New Rule 3.25. Approval of a new genus must be accompanied by the approval of a type species.In addition, the ART group was reminded that changes were needed to some other existing rules in the ICVCN, in order to prevent inconsistencies between the new Rules described above and existing rules. The following changes are proposed to existing ICVCN Rules not in Section IV:Old and new Rule 3.2. The universal virus classification system shall employ the hierarchical levels of realm, subrealm, kingdom, subkingdom, phylum, subphylum, class, subclass, order, suborder, family, subfamily, genus, subgenus and species.Old Rule 3.33, new Rule 3.27. The formal endings for taxa of viroids are the suffixes "-*viroidia*" for realms, "-*viroida*" for subrealms, "-*viroidiae*" for kingdoms, "-*viroidites*" for subkingdoms, "-*viroidicota*" for phyla, "-*viroidicotina*" for subphyla, "-*viroidicetes*" for classes, "*-viroidicetidea*" for subclasses, "-*viroidales*" for orders, "*viroidineae*" for suborders, "-*viroidae*" for families, "-*viroidinae*" for subfamilies, *"-viroid*" for genera and subgenera, and the word "*viroid*" for species.Old Rule 3.34, new Rule 3.28. The formal endings for taxa of satellite nucleic acids are the suffixes "-*satellitia*" for realms, "-*satellita*" for subrealms, "-*satellitiae*" for kingdoms, "*-satellitites*" for subkingdoms, "-*satelliticota*" for phyla, "-*satelliticotina*" for subphyla, "-*satelliticetes*" for classes, "*-satelliticetidea*" for subclasses, "-*satellitales*" for orders, "-*satellitineae*" for suborders,"-*satellitidae*" for families, "-*satellitinae*" for subfamilies, and "-*satellite*" for subgenera and genera.Old Rule 3.35, new Rule 3.30. In formal taxonomic usage, the accepted names of virus, viroid and satellite realms, subrealms, kingdoms, subkingdoms, phyla, subphyla, classes, subclasses, orders, suborders, familes, subfamilies, genera and subgenera are printed in italics and the first letters of the names are capitalized.Moreover, the old Rule 3.6 has to be deleted as it is no longer compatible with the new rules.**Conclusions** As a result of the proposed change to the number and the scope of ranks, and for the first time, virus taxonomy will encompass the entire spectrum of virus diversity by accommodating taxa at any level of virus diversity from the very narrow (species) to the extremely wide (realms). The availability of a greater number of ranks will mean more work for the ICTV and community but will improve the connection between taxonomy development and evolutionary studies. In the future, after reviewing the acquired experience, this new rank structure could be further refined to improve its representation of the evolutionary relationships of viruses resulting from the ever-increasing sampling of virus diversity and from technical advancements. One particular area not addressed here but worth revisiting in the future is the possible creation of a sub-species rank. |

**Part 4:** **APPENDIX A**: supporting material

| additional material in support of this proposal |
| --- |

**Additional ranks: their number and relation to currently known virus diversity**

The ART group revisited the issue of increasing the number of ranks available for virus taxonomy and confirmed its full support for such an undertaking. Then the group discussed extensively the number of ranks that could, and should, be introduced. This discussion was conducted with the assumption that virus taxonomy would continue to be developed to reflect the evolutionary relationships/phylogeny of viruses. The group simultaneously acknowledged:

1. the considerable complexity and unresolved nature of many questions related to the origin(s) and evolution of viruses, due to the high rates of mutation and recombination associated with many of the known viral taxa, sparsely populated viral sequence space resulting from limited sampling, and other factors;
2. the unmet technical challenges of reconstructing the arrangement of deep-branching virus clades, its reflection in virus classification, and the lack of an independent “gold” standard for classification.

The ART group noted that virus evolutionary studies and classification continue to advance using primarily sequence-based analyses of conserved genes and proteins that includes gene phylogeny, gene synteny, and/or shared gene content. However, it is expected that, at the level of ranks that encompass the most distant relationships, additional approaches, including structural comparisons, genome network analyses and employing new algorithms and statistics may yield complementary information to guide the creation of taxa.

Given the limitations listed above, the ART group noted that it is difficult to foresee, with confidence, the number of ranks that will eventually be required to accommodate the entire, or even the currently known, spectrum of virus diversity. Therefore, to fulfill its mandate, the ART group then asked whether the current five-rank system should be extended above the order rank with just one or two ranks, or all four primary ranks of the Linnaean system (as proposed in 2016.003aG), or even a larger number of ranks to classify the largest possible subset of the already known virus diversity. This exercise was conducted purely for the purpose of this report and in no way should it be considered to validate or invalidate certain groupings, or preempt future proposals on virus classification.

**Additional ranks: number required to accommodate known viruses related to members of the *Picornavirales* order (Table 1)**

In this section, a "use case" analysis is presented for illustrative purposes. First, consideration was given to the choice of the subset of viruses for which higher-rank taxa could be tentatively constructed. In this respect, RNA viruses and particularly +RNA viruses stand out. These viruses are currently members of three orders and a number of informal supergroups (“superfamilies”) of viruses with deeper links to other RNA viruses, as well as viruses with reverse-transcribing genomes that have been described as a result of numerous comparative genomics studies produced over a period of 30 years (see Argument 3 in 2016.003G.N.v1). The ART group then chose the *Picornavirales* order as the starting point of the exercise because of its large and diverse family base, covering viruses of a very large range of eukaryotes, and its multi-layered connections to many other more distantly related viruses.

A tentative hierarchical classification was considered, in which ranks above the order rank could be filled with clades of viruses related, more and more distantly, to members of the *Picornavirales* order. Obviously, the degree of uncertainty regarding composition and rank assignment for each clade increases along with the distance separating the corresponding viruses.

With all these reservations in place, the ART group has agreed that up to **eight ranks** above the existing orderrank might be required to accommodate a hypothetical taxonomic arrangement of currently known viruses that will include the members of the order *Picornavirales* as their subset. Groups of viruses that were provisionally added to the *Picornavirales* at each higher rank, and thus with a decreasing level of similarity, are listed in Table 1. Using this step-wise addition of virus groups, a taxon that includes *all* RNA viruses plus possibly other viruses may be created at a basal rank. It should be noted that existing data suggests that adequate classification of highly diverse eukaryotic ssDNA viruses as well as viruses with large dsDNA genomes also necessitates the introduction of additional taxonomic ranks, emphasizing the legitimacy and timeliness of the task undertaken by the ART group.

Eight ranks above the order rank could be accommodated in the Linnaean taxonomic structure if its four primary ranks are supplemented with four additional ranks. This could be done in several ways depending on various considerations. For instance, “secondary” and “tertiary” ranks, as outlined in TaxoProp 2016.001aG(**Table 1**), provide for very large number of potential ranks above and below primary ranks to achieve any desirable resolution. Alternatively, these eight additional ranks may be introduced in a manner similar to that used for the family rank in virus taxonomy, which is immediately above the non-primary “subfamily” rank. The choice of the introduction of non-primary ranks might become important for the long-term development of virus taxonomy, which may be evident from the description of possible changes to the nomenclature of ranks of virus taxonomy (see below). Regardless, the ART group currently recommends the introduction of four “sub-“ ranks above the order rank.

This extended Linnaean taxonomic structure, including primary and non-primary ranks, could also be applied below the order rank in a consistent manner. The ART expects the resulting two or three additional ranks, i.e., suborder, subgenus, and possibly subspecies, to become particularly popular for the fine structuring of virus families and orders that are more extensively sampled. The introduction of a "subspecies" rank is likely to be controversial and of practical difficulty, due to sheer number of prospective taxa at this level, which might exceed the number of all other taxa combined. Because of these considerations, the ART group decided not to propose the creation of this rank but rather stress that a separate proposal on subspecies accompanied by extensive deliberation may be warranted in the future.

In total, this extended taxonomy structure could include 15 ranks, eight primary ranks and seven “sub-“ derivatives. In the future, if necessary, the resolution of this scheme could be further improved across the entire diversity rank spectrum with the addition of extra ranks. This possible further expansion will benefit from the experience acquired through the use of the proposed extended taxonomy rank structure.

**Practical consequences of the introduction of additional ranks into virus taxonomy: ICTV website and its database, the online ICTV Report, Study Groups and utilization of the new rank structure**

The full implications of the introduction of additional ranks may be realized only gradually. It is clear to the ART group that, as a result of expanding the ranks available for taxonomy assignment, the number of taxonomy proposals are likely to increase, both for creating new taxa and refining old ones. Particularly, using the subgenus rank might considerably increase the amount of work for Study Groups, especially depending on the demands for rank descriptions. Furthermore, working with these ranks may require particular caution since decisions on whether to choose between, for example, a subgenus or genus, or between a subgenus or species, may influence the naming of species (in particular if the species name is binominal). Another aspect concerns the processes of initiation, evaluation and oversight of the creation of taxa above the order rank. Who will be in charge of these processes? Should dedicated Study Groups be created with a mandate to consider taxonomy for the ranks above the order rank, or should it only be done in a bottom-up fashion, as a joint effort of all Study Groups that may be affected by the changes? One of the approaches, compatible with the current ICTV structure and favored by the **entire** ART group, is to mandate that whenever a taxonomic proposal to create taxa above the family rank is contemplated, the authors of such proposal should seek feedback from the Chairs of all relevant Study Groups within a reasonable time-frame. This response should be summarized in the filed proposals.

As required, the ART Chair has contacted EC Data Secretary Elliot J. Lefkowitz on possible implications of the proposed changes to the taxonomic rank structure for the database, website, and ICTV Report, and, additionally, on the impact of ICTV interaction with NCBI databases. In his response, and based on inquiries, the Data Secretary has assured the ART group that the anticipated changes could be accommodated without harm to the products and activities of the ICTV.

Specialist in the area of viroid and satellite classification who have seen and support this proposal:

Rob Briddon: Member Geminiviridae and Tolecusatellitidae Study Group

Francesco Di Serio; Chair Avsunviroidae and Pospiviroidae Study Group

Jesús Navas-Castillo: Member Geminiviridae and Tolecusatellitidae Study Group

Ricardo Flores: Member Avsunviroidae and Pospiviroidae Study Group

# Elvira Fiallo-Olivé: Chair Geminiviridae and Tolecusatellitidae Study Group

# John W Randles: Member Avsunviroidae and Pospiviroidae Study Group

# Matthias Fischer: Chair Mimiviridae Study Group

# Robert Owens: Member Avsunviroidae and Pospiviroidae Study Group

**Table 1. Proposed rank structure of virus taxonomy: illustrated by putative high-rank taxa including the *Picornavirales* order**

1 Primary ranks are left indented; already ICTV approved ranks are in green.

2 the hierarchical assignment of listed virus groups in this column is to illustrate different scales of virus diversity. While these clustering may have support in literature, they are presented here without implicit taxonomic meaning and without suggesting any names for the putative taxa.

|  |  |  |  |
| --- | --- | --- | --- |
| **Rank #** | **Proposed & used ranks1** | **Starting taxon** | **Group tentatively & consecutively added to starting taxon2** |
| **1** | realm |  | Bacterial RNA viruses? +RNA-RT? |
| **2** | subrealm |  | (-)RNA viruses? |
| **3** | kingdom |  | dsRNA *Reoviridae*?  |
| **4** | subkingdom |  | Other eukaryotic +RNA viruses & dsRNA *Totiviridae*? |
| **5** | phylum |  | *Permutotetraviridae* & dsRNA *Birnaviridae* |
| **6** | subphylum |  | *Nidovirales*, *Astroviridae* & provisional Sobemoviridae |
| **7** | class |  | *Potyviridae* & some other |
| **8** | subclass |  | *Caliciviridae* & some other |
| **9** | order | *Picornavirales* |  |
| **10** | suborder |  |  |
| **11** | family |  |  |
| **12** | subfamily |  |  |
| **13** | genus |  |  |
| **14** | subgenus |  |  |
| **15** | species |  |  |

**Table 2. Suffixes for taxon names of proposed and used ranks**

|  |  |  |
| --- | --- | --- |
| **Rank #** | **Proposed & used ranks** | **Suffixes** |
| **1** | realm | *....viria*  |
| **2** | subrealm | *....vira*  |
| **3** | kingdom | *....virae*  |
| **4** | subkingdom | *....virites*  |
| **5** | phylum | *....viricota* |
| **6** | subphylum | *....viricotina* |
| **7** | class | *....viricetes* |
| **8** | subclass | *....viricetidae* |
| **9** | order | *....virales* |
| **10** | suborder | *....virineae* |
| **11** | family | *....viridae* |
| **12** | subfamily | *....virinae* |
| **13** | genus | *....virus* |
| **14** | subgenus | *....virus*  |

**Background information for Table 2:** The ART agreed that suffixes should be used that are already in use in other taxonomies to avoid further confusion. Currently, the used suffixes are:

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Rank** | **Prokaryotes** | [Plants](https://en.wikipedia.org/wiki/Plant) | [Algae](https://en.wikipedia.org/wiki/Algae) | [Fungi](https://en.wikipedia.org/wiki/Fungus) | [Animals](https://en.wikipedia.org/wiki/Animal) |
| Division/Phylum | Not used | -phyta [/ˈfaɪtə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -phycota [/ˈfaɪkoʊtə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -mycota [/maɪˈkoʊtə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Subdivision/Subphylum | Not used | -phytina [/fᵻˈtaɪnə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -phycotina [/fᵻkoʊˈtaɪnə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -mycotina [/maɪkoʊˈtaɪnə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Class | -ia [/iə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -opsida [/ˈɒpsᵻdə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -phyceae [/ˈfaɪʃiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -mycetes [/maɪˈsiːtiːz/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Subclass | -idae [/ᵻdiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -phycidae [/ˈfɪsᵻdiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -mycetidae [/maɪˈsɛtᵻdiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Superorder | Not used | -anae [/ˈeɪniː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Order | -ales [/ˈeɪliːz/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Suborder | -ineae [/ˈɪnᵻ.iː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Infraorder | Not used | -aria [/ˈɛəriə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | Not used |
| Superfamily | Not used | -acea [/ˈeɪʃə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -oidea [/ˈɔɪdiə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Epifamily | Not used | Not used | Not used | Not used | -oidae [/ˈɔɪdiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Family | -aceae [/ˈeɪʃiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -idae [/ᵻdiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Subfamily | -oideae [/ˈɔɪdᵻiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -inae [/ˈaɪniː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Infrafamily | Not used | Not used | Not used | Not used | -odd [/ɒd/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Tribe | -eae [/ᵻiː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -ini [/ˈaɪnaɪ/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Subtribe | -inae [/ˈaɪniː/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) | -ina [/ˈaɪnə/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |
| Infratribe | Not used | Not used | Not used | Not used | -ad [/æd/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) or -iti [/ˈaɪti/](https://en.wikipedia.org/wiki/Help%3AIPA_for_English) |

**Part 4:** **APPENDIX B**: supporting material

Responses to Comments from Andrew Davison:

My concerns are as follows.

1. **The role of the BioCode.** Rule 2.2 in the code is unaffected and says:

Nomenclature of viruses is independent of other biological nomenclature. Virus taxon nomenclature is recognized as an exception in the proposed International Code of Bionomenclature (BioCode).

This reflects the early and long-lived desire of the ICTV for virus classification not to be subject to any other system. The weakening of this position evident in the proposal needs to be examined and, in my view, rejected. The Code should not declare independence from the BioCode in rule 2.2 and then express a longing to be compliant with it in new rule 3.25 (now 3.24), which, as a clear result of the background explanation of the desired involvement of the BioCode, states that classification should be “preferably in a continuous manner”.

Also, rule 2.1 in the code is unaffected and says:

The essential principles of virus nomenclature are:

(i) to aim for stability; (ii) to avoid or reject the use of names which might cause error or confusion; (iii) to avoid the unnecessary creation of names.

The encouragement in new rule 3.25 (now 3.24) to create names in a continuous manner – potentially 15 for each virus instead of the three that suffice at present – threatens the principle of avoiding the unnecessary creation of names, which is an important expression of the need for the ICTV to be useful to the whole of virology and not only to taxonomy wonks.

In addition, the comment to rule 3.2, that “it is not obligatory to use all levels of the taxonomic hierarchy” (see point 2 below), contradicts the intent of new rule 3.25 (now 3.24).

For these reasons, and because no changes have been proposed for rules 2.1, 2.2 or 3.2, the phrase “preferably in a continuous manner” should be deleted.

**Response**

The proposal does not say that virus taxonomy is dependent upon the BioCode. It states that the proposal "was devised to retain compatibility with the Draft BioCode 2011 (wherever it was possible) but **allowed deviations either to address ambiguities or accommodate specific attributes of virus taxonomy**".

The proposal does not encourage the creation of unnecessary names. Rule 3.24 now says: " The classification of a virus at the species and genus ranks is mandatory. Classification may also encompass any further number of taxa at higher hierarchical ranks". It is up to the proposers to decide how many taxa they wish to use and name.

2. **The number of ranks.** Rule 3.2 in the code is unaffected and says:

The universal virus classification system shall employ the hierarchical levels of Order, Family, Subfamily, Genus, and Species.

Comment: It is not obligatory to use all levels of the taxonomic hierarchy. The primary classification is of viruses into species. Most species are classified into genera and most genera are classified into families. Species not assigned to a genus will be "unassigned" in a family (see Rule 3.6) and genera not classified in families have the status of "unassigned" (sometimes referred to as "floating"). Some families are classified into Orders, but often the family is the highest level taxon in use. Also, families are not necessarily divided into subfamilies. This taxon is to be used only when it is needed to solve a complex hierarchical problem (see Rule 3.26).

Contrasting examples of full classifications of some negative strand RNA viruses are: (1) species *Bovine torovirus*; genus *Torovirus*; subfamily *Torovirinae*; family *Coronaviridae*; order *Nidovirales*, and (2) species *Rice stripe virus*; genus *Tenuivirus*.

Also, rule 3.7 in the code is unaffected and says:

Names will only be accepted if they are linked to taxa at the hierarchical levels described in Rule 3.2 and which have been approved by the ICTV.

Similarly, rule 3.35 in the code is unaffected and says:

In formal taxonomic usage, the accepted names of virus Orders, Families, Subfamilies, and Genera are printed in italics and the first letters of the names are capitalized.

Comment: See Rule 3.8 for the definition of an "accepted" name.

Adoption of the proposal would leave these rules contradicting or inconsistent with the ranks listed in new rule 3.24. Adjustments should be proposed.

**Response**

Old and new Rule 3.2 has been modified to be consistent

Old Rule 3.7, new Rule 3.6 is now consistent as Rule 3.2 has been modified

Old Rule 3.35, new Rule 3.30 has been modified to be consistent with the extended ranks

3. **Unassigned species.** Rule 3.6 in the code is unaffected and says:

When it is uncertain how to classify a species into a genus but its classification in a family is clear, it will be classified as an unassigned species of that family.

Comment: A species can be classified as an unassigned member of a family when no genus has been devised. For example, *Groundnut rosette assistor virus* is classified in the family *Luteoviridae* but not within any of the current genera of that family.

Adoption of the proposal would leave this rule, as well as rule 3.2 (see point 2, above), at odds with the demand for all species to be placed into genera in new rule 3.24. It is not clear from the proposal why the twice-stated instruction in the present rules – that species not assigned to genera are permitted – should be abolished. This question and its solution should be addressed.

**Response**

Knowing that members of a virus species do not to belong to any existing genus, deems it logical to create a new genus. The status as well as the name of such a genus, like those of any other taxon, can be revised when new knowledge is obtained. If the old Rule 3.6 is deleted, there is no longer any inconsistency. This is justified because it is illogical to have an optional rule that allows for taxonomic "uncertainty" at one, and only one, particular rank. Either, we should have similar rules for all ranks, or, as the new Rule 3.24 implies, only allow for certainty when creating taxa at the two lowest ranks

However, we accept that this is a significant change to current practice and would also call for a genus assignment for circa 240 virus species that are currently "floating" without a genus. If this proposal is adopted, the Study Groups could be given a specific time frame (e.g., more than one and a half years, between this rule ratification and the early summer of the next but one calendar year) to comply by submitting new-genera proposals.

4. **Definition of ranks.** Rules 3.23, 3.26 and 3.28 in the code would be replaced and say:

A genus is a group of species sharing certain common characters.

Comment: It is acceptable for a genus to contain a single species.

A subfamily is a group of genera sharing certain common characters. The taxon shall be used only when it is needed to solve a complex hierarchical problem.

Comment: It is acceptable for a subfamily to contain a single genus.

A family is a group of genera (whether or not these are organized into subfamilies) sharing certain common characters.

Comment: It is acceptable for a family to contain a single genus.

The replacement of the rule and the comment in each of these, in which a rank is first defined and then permitted in the comments to contain a single lower taxon, by taxa that are not defined and on which it is unclear whether a higher rank may contain a single lower rank, is unsatisfactory.

Also, implementation of a system in which all ranks may be used, whether or not they solve complex hierarchical problems (or, indeed, any problems at all), fosters the unnecessary creation of names (see point 1, above).

**Response**

The new Rules dispense with the need to list, individually, the endings that are to be used for each rank (now covered in new Rules 3.23, 3.27 and 3.28). We do not think that we need to have Rules that state that a rank is a group of lower ranks? Is that not the meaning of the word hierarchical? Nor do we need to say that a rank may contain a single lower rank. Why not? Thus, we see no problem in deleting the old Rules 3.23 to 3.31.

In removing old Rule 3.26, we have removed the reference to solving "complex hierarchical problems". What are these? As the number of known viruses increases, so will the number of taxa and, as we become aware of increasing diversity ("complexity"), the number of taxa required to accommodate only one or a few viruses may increase and the framework to create such taxa should be provided. It may be expected that, with time, some of these taxa will become more heavily populated. Why is this a complex problem? The ART group wishes to note that, for example, the current taxonomy of the *Picornaviridae*, includes many genera with single species. It is the responsibility of the EC to evaluate proposals and ensure that ranks are only filled with taxa when there is sound scientific reasoning.

5. **Type species.** Rule 3.25 in the code would be subsumed into new rule 3.24 and says:

Approval of a new genus must be accompanied by the approval of a type species.

This is an entirely separate consideration from the rest of new rule 3.24, and should be retained as a separate item (with renumbering if necessary).

**Response**

This Rule has been retained

6. **Unnecessary rules.** Rules 3.29, 3.30 and 3.31 in the code would be retained and say:

A family name shall be a single word ending in *...viridae*.

An order is a group of families sharing certain common characters.

An order name shall be a single word ending in *...virales*.

Under the new proposals, rules 3.29 and 3.31 are redundant and should be abolished, and rule 3.30 should receive the same consideration as the equivalent rules for other ranks (see point 4, above).

**Response**

This has been addressed in this revision

7. **Subviral agents.** Rules 3.32, 3.33 and 3.34 in the code are unaffected and say:

Rules concerned with the classification of viruses shall also apply to the classification of viroids and satellite nucleic acids.

The formal endings for taxa of viroids are the word "viroid" for species, the suffix "-viroid" for genera, the suffix "-viroinae" for sub-families (should this taxon be needed) and "-viroidae" for families.

Comment: For example, the species *Potato spindle tuber viroid* is classified in the genus *Pospiviroid*, and the family *Pospiviroidae*.

The formal endings for taxa of satellite nucleic acids are the suffix "-satellite" for genera, the suffix "-satellitinae" for sub-families (should this taxon be needed) and "-satellitidae" for families.

Comment: For example, the species *Ageratum yellow vein betasatellite* is classified in the genus *Betasatellite*, and the family *Tolecusatellitidae*.

Rule 3.32 implies that equivalents to the new ranks would also apply to subviral agents. This would leave rules 3.33 and 3.34 incomplete. Also, the lesser importance placed on the rank of subfamily in these rules is inconsistent with new rules 3.24 and 3.25.

**Response**

The additional ranks have also been applied to viroids and satellite nucleic acids (new Rules 3.27 and 3.28). The ART group have contacted eight leading scientists (see appendix) in the field of viroids and satellites, and they have unanimously replied in favour of including both of these subviral agents in the proposed reorganization.

Response to comments from Andrew King:

**Response**

Andrew King's concerns regarding several taxonomic proposals, including 2017.005G.U., were detailed in an email from 14/12/2017. Many of them are related to what are termed description-less TPs and/or the unnecessary creation of taxa. We would like to reiterate that this proposal is to increase the number of ranks available in virus taxonomy for the community to use, and this is entirely separate from how new, or existing, taxa will be assigned to these ranks. We must distinguish between modifications to the framework in which we operate, and the methods we use to populate that framework. Our current rules and practices allow for proposals that deal with either aspect (e.g., proposal 2017.003G.A.v2.ICVCN\_Rule\_3.11\_Change, which was ratified earlier this year).

Several other of Andrew King's concerns are the same as Andrew Davison's, and have been addressed above: yet others, which are both extensive and complex, were discussed in relation to this proposal at EC49, and did not alter the majority view in favour of the proposal.

**Part 4:** **APPENDIX C**: supporting material

| Draft ICVCN |
| --- |

Explanatory note.

Text in black is the original text of the latest ICVCN (April 2018). Some text may be struck-through if it describes a Rule that would be deleted as a result of approving 2017.005G.U.v4.AdditionalTaxonomyRanks. Text that is NOT struck-through would remain in the revised ICVCN

Text in blue are the comments contained in the original text of the latest ICVCN (April 2018). Some text may be struck-through if the ART group suggests this as a necessary change. Text that is NOT struck-through would remain in the revised ICVCN

Text in red are new rules that would be created as a result of approving 2017.005G.U.AdditionalTaxonomyRanks. ALL of this text would be included in the revised ICVCN

Text in green is explanatory. In some cases, these comments are expanded upon in the "Responses to comments" section of the appendix. NONE of this text would remain in the revised ICVCN

ICTV Code

The International Code of Virus Classification and Nomenclature
XXXX 20XX

1. Statutory basis for the International Committee on Taxonomy of Viruses (ICTV)

1.1

The International Committee on Taxonomy of Viruses (ICTV) is a committee of the Virology Division of the International Union of Microbiological Societies. ICTV activities are governed by Statutes agreed with the Virology Division.

1.2

The Statutes define the objectives of the ICTV. These are:
(i) to develop an internationally agreed taxonomy for viruses; (ii) to develop internationally agreed names for virus taxa; (iii) to communicate taxonomic decisions to the international community of virologists; (iv) to maintain an Index of agreed names of virus taxa.

1.3

The Statutes also state that classification and nomenclature will be subject to Rules set out in an International Code.

Comment: Ratified changes will be published in Virology Division News in Archives of Virology, and in subsequent ICTV Reports.

2. Principles of Nomenclature

2.1

The essential principles of virus nomenclature are:
(i) to aim for stability; (ii) to avoid or reject the use of names which might cause error or confusion; (iii) to avoid the unnecessary creation of names.

2.2

Nomenclature of viruses is independent of other biological nomenclature. Virus taxon nomenclature is recognized as an exception in the proposed International Code of Bionomenclature (BioCode).

2.3

The primary purpose of naming a taxon is to supply a means of referring to the taxon, rather than to indicate the characters or history of the taxon.

2.4

The name of a taxon has no official status until it has been approved by ICTV.

Comment: see section 3.8

3. Rules of Classification and Nomenclature

I - General Rules

The universal scheme

3.1

Virus classification and nomenclature shall be international and shall be universally applied to all viruses.

3.2

The universal virus classification system shall employ the hierarchical levels of realm, subrealm, kingdom, subkingdom, phylum, subphylum, class, subclass, order, suborder, family, subfamily, genus, subgenus and species.

Comment: It is not obligatory to use all levels of the taxonomic hierarchy. The primary classification is of viruses into species. Species are classified into genera and most genera are classified into families. ~~Species not assigned to a genus will be "unassigned" in a family (see Rule 3.6) and genera not classified in families have the status of "unassigned" (sometimes referred to as "floating"). Some families are classified into Orders, but often the family is the highest level taxon in use. Also, families are not necessarily divided into subfamilies. This taxon is to be used only when it is needed to solve a complex hierarchical problem (see Rule 3.26).~~

Contrasting examples of full classifications of some positive-strand RNA viruses are: (1) species *Cocoa necrosis virus*; genus *Nepovirus*; subfamily *Comovirinae*; family *Secoviridae*; order *Picornavirales*, and (2) species *Tobacco albetovirus 1*; genus *Albetovirus*.

Deletion of some comments as old Rule 3.6 and old rule 3.26 have been deleted

Scope of the classification

3.3

The ICTV is not responsible for classification and nomenclature of virus taxa below the rank of species. The classification and naming of serotypes, genotypes, strains, variants and isolates of virus species is the responsibility of acknowledged international specialist groups.

Comment: A variety of subspecific entities may be identified within a single virus species. These may be described as viruses (e.g. peanut stripe virus, which is classified in the species *Bean common mosaic virus*, genus *Potyvirus*, family *Potyviridae*) or as serotypes, genotypes, strains, variants, isolates etc. Naming of such entities is not the responsibility of the ICTV but of international specialty groups. It is the responsibility of ICTV Study Groups to consider how these entities may best be classified into species.

3.4

Artificially created viruses and laboratory hybrid viruses will not be given taxonomic consideration. Their classification will be the responsibility of acknowledged international specialist groups.

Limitations

3.5

Taxa will be established only when representative member viruses are sufficiently well characterized and described in the published literature so as to allow them to be identified unambiguously and the taxon to be distinguished from other similar taxa.

~~3.6~~

~~When it is uncertain how to classify a species into a genus but its classification in a family is clear, it will be classified as an unassigned species of that family.~~

~~Comment: A species can be classified as an unassigned member of a family when no genus has been devised. For example,~~*~~Groundnut rosette assistor virus~~*~~is classified in the family~~*~~Luteoviridae~~*~~but not within any of the current genera of that family.~~

This rule should be deleted.

New rule 3.24 states that "The classification of a virus at the species and genus ranks is mandatory. Classification may also encompass any further number of taxa at higher hierarchical ranks."

3.6

Names will only be accepted if they are linked to taxa at the hierarchical levels described in Rule 3.2 and which have been approved by the ICTV.

II - Rules about naming Taxa

Status of Names

3.7

Names proposed for taxa are "valid names" if they conform to the Rules set out in the Code and they pertain to established taxa. Valid names are "accepted names" if they are recorded as approved International Names in the 9th ICTV Report or have subsequently become "accepted names" by an ICTV vote of approval for a taxonomic proposal.

Comment: A valid taxon name is one that has been published, one that is associated with descriptive material, and one that is acceptable in that it conforms to the Rules in the Code. Accepted names will be kept in an "Index" by the ICTV.

3.8

Existing names of taxa shall be retained whenever feasible.

Comment: A stable nomenclature is one of the principal aims of taxonomy and therefore changes to names that have been accepted will only be considered if the accepted name conflicts with the Rules or if a change is necessary to remove ambiguities or confusion.

3.9

The rule of priority in naming taxa shall not be observed.

Comment: The earlier of candidate names for a taxon may be chosen as a convenience to virologists, but the Rule ensures that it is not possible to invalidate a name in current use by claiming priority for an older name that has been superseded.

3.10

A person's name may be used when devising a name for new taxon. If the person is alive at the time of the proposal, the person’s written consent for use of his/her name must be provided together with the official taxonomic proposal. Whether the use of a person’s name for taxon naming is appropriate will be judged by the responsible ICTV Study Group, the respective ICTV Subcommittee, and the ICTV Executive Committee and approved or disapproved following established taxonomic proposal procedures. Furthermore, a) An individual may not propose his/her own name as the basis for any new taxon name; and, b) A taxon may not be named wholly or in part after any current member of an ICTV Study Group or committee.

3.11

Names for taxa shall be easy to use and easy to remember. Euphonious names are preferred.

Comment: In general, short names are desirable and the number of syllables should be kept to a minimum.

3.12

Ligatures, diacritical marks, punctuation marks (excluding hyphens), subscripts, superscripts, oblique bars and non-Latin letters (i.e. those not included in the ISO basic Latin alphabet) may not be used in taxon names. Numbers and hyphens are allowed but hyphens should not be used when attaching numbers or letters to the end of a series of species names and should never be used in names of genera and higher taxonomic ranks.

Comment: The Rule is intended to make text unambiguous and easy to sort electronically; its application should often make names more pronounceable, in agreement with Rule 3.12.

3.13

New names shall not duplicate approved names. New names shall be chosen such that they are not closely similar to names that are in use currently or have been in use in the recent past.

Comment: The name selected for a new taxon should not sound indistinguishable from the name of another taxon at any rank or from any taxon. For example, the existence of the genus *Iridovirus* means that forms of new name such as "irodovirus" or "iridivirus" are unacceptable as they are too easily confused with an approved name. Confusion can also be between species and genus names as both end in "virus". Thus, for example, a genus typified by the imaginary species Omega virus would not be named Omegavirus because species and genus would then be too readily confused.

3.14

Sigla may be accepted as names of taxa, provided that they are meaningful to virologists in the field, normally as represented by Study Groups.

Comment: Sigla are names comprising letters and/or letter combinations taken from words in a compound term. The name of the genus *Comovirus* has the sigla stem "Co-" from cowpea and "-mo-" from mosaic; the name of the family *Reoviridae* has the sigla stem "R" from "Respiratory, "e" from "enteric" and "o" from "orphan".

Decision making

3.15

In the event of more than one candidate name being proposed, the relevant Subcommittee will make a recommendation to the Executive Committee of the ICTV, which will then decide among the candidates as to which to recommend to ICTV for acceptance.

Comment: When there is more than one candidate name for the same taxon, the choice of name to be approved will usually be based on the recommendations of a particular Study Group working on behalf of the ICTV. The Study Group will be expected to consult widely so as to ensure the acceptability of names, subject to the Rules in the Code. The policy of the ICTV is that, as far as is possible, decisions on questions of taxonomy and nomenclature should reflect the majority view of the appropriate virological constituency

Procedures for naming taxa

3.16

New names shall be selected such that they, or parts of them, do not convey a meaning for the taxon which would either (1) seem to exclude viruses which lack the character described by the name but which are members of the taxon being named, or (2) seem to exclude viruses which are as yet undescribed but which might belong to the taxon being named, or (3) appear to include within the taxon viruses which are members of different taxa.

3.17

New names shall be chosen with due regard to national and/or local sensitivities. When names are universally used by virologists in published work, these or derivatives shall be the preferred basis for creating names, irrespective of national origin.

3.18

All relevant ICTV subcommittees and study groups will be consulted prior to a decision being taken on any taxonomic proposal submitted to the Executive Committee of the ICTV.

Comment: Proposals concerning a family containing genera of viruses that infect diverse types of host (e.g. plants and vertebrates, fungi and plants, and so on) must be considered by the Subcommittees responsible for viruses of each host type (i.e. Plant viruses, Vertebrate viruses, and so on). For example, taxonomic proposals concerned with the family *Partitiviridae* would be considered by the Fungal Virus Subcommittee and one of its Study Groups but because some genera in the family contain viruses of plants, proposals affecting the family would also be considered by the Plant Virus Subcommittee.

III - Rules about Species

Definition of a virus species

3.19

Species shall be created in accordance with the following definition:
"A species is the lowest taxonomic level in the hierarchy approved by the ICTV. 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. The criteria used should be published in the relevant section of the ICTV Report and reviewed periodically by the Study Group.

Construction of a name

3.20

A species name shall consist of as few words as practicable but be distinct from names of other taxa. Species names shall not consist only of a host name and the word "virus".

Comment: Species names normally comprise more than one word (e.g. *Bunyamwera virus*).

3.21

A species name must provide an appropriately unambiguous identification of the species.

Comment: Species names should be distinctive. They should not be in a form that could be easily confused with the names of other taxa.

IV - Rules about ranks other than species

3.22.Every individual virus is a physical entity and treated as belonging to a number of taxa of hierarchical ranks, some of which may remain undefined.

3.23. Other than species, the ranks currently in use in virus taxonomy, from most to least diverse, are realm, subrealm, kingdom, subkingdom, phylum, subphylum, class, subclass, order, suborder, family, subfamily, genus and subgenus. The names for these ranks shall be single words ending with the suffixes “-*viria*”, “-*vira*”, “-*virae*”, “-*virites*”, “-*viricota*”, “-*viricotina*”, “-*viricetes*”, “-*viricetidae*”, “-*virales*”, “-*virineae*”, “-*viridae*”, “-*virinae*”, “-*virus*" and “-*virus*”, respectively.

3.24. The classification of a virus at the species and genus ranks is mandatory. Classification may also encompass any further number of taxa at higher hierarchical ranks.

3.25. Approval of a new genus must be accompanied by the approval of a type species.

~~V - Rules about Subfamilies~~

~~3.26~~

~~A subfamily is a group of genera sharing certain common characters. The taxon shall be used only when it is needed to solve a complex hierarchical problem.~~

~~Comment: It is acceptable for a subfamily to contain a single genus.~~

~~3.27~~

~~A subfamily name shall be a single word ending in ...virinae.~~

Delete.

The new Rules dispense with the need to list, individually, the endings that are to be used for each rank (now covered in Rules 3.23, 3.27 and 3.28). We do not think that we need to have Rules that state that a rank is a group of lower ranks? Is that not the meaning of the word hierarchical? Nor do we need to say that a rank may contain a single lower rank. Why not? Thus, we see no problem in deleting the old Rules 3.23 to 3.31.

In removing old Rule 3.26, we have removed the reference to solving "complex hierarchical problems". What are these? As the number of known viruses increases, so will the number of taxa and, as we become aware of increasing diversity ("complexity"), the number of taxa required to accommodate only one or a few viruses may increase and the framework to create such taxa should be provided. It may be expected that, with time, some of these taxa will become more heavily populated. Why is this a complex problem? The ART group wishes to note that, for example, the current taxonomy of the *Picornaviridae*, includes many genera with single species. It is the responsibility of the EC to evaluate proposals and ensure that ranks are only filled with taxa when there is sound scientific reasoning.

~~VI - Rules about Families~~

~~3.28~~

~~A family is a group of genera (whether or not these are organized into subfamilies) sharing certain common characters.~~

~~Comment: It is acceptable for a family to contain a single genus.~~

~~3.29~~

~~A family name shall be a single word ending in ...viridae.~~

~~VII - Rules about Orders~~

Delete. See above.

V - Rules about Sub-viral Agents

Viroids and satellite nucleic acids

3.26

Rules concerned with the classification of viruses shall also apply to the classification of viroids and satellite nucleic acids.

3.27

The formal endings for taxa of viroids are the suffixes "-*viroidia*" for realms, "-*viroida*" for subrealms, "-*viroidiae*" for kingdoms, "-*viroidites*" for subkingdoms, "-*viroidicota*" for phyla, "-*viroidicotina*" for subphyla, "-*viroidicetes*" for classes, "*-viroidicetidea*" for subclasses, "-*viroidales*" for orders, "*viroidineae*" for suborders, "-*viroidae*" for families, "-*viroidinae*" for subfamilies, *"-viroid*" for genera and subgenera, and the word "*viroid*" for species.

Comment: For example, the species *Potato spindle tuber viroid*is classified in the genus *Pospiviroid*, and the family *Pospiviroidae*.

3.28

The formal endings for taxa of satellite nucleic acids are the suffixes "-*satellitia*" for realms, "-*satellita*" for subrealms, "-*satellitiae*" for kingdoms, "*-satellitites*" for subkingdoms, "-*satelliticota*" for phyla, "-*satelliticotina*" for subphyla, "-*satelliticetes*" for classes, "*-satelliticetidea*" for subclasses, "-*satellitales*" for orders, "-*satellitineae*" for suborders,"-*satellitidae*" for families, "-*satellitinae*" for subfamilies, and "-*satellite*" for sugenera and genera.

Comment: For example, the species *Ageratum yellow vein betasatellite* is classified in the genus *Betasatellite*, and the family *Tolecusatellitidae*.

Other sub-viral Agents

3.29

Retrotransposons are considered to be viruses in classification and nomenclature

IX - Rules for Orthography

3.30

In formal taxonomic usage, the accepted names of virus, viroid and satellite realms, subrealms, kingdoms, subkingdoms, phyla, subphyla, classes, subclasses, orders, suborders, familes, subfamilies, genera and subgenera are printed in italics and the first letters of the names are capitalized.

Comment: See Rule 3.7 for the definition of an "accepted" name.

3.31

Species names are printed in italics and have the first letter of the first word capitalized. Other words are not capitalized unless they are proper nouns, or parts of proper nouns.

Comment: The species names *Tobacco mosaic virus* and *Murray Valley encephalitis virus* are in the correct form and typographical style. Examples of incorrect forms are Ustilago maydis virus H (not italicized), *Murray valley encephalitis virus* (Valley is a proper noun) or tobacco mosaic virus (not capitalized or italicized).
When taxon names are used informally, italics and capital initial letters are not needed. This applies at all taxonomic levels; examples are: (1) "the tobacco mosaic virus polymerase", when describing the properties of the polymerase in members of the species *Tobacco mosaic virus* and (2) "three pestiviruses", to describe viruses that are members of the genus *Pestivirus*.