This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

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| --- | --- | --- | --- |
| **Code assigned:** | ***2019.006G*** | |  |
| **Short title:** Create a megataxonomic framework, filling all principal taxonomic ranks, for realm *Riboviria* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Koonin EV, Dolja VV, Krupovic M, Varsani A, Wolf YI, Yutin N, Zerbini M, Kuhn JH | | [koonin@ncbi.nlm.nih.gov](mailto:koonin@ncbi.nlm.nih.gov); [doljav@science.oregonstate.edu](mailto:doljav@science.oregonstate.edu); [mart.krupovic@pasteur.fr](mailto:mart.krupovic@pasteur.fr); [Arvind.Varsani@asu.edu](mailto:Arvind.Varsani@asu.edu);  [wolf@ncbi.nlm.nih.gov](mailto:wolf@ncbi.nlm.nih.gov);  [yutin@ncbi.nlm.nih.gov](mailto:yutin@ncbi.nlm.nih.gov);  [zerbini@ufv.br](mailto:zerbini@ufv.br); [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov) | |
| **Corresponding authors** | | | |
| Koonin, Eugene V.; [koonin@ncbi.nlm.nih.gov](mailto:koonin@ncbi.nlm.nih.gov)  Kuhn, Jens H.; [kuhnjens@mail.nih.gov](mailto:kuhnjens@mail.nih.gov) | | | |
| **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) | | **ICTV *Alphatetraviridae*, *Amalgaviridae, Arenaviridae*, *Artoviridae*, *Aspiviridae, Astroviridae*, *Barnaviridae*, *Bornaviridae, Botourmiaviridae*, *Bromoviridae*, *Bunyavirales, Caliciviridae, Carmotetraviridae, Caulimoviridae, Chrysoviridae, Closteroviridae, Cystoviridae, Endornaviridae, Filoviridae, Fimoviridae, Flaviviridae, Hantaviridae, Hepadnaviridae, Hepeviridae, Hypoviridae, Leviviridae, Luteoviridae, Monjiviricetes, Mymonaviridae, Nairoviridae, Narnaviridae, Negarnaviricota, Nidovirales, Nodaviridae, Nyamiviridae, Orthomyxoviridae, Paramyxoviridae, Partitiviridae, Peribunyaviridae, Picobirnaviridae, Phasmaviridae, Phenuiviridae, Picornavirales, Pneumoviridae, Potyviridae, Reoviridae, Retroviridae, Rhabdoviridae, Sobemovirus, Tenuivirus, Togaviridae, Tombusviridae, Tospoviridae, Totiviridae, Tymoviridae, and Virgaviridae* Study Group Chairs, ICTV Bacterial and Archaeal Viruses Subcommittee; ICTV Animal dsRNA and ssRNA- Viruses Subcommittee Chair; ICTV Animal DNA Viruses and Retroviruses Subcommittee Chair; ICTV Plant Viruses Subcommittee Chair; ICTV Fungal and Protist Viruses Subcommittee Chair**  **This is a direct submission to the entire ICTV Executive Committee** | |
| **ICTV Study Group/Author comments (if any) and response of the proposer:** | | | |
| Here we propose a megataxonomic framework for the only currently established viral realm, *Riboviria*, by assigning ICTV-ratified taxa (i.e., species, genera, subfamilies, families, orders, and one phylum) to available, but presently unfilled major megataxonomic ranks (orders, classes, phyla, and kingdoms). The goal of this proposal is to provide taxonomic “buckets” or “place holders” that enable ICTV Study Groups to accommodate the close-to-exponentially increasing number of novel viruses that are related to, but distinct from, viruses that constitute the already established taxa. The awareness of these novel viruses often goes hand-in-hand with the realization that current orders might have to be promoted to orders(e.g., *Reoviridae*) or that entire family structures need to be completely re-evaluated (e.g., *Orthomyxoviridae*). We surmise that the absence of established higher taxa and the absence of ICTV Study Groups for such taxa may have had an adverse effect, leading to large groups of classifiable viruses not becoming classified. Vice versa, placing currently established taxa together into higher-rank taxa may initiate long-overdue, likely intense, discussions between currently non-interacting ICTV Study Groups to examine higher-rank evolutionary relationships of the viruses they are engaged with. The megataxonomy outlined in this proposal is to be seen only as an initial step and we fully expect this framework to change substantially over time.  We:   * aim to bring virus taxonomy into better accordance with other biological taxonomies, which require novel organisms to be classified into all available principle/primary ranks even if this means that certain higher-ranked taxa only include single lower-ranked taxa. For instance, in animal taxonomy, the unranked supergroup Hemimastigophora includes a single class Hemimastigidea, which includes a single order Hemimastigida, which includes a single family Spironem(atelli)idae (which includes 4 genera). Likewise, in prokaryotic taxonomy, the bacterial species *Elusimicrobium minutum* is the only included species in genus *Elusimicrobium*, which is the only genus in family *Elusimicrobiaceae*, which is the only family in order *Elusimicrobiales*—that order is the only order in class *Elusimicrobia*, which is the only class in phylum *Elusimicrobia*. Obviously, taxon demarcation criteria cannot be established for single taxon-including higher-ranked taxa and hence their definitions are identical to those of the higher-ranked taxa for the time being, i.e., until the discovery of novel organisms requires the creation of sister taxa. However, filling all principle ranks provides a sense of “scaling”, i.e. a current assessment of how distant a particular organism is from other classified taxa; this “scaling” argument was used successfully previously in TaxoProps establishing the availability of taxonomic ranks above order and the establishment realm *Riboviria*; * deliberately propose the creation of higher-ranked taxa that currently include only single lower-ranked taxa, either because we are aware from the literature that an existing lower-rank taxon will have to be promoted to a higher rank in the near future due to overbearing virus diversity (e.g., *Reoviridae*), or because we are aware from the literature of large virus groups for which higher-rank taxa will have to be established shortly (e.g., “weiviruses”/“yanviruses”/”zhaoviruses”); we hope that the created higher-ranked taxa will provide an impetus for the community to classify already known highly divergent virus groups; * deliberately did not fill any secondary (sub-)ranks as the filling of such ranks is not mandatory in other biological taxonomies; * deliberately focus this proposal only on official taxa (rather than, for instance, proposing novel species that could become the founding members of “obvious” novel higher-rank taxa we are certain will need to be established) to keep this proposal relatively simple; * emphasize that, although we posit that RNA-directed RNA polymerase (RdRp)/RNA-directed DNA polymerases/reverse transcriptase (RTs) phylogenies are initially sufficient for creation of RNA virus megataxonomy (from the highest rank, realm, down to approximately class/order), such a focus must be seen as a rough guide for lower-rank taxonomy, so that other methods (e.g., sequence-based methods such as GRAViTy, pairwise genome sequence comparisons, phylogenies of individual ORFs or proteins; structural comparisons of encoded proteins or virions; phenotypic virus characteristics) will have to be used to resolve lower-rank relationships and likely to refine higher-rank relationships. | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 19, 2019 |
| Date of this revision (if different to above): | | | October 18, 2019 |

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| --- |
| **ICTV-EC comments and response of the proposer:** |
| Per the minutes of the last ICTV Executive Committee meeting (EC51, July 15–17, 2019, Berlin, Germany), the EC voted for minor revisions of this proposal (Uc) with 12/19 votes in favor. The EC asked for the following steps to be taken prior to submission of this revision:   1. Consult all affected Study Group once again for feedback   Response: all relevant Study Group Chairs were contacted for a second time and asked to provide input and criticisms. None of the Study Groups disagreed with the overall taxonomic proposal, i.e., the proposed relationship between officially established taxa. Concerns were voiced about certain proposed taxon names and the Study Groups’ suggestion were mostly followed and names were changed accordingly for this revision.   1. Provide any feedback from Study Groups to the ICTV President   Response: all relevant Study Group responses (and all TaxoProp author rebuttals or explanations) were forwarded to the ICTV President and the ICTV Executive Committee per email.   1. Regarding proposed taxon names using people’s names, provide permissions from these people (if alive) to use their names to the ICTV President and the ICTV Proposals Secretary   Response: all relevant permissions were forwarded to the ICTV President, the ICTV Proposal Secretary, and the ICTV Executive Committee per email.   1. Several ICTV Executive Committee members correctly pointed out that are paraphyletic clades within the realm, in particular the dsRNA virus clades in Branches 4–5.   Response: This issue had already been discussed in the literature [[24](#_ENREF_24)]: this issue indeed needs to be resolved in the near future, but while the RdRp-tree suggests Branches 4 and 5 to be one clade rather than 2, the fundamentally different genomic organization of the dsRNA viruses compared to those in phylum *Negarnaviricota* and the conservation of the dsRNA virus CP structure and capsid organization, with 60 homo- or heterodimers of the CP organized on an unusual, so-called pseudo T=2 lattice, justifies, at least for now, to separate these two supergroups until further analysis are done using different genes and protein. One solution to this issue would be to create multiple phyla for dsRNA viruses (i.e., to dissolve Branch 4 into three separate branches/phyla), but this solution was considered too excessive by the coauthors at this point in time.   1. Several ICTV Executive Committee members requested Figure 1 to be replaced with a new version showing expanded branches.   Response: done. |

**Part 3:** **PROPOSED TAXONOMY**

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| **Name of accompanying Excel module:** 2019.006G.A.v1.Riboviria.xlsx |

**INTRODUCTION**

Recent advances of comparative genomics and metagenomics uncover a close-to-exponentially increasing number of diverse viruses. These discoveries not only vastly improve our understanding of the evolutionary relationships within the virosphere, but also emphasize that the existing taxonomic framework is inadequate to depict the relationships within the virosphere. The currently available dataset of virus genome sequences and increasingly sophisticated methods for analysis beyond “simple” phylogenies (e.g., gene network analysis, iterative and self-optimizing sequence alignments) enable us now to roughly outline the global organization of the virus world in its entirety, including key evolutionary events that resulted in the emergence of major virus clades.

Depicting the evolutionary relationships among viruses necessarily depends on the identification of hallmark genes/proteins that connect them. In contrast to cellular organisms, such hallmark genes are not universally shared among all viruses [[9](#_ENREF_9)] and it is therefore currently presumed that viruses have several distinct points of origin, i.e., that they cannot be united under a single highest taxon rank on evolutionary grounds. Nevertheless, extensive analyses of the evolution of large groups of viruses, rather than all of them, have proved productive. The primary approach taken in such studies is the phylogenetic analysis of genes that are conserved across those groups, known as Virus Hallmark Genes (VHGs), which are responsible for the key functions in virus replication and virion morphogenesis [[9](#_ENREF_9)]. The most widely spread VHGs are:

* RNA-directed RNA polymerases (RdRps);
* RNA-directed DNA polymerases/reverse transcriptases (RTs) that are homologous to RdRps;
* superfamily 3 helicases (S3Hs);
* single jelly-roll major capsid proteins (SJR-MCPs);
* double jelly-roll major capsid proteins (DJR-MCPs); and
* rolling-circle replication initiation endonucleases (RCREs) [[9](#_ENREF_9), [11](#_ENREF_11), [12](#_ENREF_12)].

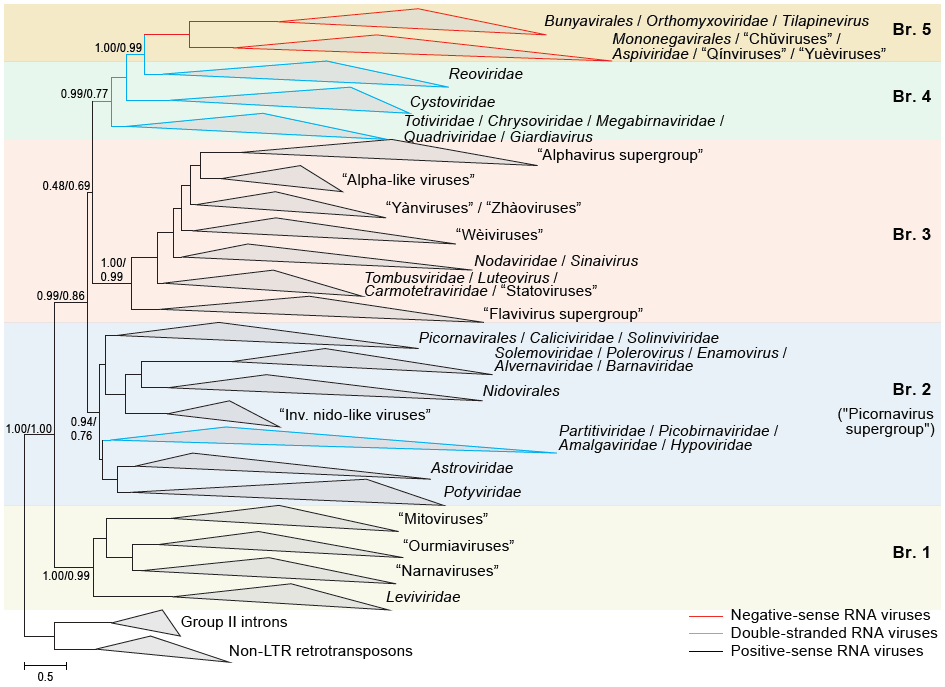
Using these VHGs, megataxonomic scaffolds can be established that are further informed, if necessary, by dissection of bipartite gene-genome networks of viruses into distinct modules [[4-6](#_ENREF_4), [10](#_ENREF_10), [21](#_ENREF_21)]. These analyses indicate that a substantial majority of currently classified viruses can be assigned to one of four, likely, evolutionarily independent virus realms. Because the International Committee on Taxonomy of Viruses (ICTV) has recently formally approved creation of taxa above the rank of order, the door is now open to formalize the megataxonomic scaffolds that resulted from VHG analyses within the official ICTV-supported taxonomy.

Here we propose a megataxonomic structure for one of these groups: RNA and reverse-transcribing viruses.

**MEGATAXONOMY OF *Riboviria***

Recently, all currently classified RNA viruses have been formally unified in a realm (*Riboviria*), the now highest officially available taxon rank supported by the ICTV [[22](#_ENREF_22)]. The establishment of this realm was based on the realization that a) ranks higher than order will be needed to appropriately classify the increasing number of RNA viruses and b) on the logical need that any classification scheme needs to have a top and bottom between which all ranks must be situation (“crown of the tree”/species, “root of the tree”/realm) [[5](#_ENREF_5)](TaxoProps 2017.006G by Gorbalenya *et al*.; and 2017.005G by Gorbalenya *et al*.). However, the creation of the realm was also justified because all then-classified RNA viruses could be connected via their major VHG encoding an RdRp or RT [[6](#_ENREF_6), [7](#_ENREF_7)]. One phylum, *Negarnaviricota*, was included in the realm encompassing all negative-sense RNA viruses with the exception of hepatitis D virus [[13](#_ENREF_13), [22](#_ENREF_22)]. However, this phylum was not assigned to a kingdom, and all other RNA viruses were not assigned to any higher rank.

Comparison of RdRp/RT sequences and of the structures of these polymerases from diverse RNA viruses and retroelements revealed the monophyly of these enzymes [[24](#_ENREF_24), [26](#_ENREF_26)]. The RdRp/RT phylogenetic trees, in which the most highly conserved RTs (group II introns) are included as the outgroup, have a well-defined structure that were published previously [[24](#_ENREF_24), [25](#_ENREF_25)]. The monophyly of the two main groups (RdRp viruses and RT viruses, here proposed to be kingdoms) and the five RdRp branches (here proposed to be phyla) is strongly supported by the used sequence data analysis [[24](#_ENREF_24)] (Figures 1 and 2), whereas the relationships between the branches are much less clear.



**Figure 1.** Phylogeny of RdRps of RNA viruses (*Riboviria*, proposed kingdom *Orthornavirae*): each of the 5 main branches (proposed to represent 5 distinct phyla) represents collapsed sequences of the corresponding set of RdRps (for details and methods see [[24](#_ENREF_24)]).

**RdRp VIRUSES (PROPOSED KINGDOM *Orthornavirae*)**

**Branch 1 (proposed phylum *Lenarviricota*)**

Branch 1 is dominated by RdRps of prokaryotic (+)RNA viruses assigned to the *Leviviridae* and a dramatically increasing number of levivirid-like viruses, plus their apparent descendants that infect eukaryotes (viruses currently classified in *Botourmiaviridae* and *Narnaviridae* and their immediate relatives that already outnumber classified viruses). Based on the phylogenetic tree, we propose the creation of four classes for levivirids and relatives, narnaviruses and relatives, mitoviruses and relatives (removed from *Narnaviridae*), and botourmiavirids and relatives, respectively.

**Branch 2 (proposed phylum *Pisuviricota*)**

Branch 2 of the RdRp tree represents what is sometimes referred to as the “picornavirus supergroup” [[4](#_ENREF_4), [7-9](#_ENREF_7)], which includes the large established orders *Nidovirales* and *Picornavirales*. The most notable features of this branch is the interleaving of a clade of bipartite dsRNA viruses that includes *Partitiviridae* and (likely prokaryotic) *Picobirnaviridae* embedded among (+)RNA viruses [[24](#_ENREF_24)], and the inclusion of *Amalgaviridae*, a family of dsRNA viruses infecting plants and protists that encode an RdRp confidently affined with that of partitivirids but a capsid protein derived from nucleocapsid proteins of (-)RNA viruses of the *Phenuiviridae* [[10](#_ENREF_10)]. Based on the phylogenetic tree, we propose the creation of three classes for 1) *Picornavirales* (now including *Caliciviridae* and *Solinviviridae*), *Nidovirales*, *Alvernaviridae*, *Barnaviridae*, and *Solemoviridae*, 2) *Astroviridae* and *Potyviridae*, and 3) *Amalgaviridae*, *Hypoviridae*, *Partitiviridae*, and *Picobirnaviridae*.

**Branch 3 (proposed phylum *Kitrinoviricota*)**

Branch 3 of the RdRp tree consists of eukaryotic (+)RNA viruses representing what are often referred to as the “alphavirus supergroup” and “flavivirus supergroup” [[3](#_ENREF_3), [7](#_ENREF_7), [8](#_ENREF_8)]. Apart from these supergroups, Branch 3 includes *Tymovirales* and an assortment of lineages that all represent short-genome viruses, such as *Nodaviridae* and *Tombusviridae*. Based on the phylogenetic tree, we propose the creation of four classes for 1) “flavivirus supergroup”: *Flaviviridae* and their rapidly increasing number of relatives, 2) *Carmotetraviridae*, *Luteoviridae*, and *Tombusviridae*, 3) *Nodaviridae* and *Sinaivirus*, and 4) “alphavirus supergroup”: *Tymovirales*, *Alphatetraviridae*, *Benyviridae*, *Bromoviridae*, *Closteroviridae*, *Endornaviridae*, *Hepeviridae*, *Kitaviridae*, *Matonaviridae*, *Mayoviridae* (proposed), *Togaviridae*, and *Virgaviridae*.

**Branch 4 (proposed phylum *Duplornaviricota*)**

Branch 4 of the RdRp tree exclusively represents dsRNA viruses. Apart from the RdRp tree topology, the key evidence that supports the monophyly of dsRNA viruses in Branch 4 is the conservation of the CP structure and capsid organization, with 60 homo- or heterodimers of the CP organized on an unusual, so-called pseudo T=2 lattice [[15](#_ENREF_15), [17](#_ENREF_17)]. Notably, this branch also includes the viruses of the family *Cystoviridae*, the only known dsRNA viruses that infect prokaryotes [[16](#_ENREF_16)]. Based on the phylogenetic tree, we propose the creation of three classes for 1) *Chrysoviridae*, *Megabirnaviridae*, *Quadriviridae*, and *Totiviridae*, 2) *Cystoviridae*, and 3) *Reoviridae*.

**Branch 5 (*Negarnaviricota*)**

This phylum is already established.

**RT VIRUSES (PROPOSED KINGDOM *Pararnavirae*)**

The phylogenetic tree of RTs consists of five major branches, four of which include non-viral retroelements [[2](#_ENREF_2), [12](#_ENREF_12)]. The remaining, strongly supported branch encompasses all RT viruses, which appear to have evolved from retrotransposons on a single occasion. The RT virus branch consists of four clades represented by currently established virus families: 1) *Caulimoviridae*/*Metaviridae*/*Retroviridae*, 2) *Belpaoviridae*, 3) *Pseudoviridae*, and 4) *Hepadnaviridae* (Figure 2) [[12](#_ENREF_12), [14](#_ENREF_14)].

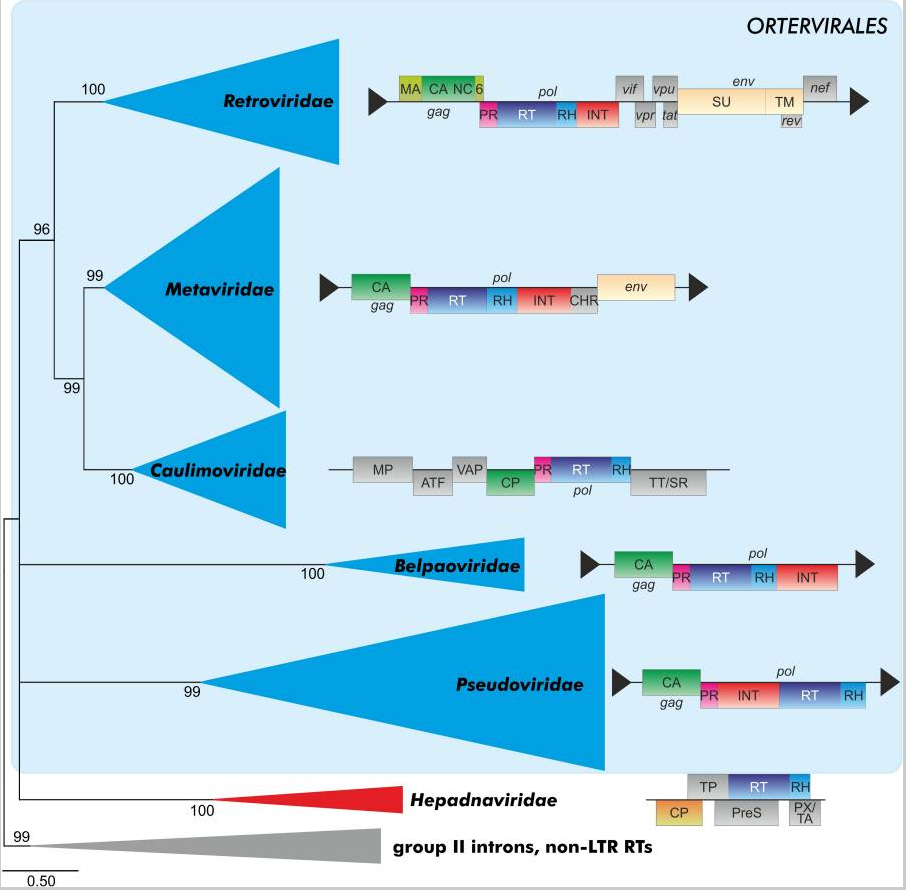


Figure 2. Maximum-likelihood phylogeny of virus RTs (for details and methods see [[12](#_ENREF_12)]).

The genomes of viruses in all these families, except for hepadnavirids, share not only the RT gene but also genes encoding two core virion components, the capsid protein and nucleocapsid proteins (the latter apparently lost in spumaretrovirins) [[11](#_ENREF_11)]. Because belpaovirids, caulimovirids (with dsDNA genomes), metavirids, pseudovirids, and retrovirids also share the same mechanism of replication priming, they already have been grouped in an order, *Ortervirales* [[12](#_ENREF_12)]. In contrast, hepadnavirids use a protein-priming mechanism that is mediated by the terminal protein domain of the RT [[14](#_ENREF_14)]. Although hepadnavirids package dsDNA genomes into their virions and have capsid proteins unrelated to those of *Ortervirales*, the monophyly of all viruses in the RT tree supports the grouping of ortervirals with hepadnavirids (proposed class *Revtraviricetes* included in proposed phylum *Artverviricota*).

This proposal is to be considered as an operational move to formalize an obvious relationship between the mentioned DNA viruses based on common VHGs.

**VIRUSES OF UNCLEAR AFFILIATION**

Until additional genomic data are acquired and detailed analyses are performed, we propose not to assign genus *Deltavirus* to the realm *Riboviria*; to keep taxa *Albetovirus*, *Aumaivirus*, *Papanivirus*, *Sarthroviridae*, and *Virtovirus* unassigned to higher-ranked taxa within realm *Riboviria*; and to assign *Birnaviridae*, *Botybirnavirus*, *Permutotetraviridae*, and *Polymycoviridae* [proposed] to kingdom *Orthornavirae* but to leave them unassigned to higher ranks within this kingdom.

**Taxon demarcation criteria:**

The International Code of Virus Classification and Nomenclature (ICVCN) is currently ambiguous regarding the need for taxon demarcation criteria at higher ranks. Three Rules appear to be applicable (emphasis in italics is ours):

“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*”;

“3.22 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*”;

and

“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*”

Because our proposal only encompasses already established taxa, all viruses affected by our proposal have been “sufficiently well characterized” as otherwise they would not have been classified into these established taxa in the first place. Furthermore, Rule 3.22 permits establishing ranks that for the moment remain undefined; and Rule 3.24 indicates no restriction of ranks to be established.

Overall, the taxon demarcation of high taxonomic ranks (order rank or higher) is for now defined by the phylogenetic trees. In addition, for the time being, we suggest the following additional provisional taxon demarcation criteria for some major taxa while being aware that these may have to be revisited whenever new members of the realm are being proposed:

1. *Riboviria*: a virus is a member of this realm if encodes an RT or an RdRp
2. *Orthornavirae*: a *Riboviria* member is a member of included kingdom *Orthornavirae* if it has an RNA genome and encodes an RdRp
3. *Lenarviricota*: an *Orthornavirae* member is a member of included phylum *Lenarviricota* if it has a positive-sense RNA genome and infects prokaryotes, and does not cluster in RdRp trees with members of *Kitrinoviricota*
4. *Pisuviricota*: an *Orthornavirae* member is a member of included phylum *Pisuviricota* if it has a positive-sense or double-stranded RNA genome and does not infect prokaryotes
5. *Kitrinoviricota*: an *Orthornavirae* member is a member of included phylum *Kitrinoviricota* if it has a positive-sense, does not infect prokaryotes, and does not cluster in RdRp trees with members of *Pisuviricota*
6. *Duplornaviricota*: an *Orthornavirae* member is a member of included phylum *Duplornaviricota* if it has a double-stranded RNA genome, infect prokaryotes or eukaryotes, does not cluster with members of *Pisuviricota*, and encodes a capsid composed of 60 homo- or heterodimers of capsid protein organized on an unusual, so-called pseudo T = 2 lattice
7. *Negarnaviricota*: an *Orthornavirae* member is a member of included phylum *Negarnaviricota* if it has a negative-sense RNA genome
8. *Pararnavirae*: a *Riboviria* member is a member of included kingdom *Orthornavirae* if it encodes an RT
9. *Blubervirales*: a *Pararnavirae* member is a member of included order *Blubervirales* if it does not use tRNA molecules as primers for reverse transcription as members of order *Ortervirales*, but uses a protein-priming mechanism that is mediated by the terminal protein domain of the RT

If a principle rank taxon includes only a single lower-ranked taxon, then the definition of the lower-ranked taxon is, for now, identical to the definition of the higher-ranked taxon.

Truly useful taxon demarcation criteria will have to be established in the future, likely by incorporating yet-unclassified virus groups into the realm.

**ETYMOLOGY OF PROPOSED TAXA**

* *Orthornavira**e*; from Greek ὀρθός [orthós] meaning straight; and the suffix -*virae* for kingdom taxa
* *Lenarviricota*; a portmanteau of *Leviviridae* and *Narnaviridae*; and the suffix -*viricota* for phylum taxa
* *Allassoviricetes*; from Greek αλλάσσω [allásso] meaning mutate (a reference to the high mutation rate of levivirids); and the suffix -*viricetes* for class taxa
* *Levivirales*; after *Leviviridae*, assuming that *Leviviridae* will have to promoted shortly to accommodate the rapidly expanding diversity of this taxon; and the suffix -*virales* for order taxa
* *Howeltoviricetes*; after Howell Township, New Jersey, USA, where a fungus (*Cryphonectria parasitica*) was isolated that was infected with the type mitovirus, [[19](#_ENREF_19)]; and the suffix -*viricetes* for class taxa
* *Cryppavirales*; a portmanteau of *Cryphonectra parasitica*, the species of the fungus in which the first mitovirus was discovered; and the suffix -*virales* for order taxa
* *Mitoviridae*; after *Mitovirus*; and the suffix -*viridae* for family taxa
* *Miaviricetes*; from ourmiavirus; and the suffix -*viricetes* for class taxa
* *Ourlivirales*; a portmanteau of ourmiavirus-like; and the suffix -*virales* for order taxa
* *Amabiliviricetes*; after Zulu amabili meaning twenty, a reference to W/20S RNA of baker’s yeast (*Saccharomyces cerevisiae*), which turned out to be an RNA-directed RNA polymerase [[18](#_ENREF_18), [20](#_ENREF_20)]); and the suffix -*viricetes* for class taxa
* *Wolframvirales*; a tongue-in-cheek reference to the element wolfram, which is abbreviated W: the type narnavirus was found after sequencing “W dsRNA” in baker’s yeast (*Saccharomyces cerevisiae*); and the suffix -*virales* for order taxa
* *Pisuviricota*; a portmanteau of “picornavirus supergroup”; and the suffix -*viricota* for phylum taxa
* *Pisoniviricetes*; a portmanteau of the names of the founding orders (*Picornavirales*, *Sobelivirales*, *Nidovirales*); and the suffix -*viricetes* for class taxa
* *Sobelivirales*: a portmanteau of sobemovirus-like; and the suffix -*virales* for order taxa
* *Stelpaviricetes*; a portmanteau of the names of the founding orders (*Stellavirales*, *Patatavirales*); and the suffix -*viricetes* for class taxa
* *Patatavirales*; from Italian patata meaning potato, a reference to potato virus Y; and the suffix -*virales* for order taxa
* *Stellavirales*; from Latin stella meaning star (a reference to astroviruses—astro also means star); and the suffix -*virales* for order taxa
* *Duplopiviricetes*; from Italian duplo meaning double (a reference to double-stranded RNA) and the first two letters of picobirnaviruses; and the suffix -*viricetes* for class taxa
* *Durnavirales*; from Italian duplo meaning double (a reference to double-stranded RNA) and RNA; and the suffix -*virales* for order taxa
* *Kitrinoviricota*; after Greek κίτρινος [kítrinos] meaning yellow, a reference to yellow fever virus; and the suffix -*viricota* for phylum taxa
* *Flasuviricetes*; a portmanteau of “flavivirus supergroup”; and the suffix -*viricetes* for class taxa
* *Amarillovirales*; from Spanish amarillo meaning yellow, a reference to yellow fever virus; and the suffix -*virales* for order taxa
* *Tolucaviricetes*; a portmanteau of tombusviruses, luteoviruses, and carmotetraviruses; and the suffix -*viricetes* for class taxa
* *Tolivirales*; a portmanteau of tombusvirus-like; and the suffix -*virales* for order taxa
* *Magsaviricetes*; from Mag 115, the original designation of Nodamura virus, and Saitama Prefecture, Japan, where studies were performed that led to the discovery of Mag 115/Nodamura virus [[21](#_ENREF_21)] ; and the suffix -*viricetes* for class taxa
* *Nodamuvirales*; a contraction of Nodamura virus; and the suffix -*virales* for order taxa
* *Sinhaliviridae*; a portmanteau of *Sinaivirus* and *Halictivirus*; and the suffix -*viridae* for family taxa
* *Alsuviricetes*; a portmanteau of “alphavirus supergroup”; and the suffix -*viricetes* for class taxa
* *Martellivirales*; a reference to G. P. Martelli, a pioneer in closterovirid research, and a long-time ICTV EC Member and two-mandate ICTV Plant Virus SC Chair; and the suffix -*virales* for order taxa
* *Hepelivirales*; a portmanteau of hepevirus-like; and the suffix -*virales* for order taxa
* *Duplornaviricota*; from Italian duplo meaning double (a reference to double-stranded RNA) and RNA; and the suffix -*viricota* for phylum taxa
* *Chrymotiviricetes*: a portmanteau of chrysovirus, megabirnavirus, and totivirus; and the suffix -*viricetes* for class taxa
* *Ghabrivirales*; in honor of the late Said Ghabrial†, a pioneer in study of the viruses in this order and former ICTV Subcommittee Chair for Fungal and Protist viruses; and the suffix -*virales* for order taxa
* *Vidaverviricetes*; in honor of Anne K. Vidaver, who co-discovered Pseudomonas phage phi6 [[23](#_ENREF_23)]; and the suffix -*viricetes* for class taxa
* *Mindivirales*; a reference to Leonard Mindich, who contributed significantly to cystovirid research; and the suffix -*virales* for order taxa
* *Resentoviricetes*; derived from respiratory enteric orphan (also the phrase that gave rise to the word stem reo in reoviruses); and the suffix -*viricetes* for class taxa
* *Reovirales*; after *Reovirales*, assuming that *Reoviridae* will have to promoted shortly to accommodate the rapidly expanding diversity of this taxon; and the suffix -*virales* for order taxa
* *Pararnavirae*; from Greek παρά [pará] meaning besides/next to and RNA; and the suffix -*virae* for kingdom taxa
* *Artverviricota*; a portmanteau of reverse transcriptase read backwards; and the suffix -*viricota* for phylum taxa
* *Revtraviricetes*; a portmanteau of reverse transcriptase; and the suffix -*viricetes* for class taxa
* *Blubervirales*; in honor of Barry Blumberg† for his role in hepatitis B research [[1](#_ENREF_1)]; and the suffix -*virales* for order taxa

Three of the proposed taxon names, *Martellivirales*, *Vidaverviricetes,* and *Mindivirales* are derived from the names of living persons. The permissions of these persons to use their names have been forwarded to the ICTV Executive Committee.

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