

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

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| **Code assigned:** | **2022.004F** |  |
| **Short title:** Create 3 new families, 3 subfamilies, 13 genera, and 20 new species within the order *Imitervirales* (phylum *Nucleocytoviricota*) and rename two existing species.  |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Fungal and Protist Viruses SC Chair |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

|  |  |
| --- | --- |
| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| SG *Imitervirales* | 7 | 0 | 0 |
|  |  |  |  |

**Authority to use the name of a living person**

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| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | May 16th, 2022 |
| Date of this revision (if different to above) | September 23rd, 2022 |

**ICTV-EC comments and response of the proposer**

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| ICTV-EC Comments:1. Please change name of the proposed genus “Cronusvirus” (already exist taxon with identical name of prokaryotic viruses in the class *Caudoviricetes,* as well as another taxon named *“Cronosvirus”*)
2. Please consider proposed minor changes in species names.
3. Please adjust irregularities in the Excel file.

Authors response:All three recommendations/suggestions were addressed in this and accompanying Excel files.  |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2022.004F.N.v2.Imitervirales\_reorg.xlsx |

**Abstract**

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| “Giant viruses” within the order *Imitervirales* have been the subject of intense study over the last decade, but currently only two members of this order are formally classified by ICTV. The creation of several new taxonomic ranks is therefore warranted in order to capture the high level of diversity within this group. We propose the creation of 3 new families, 3 subfamilies, 13 genera, and 20 species within the order *Imitervirales*. We propose binomial names for all new species and rename two existing species. The new families, subfamilies, genera, and species are all consistently defined within a phylogenetic framework that has recently been proposed [8].  |

**Text of proposal**

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| Large dsDNA viruses belonging to the phylum *Nucleocytoviricota*, often referred to as “giant viruses”, include the largest viruses that have yet been characterized, both in terms of virion size and genome length [[1]](https://paperpile.com/c/GI5oRD/e1e7). Of particular interest are viruses in the order *Imitervirales*, which are particularly abundant and widespread in ecosystems around the globe [[2–5]](https://paperpile.com/c/GI5oRD/ixn8%2BZvDT%2B6vpN%2BCFfW). Despite their importance, only two members of the *Imitervirales* are currently classified: Acanthamoeba polyphaga mimivirus (APMV) and Cafeteria roenbergensis virus (CroV). These viruses belong to two homonymous species, both classified in the family *Mimiviridae*, but a large number of recently-characterized members of the *Imitervirales* are only distantly related to either APMV or CroV, and these viruses are sometimes referred to as “extended *Mimiviridae*” or “extended family *Mimiviridae*” [[6–8]](https://paperpile.com/c/GI5oRD/vFeK%2BjELY%2BKUPs). There is therefore an urgent need to update the taxonomy of the *Imitervirales* by establishing new species, genera, subfamilies and families to encompass current diversity of these viruses. To this end we analyzed 43 *Imitervirales* genomes using both a concatenated phylogenetic approach (Figure 1) and by examining pairwise average nucleotide identity (ANI; Figures 2 and 3)). The concatenated tree is based on 7 marker genes: DNA polymerase family B (PolB), RNA polymerase large subunit (RNAPL), A32-like packaging enzyme (A32), Topoisomerase family II (TopoII), Virus Late Transcription Factor 3 (VLTF3), Transcription Factor IIB (TFIIB), and a superfamily II helicase (SFII). These marker genes have previously been benchmarked and shown to provide high fidelity phylogenetic trees of the *Nucleocytoviricota* [[9]](https://paperpile.com/c/GI5oRD/Ilwk). Families, subfamilies, and genera are demarcated such that they have approximately equivalent phylogenetic depths (i.e., distance from the root). We only propose classification of viral isolates here, but for our concatenated phylogenetic approach we also included metagenome-derived viral genomes. This was done to improve phylogenetic reconstruction by providing additional evolutionary context and to avoid long branches that arise when only isolates are used. For this purpose a manually-selected set of metagenome-derived genomes were taken from the Giant Virus Database (<https://faylward.github.io/GVDB/>).**Guidelines used for new names:**Proposed family names have the “-mimiviridae” suffix to denote evolutionary relatedness to the *Mimiviridae* (*Allomimiviridae, Mesomimiviridae, Schizomimiviridae*). Proposed subfamily names are either based on names commonly used in the literature (*Megamimivirinae, Klosneuvirinae*) or use a simple Latin prefix (*Aliimimivirinae*; alii- Latin for “other”). Subfamilies are proposed for the family *Mimiviridae* only because the most viral isolates are available for this family. For species we adopted Latinized binomial names. Genus names refer to the names of Titans in Greek mythology (*Biavirus, Kratosvirus, Heliosvirus, Oceanusvirus, Rheavirus, Tethysvirus*, and *Theiavirus*) unless another genus name was already in common usage in the literature (*Megavirus*, *Moumouvirus, Fadolivirus, Yasminevirus, Cotonvirus*, and *Tupanvirus*). The species epithet in the binomial name refers to features or geography where viruses were sampled or isolated (i.e., *sinusmexicanus* denoting isolation from the Gulf of Mexico). For consistent use of binomial names, we also propose renaming species for classifying APMV and CroV to *Mimivirus bradfordmassiliense* and *Rheavirus sinusmexicani*, respectively. A full list of all proposed binomial names can be found in Table 1.**Proposed Families:****Family *Allomimiviridae***“Allo-“ from Greek allos "other, different". This family contains two monospecific genera to classify species *Heliosvirus raunefjordenense* and *Oceanusvirus keneoense*. Members of both species are marine viruses that infect green algae (*Pyramimonas orientalis* and *Tetraselmis* sp. respectively). The name denotes broad phylogenetic affinity of this family for the *Mimiviridae*.**Family *Schizomimiviridae***“Schizo-” from Greek schizo, “split”. This family contains *Biavirus raunefjordenensis* and *Kratosvirus quantuckense* classified in two new genera. Member viruses are found in marine environment infecting haptophyte or heterokont hosts, respectively. The name refers to the common description of these viruses as “extended *Mimiviridae*”.**Family *Mesomimiviridae***“Meso-“ from Greek mesos, “middle”. This family contains the three species *Tethysvirus hollandense, T. ontarioense*, and *T. raunefjordenense*, represented by aquatic viruses that infect haptophytes. These viruses form a highly-supported monophyletic clade in our concatenated phylogeny, and we therefore propose that they should be classified in the same genus. The name refers to the previous description of these viruses as “extended *Mimiviridae*”. This lineage was previously suggested to be a subfamily within the *Mimiviridae* with the name *Mesomimivirinae* [[6]](https://paperpile.com/c/GI5oRD/vFeK)*,* but analysis of the concatenated phylogeny demonstrates that this group can be clearly distinguished from the *Mimiviridae* and that a new family-level rank is therefore appropriate (Figure 1). **Proposed Subfamilies**We also propose reorganization within the *Mimiviridae* by addition of three subfamilies, which form highly-supported clades of approximately the same phylogenetic depth. The literature often refers to subfamilies “*Megamimivirinae”* and “*Klosneuvirinae”*, and we therefore feel it is appropriate to formalize these names and also introduce the *Aliimimivirinae* such that consistent reference can be made to all sub-clades within this family.**Subfamily *Megamimivirinae*:**This subfamily includes all members of the genera *Tupanvirus, Cotonvirus, Mimivirus, Megavirus*, and *Moumouvirus*, all of which infect amoeba. The name is already used frequently in the literature (e.g. [[6]](https://paperpile.com/c/GI5oRD/vFeK)). **Subfamily *Klosneuvirinae*:**This subfamily contains three species *Fadolivirus algeriomassiliense, Yasminevirus saudimassiliense*, and *Theiavirus salishense* represented by fadolivirus, yasminevirus and Bodo saltans virus. The first two of these infect amoebal hosts, while the third infects a kinetoplastid phagotrophic protozoon (*Bodo saltans*). The name of the subfamily is already used frequently in the literature (e.g. [[10]](https://paperpile.com/c/GI5oRD/ydP3)). **Subfamily *Aliimimivirinae*:**“Alii-”, Latin for “other”. This subfamily contains species *Rheavirus sinusmexicani* to classify Cafeteria roenbergensis virus (CroV) which infects a bicosoecid phagotrophic protozoon (*Cafeteria roenbergensis*). **Demarcation Criteria**Members of the same species have pairwise ANI > 95% for >75% of the predicted genes in each genome. Accordingly, the species *Mimivirus bradfordmassiliense*, *Moumouvirus moumou*, *Megavirus chilense,* and *Tethysvirus hollandense* contain multiple viral isolates that fit these criteria (Table 1, Figures 2 and 3).Families and genera are defined as monophyletic clades in the concatenated tree that have high bootstrap support (>80%) and approximately equivalent phylogenetic depth (Figure 1). Our family-level demarcations are consistent with a phylogenomic framework that has recently been proposed [[9]](https://paperpile.com/c/GI5oRD/Ilwk).The phylogenetic methodology should be adequate for adding new taxonomic levels in the future. Although it relies on 7 marker genes (PolB, A32, SFII, VLTF3, RNAPS, TopoII, and TFIIB), genomes can be included even if they encode only a subset of these genes. For example, prasinoviruses that lack RNA polymerase subunits were still included in these phylogenetic approaches, and they had robust phylogenetic placement [8]. Therefore, novel viral lineages discovered in the future could still be included using these methods even if their genomic composition differed from the viruses examined here. |

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**Supporting evidence**

**Table 1.** Proposed taxonomy

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| **Family** | **Subfamily** | **Genus** | **Species** | **Virus Isolate** | **NCBI Access.** |
| *Allomimiviridae* | *-* | *Heliosvirus* | *Heliosvirus raunefjordenense* | Pyramimonas orientalis virus 01B | MT663534:MT663543 |
| *-* | *Oceanusvirus* | *Oceanusvirus kaneohense* | Tetraselmis virus 1 | KY322437 |
| *Mesomimiviridae* | *-* | *Tethysvirus* | *Tethysvirus hollandense* | Phaeocystis globosa virus PgV-16T | KC662249 |
| Phaeocystis globosa virus PgV-12T | HQ634147 |
| Phaeocystis globosa virus PgV-14T | HQ634144 |
| *Tethysvirus ontarioense* | Chrysochromulina parva virus BQ2 | MH918795 |
| *Tethysvirus raunefjordenense* | Chrysochromulina ericina virus CeV-01B | KT820662 |
| *Mimiviridae* | *Aliimimivirinae* | *Rheavirus* | *Rheavirus sinusmexicani* | Cafeteria roenbergensis virus BV-PW1 | GU244497 |
| *Klosneuvirinae* | *Fadolivirus* | *Fadolivirus algeromassiliense* | Fadolivirus FV1/VV64 | MT418680 |
| *Theiavirus* | *Theiavirus salishense* | Bodo saltans virus strain NG1 | MF782455 |
| *Yasminevirus* | *Yasminevirus saudimassiliense* | Yasminevirus sp. GU-2018 | UPSH01000001  |
| *Megamimivirinae* | *Cotonvirus* | *Cotonvirus japonicum* | Cotonvirus japonicus | AP024483 |
| *Megavirus* | *Megavirus boshanense* | Megavirus baoshan strain SH | MH046811 |
| *Megavirus chilense* | Megavirus chilensis | JN258408 |
| Megavirus lba isolate LBA111 | JX885207 |
| Megavirus terra1 genome | KF527229 |
| Megavirus courdo11 | JX975216 |
| Acanthamoeba polyphaga mimivirus ASM381511v1 | MG602508 |
| Acanthamoeba polyphaga mimivirus ASM381513v1 | MG602507 |
| Megavirus vitis isolate vigne | MG807319 |
| *Megavirus powaiense* | Powai lake megavirus isolate 1 | KU877344 |
| *Mimivirus* | *Mimivirus bradfordmassiliense* | Acanthamoeba polyphaga mimivirus ViralProj60053 | HQ336222 |
| Mimivirus terra2 genome | KF527228 |
| Acanthamoeba castellanii mamavirus Hal-V | JF801956 |
| Acanthamoeba castellanii mimivirus kasaii | AP017644 |
| Acanthamoeba castellanii mimivirus shirakomae | AP017645 |
| Acanthamoeba polyphaga mimivirus M4 | JN036606 |
| Acanthamoeba polyphaga mimivirus Oyster | KM982401 |
| Acanthamoeba polyphaga mimivirus | AY653733 |
| Hirudovirus strain Sangsue | KF493731 |
| Mimivirus Bombay isolate 1 | KU761889 |
| Niemeyer virus | KT599914 |
| Samba virus | KF959826 |
| Acanthamoeba polyphaga mimivirus strain Amazonia | KM982403 |
| *Mimivirus lagoaense* | Acanthamoeba polyphaga mimivirus Kroon | KM982402 |
| *Moumouvirus* | *Moumouvirus australiense* | Moumouvirus australiensis isolate 10A | MG807320 |
| *Moumouvirus goulettemassiliense* | Moumouvirus goulette | KC008572 |
| *Moumouvirus moumou* | Acanthamoeba polyphaga moumouvirus | JX962719 |
| Saudi moumouvirus | KY110734 |
| *Tupanvirus* | *Tupanvirus altamarinense* | Tupanvirus deep ocean | MF405918 |
| *Tupanvirus salinum* | Tupanvirus soda lake | KY523104 |
| *Schizomimiviridae* | *-* | *Biavirus* | *Biavirus raunefjordenense* | Prymnesium kappa virus RF01 | HG999358 |
| *-* | *Kratosvirus* | *Kratosvirus quantuckense* | Aureococcus anophagefferens virus isolate BtV-01 | KJ645900 |



**Figure 1**. Phylogeny of the order *Imitervirales*, based on a concatenated alignment of seven marker genes (see main text for details). Species proposed or renamed here are in bold. The Maximum Likelihood based phylogeny was constructed using IQ-TREE 1.6.9. Black circles denote nodes with >80% ultrafast bootstrap support.



**Figure 2**. Pairwise Average Nucleotide Identity (ANI) of viral isolates in the family *Mimiviridae*. ANI was calculated only if the average alignment fraction was >75%; otherwise ANI was set to 0. Nucleotide comparisons were performed with LAST v. 959.



**Figure 3**. Pairwise Average Nucleotide Identity (ANI) of viral isolates in the proposed genus *Tethysvirus*. ANI was calculated only if the average alignment fraction was >75%; otherwise ANI was set to 0. Nucleotide comparisons were performed with LAST v. 959.

**References**

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