

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

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| **Code assigned:** | ***2023.008F*** |  |
| **Short title:** Establishing 11 new genera and 19 species in the families *Nenyaviridae, Naryaviridae* and *Vilyaviridae* | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
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**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 | 06-23-2023 |
| Date of this revision (if different to above) |  |

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

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**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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| 2023.008F.v1.Arfiviricetes*\_*11ng\_19nsp.xlsx |

**Abstract**

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| We aim to classify various new virus genomes in the families *Naryaviridae*, *Nenyaviridae* and *Vilyaviridae* whose members are likely associated with protozoan parasites *Entamoeba* and *Giardia*. We propose establishing 7 new genera and 9 new species in *Naryaviridae*, 1 new genus and 1 new species in *Nenyaviridae*, and 3 new genera and 9 new species in *Vilyaviridae.* |

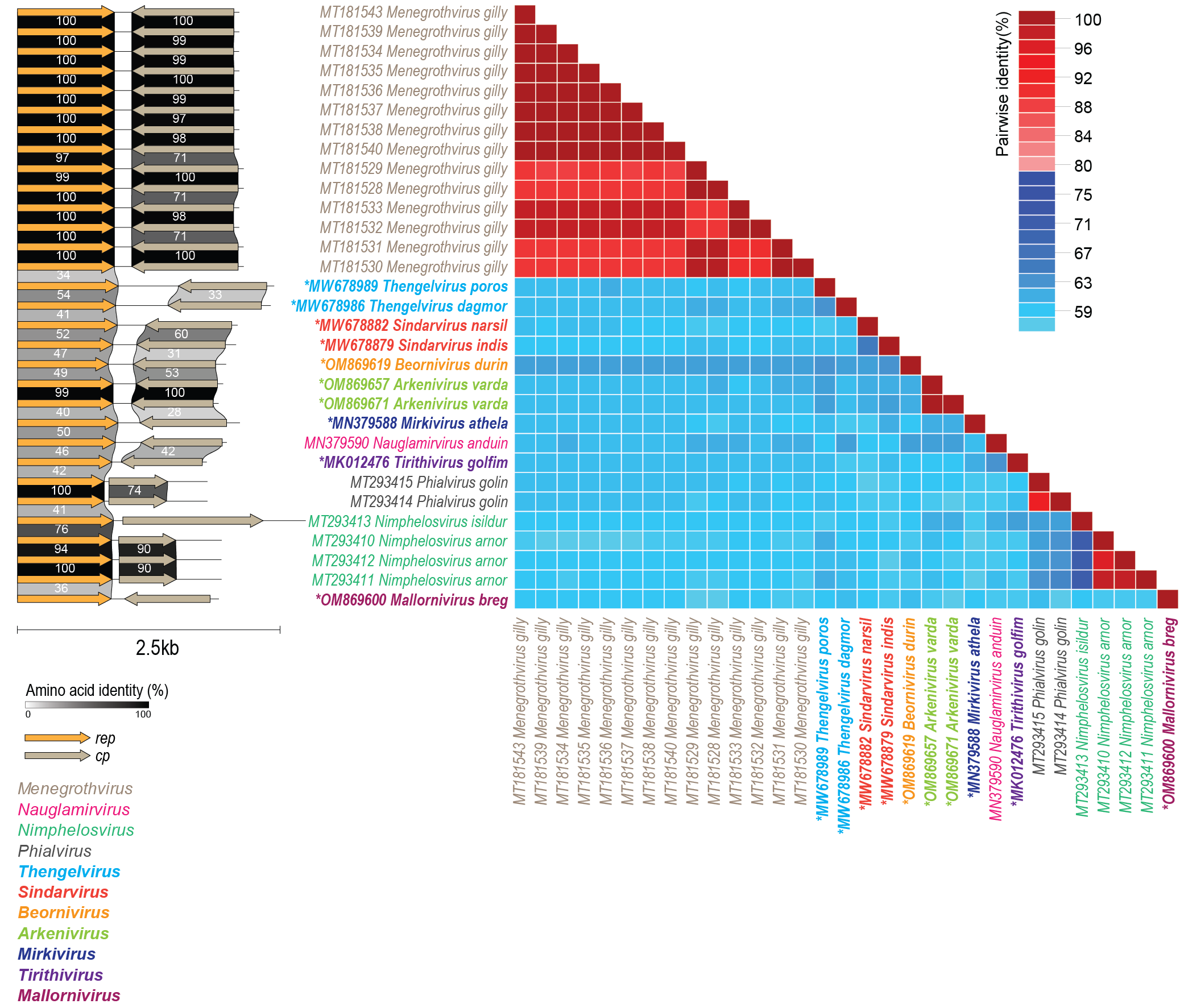
**Text of proposal**

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| |  | | --- | | Since the establishment of the families *Naryaviridae*, *Nenyaviridae* and *Vilyaviridae*, in the class *Arfiviricetes* (phylum *Cressdnaviricota*) in 2022 for classification of single-stranded DNA viruses associated with protozoan parasites *Entamoeba* and *Giardia*, a number of new virus genomes that can be assigned to these families have been identified. Namely, 11 new genomes can be classified into the family *Naryaviridae*, 1 into *Nenyaviridae* and 14 into *Vilyaviridae*. Four of the 14 in the family *Vilyaviridae* can be classified into the species *Angristvirus fangorn* (n=3) and *Aranruthvirus numenor* (n=1).  We follow the genus and species demarcation criteria outlined in Krupovic and Varsani [1], 65% pairwise nucleotide sequence identity for genus demarcation and 78% pairwise nucleotide sequence identity as a species demarcation criterion.  In this proposal we classify:   * 11 naryaviruses: we propose establishing 7 new genera and 9 new species * 1 nenyavirus: we propose 1 new genus and 1 new species * 10 vilyaviruses: we propose 3 new genera and 9 new species   **Etymology of the taxa names**  ***Naryaviridae***  Genera:  *Thengelvirus* - Thengel: 16th King of Rohan  *Sindarvirus* - Sindar: Grey Elves  *Beornivirus* - Beorn: Chieftain of the Beorning  *Arkenivirus* - Arkenstone: gem discovered in the lonely mountain  *Mirkivirus* - Mirkwood: Woodland in Rhovanion  *Tirithivirus* - Minas Tirith: Capital of Gondor  *Mallornivirus* - Mallorn: large tree in Aman  Epithets:  poros - Poros: Small river in Gondor  dagmor - Dagmor: sword belonging to Beren  narsil - Narsil: sword belonging to Isildur  indis - Indis: Elvish for ‘Great or Valient Woman’  durin - Durin: Seven Fathers of the Dwarves  varda - Varda: Queen of Valar  athela - athelas: healing herb  golfim - Golfimbul: king of the Orcs  breg - Brego: horse of Rohan  ***Nenyaviridae***  Genera:  *Cirilivirus* - Ciril: third of the Seven Rivers of Gondor  Epithet:  boffger -Concatenation of Boffin and Bolger (two prominent Hobbit families)  ***Vilyaviridae***  Genera:  *Ulaervirus* - Ulaer: The Nazgûl are known also known as Ulaer in evlish  *Ancalagonvirus* - Ancalagon: A colossal dragon known as the mightiest of its kind  *Berenvirus* - Lúthien Tinúviel: A Half-elf maiden renowned for her beauty, grace, and courage  Epithets:  earendil - Eärendil: The mariner who carried the Silmaril and became the Morning and Evening Star.  glaurung - Glaurung: A powerful and deceitful dragon who played a significant role in The Silmarillion.  auledhrim - auledhrim: A blend of Aulë, the Vala who created the Dwarves, and Oropher, father of Thranduil and grandfather of Legolas.  mirksil - Mirksil: A concatenation of Mirkwood and Nirsil the sword of Elendil  morgothanc - Morgothanc: A mix of Morgoth, the first Dark Lord, and Fangorn, the forest home of the Ents.  tuor - Tuor: a mortal hero who played a significant role in The Silmarillion  maedhros - Maedhros: one of the Sons of Fëanor from The Silmarillion  eol - Eöl: The Dark Elf of Nan Elmoth  tinúviel - Lúthien Tinúviel: A Half-elf maiden renowned for her beauty, grace, and courage. | |

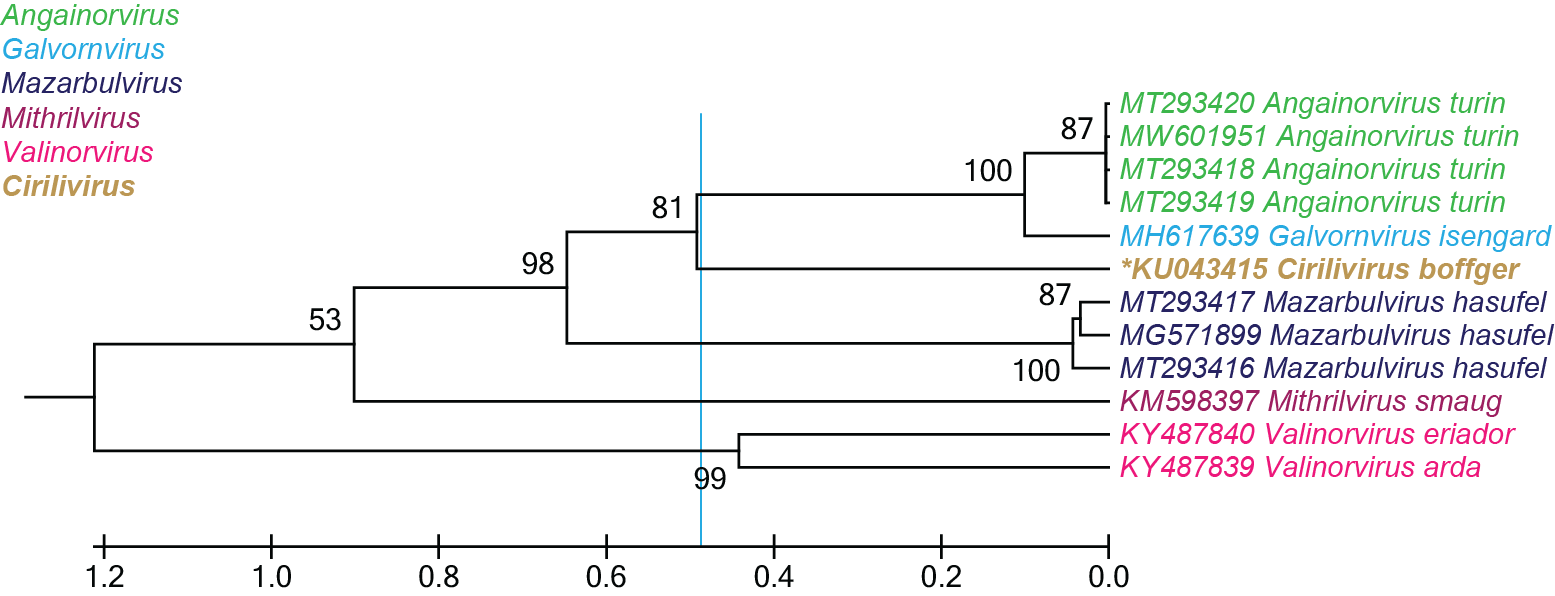
**Supporting evidence**

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**Figure 1:** Maximum likelihood tree of the Rep sequences of members of the *Naryaviridae* family inferred from the aligned Rep amino-acid sequences using PhyML [2] with VT+F is the best substitution model. Numbers at the nodes represent aLRT branch supports. The cyan line shows a proposed demarcation of genera. The new genera are in bold font and \* denotes the species assignment of the new viruses.

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**Figure 2:** Genome-wide pairwise comparison of the naryavirid genomes. Genome maps are shown on the left and. The pairwise identities were calculated using SDT [3]. The new genus is in bold font and \* denotes the species assignment of the new viruses.

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**Figure 3:** Maximum likelihood tree of the Rep sequences of members of the *Nenyaviridae* family inferred from the aligned Rep amino-acid sequences using PhyML [2] with VT+F is the best substitution model. Numbers at the nodes represent aLRT branch supports. The cyan line shows a proposed demarcation of genera. The new genus is in bold font and \* denotes the species assignment of the new viruses.

**A screen shot of a computer

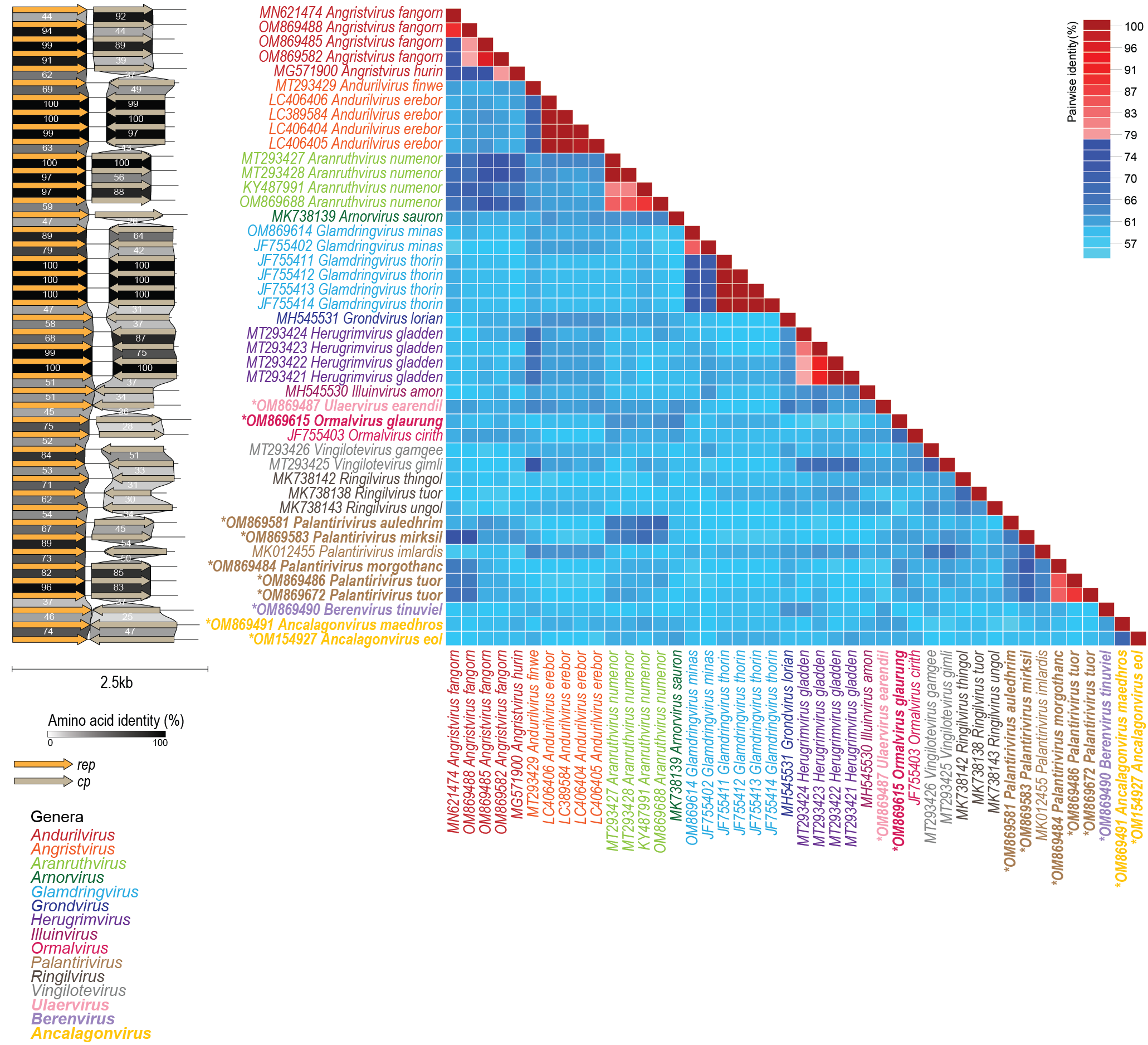
Description automatically generated with medium confidence**

**Figure 4:** Genome-wide pairwise comparison of the nenyavirid genomes. Genome maps are shown on the left and. The pairwise identities were calculated using SDT [3]. The new genus is in bold font and \* denotes the species assignment of the new viruses.

**A screen shot of a computer

Description automatically generated with low confidence**

**Figure 5:** Maximum likelihood tree of the Rep sequences of members of the *Vilyaviridae* family inferred from the aligned Rep amino-acid sequences using PhyML [2] with rtREV+I+G+F is the best substitution model. Numbers at the nodes represent aLRT branch supports. The cyan line shows a proposed demarcation of genera. The new genera are in bold font and \* denotes the species assignment of the new viruses.

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**Figure 6:** Genome-wide pairwise comparison of the vilyavirid genomes. Genome maps are shown on the left and. The pairwise identities were calculated using SDT [3]. The new genus is in bold font and \* denotes the species assignment of the new viruses.

**Table 1:** Summary of new species in the families *Naryaviridae*, *Nenyaviridae* and *Vilyaviridae*. Those in black font are exemplar viruses for their respective species.

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| **Family** | **Genus** | **Species** | **Accession #** | **Virus** | | **Country of isolation** | **Host / source** | **Isolate** | **Sample type** |
| *Naryaviridae* | *Thengelvirus* | *Thengelvirus poros* | MW678989 | | Virus sp. D1\_583 | USA | environmental | D1\_583 | airborne particulate matter |
| *Naryaviridae* | *Thengelvirus* | *Thengelvirus dagmor* | MW678986 | | Virus sp. D10\_8234 | USA | environmental | D10\_8234 | airborne particulate matter |
| *Naryaviridae* | *Sindarvirus* | *Sindarvirus narsil* | MW678882 | | Virus sp. D10\_11052 | USA | environmental | D10\_11052 | airborne particulate matter |
| *Naryaviridae* | *Sindarvirus* | *Sindarvirus indis* | MW678879 | | Virus sp. D3\_1047 | USA | environmental | D3\_1047 | airborne particulate matter |
| *Naryaviridae* | *Beornivirus* | *Beornivirus durin* | OM869619 | | Peromfec virus RodF8\_96 | USA | *Peromyscus boylii* | RodF8\_96 | feces |
| *Naryaviridae* | *Arkenivirus* | *Arkenivirus varda* | OM869657 | | Peromfec virus RodF7\_30 | USA | *Peromyscus boylii* | RodF7\_30 | feces |
| *Naryaviridae* | *Arkenivirus* | *Arkenivirus varda* | OM869671 | | Peromfec virus RodF5\_42 | USA | *Peromyscus truei* | RodF5\_42 | feces |
| *Naryaviridae* | *Mirkivirus* | *Mirkivirus athela* | MN379588 | | Chicken virus mg5\_2197 | USA | *Galus galus* | mg5\_2197 | tracheal swab |
| *Naryaviridae* | *Tirithivirus* | *Tirithivirus golfim* | MK012476 | | CRESS virus sp. ctbi77 | USA | turkey | ctbi77 | tissue |
| *Naryaviridae* | *Mallornivirus* | *Mallornivirus breg* | OM869600 | | Dipodfec virus UA23Rod\_5718 | USA | *Dipodomys spectabilis* | UA23Rod\_5718 | feces |
| *Nenyaviridae* | *Cirilivirus* | *Cirilivirus boffger* | KU043415 | Circular ssDNA virus sp. cg6319 | | USA | *Macaca mulatta* | cg6319 | feces |
| *Vilyaviridae* | *Ulaervirus* | *Ulaervirus earendil* | OM869487 | Sigmofec virus UA08Rod\_19468 | | USA | *Sigmodon arizonae* | UA08Rod\_19468 | feces |
| *Vilyaviridae* | *Ormalvirus* | *Ormalvirus glaurung* | OM869615 | Myodefec virus RodL3\_773 | | USA | *Clethrionomys gapperi* | RodL3\_773 | liver |
| *Vilyaviridae* | *Palantirivirus* | *Palantirivirus auledhrim* | OM869581 | Dipodfec virus UA06Rod\_119 | | USA | *Dipodomys ordii* | UA06Rod\_119 | feces |
| *Vilyaviridae* | *Palantirivirus* | *Palantirivirus mirksil* | OM869583 | Dipodfec virus UA06Rod\_108 | | USA | *Dipodomys ordii* | UA06Rod\_108 | feces |
| *Vilyaviridae* | *Palantirivirus* | *Palantirivirus morgothanc* | OM869484 | Sigmofec virus UA08Rod\_21233 | | USA | *Sigmodon arizonae* | UA08Rod\_21233 | feces |
| *Vilyaviridae* | *Palantirivirus* | *Palantirivirus tuor* | OM869486 | Sigmofec virus UA08Rod\_20100 | | USA | *Sigmodon arizonae* | UA08Rod\_20100 | feces |
| *Vilyaviridae* | *Palantirivirus* | *Palantirivirus tuor* | OM869672 | Peromfec virus RodF5\_41 | | USA | *Peromyscus truei* | RodF5\_41 | feces |
| *Vilyaviridae* | *Berenvirus* | *Berenvirus tinuviel* | OM869490 | Sigmofec virus UA08Rod\_17746 | | USA | *Sigmodon arizonae* | UA08Rod\_17746 | feces |
| *Vilyaviridae* | *Ancalagonvirus* | *Ancalagonvirus maedhros* | OM869491 | Sigmofec virus UA08Rod\_17037 | | USA | *Sigmodon arizonae* | UA08Rod\_17037 | feces |
| *Vilyaviridae* | *Ancalagonvirus* | *Ancalagonvirus eol* | OM154927 | Chaetfec virus UA24\_7381 | | USA | *Chaetodipus sp.* | UA24rod\_7381 | feces |

**References**

1. Krupovic M, Varsani A, 2022. Naryaviridae, Nenyaviridae, and Vilyaviridae: three new families of single-stranded DNA viruses in the phylum Cressdnaviricota. Arch. Virol. 167, 2907–2921.PMID: 36098801 DOI: 10.1007/s00705-022-05557-w
2. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol 59:307-321. PMID: 20525638; doi: 10.1093/sysbio/syq010
3. Muhire BM, Varsani A, Martin DP (2014) SDT: A Virus Classification Tool Based on Pairwise Sequence Alignment and Identity Calculation. Plos One 9:e108277. doi:10.1371/journal.pone.0108277. PMID:WOS:000342685600059