

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create new class and new order to accommodate two orphan mycoviral families |
| **Code assigned:** | 2025.007F.Ac.v3.Mycopleornaviricetes\_nclass\_Xenadelphovirales\_nord | |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses | **X** |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
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| **Submission date:** | 30/04/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **X** |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
| Please proofread and address some typos in the text. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
| All suggestions addressed. |

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| **Revision date:** | 30/08/2025 |

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

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon | **X** | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| “*Mycopleornaviricetes*” | Derived from “myco” (Greek; fungi) + “pleorna”, which is a combination of “pleon” (Greek; multiple) and “RNA” + class suffix “viricetes” |
| “*Xenadelphovirales*” | Combination of “xeno” (Greek; “alien”) and “adelphos” (Greek; brothers) + order suffix “virales” |

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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  This proposal affects primarily the phylum *Pisuviricota*, by establishing a novel class and a novel order to accommodate two established families yet unassigned to higher taxa.  *Description of current taxonomy*:  *Polymycoviridae* is an orphan family within the realm *Riboviria*, not yet assigned to taxa of the order-kingdom ranks. *Polymycoviridae* is phylogenetically related to *Hadakaviridae*, a family assigned to the phylum *Pisuviricota*, kingdom *Orthornavirae*, realm *Riboviria* but not yet assigned to an order or class.  *Proposed* *taxonomic change(s):*  We propose to move *Polymycoviridae* to the phylum *Pisuviricota* and create a novel class, “*Mycopleornaviricetes***”** and a novel order, “*Xenadelphovirales*”, to accommodate the *Polymycoviridae* and *Hadakaviridae* families.  *Justification*:  *Polymycoviridae* and *Hadakaviridae* are two families of mycoviruses, belonging to a monophyletic clade within the phylum *Pisuviricota* and more closely related to each other than to other viral families within the same phylum. Currently, *Polymycoviridae* is not assigned to order-kingdom taxa, while *Hadakaviridae* is assigned to phylum *Pisuviricota* but not to an order or class. Therefore, we propose establishing a novel class and order to accommodate this monophyletic clade of mycoviruses. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  The proposal affects primarily the phylum *Pisuviricota*. A novel class, “*Mycopleornaviricetes*” and a novel order, “*Xenadelphovirales*”, are established to accommodate families *Polymycoviridae* and *Hadakaviridae*.  *Description of current taxonomy*:  *Polymycoviridae* is an orphan family of multisegmented double-stranded (ds)RNA mycoviruses within the realm *Riboviria*, not yet assigned to order-kingdom taxa [1]. *Polymycoviridae* is phylogenetically related to *Hadakaviridae* family of multisegmented (+)RNA mycoviruses, currently classified in the phylum *Pisuviricota* and the kingdom *Orthornavirae,* but not yet assigned to order or class [2]. Ideas to group these families in the higher-level taxon have already been proposed in scientific literature [3].  *Proposed* *taxonomic change(s)*:  We propose moving the *Polymycoviridae* family to the phylum *Pisuviricota*, kingdom *Orthornavirae*. We also propose establishing a novel class, “*Mycopleornaviricetes*”, with one new order, “*Xenadelphovirales*”. The phylogenetically related families *Polymycoviridae* and *Hadakaviridae* are proposed to be classified in the proposed class “*Mycopleornaviricetes*” and order “*Xenadelphovirales*” (Table 1).  As recommended by the ICTV, the amino acid sequence of RNA-directed RNA polymerase (RdRP), the hallmark protein of non-reverse transcribing viruses across the entire *Riboviria* realm, was used for phylogenetic analyses of *Polymycoviridae*, *Hadakaviridae*, and other related families [4-6]. All members of the proposed new class (“*Mycopleornaviricetes*”) and order (“*Xenadelphovirales”)* cluster together in a monophyletic clade, confirming the close relationship between *Polymycoviridae* and *Hadakaviridae* while demonstrating a more distant relationship with other families in the phylum *Pisuviricota*, such as *Picornaviridae*, *Astroviridae*, and *Partitiviridae* (Figure 1).  The proposed order, “*Xenadelphovirales*”, represents a monophyletic clade accommodating the families *Polymycoviridae* and *Hadakaviridae* (Figure 1). Indeed, both families share molecular features, such as the conserved GDNQ amino acids in their RdRP palm domain, host, segmented RNA genome, and encode other homologous proteins. However, viruses in the family *Polymycoviridae* have double-stranded RNA (dsRNA) genome and encode a PASrp protein, which sometimes covers and protects its genome in filamentous particles [1,7]. On the other hand, members of the *Hadakaviridae* family have a (+)RNA genome and are capsidless (encode no capsid-like protein) [2,8-11].  Therefore, the name of the proposed order “*Xenadelphovirales*” is a combination of the Greek words “Xeno” and “Adelphos” (“alien brothers”), representing their close evolutionary relationship despite their differences in genome structure and virion formation.  *Demarcation criteria:*  To be classified in the class “*Mycopleornaviricetes*” and the order “*Xenadelphovirales*”, a virus should cluster in a highly supported monophyletic clade with other viruses in *Hadakaviridae* or *Polymycoviridae*.  *Justification:*  This proposal aims to assign the orphan families *Polymycoviridae* and *Hadakaviridae* to higher-level taxa based on their evolutionary relationships with other viral groups. *Polymycoviridae* is a fast-growing family, with recent studies identifying a large diversity of new members [1,3,7,12]. The current taxonomic positions of *Polymycoviridae* and *Hadakaviridae* do not accurately represent their phylogenetic relationship with other groups within the *Riboviria* realm, as *Polymycoviridae* is not yet assigned to any order-kingdom and *Hadakaviridae* is not yet assigned to order-class taxa.  Therefore, we propose creating a novel class and order based on the phylogenetic relationship between *Hadakaviridae* and *Polymycoviridae*. Members of *Polymycoviridae* and *Hadakaviridae,* in addition to the phylogenetic relationship, share other characteristics. Both infect fungi, have multisegmented genomes and encode a methyltransferase and other homologous proteins. Both groups of viruses also have conserved GDNQ amino acids in motif VI of their RdRP palm domain instead of a characteristic GDD triplet present in other viruses of the phylum *Pisuviricota* [1,2,10]. This RdRP motif is common in (–)RNA viruses within the order *Mononegavirales*; however, phylogenetic analyses do not support an evolutionary relationship between *Hadakaviridae* and *Polymycoviridae* with other viruses in *Mononegavirales* [1,2,10,13].  Nevertheless, members of *Polymycoviridae* and *Hadakaviridae* differ in genome structure: polymycoviruses have a dsRNA genome and encode a PASrp sometimes forming filamentous particles, while hadakaviruses have a (+)RNA genome and encode no capsid protein (capsidless) [2,7-9,13]. Therefore, the novel class *“Mycopleornaviricetes”* will comprise a single novel order (“*Xenadelphovirales*”) to accommodate *Polymycoviridae* and *Hadakaviridae*. |
| **References:** |
| [1] I. Kotta-Loizou and R. H. A. Coutts, “ICTV Virus Taxonomy Profile: *Polymycoviridae* 2022,” *Journal of General Virology*, vol. 103, no. 5, p. 001747, May 2022, doi: 10.1099/JGV.0.001747/CITE/REFWORKS.  [2] Y. Sato *et al.*, “ICTV Virus Taxonomy Profile: *Hadakaviridae* 2023,” *Journal of General Virology*, vol. 104, no. 1, p. 001820, Jan. 2023, doi: 10.1099/JGV.0.001820/CITE/REFWORKS.  [3] C. N. Oliveira, Y. de Sousa Santos, R. R. de Rezende, and P. Alfenas-Zerbini, “Identification of a novel polymycovirus infecting the entomopathogenic fungus *Metarhizium robertsii*,” *Archives of Virology*, 170:3, vol. 170, no. 3, pp. 1–8, Feb. 2025, doi: 10.1007/S00705-025-06240-6.  [4] E. V. Koonin *et al.*, “Global organization and proposed megataxonomy of the virus world,” *Microbiology and Molecular Biology Reviews*, vol. 84, no. 2, May 2020, doi: 10.1128/MMBR.00061-19/SUPPL\_FILE/MMBR.00061-19-S0001.PDF.  [5] E. V Koonin, A. Varsani, and F. M. Zerbini, “Create a megataxonomic framework, filling all principal taxonomic ranks, for realm *Riboviria*,” doi: 10.13140/RG.2.2.20234.21444.  [6] P. Simmonds et al., “Four principles to establish a universal virus taxonomy,” *PLoS Biology*, vol. 21, no. 2, p. e3001922, Feb. 2023, doi: 10.1371/JOURNAL.PBIO.3001922.  [7] Z. Han, J. Jiang, and W. Xu, “Novel polymycoviruses are encapsidated in filamentous virions,” *Journal of Virology*, Dec. 2024, doi: 10.1128/JVI.01515-24.  [8] Y. Sato *et al.*, “Hadaka virus 1: A capsidless eleven-segmented positive-sense single-stranded RNA virus from a phytopathogenic fungus, *Fusarium oxysporum*,” *mBio*, vol. 11, no. 3, May 2020, doi: 10.1128/MBIO.00450-20/ASSET/CF486066-9D35-4C45-85DA-6C4C6D4C903E/ASSETS/GRAPHIC/MBIO.00450-20-F0006.JPEG.  [9] H. A. Khan, Y. Sato, H. Kondo, A. Jamal, M. F. Bhatti, and N. Suzuki, “A second capsidless hadakavirus strain with 10 positive-sense single-stranded RNA genomic segments from *Fusarium nygamai*,” *Archives of Virology*, vol. 166, no. 10, pp. 2711–2722, Oct. 2021, doi: 10.1007/S00705-021-05176-X/FIGURES/5.  [10] M. Fu *et al.*, “A novel heptasegmented positive-sense single-stranded RNA virus from the phytopathogenic fungus *Colletotrichum fructicola*,” *Journal of Virology*, vol. 96, no. 9, May 2022, doi: 10.1128/JVI.00318-22.  [11] Y. Lin, G. Pan, Y. Qi, B. Wang, C. Jin, and W. Fang, “A novel hypovirulence-associated Hadaka virus 1 (HadV1-LA6) in *Fusarium oxysporum f. sp. cubense* ,” *mSphere*, Jul. 2024, doi: 10.1128/MSPHERE.00428-24/SUPPL\_FILE/MSPHERE.00428-24-S0001.DOCX.  [12] Y. Zheng *et al.*, “Four distinct isolates of a novel polymycovirus identified in *Setosphaeria turcica*,” *Archives of Virology*, vol. 168, no. 7, pp. 1–5, Jul. 2023, doi: 10.1007/S00705-023-05819-1/FIGURES/2.  [13] M. Ouizougun-Oubari and R. Fearns, “Structures and mechanisms of nonsegmented, negative-strand RNA virus polymerases,” *Annual Reviews in Virology*, vol. 10, no. 1, pp. 199–215, Sep. 2023, doi: 10.1146/ANNUREV-VIROLOGY-111821-102603/CITE/REFWORKS. |

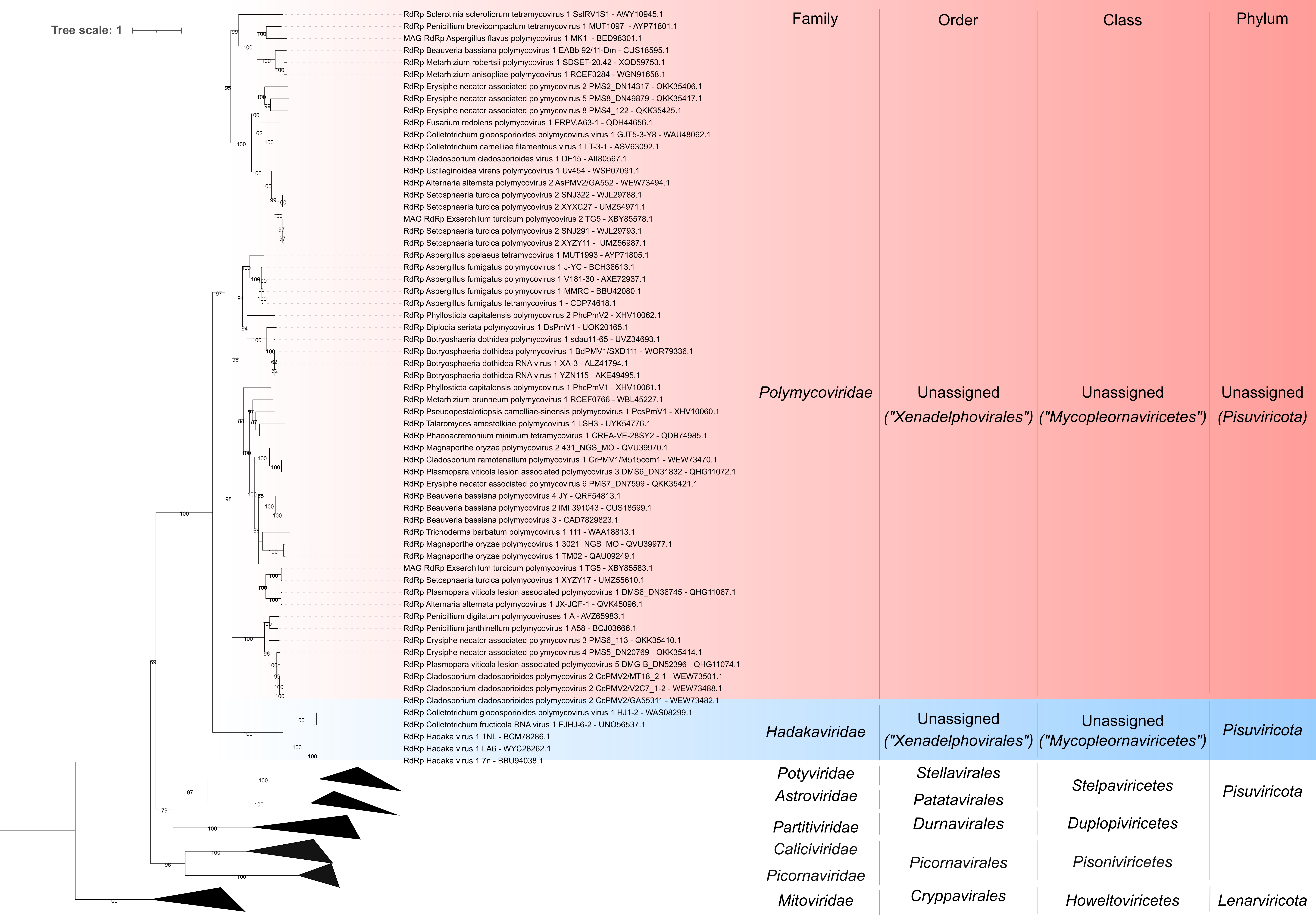
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| **accesion\_numbers\_ncbi\_phylogeny.xlsx** | **List of all NCBI accession numbers used in the phylogenetic tree analyses** |
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| **Tables, Figures:** |

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**Table 1:** Current and proposed taxonomy of the families *Polymycoviridae* and *Hadakaviridae*. text – original taxonomy; green text – new assignation to established taxa; red text – new taxa.

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| **TAXON** | **CURRENT** | **PROPOSED** | **CURRENT** | **PROPOSED** |
| Realm | *Riboviria* | *Riboviria* | *Riboviria* | *Riboviria* |
| Kingdom |  | *Orthornavirae* | *Orthornavirae* | *Orthornavirae* |
| Phylum |  | *Pisuviricota* | *Pisuviricota* | *Pisuviricota* |
| Class |  | *Mycopleornaviricetes* |  | *Mycopleornaviricetes* |
| Order |  | *Xenadelphovirales* |  | *Xenadelphovirales* |
| Family | *Polymycoviridae* | *Polymycoviridae* | *Hadakaviridae* | *Hadakaviridae* |



**Figure 1:** Phylogenetic analyses of the RdRP amino acid sequences of members of the families *Polymycoviridae*, *Hadakaviridae*, and other viral families within the phylum *Pisuviricota*. The hadakavirid and polymycovirid sequences were downloaded from NCBI on April 10th, 2025, and representative sequences of the viral families within *Pisuviricota* were selected from the VMR\_MSL\_v2 list. MAFFT v7.471 was used for multiple sequence alignment. The ML phylogenetic tree was constructed using IQ-TREE v1.6.11, which calculates the best evolutionary model (LG+F+R5). The proposed taxonomy changes are reported in parentheses, while the proposed novel class and order are also highlighted in quotation marks.