

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

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| **Title:** | Polymycoviridae\_reorganization |
| **Code assigned:** | 2025.006F.N.v2.Polymycoviridae\_3ngen\_18nsp | |

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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:** | 13/06/2025 |

**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 |  |
| 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| W - Withdrawn |  |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:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

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

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

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

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *“Polymycovirus”* | *Polymycovirus*; the prefix “poly”, representing the number of segments. The “myco” was not altered since it is the virus host. |
| *“Multimycovirus”* | It is a variation of the original genus *Polymycovirus*; in this case, the prefix “poly” was replaced with “multi”, representing the number of segments. The “myco” was not altered since it is the virus host. |
| *“Plurimycovirus”* | It is a variation of the original genus *Polymycovirus*; in this case, the prefix “poly” was replaced with “pluri”, representing the number of segments. The “myco” was not altered since it is the virus host. |

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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 family *Polymycoviridae*, splitting its sole genus *Polymycovirus* into 3 genera, renaming 5 established species and establishing 18 novel species.  *Description of current taxonomy*:  *Polymycoviridae* comprises a single genus, *Polymycovirus,* with 10 species recognized by the ICTV.  *Proposed* *taxonomic change(s):*  We propose to split genus *Polymycovirus* into three genera namely, *Polymycovirus*, “Multimycovirus”, and “Plurimycovirus” in the family *Polymycoviridae*. Consequently, we propose to move and rename the 5 established species in the family *Polymycoviridae* based on the novel genus they are assigned in. Additionally, we propose to establish 18 novel species in the family *Polymycoviridae*, 4 in the genus *Polymycovirus*, 13 in the genus “Multimycovirus”, and 1 in the genus “Plurimycovirus”.  *Justification*:  The proposed taxa better reflect the evolutionary relationships of novel polymycovirus-related isolates. and will facilitate future classifying efforts for the increasing number of polymycovirus-related isolates in public databases. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  This proposal affects primarily the family *Polymycoviridae* [1]. Its sole genus *Polymycovirus* is split into 3 genera *Polymycovirus*, “*Multimycovirus*” and “*Plurimycovirus*”. Five of ten currently established species are moved to newly created genera and renamed accordingly. Additionally, 18 novel species (nsp) are established in these 3 genera.  *Description of current taxonomy*:  *Polymycoviridae* is an orphan family of mycoviruses within the realm *Riboviria*, not yet assigned to order-kingdom taxa [1]. *Polymycoviridae* is phylogenetically related to *Hadakaviridae* family of mycoviruses (phylum *Pisuviricota*, kingdom *Orthornavirae*, realm *Riboviria*) [2]. Ideas to group these families at a high level have already been proposed [3]. Currently, *Polymycoviridae* comprises a single genus, *Polymycovirus*, with 10 species recognized by the ICTV [1].  *Proposed* *taxonomic change(s)*:  We propose reorganization of the family *Polymycoviridae* by splitting the genus *Polymycovirus* genus into 3 genera: *Polymycovirus*, “*Multimycovirus*” and “*Plurimycoviru*s”. Additionally, we propose establishing 18 new species in these 3 genera (Table 1).  As recommended by the ICTV, the amino acid sequence of RNA-dependent RNA polymerase (RdRp), the hallmark protein of non-reverse transcribing viruses across the entire *Riboviria* realm, was used for phylogenetic analyses of the members of the family *Polymycoviridae,* with *Hadakaviridae* serving as an outgroup [4,5]. The phylogenetic analyses included the representative isolates of the 10 established species in the family *Polymycoviridae* and other related isolates whose complete genome sequences were available in the National Center for Biotechnology Information (NCBI) databases. The maximum likelihood phylogenetic tree of the RdRp amino acid sequences revealed the existence of at least three well-supported monophyletic clades, each proposed to represent genera in the *Polymycoviridae* family (Figure 1A). This was supported by the heat map showing the pairwise identity values of the RdRp amino acid sequences (Figure 1B).  The proposed genus *Polymycovirus* comprises 4 new and 5 established species, *Polymycovirus penicompactii*, *Polymycovirus beauveriae*, *Polymycovirus fusarii*, *Polymycovirus colletotrichi*, and *Polymycovirus cladosporii*(Table 1).  The proposed genus “*Multimycovirus*” is the biggest genus in the family as it comprises 17 species of which 13 new. Four species previously classified in the genus *Polymycovir*us (*Polymycovirus aspelaei*, *Polymycovirus aspergilli*, *Polymycovirus botryosphaeriae*, and *Polymycovirus magnaporthis*) are moved into this genus and renamed accordingly (Table 1).  The proposed genus “*Plurimycovirus*” is the smallest genus within *Polymycoviridae*; it comprises a well-supported monophyletic clade containing 2 species of which 1 species is new, while the established species *Polymycovirus penidigitati*, previously classified in the genus Polymycovirus was renamed “*Plurimycovirus penidigitati*” to reflect new taxonomic position (Table 1).  The novel proposed genera and species are summarized in Table 1 and visualized in Figures 1A and 1B.  *Demarcation criteria:*  The species demarcation criteria remain the same as the ones originally established for the *Polymycoviridae* family: i.e., viral isolates sharing more than 70% identity in the RdRp amino acid sequence represent a single species [1]. To be classified in the proposed genera *Polymycovirus*, “*Multimycovirus*”, or “*Plurimycovirus*”, a virus should cluster in a highly supported monophyletic clade with another virus of these genera.  *Justification*:  Interest in mycovirus studies has increased in recent years due to their potential as biocontrol agents. Therefore, several novel polymycovirus-related sequences have been available in NCBI but not classified yet [1]. Taxonomy is a human-made tool to organize biological entities into groups with more similarity and a closer evolutionary history [5]. Therefore, we propose reorganization of the family by splitting the genus *Polymycovirus* into three novel genera to better reflect the evolutionary relationships among these viruses - including novel polymycovirus-related isolates. We believe this new arrangement will facilitate further work on classifying the increasing number of polymycovirids. Additionally, we propose establishing 18 new species in the *Polymycoviridae* family, representing almost threefold fold increase in species number in the family. |
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| **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,* 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] 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. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| Polymycoviridae\_3nGen\_18nsp.xlsx | Obligatory Excel template to submit the proposal |
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| **Tables, Figures:** |

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**Table 1:** Current and proposed taxonomy of the family *Polymycoviridae*. text – original taxonomy; purple text – new genera; green text – moved/renamed species; red text – new species.

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| **CURRENT TAXONOMY** | **PROPOSED TAXONOMY** |
|  |  |
|  |  |
|  | Species: *Polymycovirus aspeflavi* |
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|  |  |
|  |  |
|  | Species: *Polymycovirus erynecati* |
|  |  |
|  | Species: *Polymycovirus metarhizii* |
|  |  |
|  | Species: *Polymycovirus turcicalternatae* |
|  | Genus: *Multimycovirus* (previously part of *Polymycovirus*) |
|  | Species: *Multimycovirus alternatae* |
|  | Species: *Multimycovirus aspelaei* |
|  | Species: *Multimycovirus aspergilli* |
|  | Species: *Multimycovirus beauvessianae* |
|  | Species: *Multimycovirus botryosphaeriae* |
|  | Species: *Multimycovirus camesinensis* |
|  | Species: *Multimycovirus priphillostictae* |
|  | Species: *Multimycovirus secuphyllostictae* |
|  | Species: *Multimycovirus cladoplasmoniae* |
|  | Species: *Multimycovirus erynecati* |
|  | Species: *Multimycovirus magnaporthis* |
|  | Species: *Multimycovirus magnaporyzae* |
|  | Species: *Multimycovirus metabrunnei* |
|  | Species: *Multimycovirus miniphaeoacremonii* |
|  | Species: *Multimycovirus talaromyci* |
|  | Species: *Multimycovirus trichodermae* |
|  | Species: *Multimycovirus turcicae* |
|  | Genus: *Plurimycovirus* (previously part of *Polymycovirus*) |
|  | Species: *Plurimycovirus cladosporii* |
|  | Species: *Plurimycovirus penidigitati* |

A diagram of a tree

AI-generated content may be incorrect.

A diagram of a number of data

AI-generated content may be incorrect.

**Figure 1: (A)** Phylogenetic analyses of the RdRp amino acid sequences of members of the *Polymycoviridae* and *Hadakaviridae* families. The sequences were downloaded from NCBI on April 10th, 2025. 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+I+G4). The proposed novel genera are indicated in green for *Polymycovirus*, blue for “*Multimycovirus*”, and red for “*Plurimycovirus*”. **(B)** Heat map with the pairwise identity values of the RdRp amino acid sequences of members of the *Polymycoviridae* and *Hadakaviridae* families. STD v1.3 was used to perform the pairwise alignment.