

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Reclassifying families *Hypo*- and *Fusariviridae* into a new order “*Hypofuvirales*” (*Stelpaviricetes*: *Pisuviricota*) and their reorganization |
| **Code assigned:** | 2025.012F.Uc.v3.Hypofuvirales\_neworder |

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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:** |
| Hypoviridae |

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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** | 20/06/2025 |

**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| W - Withdrawn |  |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:** |
| Please change/update the phylogenetic tree to focus on the Hypofuvirales/Stelpaviricetes, because some higher taxa appear paraphyletic (only use one outgroup); fix typo in legend; supplementary excel file color codes and values need to be addressed |

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

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| **Response of proposer:** |
| The phylogenetic tree was simplified to focus on taxonomic position of the new proposed order, as well as the new family. Figure legend was also improved. Excel file was fixed (also two species with partial genomes removed). Color code addressed as well. |

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| **Revision date:** | 10/29/2025 |

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

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

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
| *“Hypofuvirales”* | From the initials of the two families (**Hypo**viridae and **Fu**sarviridae) that are included in the order |
| *“Parahypoviridae”* | From Greek “para” (distant) and Hypoviridae |
| *“Iotahypovirus”* | Letter of Greek alphabet and former genus name *Hypovirus* |
| *“Deltafusarivirus”* | Letter of Greek alphabet and former genus name *Hypovirus* |
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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*:  Species, Genus, Family, Order, Class  *Description of current taxonomy*:  Currently, families *Hypoviridae* and *Fusariviridae* are members of the order *Durnavirales* in the class *Duplopiviricetes* in the phylum *Pisuviricota*. Such assignment was based on a previous “megataxonomy” analysis that associated viruses in the family Hypoviridae with members of the order *Durnavirales,* yetwith rather poor statistical support.  *Proposed* *taxonomic change(s):*  We propose to move the families *Hypoviridae* and *Fusariviridae* to a newly created order “*Hypofuvirales”* in the *Stelpaviricetes* class. Additionally, we propose to create a new family “*Parahypoviridae*” to move current genus *Betahypovirus*. We also propose to create a new genus “*Iotahypovirus*” in the family *Hypoviridae* and a new genus “*Deltafusarivirus*” in the *Fusariviridae*. Finally, we propose creation of 51 new species to be classified in these three families, of which 27 in the family *Hypoviridae,* 5 in the newly proposed *“Parahypoviridae”* and 19 in the *Fusariviridae*.  *Justification*:  The original classification of the two families, *Hypoviridae* and *Fusariviridae*, (*Duplopiviricetes*; *Durnavirales*) was not well supported. A newly performed phylogenetic analysis performed on RdRPs of members of the currently recognized classes in the phylum *Pisuviricota* shows strong support for the reclassification of the two families in the class *Stelpaviricetes* and justifying creation of a new order to accommodate both families (and another newly created “*Parahypoviridae*”, proposed here) to recognize their distinction from members of orders *Stellavirales* and *Patatavirales*. Also, importantly, there is a basic difference between members of the *Hypoviridae* (which are infectious as ssRNA) and members of the *Durnavirales* (which are mostly confirmed dsRNA viruses and are not infectious as ssRNA). |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Class, Order, Family, Genus, Species  *Description of current taxonomy*:  Currently, 39 species are included in 8 genera in the family *Hypoviridae* and 34 species are classified in 3 genera in the family *Fusariviridae*. Both families are presently classified in the order *Durnavirales*, in the class *Duplopiviricetes*, the phylum *Pisuviricota*, kingdom *Orthornavirae*, and realm *Riboviria*.  *Proposed* *taxonomic change(s)*:  We propose to reclassify families *Hypoviridae* and *Fusariviridae* by moving them from the current order *Durnavirales* (class *Duplopiviricetes*) to a newly created order, named “*Hypofuvirales*” in the class *Stelpaviricetes*, phylum *Pisuviricota*.  Furthermore, propose to create a new family “*Parahypoviridae*” to move current genus *Betahypovirus.*  We also propose creating the two new genera: the “*Iotahypovirus*” in the family *Hypoviridae* and the “*Deltafusarivirus*” in the family *Fusariviridae*.  Finally, we create a total of 51 new species, of which 27 in the family *Hypoviridae* (11 in the *Alphahypovirus*, 2 in the *Deltahypovirus*, 3 in the *Gammahypovirus*, 1 in the *Etahypovirus*, 2 in the *Zetahypovirus* and 8 new species in the newly established genus “*Iotahypovirus*”), 5 in the newly proposed *“Parahypoviridae”* family (all in the *Betahypovirus* genus) and 19 new species in the family *Fusariviridae* (9 in the *Alphafusarivirus* genus, 5 in the *Betafusarivirus* genus, 4 in the *Gammafusarivirus* genus, and 1 species in the proposed “*Deltafusarivirus”* genus).  *Demarcation criteria:*  We here establish two criteria for belonging to different genera in the family *Hypoviridae* (<20% identity in pairwise alignment of RdRP encoding ORF) and *Fusariviridae* (<30% identity in pairwise alignment of RdRP encoding ORF). In both families, members of new species share below 90% aa identity threshold whole RNA dependent RNA Polymerase (RdRP) encoding ORF.  The same criteria apply for the “*Parahypoviridae*”.  *Justification*:  The family *Hypoviridae* was established with an original taxonomic proposal ratified in 1993. Although not explicitly reported in the proposal, the family was recognized as having a common ancestry with the plant virus infecting family *Potyviridae* (Koonin *et al.*, 1991). A few years later, the common ancestry had also a molecular confirmation when it was shown that plus strand RNA transcripts of the cDNA of Cryphonectria hypovirus 1 were infectious when transfected in *Cryphonectria parasitica* protoplasts (Chen *et al.*, 1994), showing that this group of viruses have a (+)RNA genome and not a dsRNA genome. (which is the replication intermediate that accumulates at high level during infection).  In 2018 the Hypoviridae was included the family in the *Riboviria* (2017.006G.A.v3.Riboviria), while in 2019 the family was associated to dsRNA viruses in the order *Durnavirales* in the *Duplopiviricetes* (2019.006G) based on a comprehensive phylogenetic analysis (Wolf *et al.*, 2018) that was later confirmed with a larger dataset of viral genome sequences (Neri *et al.*, 2022).  The family *Fusariviridae* was established a few years go (2021.001F.R.Fusariviridae\_1newfam in 2021) and was included in the *Durnavirales*/*Duplopiviricetes* because of its close phylogenetic relationship with the family *Hypoviridae*. Infectious clones are not constructed yet for members of this family.  We here revisited the current classification of the two families by comprehensive set of representative members of the families present in the phylum *Pisuviricota*, including a large number of hypovirids and fusarivirids (supplementary file). We derived a phylogenetic tree using as outgroup viruses not included in the *Pisuviricota* with the maximum likelihood methodology implemented in IQ-Tree (Minh *et al.*, 2024). The alignment with clustalOmega (Sievers *et al.*, 2011) correctly showed conservation of the RdRP motifs, thus validating the used approach.  The phylogenetic tree suggested stronger relationships of members of the *Hypoviridae* and *Fusariviridae* to members of orders *Stellavirales* and *Patatavirales*, in the class *Stelpaviricetes* rather than to those classified in the *Durnavirales* (Figure 1) confirming the original observations of evolutionary connection of *Hypoviridae* and *Potyviridae* (included in the *Patatavirales*). Furthermore, the phylogenetic tree shows that species included in the genus *Betahypovirus* are no longer in a monophyletic clade with those in other genera in the *Hypoviridae*. For this reason, we propose to move the genus *Betahypovirus* in a new family named “*Parahypoviridae*”.  A few new fusarivirids sequences are available in the NCBI database that are complete and distinct enough to represent new species. Majority of them were also already described in peer reviewed journals (Hrabakova *et al.*, 2017; Gilbert *et al.*, 2019; Fukunishi *et al.*, 2021; Gao *et al.*, 2021; Gong *et al.*, 2021; Sahin *et al.*, 2021; Abdoulaye *et al.*, 2022; De Miccolis Angelini *et al.*, 2022; Drenkhan *et al.*, 2022; Liu *et al.*, 2022; Xie *et al.*, 2022; French *et al.*, 2023; Liu, C *et al.*, 2023; Ahmed *et al.*, 2024; Buma *et al.*, 2024; Dálya *et al.*, 2024).  Similarly, a score of coding-complete genomes of new or previously unclassified hypovirids are also available in the NCBI database, of which many have been published in peer review journals (Guo *et al.*, 2021; Li *et al.*, 2021; Chen *et al.*, 2022; Liang *et al.*, 2022; Han *et al.*, 2023; Li, S *et al.*, 2023; Li, W *et al.*, 2023; Liu, H *et al.*, 2023; Ribeiro *et al.*, 2023; Wang *et al.*, 2023).  We used the <90% amino acid identity threshold for new species for both families (identity matrix *Hypoviridae* and Identity matrix *Fusariviridae*). The results of identity matrix analyses strongly justify creation of 51 new species and establishment of two new genera (one in the family *Hypoviridae* and one in *Fusariviridae*). |

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| **References:** |
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Integrative Bioinformatics Vienna MPL, University of Vienna and Medical University of Vienna, Vienna, Austria, Schrempf D, Center for Integrative Bioinformatics Vienna MPL, University of Vienna and Medical University of Vienna, Vienna, Austria, Department of Biological Physics ELU, Budapest, Hungary, et al. 2024.** IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Molecular Biology and Evolution* **37**(5): 1530-1534.  **Neri U, Wolf YI, Roux S, Camargo AP, Lee B, Kazlauskas D, Chen IM, Ivanova N, Allen LZ, Paez-Espino D. 2022.** Expansion of the global RNA virome reveals diverse clades of bacteriophages. *Cell* **185**(21): 4023-4037. e4018.  **Ribeiro JM, Hartmann D, Bartošová-Sojková P, Debat H, Moos M, Šimek P, Fara J, Palus M, Kučera M, Hajdušek O. 2023.** Blood-feeding adaptations and virome assessment of the poultry red mite Dermanyssus gallinae guided by RNA-seq. *Communications Biology* **6**(1): 517.  **Sahin E, Keskin E, Akata I. 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*Frontiers in Plant Science* **13**: 996862. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.012F.Uc.v3.Hypofuvirales\_neworder.xlsx |  |
| 2025.012F.N.v2.Hypofuvirales\_neworder\_S1\_IdentitymatrixFusariwithgenera.xlsx |  |
| 2025.012F.N.v2.Hypofuvirales\_neworder\_S2\_IdentitymatrixGeneraHypo.xlsx |  |

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| **Tables, Figures:** |

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**Figure 1:** ML-Phylogenetic trees generated by IQ-Tree (Minh *et al.*, 2024) and visualized with iTOL. The trees were constructed on 215 RdRP amino acid sequences aligned with Clustal-Omega. Best-fit model (Q.pfam+F+R9) for this dataset was determined using Model Finder (Kalyaanamoorthy *et al.*, 2017). Panel A depicts the relationships of the viruses in the proposed new order “*Hypofuvirales*” (red font) with members of orders in the three classes, justifying its classification in the class *Stelpaviricetes*. Essentially the same tree with the expanded “*Hypofuvirales*” clade, to showcase the three families comprised in this order, is presented in the panel B. The three classes are shaded with different colors (see the color key on the lower part of the figure). Presence of red circles illustrates the ultrafast bootstrap support above 92%.