

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create new family “*Potyliviridae”* in the order *Patatavirales* |
| **Code assigned:**  | 2025.009F.Ac.v3.Potyliviridae\_newfam |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
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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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| **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:** |  25/06/2025 |

**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 | **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| W - Withdrawn |  |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 run the quality check and address some typos. |

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

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

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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 |  | 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** |
| *“Potyliviridae”* | Coined from ‘**poty**-**li**ke’ and universal family-rank suffix  |
| *“Potylivirus”* | Coined from ‘**poty**-**li**ke’ and universal genus-rank suffix |
| *“Potylivirus italicum”* | From Italia, a country of sample provenience |
| *“Potylivirus uromyci”* | From the genus name of the host *- Uromyces* |

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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*: Order*Description of current taxonomy*: Order *Patatavirales* currently includes a single family, *Potyviridae* (13 genera; 259 species). *Proposed* *taxonomic change(s):* To create a second family in the order *Patatavirales*, with proposed name “*Potyliviridae*” comprising one new genus (“*Potylivirus*”) to classify two new species.*Justification*:Creation of a new family “*Potyliviridae*” comprising a new genus “*Potylivirus*” with two species is proposed to classify recently discovered group of viruses with monocistronic (+)RNA genomes of ≈7.5-8.0 kb in length. Members of the “*Potyliviridae*” are distantly related to members of the family *Potyviridae*, in particular to viruses belonging to the genus *Potyvirus*. The creation of a new family is strongly supported by phylogenetic analyses.  |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Order*Description of current taxonomy*: Order *Patatavirales* currently includes a single family, *Potyviridae* (13 genera and 259 species). *Proposed* *taxonomic change(s)*: To create a second family in the order *Patatavirales*, with proposed name “*Potyliviridae*”, comprising one new genus (“*Potylivirus*”) with two new species.*Demarcation criteria:*Proposed species demarcation criteria are similar to those currently adopted in the closest taxon, family *Potyviridae*. Therefore, genomes of viruses belonging to different species differ by up to 25% in nucleotide sequences of complete ORFs and/or 20% amino acid sequences of the entire polyproteins. Viruses of the family must be monophyletic in RdRP-based phylogenetic analyses. *Justification*: *Potyviridae* is the largest family of plant-infecting viruses with (+)RNA genomes, with 259 currently established species included in 13 genera, of which more than 80% (total of 214) belong to the “founding” genus *Potyvirus* [5,11]. Currently, *Potyviridae* is the sole taxon in the order *Patatavirales* and its viruses are distantly related to those of *Astroviridae*, a family of animal-infecting viruses classified in the order *Stellavirales*. Potyviruses are naturally transmitted by aphids in a non-persistent manner. Many members of this genus can cause substantial economic damage, in terms of yield quality and quantity, to various major crops worldwide. Potyviruses are characterized by their filamentous, flexuous virions of ca 700–900 x 11–13 nm in size and non-segmented polyadenylated RNA genomes of 9.7–11 kb with a virus protein (VPg) covalently linked to the 5’ ends of the genomes. The major ORF, encompassing >90% of the genome, codes for a long polyprotein that is self-cleaved into a set of 10 functional proteins (Figure 1). An additional small ORF, named PIPO (pretty interesting *Potyviridae* ORF) is expressed via translational slippage mechanism as a *trans*-frame P3N-PIPO protein [5,11]. Recent exploration of the fungal virome has revealed several potyvirus-related viruses via determination and analysis of coding-complete [2,6], or partial [10] genome sequences. In addition, there are several unpublished sequences available in GenBank as well as those generated in recent studies by the authors of this proposal (Aboughanem-Sabanadzovic et al, unpublished data). Genomes of these viruses, reported in literature as ‘poty-like’ viruses (PLVs), are shorter than those of potyviruses (7.8–8.0 kb versus 10–11 kb) and lack the 3’-terminal polyA tails. They have a uniform genome organization and code for a single major polyprotein of ≈280K with conserved domains of DEAD-like helicase, C4 peptidase and RNA-directed RNA polymerase [2,6,10], as revealed by searches against the NCBI’s Conserved Domain Database. PLVs are most closely related to each other (percentage identities reported in Table 1). However, BLASTp searches revealed that PLV polyproteins also share similarities with counterparts encoded by bona fide potyviruses, especially in their C-terminal halves. Indeed, sometimes these viruses are erroneously considered as members of a putative new genus in the family *Potyviridae* [10].Phylogenetic analyses performed on viral RdRPs of PLVs and selected representative viruses of genera in the families *Potyviridae* and *Astroviridae* showed that PLVs share an immediate common ancestor with the potyvirids, but belong to a different evolutionary lineage in the order *Patatavirales* (Figure2), supporting the establishment of a second family. Pairwise comparisons of ≈180–200 C-terminal amino acid sequences revealed high level of conservation (52–65%) between the polyproteins of all 5 PLVs used in the current analyses. Structural modeling of the C-terminal region (230 aa) of the polyprotein encoded by Plasmopara viticola lesion associated ‘poty-like’ virus 1 (PvLaPLV1) using AlphaFold3 yielded a good quality model with a central alpha-helical domain and unstructured N- and C-terminal extensions. DALI search using this model produced significant hits (Z scores of 10-12) to the experimentally determined capsid protein structures of potyvirids (Figure 3) and other plant viruses with flexible filamentous virions. Notably, the unstructured N- and C-terminal regions typical of flexible filamentous virus CPs are known to be important for capsid protein polymerization and virion flexibility [3,12]. The presence of similar extensions in the PLV CPs suggests that they also form flexible filamentous virions, similar to those of potyvirids.In summary, based on literature review and our own analyses, we propose creation of a new (second) family “*Potyliviridae*” in the order *Patatavirales,* comprising one genus and two species to classify viruses represented by coding-complete genomes and described in peer-reviewed publications [2,6]. The number of family members is destined to grow in the near future, as supported by data of some additional related viruses that are currently incompletely sequenced [10], or awaiting official publication (Aboughanem-Sabanadzovic et al, unpublished data). |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
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| **Tables, Figures:**  |

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**Figure 1.** Schematic representation of genome organization of potato virus Y (PVY; X12456.1) and Plasmopara viticola lesion associated poty-like virus 1 (PvLaPLV1), typical members of the genus *Potyvirus* (family *Potyviridae*) and proposed genus “*Potylivirus”* (family “*Potyliviridae*”). Overall genome lengths (in case of PVY excluding polyA tail) and molecular weight of respective polyproteins encoded by long ORFs are indicated in parentheses. Genomes are represented by lines and the long ORFs coding for polyproteins by boxes with the mature proteolytic products indicated with different colors. The non-translated regions (NTRs) are represented by short lines on each end of the long ORFs. Circles at the 5’ end of the PVY genome depict virus-encoded VPg covalently attached to the initial (5’-terminal) nucleotide. 6K1: 6kDa peptide 1; 6K2: 6kDa peptide 2; C4: C4 peptidase; CI: cylindrical inclusion CP: coat protein; DEXDc: DEXDc helicase; HC-Pro: helper component protease; NIa-Pro: nuclear inclusion a protease; NIb: nuclear inclusion b; P1: protein 1 protease; P3: protein 3; PIPO: pretty interesting *Potyviridae* ORF; RdRP: RNA-directed RNA polymerase; VPg: virus protein-genome linked.

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**Figure 2.** Maximum-likelihood phylogenetic tree showing the relationships of members of the proposed family “*Potyliviridae*” (shaded in pink) with viruses classified in the *Potyviridae*, a sole currently recognized family in the order *Patatavirales*. Viruses of the family *Astroviridae* were used as an outgroup from a sister-order, *Stellavirales*. “Potylivirids” form a strongly supported clade distinct from the family *Potyviridae*. The tree was constructed on a dataset of MAFFT-aligned amino acid sequences of RNA-directed RNA polymerases using IQ-TREE v 1.6.11 [7] with the 1,000 replicates ultrafast bootstrap [3] under best-fit model “LG+I+G4” and visualized with iTOL v7 [6]. The GenBank accession numbers of RdRP amino acid sequences used for analyses along with virus names are indicated at the tips of branches. Ultrafast bootstrap values above 95% are indicated. Viruses proposed to represent two new species are indicated in bold. PvLaPLV1: Plasmopara viticola lesion associated poty-like virus 1; UrPVA: Uromyces potyvirus A; MpPLV1: Macrophomina phaseolina poty-like virus 1; SwPaPLV1: sweet potato associated poty-like virus 1.



**Figure 3.** The comparison of the predicted structure of a putative coat protein (CP) of Plasmopara viticola lesion associated poty-like virus 1 (PvLaPLV1, left) with the experimentally determined CP structure of a representative potyvirus, watermelon mosaic virus (right). Structural similarity between the two proteins strongly suggests that members of the proposed family “*Potyliviridae*” form filamentous and flexuous virions similar to those of potyvirids. The structure of PvLaPLV1 CP was predicted using AlphaFold3 [1]. The central alpha-helical domains of the CPs are colored using the rainbow scheme from blue (N-terminus) to red (C-terminus), whereas the N- and C-terminal unstructured extensions are shown in grey. **Table 1.** Percentage (%) identity between ‘poty-like’ viruses in the complete nucleotide sequences (above the diagonal) and amino acids of the polyprotein. Two viruses proposed to represent two species in the proposed genus “*Potylivirus*” are reported in red font.

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|  | PvLaPLV1 | UrPVA | MpPLV\* | SwPaPLV1\*\* | CaPLV1\*\* |
| PvLaPLV1 |  | 50.87 | 46.61 | 49.10 | 50.59 |
| UrPVA | 40.46 |  | 46.72 | 48.75 | 68.55 |
| MpPLV\* | 34.67 | 34.60 |  | 49.77 | 46.25 |
| SwPaPLV1\*\* | 41.89 | 41.17 | 37.70 |  | 49.05 |
| CaPLV1\*\* | 40.50 | 74.33 | 35.54 | 40.56 |  |

\*- Incomplete genome (missing ≈500 nt at the 5’end)

\*\*- Unpublished data (complete genomes)