

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create one new family, one genus and 9 species in the order *Martellivirales* |
| **Code assigned:**  | 2025.008F.N.v2.Tobaliviridae\_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:** |  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| W - Withdrawn |  |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:** |
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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**

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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** |
| *Tobaliviridae* | Coined from “**toba**mo-**li**ke” and universal family-rank suffix “viridae” |
| *Tobalivirus* | Coined from “**toba**mo-**li**ke”and universal genus-rank suffix “virus” |
| *Tobalivirus acidomyci* | From the name of the host genus - *Acidomyces* |
| *Tobalivirus armillariae* | From the name of the host genus - *Armillaria* |
| *Tobalivirus auricolariae* | From the name of the host genus - *Auricolaria* |
| *Tobalivirus ibericum* | From the geographic location – Iberia (Iberian Peninsula) |
| *Tobalivirus macrophominae* | From the name of the host genus - *Macrophomina* |
| *Tobalivirus lentinulae* | From the name of the host genus - *Lentinula* |
| *Tobalivirus nigrosporae* | From the name of the host genus - *Nigrospora* |
| *Tobalivirus podosphaerae* | From the name of the host genus - *Podosphaera* |
| *Tobalivirus uromyci* | From the name of the host genus - *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, family, genus, species*Description of current taxonomy*: The order *Martellivirales* currently contains seven families (*Bromoviridae, Closteroviridae, Endornaviridae, Kitaviridae, Mayoviridae, Togaviridae* and *Virgaviridae*) of (+)RNA viruses encoding alphavirus-like replicases.*Proposed* *taxonomic change(s):* We propose establishing a new family “*Tobaliviridae*” in the order *Martellivirales* to classify a growing group of “tobamo-like” viruses characterized from fungi. The proposed family will contain a single genus “*Tobalivirus*” with nine species. *Justification*:Despite obvious similarities in genome organization and possible expression strategy between tobamoviruses (family *Virgaviridae*) and “tobamo-like” mycoviruses, differences in:* primary hosts (plant versus fungi)
* genome size (6.3-6.6 versus 10-13 kb),
* size and nature of proteins encoded by ORF3,
* CP size (17 kDa versus 36 kDa),
* virion morphology (rigid versus flexuous rods) and
* phylogenetically distinct RdRP lineage

justify the proposal for creation of a new family “*Tobaliviridae*” with a single genus, “*Tobalivirus*”, containing nine species to classify a set of well-characterized viruses.  |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Order, family, genus, species*Description of current taxonomy*: The order *Martellivirales* currently contains seven families (*Bromoviridae, Closteroviridae, Endornaviridae, Kitaviridae, Mayoviridae, Togaviridae* and *Virgaviridae*) of (+)RNA viruses encoding alphavirus-like replicases.*Proposed* *taxonomic change(s)*: We propose establishing a new family “*Tobaliviridae*” to classify a growing group of viruses reported from fungi and oomycetes. The proposed family will contain a single genus, “*Tobalivirus*”, with nine species. *Demarcation criteria:*Species demarcation is based on phylogenetic relationships of their members and differences of >10% in amino acid content in all virus-encoded products. Proposed family is monogenic; therefore, genus demarcation criteria do not apply at this time. *Justification*: A group of as of yet unclassified mycoviruses with non-segmented (+)RNA genomes of approximately 10-13 kb in size and evolutionarily related to members of the family *Virgaviridae*, in particular to viruses classified in the genus *Tobamovirus*, has been reported from virome studies of several different fungi and the meta sample of grapevine leaf lesions caused by the oomycete *Plasmopara viticola*. Accordingly, in published scientific literature they are commonly referred to as “tobamo-like viruses” [2-6, 13-18] or “mycovirgaviruses” [11, 12]. However, for the sake of simplicity, in this proposal, we will use originally coined terminology “tobamo-like viruses” or TLVs. From a larger pool of TLV sequences available in the GenBank, we selected only those with complete or coding-complete genomes and with associated peer-reviewed publications representing the proposed species. Tobamoviruses are plant-infecting viruses that belong to the family *Virgaviridae* and contain non-segmented (+)RNA genomes encapsidated in rigid rod-shaped virions of 300 x 18nm in size [1]. Their quadricistronic genomes of approximately 6.3-6.6 kb in size have a “cap” at the 5’-end, whereas the 3’-terminal sequences fold to form a tRNA-like, amino acid-accepting, structure. The two 5’-proximal ORFs, coding for proteins involved in virus replication (replicase, REP), are translated directly from genomic RNA. ORF1 codes for ~125-130 kDa protein with conserved motifs of viral methyltransferase (MTR) and helicase (Hel). ORF2 encodes RNA-dependent RNA polymerase (RdRP) and is expressed by occasional readthrough of the “leaky” ORF1 termination (amber; UAG) codon as a fusion polyprotein of 180-190 kDa. ORFs 3 and 4 encode the movement (MP) and coat proteins (CP), respectively, and are translated from the two 3’-coterminal subgenomic RNAs (sgRNAs) [1].TLVs have significantly larger genomes than tobamoviruses (10-13 kb vs 6.3-6.6 kb) (Figure 1). Additionally, genomes of several TLVs do not have tRNA-like structures at their 3’ends but rather terminate with a polyA tract [5, 8,11,12,15]. Concerning the host range, tobamoviruses (and virgavirids in general) exclusively infect plants, whereas TLVs infect fungi.Nevertheless, TLVs share similarities with tobamoviruses in overall genome organization, that strongly suggest similar expression strategies too. As in tobamoviruses, genomes of most TLVs contain four ORFs (Fig 1). The two 5’-proximal ORFs code for the replicase complex and are translated directly from the genomic RNA, through a “readthrough” mechanism involving the suppression of the termination codon at the end of ORF1, yielding a large polyprotein containing hallmark domains of alphavirus-like replicases: methyltransferase (MTR; cl46422), viral helicase 1 (HEL1; cl26263) and RNA-dependent RNA polymerase 2 (RdRP\_2; cl03049). MTR and HEL1 are encoded by ORF1, whereas RdRP\_2 is likely translated from ORF2 via readthrough mechanism to give rise to a large (240-270 kDa) polyprotein with a role in virus replication. Expression products of ORFs 1 and 2 of TLVs are homologous to the counterparts encoded by members of the plant-infecting tobamoviruses. In phylogenetic analyses of the viral RdRPs with those of members of the order *Martellivirales* (Figure 2), all studied TLVs grouped together to form a sister-clade to virgavirids indicating that they belong to a taxon distinct from the family *Virgaviridae*. Monophyly of TLVs used in the dataset was supported by 100% bootstrap value. ORFs 3 and 4 are likely expressed from corresponding subgenomic RNA templates. ORF3 of TLVs codes for a large protein (90-115 kDa, depending on the virus) which is conserved among all known tobamo-like viruses and characterized by the presence of the DEXDc helicase motifs (cl28899). In the original literature, ORF3 has been referred to as the “movement protein”, in part because of BLASTP matches to protein sequences of several gammaflexiviruses annotated as MPs (but not experimentally confirmed). Furthermore, the conserved DEXDc domain from TLVs was identities with the CIs of plant viruses in the *Potyviridae* family [8]. The real function of this protein is yet to be experimentally ascertained. ORF4 homologs code for a protein of uniform size (36-38 kDa) with shared amino acid sequences among TLVs and assumed to be a structural (coat) protein involved in virion formation. However, TLV-encoded proteins are double in size (36-38 kDa vs 17kDa) and lack significant identities with tobamovirus CPs, suggesting a different virion morphology. Indeed, a recent study on characterization of Nigrospora aurantiaca tobamo-like virus 1 (NaTLV1) provided an experimental proof for the flexuous nature of NaTLV1 virions based on results of electron microscopy observations of 1,100 nm long filamentous virus-like particles and presence of a major ~37 kDa band in SDS-PAGE analyses of purified virus preparations [8]. In conclusion, despite obvious similarities in genome organization and possible genome expression between plant-infecting tobamoviruses and a group of “tobamo-like” mycoviruses, we think that differences in:* genome size
* size and nature of proteins encoded by ORF3,
* CP size and virion morphology
* RdRP-based phylogeny and
* host

justify the creation of a new family “*Tobaliviridae*” with a single genus “*Tobalivirus*” containing nine species to classify a set of well-characterized viruses.  |
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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
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| **Tables, Figures:**  |

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**Figure 1**. Schematic depiction of genome organization of tobacco mosaic virus (TMV), a typical tobamovirus (panel A), and a few representative members of the proposed family “*Tobaliviridae*” (panel B). Black circle in TMV genome depicts the 5’ cap, while black rectangle indicates 3’ tRNA-like structure. CP: coat protein; DEXDc: DEXDc helicase; Hel: viral helicase 1; MTR: methyltransferase; ORF: open reading frame; RdRP: RNA-dependent RNA polymerase 2; AAAA: short poly A tail. For extended virus names of tobaliviruses please refer to Table 1 and associated Excel spreadsheet.

**Figure 2.** Maximum-likelihood phylogenetic tree showing the relationships of members of the proposed family “Tobaliviridae” (shaded in yellow) with viruses classified in seven currently recognized families of the order *Martellivirales*. “Tobaliviruses” form a strongly supported monophyletic clade, evolutionarily distinct from other families in the order. The tree was constructed on the MAFFT-aligned amino acid sequences of RdRPs using IQ-TREE v 1.6.11 [14] with the 1,000 replicates ultrafast bootstrap [7] under best-fit model “LG+F+I+G4” according to BIC as estimated by ModelFinder [9] and visualized with iTOL v7 [10]. The GenBank accession numbers of RdRP amino acid sequences used for analyses along with virus names are indicated at the tips of branches. Presence of red dot on branching point indicates statistical support of >90% with size corresponding to level of bootstrap values. Names of viruses proposed to represent new species listed in this proposal are indicated in bold.

**Table 1.** List of the species in the proposed new family “*Tobaliviridae*”, along with exemplar viruses, their acronyms, corresponding GenBank accessions and associated publications.

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| **Genus** | **Species name** | **Virus name** | **Acronym** | **GenBank** | **Ref** |
| *Tobalivirus* | *Tobalivirus acidomyci* | Acidomyces richmondensis tobamo-like virus 1 | ArTLV1 | MK279511 | 5 |
|  | *Tobalivirus armillariae* | Armillaria borealis mycovirgavirus 1 | AbMV1 | MW423800 | 12 |
|  | *Tobalivirus auricolariae* | Auricularia heimuer mycovirgavirus 1 | AhMV1 | MN928963 | 11 |
|  | *Tobalivirus ibericum* | Plasmopara viticola lesion associated tobamo-like virus 1 | PvLaTLV1 | MN565665 | 2 |
|  | *Tobalivirus macrophominae* | Macrophomina phaseolina tobamo-like virus | MpTLV | KF537660 | 13 |
|  | *Tobalivirus lentinulae* | Lentinula edodes tobamo-like virus 1 | LeTLV1 | MN744727 | 6 |
|  | *Tobalivirus nigrosporae* | Nigrospora aurantiaca tobamo-like virus 1 | NaTLV1 | OR228589 | 8 |
|  | *Tobalivirus podosphaerae* | Podosphaera prunicola tobamo-like virus | PpTLV | KY420046 | 15 |
|  | *Tobalivirus uromyci* | Uromyces fabae virus | UFV | OQ995224 | 17 |