

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Botourmiaviridae reorganization |
| **Code assigned:** | 2025.013F.N.v2.Botourmiaviridae\_reorgan | |

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| **Author(s), affiliation and email address(es):** | | | | |
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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:** |
| *Botourmiaviridae* Study Group |

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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** |
| All members | 7 | 0 | 0 |

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| **Submission date:** | 10/06/2025 |

**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| W - Withdrawn |  |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 |  |
| 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** |
| Ourmiaviridae | Derived from *Ourmiavirus* |
| Rhizouliviridae | Derived from *Rhizoulivirus* |
| Alphaourmiavirus |  |
| Betaourmiavirus |  |
| Gammaourmiavirus |  |
| Deltaourmiavirus |  |
| Epsilonourmiavirus |  |
| Zetaourmiavirus |  |
| Etaourmiavirus |  |
| Thetaourmiavirus |  |
| Iotaourmiavirus |  |
| Kappaourmiavirus |  |

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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*:  Genus, Family, Order  *Description of current taxonomy*:  The family *Botourmiaviridae* currently the only family in the order *Ourlivirales.* It includes twelve genera with 159 species: *Ourmiavirus*, *Botoulivirus*, *Betabotoulivirus*, *Magoulivirus*, *Scleroulivirus*, *Betascleroulivirus*, *Deltascleroulivirus*, *Gammascleroulivirus*, *Epsilonscleroulivirus*, *Rhizoulivirus*, *Betarhizoulivirus*, and *Penoulivirus*.  *Proposed* *taxonomic change(s):*  We propose to create two new families “*Ourmiaviridae”* and *“Rhizouliviridae”* in the order *Ourliviriales* by reorganizing current family *Botourmiaviridae* to better reflect phylogenetic relationships among members of this order of (+)RNA viruses.  *Justification*: Results of updated phylogenetic analyses of the RNA dependent RNA polymerases (RdRPs) of viruses belonging to the family *Botourmiaviridae* and newly characterized, related and yet unclassified, viruses showed three main clades supported by high bootstrap values. One group includes ten genera currently classified in the family *Botourmiaviridae,* second clade is composed of the two genera (*Rhizoulivirus* and *Betarhizoulivirus*) of viruses exclusively reported from the basidiomycetous hosts*,* while the third comprises members of the three plant-infecting members of a current genus *Ourmiavirus* along withseveral recently sequenced closely related viruses*.* The three well-supported clades are proposed to represent three families in the order *Ourlivirales*. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus, Family, Order  *Description of current taxonomy*:    The family *Botourmiaviridae* currently includes twelve genera with 159 species: *Ourmiavirus*, *Botoulivirus*, *Betabotoulivirus*, *Magoulivirus*, *Scleroulivirus*, *Betascleroulivirus*, *Deltascleroulivirus*, *Gammascleroulivirus*, *Epsilonscleorulivirus*, *Rhizoulivirus*, *Betarhizoulivirus*, and *Penoulivirus*. With the exception of the genus *Ourmiavirus*, that includes plant viruses with a genome divided in three segments, the remaining members of the family are viruses that infect fungi. Genera *Rhizoulivirus* and *Betarhizoulivirus* include exclusively viruses that infect fungi of the *Basydiomicota* division, specifically, genera *Armillaria* and *Rhizoctonia*.  *Proposed* *taxonomic change(s)*:  We propose creation of two new families in the order *Ourliviriales* by reorganization of current complex family *Botourmiaviridae* by moving/reclassifying genera *Rhizoulivirus and Betarhizoulivirus* to a new family *“Rhizouliviridae”* and a genus *Ourmiavirus* in the new family *“Ourmiaviridae”.*  Furthermore, we propose creation of 10 new genera comprising 25 new species in the family “*Ourmiaviridae*” to classify newly characterized viruses.  *Demarcation criteria:*  The demarcation criteria for genera in the families “*Ourmiaviridae*” and “*Rhizouliviridae*” have been stablished at >35% amino acid identity of the RdRP.  Amino acid sequence identities of putative RdRP proteins between viruses belonging to different species is less that 80%.  *Justification*:    Phylogenetic analysis of the amino acid sequences of the RNA-directed RNA polymerase (RdRP) of viruses inside the current family *Botourmiaviridae* (Ayllón et al. 2020; Donaire et al. 2024), and viruses related to ourmiaviruses, show a phylogenetic tree with three independent main groups supported by bootstrap values >97% (Figure 1).  One of the main groups with a strong statistical support is constituted by two genera, *Rhizoulivirus* and *Betarhizoulivirus*, based in this clear differentiation we propose the creation of a new family, “*Rhizouliviridae*”, to include both genera. This new classification is additionally supported by the fact that these two genera include only mycoviruses infecting fungi of the *Basidiomycota* division (*Armillaria* and *Rhizoctonia*).  Other main group, supported by a bootstrap value of 100%, included members of the genus *Ourmiavirus*, and many other related ourmia-like viruses. This clear phylogenetic separation prone us to propose the creation of the new family “*Ourmiaviridae*” to include the genus *Ourmiavirus* and related viruses reported from numerous HTS-based studies on “viromes”-associated with different plants and animals (birds, fishes, arthropods, mollusks) (Shi et al. 2016; François et al. 2019; Stanojević et al. 2020; Yang et al. 2022; Lu et al. 2024; Zhang et al. 2024; Mao et al. 2024; Martínez-Fajardo et al. 2024), riverbank sediments or water, or different soil ecosystems(Chen et al. 2022; French et al. 2022; Sadiq et al. 2024). To classify new viruses, we propose to create 25 new species in 10 new genera in the family “Ourmiaviridae”. Anyway, the original hosts of these viruses is yet to be experimentally ascertained. Except for the members of the genus O*urmiavirus*, which have three-segmented genomes, the viruses in other genera of all three families have nonsegmented, RdRP-encoding genomes.  Comparison between current and proposed organization of the order *Ourliviriales* with reorganized current family *Botourmiaviridae* and additional two new families “*Rhizouliviridae*” and “*Ourmiaviridae*” is presented in Table 1. |

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| * Ayllón MA, Turina M, Xie J, Nerva L, Marzano SL, Donaire L, Jiang D, Consortium IR. ICTV Virus Taxonomy Profile: Botourmiaviridae. J Gen Virol. 2020 May;101(5):454-455. doi: 10.1099/jgv.0.001409. Epub 2020 Apr 24. PMID: 32375992; PMCID: PMC7414452. * Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T. trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics. 2009 Aug 1;25(15):1972-3. doi: 10.1093/bioinformatics/btp348. Epub 2009 Jun 8. PMID: 19505945; PMCID: PMC2712344. * Chen YM, Sadiq S, Tian JH, Chen X, Lin XD, Shen JJ, Chen H, Hao ZY, Wille M, Zhou ZC, Wu J, Li F, Wang HW, Yang WD, Xu QY, Wang W, Gao WH, Holmes EC, Zhang YZ. RNA viromes from terrestrial sites across China expand environmental viral diversity. Nat Microbiol. 2022 Aug;7(8):1312-1323. doi: 10.1038/s41564-022-01180-2. Epub 2022 Jul 28. PMID: 35902778. * Donaire L, Xie J, Nerva L, Jiang D, Marzano SL, Sabanadzovic S, Turina M, Ayllón MA. 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| **Accompanying files:** | |
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| **Tables, Figures:** |

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**Figure 1.** Phylogenetic tree of the order *Ourlivirales*, including the family *Botourmiaviridae* and two proposed families “*Ourmiaviridae*” and “*Rhizouliviridae*”. Included are only viruses proposed as representative of species in each of the two proposed families.

![A blue and green graph

AI-generated content may be incorrect.]()**Figure 2**. Matrix diagram of amino acid identities of RNA dependent-RNA polymerase (RdRP) proteins among members of the genera in the families *Botourmiaviridae*, and “*Rhizouliviridae*” and “*Ourmiaviridae*”. The percent identity matrixes were created via multiple sequence alignment in R.



**Figure 3.** Identity matrix of amino acid identities of RNA dependent-RNA polymerase (RdRP) proteins among members of the proposed family “*Ourmiaviridae*”.

**Table 1.** Current and proposed organization of the order *Ourlivirales*. Proposed new taxa are reported in red font, those moved from current family *Botourmiaviridae* are listed in blue.

**Current Proposed**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Family** | **Genus** |  | **Family** | **Genus** |
| *Botourmiaviridae* | *Betabotoulivirus* |  | *Botourmiaviridae* | *Betabotoulivirus* |
| (12 genera) | *Betarhizoulivirus* |  | (9 genera) | *Betascleroulivirus* |
|  | *Betascleroulivirus* |  |  | *Botoulivirus* |
|  | *Botoulivirus* |  |  | *Deltascleroulivirus* |
|  | *Deltascleroulivirus* |  |  | *Epsilonscleroulivirus* |
|  | *Epsilonscleroulivirus* |  |  | *Gammascleroulivirus* |
|  | *Gammascleroulivirus* |  |  | *Magoulivirus* |
|  | *Magoulivirus* |  |  | *Penoulivirus* |
|  | *Ourmiavirus* |  |  | *Scleroulivirus* |
|  | *Penoulivirus* |  |  |  |
|  | *Rhizoulivirus* |  | “*Rhizouliviridae*” | *Betarhizoulivirus* |
|  | *Scleroulivirus* |  |  | *Rhizoulivirus* |
|  |  |  |  |  |
|  |  |  | “*Ourmiaviridae*” | *Ourmiavirus* |
|  |  |  |  | *“Alphaourmiavirus”* |
|  |  |  |  | *“Betaourmiavirus”* |
|  |  |  |  | *“Gammaourmiavirus”* |
|  |  |  |  | *“Deltaourmiavirus”* |
|  |  |  |  | *“Epsilonourmiavirus”* |
|  |  |  |  | *“Etaourmiavirus”* |
|  |  |  |  | *“Iotaourmiavirus”* |
|  |  |  |  | *“Kappaourmiavirus”* |
|  |  |  |  | *“Thetaourmiavirus”* |
|  |  |  |  | *“Zetaourmiavirus”* |