

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create eight [8] new species in the genus *Orthotospovirus* (*Elliovirales*: *Tospoviridae*) |
| **Code assigned:** | 2025.007P.Tospoviridae\_8nsp | |

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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 |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
| *Tospoviridae* 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** |
| *Tospoviridae* | **7** | **-** | **-** |
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| **Submission date:** | 15/06/2025 |

**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| W - Withdrawn |  |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** |
| *Orthotospovirus tomatonecroanuli* | host plant, symptom |
| *Orthotospovirus limonii* | host plant genus where it was first described |
| *Orthotospovirus barlerichlorosis* | host plant genus where it was first described, symptom |
| *Orthotospovirus scadoxiflavianuli* | host plant genus where it was first described, symptom |
| *Orthotospovirus macadamianuli* | host plant genus where it was first described, symptom |
| *Orthotospovirus mercurialis* | host plant genus where it was first described |
| *Orthotospovirus capsiciflavianuli* | host plant genus where it was first described, symptom |
| *Orthotospovirus tomatonecromaculae* | host plant where it was first described, symptom |

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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  *Description of current taxonomy*:  *Negarnaviricota, Polyploviricotina, Bunyaviricetes, Elliovirales, Tospoviridae, Orthotospovirus.*  The genus *Orthotospovirus*, in the family *Tospoviridae,* currently includes 28 virus species.  *Proposed* *taxonomic change(s):*  Classification of eight (8) novel orthotospoviruses into new species in the genus *Orthotospovirus*, on the basis of the species demarcation criterion in the % amino acid sequence identity (<90%) of the nucleocapsid protein (N).  *Justification*:  The identity value of the nucleocapsid (N) protein sequence of the eight novel orthotospoviruses to other established orthotospoviruses and across themselves, is below 90%, satisfying the criterion for novel species demarcation in the genus *Orthotospovirus* based on sequence identity of the amino acid sequence of the N protein. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus, species  *Description of current taxonomy*: The genus *Orthotospovirus* in the family *Tospoviridae* currently includes 28 species: *Orthotospovirus alstroemeriflavi, Orthotospovirus alstroemerinecrosis, Orthotospovirus arachianuli, Orthotospovirus arachiflavamaculae, Orthotospovirus arachiflavi, Orthotospovirus arachinecrosis, Orthotospovirus callaflavi, Orthotospovirus capsiciflavi, Orthotospovirus capsicimaculaflavi, Orthotospovirus chrysanthinecrocaulis, Orthotospovirus citrullomaculosi, Orthotospovirus citrullonecrosis, Orthotospovirus cucurbichlorosis, Orthotospovirus eustomae, Orthotospovirus fatsiae, Orthotospovirus glycininecrovenae, Orthotospovirus hippeflavi, Orthotospovirus impatiensnecromaculae, Orthotospovirus iridimaculaflavi, Orthotospovirus meloflavi, Orthotospovirus melotessellati, Orthotospovirus morivenae, Orthotospovirus phaseolinecrotessellati, Orthotospovirus polygonianuli, Orthotospovirus tomatanuli, Orthotospovirus tomatoflavi, Orthotospovirus tomatomaculae, Orthotospovirus tomatozonae*  *Proposed* *taxonomic change(s)*:  Following examination of the literature and NCBI GenBank sequence repository, we here propose the classification of eight novel orthotospoviruses as members of eight new species in the genus *Orthotospovirus*  *Demarcation criteria:*  Species demarcation criteria: % amino acid sequence identity (<90%) of the nucleocapsid protein (N).  *Justification*:  **Creation of a first novel species in the genus *Orthotospovirus***  The complete genome sequence of tomato necrotic ringspot virus (TNRV) was determined from chilli plants (*Capsicum annuum*) by high-throughput sequencing and Sanger sequencing of cDNA amplicons [1] and is available in NCBI GenBank under accession numbers MW256413, MW256414, MW256415. The highest identity value of the N protein sequence between TNRV and other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), TNRV falls into the “Asian clade 1”. We propose to classify TNRV as a member of a novel species, named “*Orthotospovirus tomatonecroanuli*”, from the host plant where it was first described and the symptom observed.  **Creation of a second novel species in the genus *Orthotospovirus***  The complete genome sequence of Limonium orthotospovirus 1 (LOV1) was determined from *Limonium sinuatum* using high-throughput sequencing [2], and is available in NCBI GenBank under accession numbers PQ587430, PQ587431, PQ587432. The highest identity value of the N protein sequence to other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), LOV1 falls into the “American clade”. We propose to classify LOV1 as a member of a novel species, named “*Orthotospovirus limonii*”, from the host plant genus where it was first described, adopting the name proposed by the authors in the original publication.  **Creation of a third novel species in the genus *Orthotospovirus***  The complete genome sequence of Barleria chlorosis-associated virus (BCaV) was determined by RNAseq [3] and is available in NCBI GenBank under accession numbers MW251496, MW251497, MW251498. The highest identity value of the N protein sequence between BCaV and other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), BCaV appears as the unique member of a novel branch. We propose to classify BCaV as a member of a novel species, named “*Orthotospovirus barlerichlorosis*”, from the host plant genus where it was first described and the symptom observed.  **Creation of a fourth novel species in the genus *Orthotospovirus***  The complete genome sequence of Scadoxus chlorotic ringspot virus (ScCRV) was determined from *Scadoxus puniceus* by high-throughput sequencing and sequencing Rapid Amplification of cDNA Ends amplicon products [4], and is available in NCBI GenBank under accession numbers MW080808, MW080809, MW080810. The highest identity value of the N protein sequence between ScCRV and other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), ScCRV groups closest to members of the “Eurasian clade”. We propose to classify ScCRV as a member of a novel species, named “*Orthotospovirus scadoxiflavianuli*”, from the host plant genus where it was first described and the symptom observed.  **Creation of a fifth novel species in the genus *Orthotospovirus***  The coding-complete genome sequence of Mercurialis orthotospovirus 1 (MerV1) was determined from *Mercurialis annua* by metatranscriptome analyses [5], and is available in NCBI GenBank under accession numbers OL471964, OL471965, OL471966 (Metagenome Assembled Genome). The highest identity value of the N protein sequence between MerV1 and orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), MerV1 groups closest to ScCRV and members of the “Eurasian clade”. We propose to classify MerV1 as a member of a novel species, named “*Orthotospovirus mercurialis*”, from the host plant genus where it was first described.  **Creation of a sixth novel species in the genus *Orthotospovirus***  The complete genome sequence of Macadamia ringspot-associated virus (MRSV) was determined from *Macadamia integrifolia* by high-throughput sequencing [6], and is available in NCBI GenBank under accession numbers OP604037, OP604038, OP604039 (Metagenome Assembled Genome). The highest identity value of the N protein sequence between MRSV and other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), MRSV groups closest to members of the “Asian clade 2”. We propose to classify MRSV as a member of a novel species, named “*Orthotospovirus macadamianuli*”, from the host plant genus where it was first described and the symptom observed.  **Creation of a seventh novel species in the genus *Orthotospovirus***  The complete genome sequence of chilli yellow ringspot virus isolate (CYRSV) was determined by high-throughput sequencing and sequencing of cloned cDNA amplicons [7], and is available in NCBI GenBank under accession numbers MH779495, MH779496, MH779497. The highest identity value of the N protein sequence between CYRSV and other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), CYRSV falls into the “Asian clade 1”. We propose to classify CYRSV as a member of a novel species, named “*Orthotospovirus capsiciflavianuli*”, from the host plant genus where it was first described and the symptom observed.  **Creation of an eight novel species in the genus *Orthotospovirus***  The complete genome sequence of tomato necrotic spot-associated virus (TNSaV) was determined via sequencing of cloned cDNA amplicons [8, 9]), and is available in NCBI GenBank under accession numbers KM355773, KT984753, KT984754. The highest identity value of the N protein sequence between TNSaV and other orthotospoviruses is below the species demarcation criterion of the genus *Orthotospovirus* (Table 1). In the phylogenetic tree (Fig.1), TNSaV falls into the “Asian clade 1”. We propose to classify TNSaV as a member of a novel species, named “*Orthotospovirus tomatonecromaculae*”, from the host plant and associated symptom. |

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| **References:** |
| [1] Maneechoat P, Chiemsombat P, Lopez Jr S, Adkins S. (2024) The complete genome sequence of tomato necrotic ringspot virus in chilli in Thailand derived from next-generation sequencing. Archives of Virology, 169(3), 64.  [2] Botermans M, Krom C D, Oplaat C, Swier J, Quaedvlieg W, Roenhorst A, Westenberg M (2025) Complete genome sequence of a putative novel orthotospovirus species identified in *Limonium sinuatum* from Colombia. Microbiology Resource Announcements, e01263-24.  [3] Read D A, Roberts R, Thompson G (2021a) Genomic characterization of two novel viruses infecting *Barleria cristata* L. from the genera *Orthotospovirus* and *Polerovirus*. Archives of Virology, 166(9), 2615-2618.  [4] Read D A, Roberts R, Swanevelder D, Pietersen G, Thompson G D (2021b) Novel viruses associated with plants of the family *Amaryllidaceae* in South Africa. Archives of Virology, 166(10), 2817-2823.  [5] Rivarez M P S, Pecman A, Bačnik K, Maksimović O, Vučurović A, Seljak G, Mehle N, Gutiérrez-Aguirre I, Ravnikar M, Kutnjak D. (2023) In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem. Microbiome, 11(1), 60.  [6] Roberts R, Robbertse N, Thompson G D, Read D A (2024) Characterization of macadamia ringspot-associated virus, a novel orthotospovirus associated with *Macadamia integrifolia* in South Africa. European Journal of Plant Pathology, 169(2), 347-357.  [7] Zheng K., Chen, T. C., Wu, K., Kang, Y. C., Yeh, S. D., Zhang, Z., & Dong, J. (2020) Characterization of a new orthotospovirus from chilli pepper in Yunnan Province, China. Plant Disease, 104(4), 1175-1182.  [8] Yin Y, Zheng K, Dong J, Fang Q, Wu S, Wang L, Zhang Z (2014) Identification of a new tospovirus causing necrotic ringspot on tomato in China. Virology Journal, 11, 213.  [9] Zheng K, Liu H, Yin Y, Chen T C, Yeh S D, Zhang Z, Dong J (2016) Full-length M and L RNA sequences of tospovirus isolate 2009-GZT, which causes necrotic ringspot on tomato in China. Archives of virology, 161(5), 1411-1414.  [10] Tamura K, Stecher G, Kumar S (2021) MEGA11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution, 38(7), 3022–3027. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.007P.N.v2.Tospoviridae\_8nsp | spreadsheet |
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| **Tables, Figures:** |

**Table 1.** Amino acid identity (%) matrix generated from the nucleocapsid protein sequences of representative members of accepted and proposed new (in bold) species in the genus *Orthotospovirus*.



**Fig.1** The evolutionary history was inferred by using the Maximum Likelihood method. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the JTT model, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (4 categories (+*G*, parameter = 1,3360)). The rate variation model allowed for some sites to be evolutionarily invariable ([+*I*], 1,75% sites). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 36 amino acid sequences. Evolutionary analyses were conducted in MEGA11 [10]. Representative members of proposed new species are highlighted in bold.

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Il contenuto generato dall'IA potrebbe non essere corretto.