

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Create five new species in the genus *Olpivirus* (*Hareavirales*: *Konkoviridae*] |
| **Code assigned:**  | 2025.003M.N.v2.Konkoviridae\_5nsp |

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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 | **X** | 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:**  |
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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** |
| Phenuiviridae SG | 10 | 0 | 0 |
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| **Submission date:** |  05/06/2025 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| 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| W - Withdrawn |  |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** |
| *Olpivirus freesiae* | Named after plant host genus *Freesia*, in which FreKV1 was first discovered |
| *Olpivirus lachenaliae* | Named after plant host genus *Lachenalia*, in which LacPhV1 was first discovered. |
| *Olpivirus soli* | Named after soil isolation source, in which SaKV was first discovered (in latin "form soil" is "soli") |
| *Olpivirus tripterocalicis* | Named after plant host genus *Tripterocalyx*, in which TaKV1 was first discovered. |
| *Olpivirus waitziae* | Named after plant host genus *Waitzia*, in which WaKV1 was first discovered. |

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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** X |
| NA | NA |  |

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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: Species*Description of current taxonomy*: Two virus species are currently classified in the genus *Olpivirus,* infect tulip and lettuce plants. The assignment of viruses to this genus is based on the placement of the viruses on a Neighbor-joining tree inferred from the complete RdRP protein sequences.*Proposed* *taxonomic change(s):*Classify five newly discovered konkoviruses into the new species in the genus *Olpivirus.**Justification*: Recently, five new putative konkoviruses were discovered. We propose the creation of five new species within the genus *Olpivirus.* |

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| **Text of Taxonomy proposal:**  |
| *Taxonomic rank(s) affected*: Species*Description of current taxonomy*: Two virus species are currently classified in the genus *Olpivirus,* infect tulip and lettuce plants. The genus *Olpivirus* is presently the only genus belonging to the family *Konkoviridae*. The assignment of viruses to this genus is based on the placement of the viruses on a Neighbor-joining tree inferred from the complete RdRP protein sequences. Different species demarcation criterion is <90% identity in the amino acid sequence of the RdRP.*Proposed* *taxonomic change(s):*Classify five newly discovered konkoviuses as the new species in the genus *Olpivirus.**Justification*: Recently, five new putative konkoviruses were discovered [1,2]. We propose the creation of five new species within the genus *Olpivirus* to accommodate the following recently identified viruses: **Freesia konkovirus 1 (FreKV1)** was identified from the analysis of transcriptome data of the necrotic leaf tissue of freesia [iridaceaen *Freesia refracta* (Jacq.) Klatt, 1866] from Liguria, Italy [1]. The complete genome (CG) sequence of FreLV1 comprises four genomic segments of negative-sense RNA; RNA1 (PQ490803), 6339 nt in length, encodes the RdRP protein; RNA2 (PQ490804), 1042 nt in length, encodes the nucleocapsid protein (NP); RNA3 (PQ490805), 1357 nt in length, encodes a putative movement protein (pMP); and RNA4 (PQ490806), 1288 nt in length, encodes a protein of unknown function (**Figure 1**). The RdRP aa sequence of FreKV1 shows the highest sequence identity (73.5%) with that of Lachenalia Phenuivirus 1 (LacPhV1). Based on NJ tree generated from the complete RdRP aa sequences, FreKV1 is placed within the konkovirus clade that includes tulip streak virus (TuSV) [3] and Lactuca big vein associated phlebovirus (LBVaPV) [4] (**Figure 2**).**Lachenalia phenuivirus 1 (LacPhV1)** was identified from the analysis of transcriptome data of the leaves of *Lachenalia* plants (asparagaceaen *Lachenalia kliprandensis* W.F.Barker, 1987) from Hortus Botanicus, a botanic garden in Amsterdam, The Netherlands [2]. The CG sequence of LacPhV1 comprises four genomic segments of negative-sense RNA; RNA1 (PQ067367), 6342 nt in length, encodes the RdRP protein; RNA2 (PQ067368), 1090 nt in length, encodes the NP and a protein of unknown function; RNA3 (PQ067369), 1475 nt in length, encodes a pMP; and RNA4 (PQ067370), 1291 nt in length, encodes a protein of unknown function (**Figure 1**). The RdRP aa sequence of LacPhV1 shows the highest sequence identity (73.5%) with that of FreKV1. Based on NJ tree generated from the complete RdRP protein sequences, LacPhV1 is placed within the konkovirus clade (**Figure 2**).**Soil associated konkovirus (SaKV)** was identified from the analysis of transcriptome data of the soil [1]. The coding-complete genome (CCG) sequence of SaKV comprises four genomic segments of negative-sense RNA; RNA1 (BK070195), 6356 nt in length, encodes the RdRP protein; RNA2 (BK070196),1152 nt in length, encodes the NP; RNA3 (BK070197), 1003 nt in length, encodes a pMP; and RNA4 (BK070198), 1342 nt in length, encodes a protein of unknown function (**Figure 1**). The RdRP aa sequence of SaKV shows the highest sequence identity (63.0%) with that of FreKV1. Based on NJ tree generated from the complete RdRp protein sequences, SaKV is placed within the konkovirus clade (**Figure 2**).**Tripterocalyx associated konkovirus 1 (TaKV1)** was identified from the analysis of transcriptome data of the Lassen sandverbena [nyctaginaceaen *Tripterocalyx crux-maltae* (Kellogg) Standl., 1909] [1]. The CCG sequence of TaKV1 comprises three genomic segments of negative-sense RNA; RNA1 (BK070397), 6322 nt in length, encodes the RdRP protein; RNA2 (BK070398), 1038 nt in length, encodes the NP; and RNA3 (BK070399), 1375 nt in length, encodes a pMP (**Figure 1**). The RdRP aa sequence of TaKV1 shows the highest sequence identity (51.3%) with that of SaKV. Based on NJ tree generated from the complete RdRP protein sequences, TaKV1 is placed within the konkovirus clade (**Figure 2**).**Waitzia associated konkovirus 1 (WaKV1)** was identified from the analysis of transcriptome data of the golden immortelle (asteraceaen *Waitzia nitida* Paul G.Wilson, 1992) [1]. The CCG sequence of WaKV1 comprises four genomic segments of negative-sense RNA; RNA1 (BK070191), 6381 nt in length, encodes the RdRP protein; RNA2 (BK070192), 1324 nt in length, encodes the NP; RNA3 (BK070193), 1587 nt in length, encodes a pMP; and RNA4 (BK070194), 1311 nt in length, encodes a protein of unknown function (**Figure 1**). The RdRP aa sequence of WaKV1 shows the highest sequence identity (62.4%) with that of SaKV. Based on NJ tree generated from the complete RdRP protein sequences, WaKV1 is placed within the konkovirus clade (**Figure 2**).FreKV1, LacPhV1, SaKV, TaKV1 and WaKV1 meet the species demarcation criterion of <90% identity in the amino acid sequence of the RdRP. Thus, we propose to classify FreKV1, LacPhV1, SaKV, TaKV1 and WaKV1 in the new species, *Olpivirus freesiae*, *Olpivirus lachenaliae*, *Olpivirus soli*, *Olpivirus tripterocalicis* and *Olpivirus waitziae,* in the family *Konkoviridae*. |

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| **References:**  |
| 1. Marra M, Rotunno S, Frascati F, Pierro R, Restuccia P, Hammond J, Vaira AM, Miozzi L (2025). The *Freesia refracta* virome analysis sheds new light on the phylogenetic relationships in the *Konkoviridae* and *Yueviridae* families. bioRxiv, 2025-03. doi: 10.1101/2025.03.19.644121
2. Dekker RJ, de Leeuw WC, van Olst M, Ensink WA, van Leeuwen S, Breit TM, Jonker MJ (2024). Discovery of a new *Phenuivirus* species in *Lachenalia* plants reveals possible co-evolution between 5’ and 3’RNA sequence motifs. bioRxiv, 2024-09. doi: 10.1101/2024.09.04.611151
3. Neriya Y, Morikawa T, Hamamoto K, Noguchi K, Kobayashi T, Suzuki T, Nishigawa H, Natsuaki T (2020) Characterization of tulip streak virus, a novel virus associated with the family *Phenuiviridae*. J Gen Virol 102:001525. PMID: 33226319. doi: 10.1099/jgv.0.001525.
4. Schravesande WEW, de Heer P, Verhage A, van den Burg HA (2024) Genome sequence of a novel phlebovirus associated with lettuce big vein disease infecting lettuce (*Lactuca* spp.). Microbiol Resour Announc 13 (2): e0097923. PMID: 38132566. doi:10.1128/mra.00979-23.

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

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**Figure 1.** Genome structures of TuSV (a) and the five new species (b). The vcRNAs (green lines) are depicted in 3′→5′ direction and mRNAs are depicted in a 5′→3′ direction. Arrows on the mRNAs depict ORFs that encode structural proteins; NP, nucleocapsid protein; RdRP, RNA-directed RNA polymerase; pMP, putative movement protein; p11, p20, p43 and p44, unknown proteins.

**Figure 2.** The neighbor-joining phylogenetic tree of RdRP amino acids of *Hareavirales*. GENETYX-MAC and MEGA11 was used to align the sequences and to generate phylogenetic tree. Numbers on branches are bootstrap values (%) obtained from 1,000 replicates. The five new species are written in red.