

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create one new species in the genus *Olpivirus* (*Hareavirales*: *Konkoviridae*) |
| **Code assigned:** | 2024.004P.A.v1.Konkoviridae\_1nsp | |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
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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:** |
| There is currently no Study Group for these taxa |

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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:** | 13/06/2024 |

**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| W - Withdrawn |  |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:** |
| The EC invites the Study Group to define genus demarcation criteria in addition to species demarcation criteria. |

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

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| **Response of proposer:** |
| [Species demarcation criteria] Viruses assigned to different species have less than 90% identity in the amino acid sequence of the RdRP.  [Genus demarcation criteria] Not applicable (the family includes only a single genus). |

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| **Revision date:** | 07/10/2024 |

**Part 3:** **TAXONOMIC PROPOSAL**

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| **Name of accompanying Excel module:** |
| 2024.004P.A.v1.Konkoviridae\_1nsp.xlsx |

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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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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| We propose the classification of one newly discovered konkovirid into a new species in the genus *Olpivirus*, on the base of a species demarcation criterion of <95% identity in the amino acid sequence of the RNA-directed RNA polymerase (RdRp). |

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| **Text of Taxonomy proposal:** |
| **Create one new species, *Olpivirus lactucae,* in the genus *Olpivirus***  A genomic sequence of a four-segmented negative-sense bunyaviral-like RNA virus named Lactuca big vein associated phlebovirus (LBVaPV) was obtained from the leaves of lettuce (*Lactuca sativa* L.) inoculated with the virus-vector fungus (*Olpidium virulentus*) from lettuce big-vein disease (LBVD)-infected fields [5].  **Biology**  Big-vein disease of lettuce occurs in major lettuce-growing areas in cool to temperate and, sometimes, subtropical regions, and has become an important problem in lettuce production during cooler periods of the year. The big-vein symptoms appear as white-to-yellow elongated chlorosis along the leaf veins, stunted growth, and absence of heads [1]. Two unrelated negative-stranded RNA viruses, lettuce big vein associated virus and Mirafiori lettuce big vein virus, were associated with LBVD, and the third virus, LBVaPV was recently confirmed in the diseased lettuce [3-6]. These viruses are transmitted by soil-inhabitant fungi, olpidiaceaean *Olpidium virulentus* (synonym *O. brassicae*) [1].  **Genome:**  The genomes of LBVaPV comprise four segments of negative-sense RNAs (Fig. 1). RNA1 (6,408 nt) encodes a protein with a predicted molecular mass of 240 kDa that shares the bunyaviral RdRp domain. The amino acid identity value obtained with the RdRp of a classified viruses in the order *Hareavirales* is below the species demarcation criterion (<95% identity), and the highest identity value obtained with the RdRp encoded by tulip streak virus (TuSV) is 84.6% [2]. RNA2 (1,107 nt) encodes a protein of 29.8 kDa that shares the tenuivirus/phlebovirus N domain. RNA3 (1,429 nt) encodes a protein of 39.4 kDa that shares sequence homology and/or structural characteristics with the cell-to-cell movement of plant viruses. RNA4 (1,282 nt) encodes a protein of 43.5 kDa that do not possess any viral motifs or domains and is not identified any homologous proteins by the BLASTP analysis.  The genome of TuSV was reported to consist of two segments but it was recently found to consist of four segments, and thus the genomic structure of the two viruses, LBVaPV and TuSV, is similar (Fig. 1).  **Phylogenetic relationships:**  A neighbor-joining phylogenetic tree was generated using amino acid sequences of the putative RdRp encoded by LBVaPV and representative members of all the genera of the *Hareavirales* order. LBVaPV is in the same clade with TuSV, and the high bootstrap values in the phylogenetic tree strongly support the classification of LBVaPV in the genus *Olpivirus* (Fig. 2)  For these reasons, we propose to classify LBVaPV as a member of a novel species, named *Olpivirus lactucae*.  **Origin of the name**: the epithet *lactucae* is named after host plant genus *Lactuca*, in which LBVaPV was first discovered. |

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| **References:** |
| 1. Huijberts N, Blystad DR, Bos L (1990) Lettuce big-vein virus: mechanical transmission and relationships to tobacco stunt virus. Ann Applied Biology 116:463–475.doi: 10.1111/j.1744-7348.1990.tb06629.x 2. 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 Ge Virol 102:001525. PMID: 33226319. doi: 10.1099/jgv.0.001525. 3. Sasaya T, Ishikawa K, Koganezawa H (2002) The nucleotide sequence of RNA1 of lettuce big-vein virus, genus varicosavirus, reveals its relation to nonsegmented negative-strand RNA viruses. Virology 297: 289–297. PMID: 12083827. doi: 10.1006/viro.2002.1420. 4. Sasaya T, Kusaba S, Ishikawa K, Koganezawa H (2004) Nucleotide sequence of RNA2 of lettuce big-vein virus and evidence for a possible transcription termination/initiation strategy similar to that of rhabdoviruses. J Gen Virol 85: 2709–2717. PMID: 15302964. doi: 10.1099/vir.0.80061-0 5. 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. 6. van der Wilk F, Dullemans AM, Verbeek M, van den Heuvel JFJM (2002) Nucleotide sequence and genomic organization of an ophiovirus associated with lettuce big-vein disease. J Gen Virol 83:2869–2877. PMID: 12388823. doi: 10.1099/0022-1317-83-11-2869. |

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| **Tables, Figures:** |

ダイアグラム

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**Figure 1.** Genome structures of LBVaPV (a) and TuSV (b). The vcRNAs 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 and RdRp, RNA-directed RNA polymerase, and non-structural proteins; pMP, putative movement protein and p10, P11, p20, p43 and p44, unknown proteins.

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