

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Creating one species in the genus *Pogseptimavirus* (Class *Caudoviricetes,* family *Demerecviridae*) |
| **Code assigned:** | 2025.063B.Pogseptimavirus\_1ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
| Zhang S | Zhang | Ocean University of China,Qingdao,China | zzhangsuqing@163.com | X |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | **X** |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| 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:** |
| Subcommittee: Bacterial Viruses  *Caudoviricetes Study Group* Members |

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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:** | 13/4/2025 |

**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| W - Withdrawn |  |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 |  | 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** |
| *“Pogseptimavirus SJ1”* | *Derived from the name of this virus* |
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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*:  Family *Demerecviridae*, class *Caudoviricetes*, phylum *Uroviricota*, kingdom *Heunggongvirae*, realm *Duplodnaviria*.  *Description of current taxonomy*:  Under the genus *Pogseptimavirus* in the family *Demerecviridae*, class *Caudoviricetes*, phylum *Uroviricota*, order *Heunggongvirae*, there are currently only two species: *Pogseptimavirus* PG07 and *Poaseptimavirus* VspSwp.  *Proposed* *taxonomic change(s):*  Add a species “*Pogseptimavirus SJ1”* under the genus *Pogseptimavirus* in the family *Demerecviridae*, class *Caudoviricetes*, phylum *Uroviricota*, order *Heunggongvirae*.  *Justification*:  A novel phage Pogseptimavirus SJ1 was isolated from surface coastal waters of Qingdao, China, and is capable of infecting the marine bacterium Vibrio hyugaensis. Here, we combined the results from phylogenetic analysis using Viptree and VIRIDIC, as well as network analysis with vConTACT 2.0, to propose that Pogseptimavirus SJ1 belongs to the same genus as Pogseptimavirus PG07 and Poaseptimavirus VspSwp. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Add a species, Vibrio phage vB\_VhyM\_SJ1, under the genus *Pogseptimavirus* in the family *Demerecviridae*, class *Caudoviricetes*, phylum *Uroviricota*, kingdom *Heunggongvirae*, realm *Duplodnaviria*.  *Description of current taxonomy*:  Under the genus *Pogseptimavirus* in the family *Demerecviridae*, class *Caudoviricetes*, phylum *Uroviricota*, order *Heunggongvirae*, there are currently only two species: *Pogseptimavirus* PG07 and *Poaseptimavirus* VspSwp.  *Proposed* *taxonomic change(s)*:  Add a species *Pogseptimavirus SJ1* under the genus *Pogseptimavirus* in the family *Demerecviridae*, class *Caudoviricetes*, phylum *Uroviricota*, order *Heunggongvirae*.  *Demarcation criteria:*  Viptree and VIRIDIC, as well as network analysis with vConTACT 2.0  *Justification*:  The marine bacteriophage vB\_VhyM\_SJ1 was isolated from surface coastal waters of Qingdao, China (120.239°E, 35.952°N), with Vibrio hyugaensis as the host. The vB\_VhyM\_SJ1 phage has a double-stranded DNA genome, with a genome length of 121,361 bp and a G+C content of 43.84%. A total of 174 open reading frames (ORFs) were predicted. The complete genome of vB\_VhyM\_SJ1 has been deposited in the GenBank database under accession number PP712102.  First, a global evolutionary analysis based on the genome sequences was carried out using Viptree (<https://www.genome.jp/viptree>) (version 2.0) [1]. The phylogenetic tree showed that vB\_VhyM\_SJ1 is most closely related to Vibrio phage vB\_VpaS\_PG07 (Pogseptimavirus PG07) and Vibrio phage VspSw\_1 (Poaseptimavirus VspSwp), which belong to the family Demerecviridae and the genus Pogseptimavirus.  To explore the relationship between vB\_VhyM\_SJ1 and other phages, homologs of vB\_VhyM\_SJ1 were searched in the IMG/VR and ICTV databases. A total of 99 related viral genome sequences, including 91 from ICTV and 8 UViGs from IMG/VR v4, were identified. All proteins were compared using all-versus-all DIAMOND BLASTp (E-value ≤1E-10, coverage ≥50%, amino acid identity ≥30%)[2], and the sequences were classified into different viral clusters (VCs) with vB\_VhyM\_SJ1 using vConTACT. The network diagram shows that VC\_1 and two isolated phages cluster together with vB\_VhyM\_SJ1. These phages are Vibrio phage vB\_VpaS\_PG07 and Vibrio phage VspSw\_1, respectively.  Average Nucleotide Identity (ANI) analysis was used to further define the genus and species boundaries of vB\_VhyM\_SJ1[3]. vB\_VhyM\_SJ1 had the highest ANI with Vibrio phage VspSw\_1 (NC\_048151) at 93.6%, and a high ANI with Vibrio phage vB\_VpaS\_PG07 (NC\_048041) at 84.7%. Vibrio phage vB\_VpaS\_PG07 (NC\_048041) and Vibrio phage VspSw\_1 (NC\_048151) had an ANI of 85.3% (Fig. 6C). According to the definition, when the genome similarity between phages is below 95%, they are classified into different species[4]. This result further confirmed that vB\_VhyM\_SJ1 is closely related to these two viruses and belongs to the same genus. Therefore, vB\_VhyM\_SJ1 is classified into the family Demerecviridae, genus Pogseptimavirus, based on the combined analysis. |

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| **References:** |
| 1. Nishimura, Y., et al., *ViPTree: the viral proteomic tree server.* Bioinformatics, 2017. 33(15): p. 2379-2380. 2. Bin Jang, H., et al., *Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks.* Nat Biotechnol, 2019. 37(6): p. 632-639. 3. Moraru, C., A. Varsani, and A.M. Kropinski, *VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses.* Viruses, 2020. 12(11). 4. Jain, C., et al., *High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries.* Nat Commun, 2018. 9(1): p. 5114. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| VIPtree.pdf | Proteomic tree of phage vB\_VhyM\_SJ1 by ViPTree in default mode. (A) The circular view of phage vB\_VhyM\_SJ1. The colored rings represent the virus families (inner ring) and host groups (outer ring). The red star represents the position where is phage vB\_VhyM\_SJ1. (B) Localized magnification proteomic tree layout of phage vB\_VhyM\_SJ1, the layout shows the 12 viruses that are more closely related to vB\_VhyM\_SJ1. These trees are calculated by BIONJ according to the genome distance matrix and take the midpoint as the root. The colored line represent the virus genus (left line) and host groups (right line) |
| Vcontact\_ANI.pdf | Phylogenetic and ANI analysis of vB\_VhyM\_SJ1. (A) Gene content-based viral network of phage vB\_VhyM\_SJ1 with related isolated viruses from ICTV virus database and related UViGs from IMG/VR dataset. The nodes represent the viral genomic sequences. The color of fill represent the hosts. The isolated viral sequences are indicated by filled circles, and UViGs are indicated by regular hexagons. Among those, the red star represents phage vB\_VhyM\_SJ1. (B) The heat map shows nucleotide-based intergenomic similarities of the phage vB\_VhyM\_SJ1 and other 11 related phages calculated by VIRIDIC. These values represent Average Nucleotide Identity (ANI) of each genome pair. |

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| **Tables, Figures:** |