This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2018.096B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Napahaivirus*, containing one (1) species in the family *Podoviridae*** | | | |
|  | | | |
| **Author(s):** | | | |
| Andrew M. Kropinski, University of Guelph, Canada  Evelien M. Adriaenssens, University of Liverpool, UK  Rob Lavigne, KU Leuven, Belgium  Dann Turner, University of the West of England, Bristol, UK  Yigang Yong, State Key Laboratory of Pathogen and Biosecurity, People's Republic of China | | | |
| **Corresponding author with e-mail address:** | | | |
| Andrew M. Kropinski Phage.Canada@gmail.com | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | **Bacterial and Archaeal Viruses Subcommittee** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 2018 |
| Date of this revision (if different to above): | | |  |

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| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module: 2018.096B.N.v1.Napahaivirus** |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Species demarcation criteria** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

**Source of the name of this taxon:** The name derives from place (Napahai wetland, Kunming, Yunnan, China) where first isolate of this type, Pseudomonas phage VSW-3, was isolated.

**History:** Lytic phage VSW-3 was isolated by Kunhao Qin et al. (Kunming University of Science and Technology, Kunming, Yunnan, People’s Republic of China) in 2016 using Pseudomonas fluorescens SW-3 as the host bacterium and a water sample obtained from the Napahai wetland [1]. “A morphological characterization of phages based on TEM images showed that VSW-3 has an icosahedral head that is 56 nm in diameter and a tail that is 20 nm × 12 nm in length, a typical morphology characteristic of the family Podoviridae” [1]. The presence of a gene encoding a single-subunit RNA polymerase suggests that it VSW-3 is part of the subfamily *Autographivirinae* [2].

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| VSW-3 | KX066068.1 | 40.56 | 57.5 | 46 | 0 |

**BLASTN homologs:** A neighbour joining tree was constructed on the basis of the BLASTN analysis at NCBI, indicating a peripheral relationship to several unclassified phages. The closest relative based upon BLASTN analysis is Pseudomonas phage Andromeda. We do not intend to create a higher taxon at this time.



**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the major capsid protein homologs of VSW-3 and related phages.



| **References:** |
| --- |
| [1] Qin K, Ji X, Zhang C, Ding Y, Kuang A, Zhang S, et al. Isolation and characterization of wetland VSW-3, a novel lytic cold-active bacteriophage of Pseudomonas fluorescens. Can J Microbiol 2017;63:110-8.  [2] Zhang C, Zhang Z, Li J, Qin K, Wei Y, Zhang Q, et al. Complete genome sequence of the lytic cold-active Pseudomonas fluorescens bacteriophage VSW-3 from Napahai plateau wetland. Virus Genes 2017;53:146-50. |