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:** | ***2018.134B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Cetovirus*, consisting of three (3) species in the family *Siphoviridae*.** | | | |
|  | | | |
| **Author(s):** | | | |
| Andrew M. Kropinski, University of Guelph  Evelien M. Adriaenssens, University of Liverpool | | | |
| **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: 2018.134B.N.v1.Cetovirus** |

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 is directly derived from that of the first isolate of its type: Vibrio harveyi phage Ceto

**History:** T5-like siphoviruses are characterized by possessing linear ds-DNA genomes of ca. 120 kb with long (>10 kb) direct terminal repeats (LTR). “Coliphage T5 injects its DNA in 2 steps: the first step transfer (FST) region 7.9% is injected and its genes are expressed and only then does the remainder (second step transfer, SST) of its DNA enter the cell. In the FST region, only 2 essential genes (*A1* and *A2*) have been identified and a third (*dmp*) non-essential gene codes for a deoxyribonucleotide 5' monophosphatase. Thirteen additional putative ORFs are present in the FST region. Numerous properties have been attributed to FST region, including SST, host DNA degradation, inhibition of host RNA and protein synthesis, restriction insensitivity and protection of T5 DNA. These effects do not occur following infection with an *A1* mutant. The *A2* gene seems only to be involved in SST transfer.” [1].

Lytic Vibrio harveyi phage Ceto was isolated from a Chesapeake Bay oyster by G. W. Broussard et al. (The Pennsylvania State University, University Park, PA, USA). Lytic Vibrio phage Thalassa was isolated by the same group on the same host.

Vibrio parahaemolyticus phage pVp-1 was isolated from seawater in South Korea by Jun Jin Woo and colleagues (Seoul National University, Aquatic Animal Medicine Laboratory, Seoul, South Korea) [2].

We have not included Vibrio ordalii phage vB\_VorS-PVo5 (KT345706), which was isolated in Antofagasta, Chile among these phages though it is clearly a member of this genus. The reason for this is that its genome (80578 bp) is considerably smaller than that of other members of this genus, and progressiveMauve analysis (see below; PVo5 [TOP], Ceto

[BOTTOM]) indicates that it is only a partial sequence.

None of the annotations for these viruses indicate the presence of LTRs. Though these viruses are clearly part of the T5-super family of phages, we do not intend to create a higher taxon, at this time.



**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | % DNA sequence identity (\*) | % common proteins(\*\*) |
| Ceto |  | MG649966 | 128.24 | 39.9 | 195 | 25 | 100 | 100 |
| Thalassa |  | MG649967 | 128.6 | 40.2 | 203 | 23 | 70 | 76.4 |
| pVp-1 | NC\_019529 | JQ340389 | 111.51 | 39.7 | 157 | 24 (\*\*\*) | 64 | 70.3 |

**(\*) determined using BLASTN at NCBI; (\*\*) determined using CoreGenes 3.5; (\*\*\*), the GenBank record does not list RNAs. They were discovered using tRNAscan-SE.**

**BLASTN homologs:** A fast minimum evolution tree was constructed on the basis of the BLASTN analysis at NCBI.



**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the large subunit terminase protein of phage Ceto and its homologs.



| **References:** |
| --- |
| 1: Davison J. Pre-early functions of bacteriophage T5 and its relatives.  Bacteriophage. 2015 Aug 25;5(4):e1086500. Erratum in: Bacteriophage. 2017; 6(4): e1271201.  2: Kim JH, Jun JW, Choresca CH, Shin SP, Han JE, Park SC. Complete genome  sequence of a novel marine siphovirus, pVp-1, infecting Vibrio parahaemolyticus.  J Virol. 2012 Jun;86(12):7013-4. |