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:** | ***2018.116B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Jesfedecavirus*, containing two 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: 2018.116B.N.v1.Jesfedecavirus** |

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 taken directly from Vibrio phage JSF10.

**History:** T5-like siphoviruses are characterized by possessing linear ds-DNA genomes of ca. 120 kb with long (>10 kb) direct terminal repeats. “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 cholerae phage phi 3 was identified on Vibrio cholerae 1051 by Tom Cheasty (HPA (PHE), London, UK) and then sequenced by S.G. Bhandare et al. (University of Nottingham, Sutton Bonington, Leicestershire, United Kingdom). It possesses many of T5-like characteristics (116 kb genome with 7,769 bp long terminal repeats.

Vibrio cholerae phage JSF10 was isolated from water in Dhaka, Bangladesh and characterized by I.B. Naser et al. [2] In addition it shares 54 protein homologs (33%) with coliphage T5 including A1 and A2. A reassessment of the relationship between the T5-like genera needs to occur before we propose higher taxa.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA identity (\*\*) | % common proteins (\*\*\*) |
| JSF10(\*) |  | KY883654.1 | 111.67 | 42.7 | 149 | 17 | 100 | 100 |
| phi 3 | NC\_028895.1 | KP280063.1 | 116.14 | 42.8 | 156 | 8 | 88 | 87.9 |

**(\*) phage JSF12 should be considered a strain within this genus; (\*\*) determined using BLASTN at NCBI; (\*\*\*) determined using CoreGenes 3.5**

**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 JSF10 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: Naser IB, Hoque MM, Nahid MA, Tareq TM, Rocky MK, Faruque SM. Analysis of the  CRISPR-Cas system in bacteriophages active on epidemic strains of Vibrio cholerae  in Bangladesh. Sci Rep. 2017;7(1):14880. |