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:** | ***2018.130B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create three (3) new genera in the subfamily *Tunavirinae*, 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): | | |  |

|  |
| --- |
| **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: 2018.130B.N.v1.Tunavirinae\_3gen** |

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 these taxa:**

*Eclunavirus:* Name derived directly from that of the first isolate of its type: Enterobacter phage Ec\_L1.

*Hanrivervirus:* Named after the location, Han River, in Korea where Shigella phage pSf-1 was found [1]

*Sertoctavirus:*  Name derived directly from that of the first isolate of its type: Escherichia phage SRT8 [2]

**History:** Enterobacter cloacae phage Ec\_L1 was isolated in China by Z. Li, H. Ren and Y. Xu (Dalian University of Technology, Dalian, Liaoning, China) and deposited in GenBank as “unclassified bacterial viruses.” Phage pSf-1 “ was isolated in 2012 from the Han River in Korea and was found to infect S. flexneri, Shigella boydii, and Shigella sonnei.” [1] The tail length and width are 103 x 6 nm; and, the head diameter is 73 nm. The authors state that its closest relative is Shigella phage Shfl1, but our phylogenetic analysis does not support this. “Escherichia coli virulent phage, SRT8, was isolated from sewage sludge samples collected from Jinan, Shandong Province, China.”[2] This phage is classified by NCBI as “unclassified bacterial viruses” in spite of the fact that the authors state “Comparative genomics analysis showed that the E. coli phage SRT8 is a member of a new species and belongs to the subfamily Tunavirinae, which includes T1-like phages.”[2]

**GenBank Summary:**

1. ***Eclunavirus***

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | % DNA sequence identity (\*) | % Common proteins (\*\*) |
| Ec\_L1 |  | MG732930 | 51.89 | 48.2 | 85 | 41 | 59.0 |
| T1 | NC\_005833 | AY216660 | 48.84 | 45.6 | 78 | 100 | 100 |

**(\*) determined using BLASTN at NCBI; (\*\*) determined using CoreGenes 3.5**

1. ***Hanrivervirus***

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | % DNA sequence identity (\*) | % Common proteins (\*\*) |
| pSf-1 | NC\_021331 | KC710998 | 51.82 | 44.0 | 94 | 37 | 64.1 |
| T1 | NC\_005833 | AY216660 | 48.84 | 45.6 | 78 | 100 | 100 |

**(\*) determined using BLASTN at NCBI; (\*\*) determined using CoreGenes 3.5**

1. ***Sertoctavirus***

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | % DNA sequence identity (\*) | % Common proteins (\*\*) |
| SRT8 |  | MF996376 | 49.58 | 48.0 | 84 | 45 | 80.8 |
| T1 | NC\_005833 | AY216660 | 48.84 | 45.6 | 78 | 100 | 100 |

**(\*) determined using BLASTN at NCBI; (\*\*) determined using CoreGenes 3.5**

**BLASTN homologs:** (see above).

**Phylogeny:** A phylogenetic tree was constructed, using phylogeny.fr, using the large subunit terminase proteins of these and related phages. **Red box** (*Eclunavirus*), **green box** (*Sertoctavirus*) and **blue box** (*Hanrivervirus*).



| **References:** |
| --- |
| 1: Jun JW, Kim JH, Shin SP, Han JE, Chai JY, Park SC. Characterization and  complete genome sequence of the Shigella bacteriophage pSf-1. Res Microbiol. 2013;164(10):979-86.  2: Zhao K, Song S, Zhao Z, Gu P, Fan X, Li Q. Complete genome sequence of SRT8, a  novel T1-like Escherichia coli bacteriophage. Arch Virol. 2018;163(6):1705-1708. |