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:** | ***2018.092B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To remove two species from the genus *Xp10virus*, and reassign them to two (2) new genera, 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: | | | May 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: 2018.092B.N.v1.Siphoviridae\_2gen** |

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.

**History:**  As currently recognized by ICTV the genus *Xp10virus* contains five species: Xanthomonas virus Xp10, Xanthomonas virus CP1, Xanthomonas virus OP1, Xanthomonas virus phil7, and Xanthomonas virus Xop411. These siphoviruses are united by the presence of a single subunit RNA polymerase, similar to the podoviruses belonging to the subfamily *Autographivirinae*. We have reassessed the relationship between these phages based upon overall DNA sequence identity and phylogeny, and have decided that the genus *Xp10virus* sensu strictu should only include Xp10, Xop411 and OP1. Phages CP1 [1] and phiL7 [2] are sufficiently different to be considered members of new genera. Based upon the overall protein homology determined using CoreGenes 3.5 these five phages probably belong to the same subfamily, but at this time we intend to consider them as three genera within the family *Siphoviridae*.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity(\*) | Overall Protein sequence conservation(\*\*) |
| Xp10 | AY299121.1 | 44.37 | 52.0 | 60 | 0 | 100% | 100% |
| Xop411 | DQ777876.1 | 44.52 | 51.9 | 58 | 0 | 86 | 85.0 |
| OP1 | AP008979.1 | 43.79 | 51.1 | 59 | 0 | 82 | 85.0 |
| CP1 | AB720063.2 | 43.87 | 53.3 | 47 | 0 | 20 | 61.7 |
| PhiL7 | EU717894.1 | 44.08 | 55.6 | 58 | 0 | 16 | 58.3 |

(\*) determined using NCBI BLASTn, (\*\*) determined using CoreGenes 3.5 (http://binf.gmu.edu:8080/CoreGenes3.5/index.html)

**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the major capsid protein (Top) and RNA polymerase protein (Bottom) homologs of these and related phages.





**Names of new genera:** *Klementvirus; Eisenstarkvirus*

**Origin of names:** Named in honour of two scientists who were the first to isolate a study Xanthomonas phages: Z. Klement from the Research Institute for Plant Protection, Budapest, Hungary; and, Abraham Eisenstark (b. 1919, Warsaw, Poland) University of Missouri; Columbia, Missouri, USA professor emeritus, since 1990. Director Cancer Research Center, since 1990. Senior scientist Laboratory and Environmental Technology, Inc., since 1990. [3].

***Klementvirus*:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Proteins | tRNAs | Overall DNA sequence identity(\*) | Overall Protein sequence conservation(\*\*) |
| CP1 | NC\_019933.2 | AB720063.2 | 43.87 | 53.3 | 47 | 0 | 100% | 100% |
| PhiL7 | NC\_012742 | EU717894.1 | 44.08 | 55.6 | 58 | 0 | 36.0 | 78.7 |

Unique proteins:

PI:BAM29075.1 hypothetical protein

PI:BAM29077.1 hypothetical protein

PI:BAM29094.1 hypothetical protein

PI:BAM29096.1 hypothetical protein

PI:BAM29102.1 hypothetical protein

PI:BAM29103.1 hypothetical protein

PI:BAM29104.1 hypothetical protein

PI:BAM29106.1 hypothetical protein

PI:BAM29116.1 hypothetical protein

PI:BAM29117.1 hypothetical protein

***Eisenstarkvirus*:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Proteins | tRNAs | Overall DNA sequence identity(\*) | Overall Protein sequence conservation(\*\*) |
| PhiL7 | NC\_019933.2 | EU717894.1 | 44.08 | 55.6 | 58 | 0 | 100% | 100% |
| CP1 | NC\_012742 | AB720063.2 | 43.87 | 53.3 | 47 | 0 | 36.0 | 63.8 |

Unique proteins:

PI:ACE75761.1 P21

PI:ACE75765.1 P25

PI:ACE75766.1 P26

PI:ACE75767.1 P27

PI:ACE75770.1 P30

PI:ACE75771.1 p31

PI:ACE75772.1 P32

PI:ACE75773.1 P33

PI:ACE75774.1 P34

PI:ACE75776.1 P36

PI:ACE75777.1 P37

PI:ACE75778.1 P38

PI:ACE75782.1 P42

PI:ACE75785.1 P45

PI:ACE75790.1 P50

PI:ACE75791.1 P51

PI:ACE75792.1 P52

PI:ACE75794.1 P54

PI:ACE75795.1 P55

PI:ACE75798.1 P58

| **References:** |
| --- |
| 1: Ahmad AA, Ogawa M, Kawasaki T, Fujie M, Yamada T. Characterization of  bacteriophages Cp1 and Cp2, the strain-typing agents for Xanthomonas axonopodis  pv. citri. Appl Environ Microbiol. 2014 Jan;80(1):77-85.  2: Lee CN, Lin JW, Weng SF, Tseng YH. Genomic characterization of the  intron-containing T7-like phage phiL7 of Xanthomonas campestris. Appl Environ  Microbiol. 2009 Dec;75(24):7828-37.  3: Eisenstark A. Life in Science: Abraham Eisenstark. Bacteriophage. 2014 Jul  28;4:e29009. |