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:** | ***2018.100B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Thornevirus* and one (1) new species in the family *Myoviridae*** | | | |
|  | | | |
| **Author(s):** | | | |
| Andrew M. Kropinski, University of Guelph  Hans-Wolfgang Ackermann, Université Laval  Evelien Adriaenssens, University of Liverpool  Kenneth Ehrlich, Tulane University  Melanie Ehrlich, Tulane University | | | |
| **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:** |
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**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: 2018.100B.N.v1.Thornevirus** |

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** Named in honour of Curtis B. Thorne (1912-2008). He was the branch chief at the Fort Detrick biolabs from 1948-1961 and 1963-1966 where his research focused on *Bacillus anthracis*. Hethen took up an academic position in Microbiology at the University of Massachusetts (Amherst) until his retirement in 1994. He isolated phage SP-15. (https://www.umass.edu/newsoffice/article/obituary-curtis-b-thorne-professor-emeritus-microbiology)

| **References:** |
| --- |
| 1. Taylor, M.J.; Thorne, C.B. Transduction of Bacillus licheniformis and Bacillus subtilis by each of two phages. Journal of Bacteriology 1963, 86:452-61., 452-461.  2. Marmur, J.; Brandon, C.; Neubort, S.; Ehrlich, M.; Mandel, M.; Konvicka, J. Unique properties of nucleic acid from Bacillus subtilis phage SP-15. Nature New Biology 1972, 239, 68-70.  3. Hayashi, H.; Nakanishi, K.; Brandon, C.; Marmur, J. Structure and synthesis of dihydroxypentyluracil from bacteriophage SP-15 deoxyribonucleic acid. Journal of the American Chemical Society 1973, 95, 8749-8757.  4. Brandon, C.; Gallop, P.M.; Marmur, J.; Hayashi, H.; Nakanishi, K. Structure of a new pyrimidine from Bacillus subtilis phage SP-15 nucleic acid. Nature New Biology 1972, 239, 70-71.  5. Walker, M.S.; Mandel, M. Incorporation of label from ribose into 5-(4',5'-dihydroxypentyl) uracil of bacteriophage SP15 DNA. Journal of Virology 1978, 25, 695-697.  6. Walker, M.S.; Mandel, M. Biosynthesis of 5-(4'5'-dihydroxypentyl) uracil as a nucleoside triphosphate in bacteriophage SP15-infected Bacillus subtilis. Journal of Virology 1978, 25, 500-509.  7. Tyeryar, F.J., Jr.; Taylor, M.J.; Lawton, W.D.; Goldberg, I.D. Cotransduction and cotransformation of genetic markers in Bacillus subtilis and Bacillus licheniformis. Journal of Bacteriology 1969, 100, 1027-1036. |

History: Martha J. Taylor and Curtis B. Thorne isolated bacteriophage SP-15 from soil using *Bacillus subtilis* W-23 as the host [1]. SP-15 DNA was found to display extraordinary biochemical properties for a naturally occurring DNA [2]. These include a unique alkaline sensitivity, and the lowest known melting temperature of any natural DNA (61.5⁰), and a high CsCl buoyant density (1.761 g/ml). NMR and mass spectroscopic analysis revealed that the unusual DNA modification was a hypermodified uracil with a 4,5-dihydroxypentyl group attached to the 5-position of uracil [3]). This modified uracil replaces over 50% of the normal thymine residues [4-6].

Morphology: The head diameter was 105 nm between opposite apices and the slender tail 250 x 20 in the extended state, showing about 56 striations with a periodicity of 3.5 nm. In the contracted state the tail was 100 x 23 nm. Again it showed a similarly sized neck and no collar. The base plate was indistinct (27 x ca.3 nm) carrying short spikes of about 10 nm in length (Fig. 1) [7].



Fig. 1. Electron micrograph of 2% uranyl acetate stained phage SP-15

GenBank summary:

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| RefSeq | INSDC | Size (Kb) | GC% | Proteins | Genes | tRNA |
| NC\_031245.1 | KT624200.1 | 221.91 | 38.6 | 317 | 317 | 0 |

BLASTN homologs: None (genomic orphan, singleton)

Phylogeny: Phylogenetic analysis, using phylogeny.fr of the major capsid proteins (left panel) and synthases (right panel) of *Bacillus* phage SP-15 reveal the formers relationship to cyanobacterial and *Sinorizobium* phage protein, while the gp09 synthase is related to an unclassified group of *Streptomyces* phages and *Andromedavirus*.

