This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

Part 1: **TITLE, AUTHORS, etc**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.019B*** | | | | (to be completed by ICTV officers) |
| **Short title: The create a new genus, *Svunavirus*, within the family *Myoviridae*** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Evelien M. Adriaenssens, University of Liverpool (UK)  Jens H. Kuhn, National Institute of Allergy and Infectious Diseases (USA)  Andrew M. Kropinski, University of Guelph (Canada) | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Andrew M. Kropinski, [Phage.Canada@gmail.com](mailto: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) | | | **ICTV Bacterial and Archaeal Viruses Subcommittee** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.019B.N.v1.Svunavirus** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet 2017\_TP\_Template\_Excel.xlsx. Submit both this and the accompanying spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

|  |  |  |
| --- | --- | --- |
| | **References:** | | --- | | **A. General**  1. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.  2. Wang Y, Coleman-Derr D, Chen G, Gu YQ. OrthoVenn: a web server for genome wide comparison and annotation of orthologous clusters across multiple species. Nucleic Acids Res. 2015 Jul 1;43(W1):W78-84.  3. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008; 36(Web Server issue):W465-9.  4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6):e39107.  **B. This TaxoProp Specifically**  5. Liu B, Zhou F, Wu S, Xu Y, Zhang X. Genomic and proteomic characterization of a thermophilic Geobacillus bacteriophage GBSV1. Res Microbiol. 2009;160(2):166-71. |   **Introduction:** Water samples were collected from an offshore hot spring at a depth of 100 m in Xiamen, Fujian Province (China), and used in enrichments with a *Geobacillus* strain. EM revealed particles with typical myovirus morphology with a hexagonal head 60 nm in diameter and a 80–150 nm contractile tail.  The phylogenetic similarity between the major capsid proteins of members of this genus and that of Exiguobacterium phage vB\_EauS-123 (KU160495) does not indicate that these viruses are closely related.  **Species demarcation:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of each of the proposed species differ from those of other species by more than 5% at the DNA level as confirmed with the BLASTN algorithm.  **Genus demarcation:** BLASTN (Table 1), OrthoVenn (Table 1) [2], progressiveMauve alignment (Fig. 4) [1], and phylogenetic analyses (Fig. 3) [3] all indicate that the proposed genus, *Svunavirus*, is cohesive and distinct from other genera. On average, the genomes of members of this genus are 34.9 kb in length (44.6 mol% G+C) and encode 54 proteins and 0 tRNAs.  The type species *Geobacillus virus GBSV1* was chosen because it represents the first sequenced member of this genus.  The name of the new genus was based on that of its first sequenced member. |

**Table 1**. Properties of the phages belonging to the genus *Svunavirus*.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage Name | RefSeq No. | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNA | % DNA  sequence  identity\* | %  Homologous  proteins \*\* |
| Geobacillus phage GBSV1 | NC\_008376.2 | DQ340064.2 | 34.68 | 44.4 | 54 | 0 | 100 | 100 |
| Bacillus virus 1 | NC\_009737.2 | DQ840344.2 | 35.06 | 44.8 | 54 | 0 | 73 | 76 |

\* Determined using BLASTN; \*\* Determined using OrthoVenn [2]

**Fig. 1.** OrthoVenn [2] comparison of the proteomes of these two phages using a cutoff of 10-5 revealing that there are 41 homologs.

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**Fig. 2.** Phylogenetic analysis of (A) large subunit terminase proteins, and (B) tail sheath proteins of Geobacillus phage GBSV1-related viruses and variety of other phage proteins constructed using “one click” at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.) for details".

**A. TerL proteins**

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**B. Major capsid proteins**



**Fig. 4.** progressiveMauve alignment [1] of the annotated genomes of members of the *Svunavirus* genus from top to bottom: Geobacillus phage GBSV1; Bacillus virus 1. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication

