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.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.057B*** | |  |
| **Short title:** Create one new family (*Finnlakeviridae*) including one new genus (*Finnlakevirus*), and one new species | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Laanto E, Mäntynen S, Sundberg LR, Kropinski AM, Adriaenssens EM, Poranen MM, Oksanen HM | | [elina.laanto@jyu.fi](mailto:elina.laanto@jyu.fi);  ssmantynen@ucdavis.edu;  [lotta-riina.sundberg@jyu.fi](mailto:lotta-riina.sundberg@jyu.fi); phage.canada@gmail.com;  [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk);  [minna.poranen@helsinki.fi](mailto:minna.poranen@helsinki.fi); [hanna.oksanen@helsinki.fi](mailto:hanna.oksanen@helsinki.fi) | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | | Department of Microbiology and Molecular Genetics, University of California, Davis, CA 95616, USA [SM]  Center of Excellence in Biological Interactions, Department of Biological and Environmental Science and Nanoscience Center, University of Jyväskylä, FI-40014 Jyväskylä, Finland [EL, LRS]  Departments of Food Science and Pathobiology, University of Guelph, Guelph, Ontario, Canada [AMK]  Quadram Institute Bioscience, Norwich Research Park, Colney Lane, NR4 7UA Norwich, UK [EMA]  Molecular and Integrative Biosciences Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, FI-00014 Helsinki, Finland [MMP, HMO] | | | | |
| **Corresponding author** | | | |
| Hanna M. Oksanen | | | |
| **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 virus subcommittee** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 3, 2019 |
| 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:** 2019.057B.A.v1.Finnlakeviridae\_1fam**.**xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_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, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

**Species demarcation criteria and supporting evidence:**

We propose to create a new family *Finnlakeviridae* (from the English Finn, for Finnish; and from English lake), including one new genus *Finnlakevirus* and one new virus species *Flavobacterium virus FLiP*.

The *Finnlakeviridae* is a family of icosahedral, internal membrane-containing bacterial viruses with single-stranded circular DNA genomes. Flavobacterium phage FLiP [1] infects Gram-negative bacteria *Flavobacterium* sp. strain B330. FLiP and its host bacterium were isolated from a boreal freshwater habitat (Lake Jyväsjärvi) in Central Finland in 2010. FLiP is the first described ssDNA virus with an internal membrane [1].

The FLiP genome is a circular ssDNA molecule of 9174 nt (GC content 34%) and it contains 16 open reading frames (ORFs) oriented in the same direction (Figure 1) [1]. Nine of the 16 ORFs have no significant sequence identity to other sequences in the public databases. Five ORFs have been shown to encode structural proteins and thus designated as genes (genes *7-9*, *11*, *14*). By using major capsid protein sequence as a marker, FLiP forms its own group among the tailless prokaryotic DNA viruses and proviruses [2].



**Figure 1.** Circular ssDNA genome of FLiP. Numbering starts from a unique EcoRII restriction site; predicted ORFs are in blue. The genes encoding structural proteins (gene product, gp) are in purple.

The virions are sensitive to chloroform and the buoyant density of the particles is 1.21 g/ mL in CsCl and 1.18 g/mL in sucrose. The major lipid class of the virion membrane is ceramide. The viral lipid composition is different from that of the host bacterium indicating selective uptake of the lipids during virion assembly.

The FLiP virions are icosahedral (Figure 2), and the diameter of the particle is 59 nm (from vertex to vertex) [1]. The lipid bilayer membrane (5 nm thick) is enclosed by the protein shell. The outer protein shell follows a pseudo *T* = 21 dextro icosahedral capsid organization. The fold of the major capsid proteins is a double β-barrel and the capsid is formed of major capsid protein trimers. The five-fold vertices are occupied by pentameric spike complexes.



**Figure 2.** Phage FLiP particles visualized under transmission electron microscopy and negative staining (phosphotungstic acid, pH 8.5). Scale bar 100 nm.

Phylogeny: The phylogenetic tree was constructed using the major capsid protein homologs of FLiP and related phages with phylogeny.fr in “one click” mode [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 [4] for details."



| **References:** |
| --- |
| 1. Laanto E, Mäntynen S, De Colibus L, Marjakangas J, Gillum A, Stuart DI, Ravantti JJ, Huiskonen JT, Sundberg LR. 2017. Virus found in a boreal lake links ssDNA and dsDNA viruses. Proc Natl Acad Sci U S A. 114:8378-8383. 2. Yutin N, Bäckström D, Ettema TJG, Krupovic M, Koonin EV. 2018. Vast diversity of prokaryotic virus genomes encoding double jelly-roll major capsid proteins uncovered by genomic and metagenomic sequence analysis. Virol J. 15:67. 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. 2008. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. 4. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. |