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:** | ***2019.029B*** | |  |
| **Short title:** Create one new genus (*Schiekvirus*) in the subfamily *Brockvirinae*, family *Herelleviridae* | | | |
|  | | | |
| **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 | |
| Kropinski AM, Adriaenssens EM | | [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com); [Evelien.adriaenssens@quadram.ac.uk](mailto:Evelien.adriaenssens@quadram.ac.uk); | |
| **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]) | | **University of Guelph [AMK]**  **Quadram Institute Bioscience [EMA]** | | | | |
| **Corresponding author** | | | |
| Andrew M. Kropinski | | | |
| **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**  **Caudovirales Study Group** | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | |  |
| 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:** 2019.029B.A.v1.Schiekvirus.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. |

| **References:** |
| --- |
| 1. Khalifa L, Brosh Y, Gelman D, Coppenhagen-Glazer S, Beyth S, Poradosu-Cohen R,   Que YA, Beyth N, Hazan R. Targeting Enterococcus faecalis biofilms with phage  therapy. Appl Environ Microbiol. 2015 Apr;81(8):2696-705. [Enterococcus phage EFDG1]   1. Brister, J. R., Ako-adjei, D., Bao, Y. & Blinkova, O. NCBI Viral Genomes Resource. *Nucleic Acids Res.* **43**, D571–D577 (2015). 2. Dereeper, A. *et al.* Phylogeny.fr: robust phylogenetic analysis for the non-specialist. *Nucleic Acids Res.* **36**, W465-469 (2008). 3. Anisomova, M. & Gascuel, O. Approximate Likelihood-Ratio Test for Branches : A Fast , Accurate ,. *Syst. Biol.* **55**, 539–552 (2006). |

**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:** The genus is named in honour of German virologist Wolfgang Schiek, formerly of Hygiene-Institut der Universität Göttingen who was one of the first scientists to work on Enterococcus phages.

**History:** At present the subfamily *Brockvirinae* consists of a single genus,*Kochikohdavirus* and an orphan species *Enterococcus virus EFDG1*. This TaxoProp proposes the creation of a new genus *Schiekvirus* containing three species of Enterococcus viruses. Enterococcus phage EFDG1 was isolated from

sewage effluents in Israel using Enterococcus faecalis as the host bacterium. *Enterococcus faecium* was used as the host to isolate Enterococcus phage EfV12-phi1 in Canada, and Enterococcus phage EFP01 in South Korea. The lytic status of these phages is unknown, and they do encode RecA recombinases (cd00983, pfam00154, COG0468) and integration host factor-like proteins (pfam00216).

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall DNA sequence identity | % common proteins |
| Enterococcus phage EFDG1 [1] | NC\_029009 | KP339049 | 147.59 | 37.2 | 192 | 26\* | 100 | 100 |
| Enterococcus phage EfV12-phi1 |  | [MH880817.1](https://www.ncbi.nlm.nih.gov/nuccore/MH880817.1) | 152.77 | 37.0 | 191 | 24 | 92.9 | 88.0 |
| Enterococcus phage EFP01 |  | [KY549443.1](https://www.ncbi.nlm.nih.gov/nuccore/KY549443.1) | 155.05 | 37.0 | 193 | 10\* | 81.4 | 79.2 |
|  |  |  |  |  |  |  |  |  |

**\* None indicated in GenBank file summary; discovered using tRNAscan-SE2**

**BLASTN homologs:** Three. The next most closely related phage is Enterococcus phage 156 with which EFDG1 shares 39.6% DNA sequence relatedness. The following is a neighbour joining tree derived from the NCBI BLASTn results (2):



**Electron micrograph:** None available, but the manuscript [1] on EFDG1 states “TEM microscopy showed that EFDG1 has a hexagonal head with a measured diameter of 98.71 ± 8.88 nm and tail length of 118.05 ± 6.87 nm.”

**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the major capsid protein homologs of EFSG1 and related phages (3,4).

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