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:** | ***2018.113B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Efquatrovirus*, containing fourteen (14) species in the family *Siphoviridae*.** | | | |
|  | | | |
| **Author(s):** | | | |
| Andrew M. Kropinski, University of Guelph, Canada  Evelien M. Adriaenssens, University of Liverpool, UK  Yigang Tong, Beijing Institute of Microbiology and Epidemiology, China | | | |
| **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:** |
|  |

**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: 2018.113B.N.v1.Efquatrovirus** |

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:** The name is directly derived from Enterococcus phage IME-EF4, which was one of the first isolates to be sequenced.

**History:**  These phages appear to have a world-wide distribution with PMBT2 isolated in Germany; phiSHEF2, phiSHEF4, and phiSHEF5 isolated in the UK; EfaCPT1, AUEF3 and SANTOR1 isolated in the USA, and the remainder in China. The lytic *Enterococcus* phages IME-EF4 were first isolated from sewage from PLA Hospital 307 (Beijing, China) in Jan 1st, 2013, and the host bacteria was a *Enterococcus faecalis* strain isolated from clinical samples in the same hospital.

This group of phages is peripherally related to another pair of Enterococcus phages (IME-EFm1, - EFm5) but at this time we are not prepared to suggest a higher taxon.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | % DNA sequence identity (\*) | % common proteins (\*\*) |
| IME-EF4 | NC\_023551 | KF733017 | 40.69 | 34.6 | 60 | 100 | 100 |
| Ec-ZZ2 | NC\_031260 | KR131750 | 41.17 | 34.6 | 59 | 93.1 | 88.3 |
| vB\_EfaS\_AL2 |  | MH203384 | 40.84 | 34.5 | 62 | 88.3 | 86.7 |
| LY0322 |  | MH193369 | 40.93 | 34.8 | 63 | 80.6 | 85.0 |
| vB\_EfaS\_AL3 |  | MH203383 | 40.79 | 34.8 | 61 | 79.8 | 86.7 |
| AUEF3 (partial) |  | KJ127304 | 41.26 | 34.4 | 68 | 78.6 | 88.3 |
| IME\_EF3 | NC\_023595.2 | KF728385.2 | 41.69 | 34.6 | 69 | 76.4 | 86.7 |
| phiSHEF5 |  | MF678790 | 41.6 | 34.7 | 69 | 75.6 | 90.0 |
| phiSHEF4 |  | MF678789 | 41.08 | 34.7 | 63 | 75.4 | 85.0 |
| SANTOR1 | NC\_031051 | KX284704 | 37.93 | 34.5 | 60 | 74.5 | 86.7 |
| phiSHEF2 |  | MF678788 | 41.71 | 34.6 | 68 | 74.4 | 85.0 |
| PMBT2 |  | MG708276 | 41.49 | 34.7 | 67 | 73.6 | 86.7 |
| EfaCPT1 | NC\_025465 | JX193904 | 40.92 | 34.6 | 69 | 72.8 | 88.3 |
| vB\_EfaS\_IME196 | NC\_028990 | KT932701 | 38.89 | 35.0 | 57 | 67.2 | 75.0 |
|  |  |  |  |  |  |  |  |

**(\*) determined using BLASTN at NCBI; (\*\*) determined using CoreGenes 3.5**

**BLASTN homologs:** This group of phages is peripherally related to another pair of Enterococcus phages (IME-EFm1, - EFm5). A fast minimum evolution tree was produced from the NCBI BLASTN data.

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**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the large subunit terminase protein of phage IME-EF4 and its homologs.



| **References:** |
| --- |
| 1. Li X, Ding P, Han C, Fan H, Wang Y, Mi Z, Feng F, Tong Y. Genome analysis of Enterococcus faecalis bacteriophage IME-EF3 harboring a putative metallo-beta-lactamase gene. Virus Genes. 2014 Aug;49(1):145-51. 2. Zhang X, Wang Y, Li S, An X, Pei G, Huang Y, Fan H, Mi Z, Zhang Z, Wang W, Chen Y, Tong Y. A novel termini analysis theory using HTS data alone for the identification of Enterococcus phage EF4-like genome termini. BMC Genomics. 2015 May 28;16:414. |