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:** | ***2018.140B*** | | (to be completed by ICTV officers) |
| **Short title:** (e.g. “6 new species in the genus *Zetavirus”*)  **To create one (1) new genus, *Beetrevirus*, including four (4) new species in the family *Siphoviridae.*** | | | |
|  | | | |
| **Author(s):** | | | |
| Andrew M. Kropinski, University of Guelph, Canada  Evelien M. Adriaenssens, University of Liverpool, UK  Ariane Toussaint, Université Libre de Bruxelles, Belgium  Christine Pourcel, Université Paris-Sud, France | | | |
| **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: 2018.140B.N.v1.Beetrevirus** |

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:** It is directly derived from the name of the first isolate bacteriophage of this type, Pseudomonas phage B3.

**History:** Temperate transposable Pseudomonas aeruginosa phage B3 was isolated in 1960 by Holloway et al. [1] in Australia from a lysogenic culture, and shown to be a member of the Siphoviridae [2], like that of the other well-characterized Pseudomonas phage D3112. Both B3 and D3112 require pili for adsorption [3]. The genome of B3 was sequenced in the laboratory of Martha Howe [4]. Its related phages PM105 was isolated in Russia by Victor Krylov, and like B3 (and D3112) carries host DNA at the genomic termini. Phage JD18 and JBD67 were isolated in Canada.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall DNA sequence identity (\*) | % Common proteins (\*\*) |
| B3 | NC\_006548 | AF232233 | 38.44 | 63.2 | 59 | 100% | 100 |
| JD18 | NC\_027986 | JX495041 | 39.01 | 63.4 | 52 | 65 | 76.3 |
| vB\_PaeS\_PM105 | NC\_028667 | LN898172 | 39.59 | 63.1 | 56 | 63 | 79.7 |
| JBD67 | - | JX495043 | 38.23 | 63.0 | 52 | 62 | 74.6 |

**BLASTN homologs:** See above. A neighbour joining tree was derived from the NCBI BLASTn data (see below). The B3-related clade is boxed in red. Phage JBD67 was not included in this diagram because the NCBI data indicates that it is a partial genome. Our results indicated that it is substantially complete.

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**Phylogeny:** The phylogenetic tree was constructed, using phylogeny.fr, using the major capsid protein homologs of these and related phages. The B3-related phages are boxed in blue.



| **References:** |
| --- |
| 1: HOLLOWAY BW, EGAN JB, MONK M. Lysogeny in Pseudomonas aeruginosa. Aust J Exp Biol Med Sci. 1960 Aug;38:321-9.  2: Slayter, H. S., B. W. Holloway, and C. E. Hall. 1964. The structure of Pseudomonas aeruginosa phages. J. Ultrastruct. Res. 11:274-281.  3: Roncero C, Darzins A, Casadaban MJ. Pseudomonas aeruginosa transposable  bacteriophages D3112 and B3 require pili and surface growth for adsorption. J  Bacteriol. 1990 Apr;172(4):1899-904.  4: Braid MD, Silhavy JL, Kitts CL, Cano RJ, Howe MM. Complete genomic sequence of  bacteriophage B3, a Mu-like phage of Pseudomonas aeruginosa. J Bacteriol. 2004  Oct;186(19):6560-74.  5: Pourcel C, Midoux C, Bourkaltseva M, Pleteneva E, Krylov V. Complete Genome  Sequence of PM105, a New Pseudomonas aeruginosa B3-Like Transposable Phage.  Genome Announc. 2016 Mar 3;4(2). pii: e01543-15.  6: Cady KC, Bondy-Denomy J, Heussler GE, Davidson AR, O'Toole GA. The CRISPR/Cas  adaptive immune system of Pseudomonas aeruginosa mediates resistance to naturally  occurring and engineered phages. J Bacteriol. 2012 Nov;194(21):5728-38. [JBD18]  7: NCBI Resource Coordinators . Database resources of the National Center for  Biotechnology Information. Nucleic Acids Res. 2018 Jan 4;46(D1):D8-D13. |