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:** | ***2019.056B*** | |  |
| --- | --- | --- | --- |
| **Short title:** Create one new genus (*Fibralongavirus*) including two new species in the family *Siphoviridae* | | | |
|  | | | |
| **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 | |
| Zeman M, Bárdy P, Vrbovská V, Pantůček R, Adriaenssens EM, Kropinski AM, Łobocka M | | [michal.zeman91@gmail.com](mailto:michal.zeman91@gmail.com);  [bardy.pavol@mail.muni.cz](mailto:bardy.pavol@mail.muni.cz);  [veronika.vrbovska@gmail.com](mailto:veronika.vrbovska@gmail.com);  [pantucek@sci.muni.cz](mailto:pantucek@sci.muni.cz);  [Evelien.adriaenssens@quadram.ac.uk](mailto:Evelien.adriaenssens@quadram.ac.uk); [phage.canada@gmail.com](mailto:phage.canada@gmail.com);  lobocka[@](mailto:phage.canada@gmail.com)ibb.waw.pl | |
| **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 Experimental Biology, Masaryk University, Czech Republic [MZ, PB, VV, RP]**  **Quadram Institute Bioscience, UK [EMA]**  **University of Guelph, Canada [AMK]**  **Institute of Biochemistry and Biophysics, PAS, Poland [MŁ]** | | | | |
| **Corresponding author** | | | |
| Michal Zeman | | | |
| **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: | | | Mar 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**

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| --- |
| **Name of accompanying Excel module:** 2019.056B.A.v1.Fibralongavirus\_1gen2sp.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.  We propose to create a genus *Fibralongavirus* for phages vB\_SpsS\_QT1 (QT1 in short), 2638A and phages with similar properties. We have chosen 95% genome 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 and EMBOSS Stretcher algorithms.  These two phages that infect *Staphylococcus pseudintermedius* have long non-contractile tail, ending with tail terminal widening and a single long fibre (Fig. 1). Phage 2638A has been described previously by Slopek and Krzywy (7). Phage QT1 has B1 morphotype with icosahedral head with diameter 61 nm. The tail has length 282 nm and central tail fibre is about 70 nm long.  Phages of this genus have genomes of approximately 42.2 kb (36.9 mol% G+C) and encode between 55 – 61 genes and no genes for tRNA. The genome of QT1 has 10 bp long 5’ overhangs (cohesive ends). An interesting feature is that both phages encode endolysin with double translational start producing two variants of endolysin. The second variant does not contain a peptidase domain (9).  Sequence comparisons preformed with tools: BLASTn (Fig. 2), EMBOSS Stretcher (Fig. 2), progressiveMauve (Fig. 3), Gegeenes (Fig. 4), CD-HIT (Table 1) and phylogenetic analyses (Fig. 5) show that phages QT1 and 2638A (7,8) belong to a distinct and cohesive group. Because of long central tail fibre, we decided to name the genus *Fibralongavirus.*  **Table 1:** Properties of the phages belonging to the genus *Fibralongavirus*   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | **Phage** | **Accession no.** | **Genome size** | **GC content** | **tRNAs** | **CDS no.** | **Shared genes\*** | **Signature genes#** | | vB\_SpsS\_QT1 | MK450538 | 43 029 bp | 36.9 % | 0 | 60 | 41 (68 %) | *sam mt, int* | | 2638A | NC\_007051 | 41 318 bp | 36.9 % | 0 | 57 | 41 (72 %) | *int* |   \*Percentage of shared genes was calculated by CD-HIT (4) as a global alignments of proteomes with identity above 40 %,  ***#****sam mt* – SAM-dependent methyltransferase; *int* – integrase; See Fig. 2.  **Fig. 1:** Electron micrographs of negatively stained phages QT1(A) and 2638A(B) with detail on the tail fibre.    **Fig. 2:** Sequence identity of QT1 and 2638A genomes visualised by EasyFig 2.1(5). BLASTn query coverage was 79 % and nucleotide identity was 99 %. Global nucleotide alignment was done by EMBOSS Stretcher (6) with 83.5 % identity and 6.5 % gaps on 43585 nt space.    **Fig. 3:** ProgressiveMauve alignment (1) of the annotated genomes belonging to the proposed genus *Fibralongavirus* – top: *Staphylococcus* phage QT1; bottom: *Staphylococcus* phage 2638A. Locally collinear blocks are showed in different colour. Height of the column on the nucleotide position is showing sequence similarity between regions.    **Fig. 4:** Genomes of *Staphylococcus Siphoviridae* phages were compared using Gegenees 3.0(3). Fragmented all-against-all comparison was computed by BLASTn algorithm with fragment size of 50 nt and sliding step size of 25 nt. Resulting matrices were then sorted by Gegenees tool Autosort. Proposed genus *Fibralongavirus* is marked in blue circle.  1 - 187; 2 - phiSauS-IPLA88; 3 - 85; 4 - phiMR25; 5 - 69; 6 - phi11; 7 - SAP-26; 8 - phiETA2; 9 - phiNM1; 10 - phiNM2; 11 - 53; 12 - 80alpha; 13 - phiNM4; 14 - phiETA3; 15 - 96; 16 - 71; 17 - phiETA; 18 - 55; 19 - phiMR11; 20 - 29; 21 - 52A; 22 - 80; 23 - 92; 24 - 88; 25 - X2; 26 - EW; 27 - phiRS7; 28 - SpaA1; 29 - 37; 30 - IME-SA4; 31 - StB20-like; 32 - StB20; 33 - phi575; 34 - phi879; 35 - 6ec; 36 - vB\_SepS\_SEP9; **37 - QT1; 38 - 2638A**; 39 - vB\_SepiS-phiIPLA5; 40 - CNPH82; 41 - vB\_SepiS-phiIPLA7; 42 - PH15; 43 - phiSauS-IPLA35; 44 - 3A; 45 - 47; 46 - phi12; 47 - phiSLT; 48 - 42e; 49 - phiPV83; 50 - JS01; 51 - tp310-3; 52 - phi13; 53 - phiPVL108; 54 - phiPVL-CN125; 55 - PVL; 56 - tp310-1; 57 - 23MRA; 58 - phiNM3; 59 - StauST398-4; 60 - phiN315; 61 - phiBU01; 62 - P954; 63 - 77; 64 - phiSa119; 65 - phi5967PVL  **Fig. 5:** Phylogenetic analysis based on amino acid sequences of major capsid proteins and terminase large subunits of phages QT1 and 2638A and representatives of other *Staphylococcus* phage genera. Phylogenetic trees were computed and build at phylogeny.fr (2) with “one click” mode.  **A) Major capsid protein**    **B) Terminase, large subunit** |

| **References:** |
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| **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. 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.  3. 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.  4. Huang Y, Niu B, Gao Y, Fu L, Li W. CD-HIT Suite: a web server for clustering and comparing biological sequences. Bioinformatics. 2010; 26(5): 680–682. DOI: 10.1093/bioinformatics/btq003.  5. Sullivan MJ, Petty NK, Beatson EA. Easyfig: a genome comparison visualizer. Bioinformatics. 2011; 27(7): 1009–1010. DOI: 10.1093/bioinformatics/btr039.  6. Myers EW, Miller W. Optimal alignments in linear space. Computer Applications in the Biosciences : CABIOS. 1988, 4(1):11-17. PMID: 3382986.  **B. This TaxoProp Specifically -**  7. Slopek, S., and T. Krzywy. Morphology and ultrastructure of bacteriophages. An electron microscopical study. 1985; Arch. Immunol. Ther. Exp. 33:1-217. PMID: 4062505.  8. Kwan T, Liu J, DuBow M, Gros P, Pelletier J. The complete genomes and proteomes of 27 Staphylococcus aureus bacteriophages. Proceedings of the National Academy of Sciences. 2005; 102 (14) 5174-5179. DOI: 10.1073/pnas.0501140102.  9. Abaev I, Foster-Frey J,Korobova O, Shishkova N, Kiseleva N, Kopylov P, Pryamchuk S, Schmelcher M, Becker SC, Donovan DM. Staphylococcal phage 2638A endolysin is lytic for Staphylococcus aureus and harbors an inter-lytic-domain secondary translational start site. Applied Microbiology and Biotechnology. 2012; 97(8):3449-3456. DOI: 10.1007/s00253-012-4252-4. |