This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.017B*** | | | | (to be completed by ICTV officers) |
| **Short title: To create one (1) new genus, *Dfl12virus*, including one (1) new species in the family *Podoviridae*.** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Johannes Wittmann - Leibniz Institute DSMZ (Germany)  Andrew M. Kropinski – University of Guelph (Canada)  Jens H. Kuhn - National Institute of Allergy and Infectious Diseases (USA)  Evelien M. Adriaenssens – University of Liverpool (UK) | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Johannes Wittmann, jow12@dsmz.de | | | | | |
| **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) | | | ICTV Bacterial and Archaeal Viruses Subcommittee | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.017B.N.v1.Dfl12virus** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| **A. General**  1. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. [MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods.](http://www.ncbi.nlm.nih.gov/pubmed/21546353) Mol Biol Evol. 2011; 28(10):2731-9.  2. Sullivan MJ, Petty NK, Beatson SA (2011) Easyﬁg: a genome comparison visualizer. Bioinformatics 27:1009–1010 |

|  |
| --- |
| **Annex:**  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. |

| **References:** |
| --- |
| **B. This TaxoProp Specifically**  3. Complete genome sequence of Roseophage vB\_DshP-R1, which infects Dinoroseobacter shibae DFL12 Jianda Ji, Rui Zhang, Nianzhi Jiao Stand Genomic Sci. 2015; 10: 6. Published online 2015 Jan 21. doi: 10.1186/1944-3277-10-6Correction in: Stand Genomic Sci. 2015; 10: 69. PMCID: PMC4572628  4: Complete genome sequence of Roseophage vB\_DshP-R1, which infects Dinoroseobacter shibae DFL12 Jianda Ji, Rui Zhang, Nianzhi Jiao Stand Genomic Sci. 2014; 9: 31. |

**Species demarcation:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. The members of the proposed species differ from each other by less than 5% at the DNA level as confirmed with the BLASTN algorithm and are considered as isolates.

**Genus demarcation:** BLASTN (Table 1) and phylogenetic analyses (Fig. 1) indicate that the proposed genus, *Dflvirus*, is cohesive and distinct from other genera. On average, the genomes of members of this genus are 74.9 kb in length (49.2 mol% G+C) and encode approximately 85 proteins and 0 tRNAs.

Dinoroseobacter phages DFL12phi1 and phage vBDshPR2C were isolated from water from Baicheng Harbor, Xiamen, China, in May and September 2012, respectively. Their particles have morphological characteristics of N4-like viruses [3,4]. Dinoroseobacter phage vBDshPR2C is considered a strain of Dinoroseobacter paheg DFL12phi1 based on the species demarcation criteria.

The type species Dinoroseobacter phage DFL12phi1 was chosen based on the first sequenced member of this genus and the name of the new genus was based on that.

**Table 1**. Properties of the phages belonging to the genus *Dfl12virus*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage Name | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNA | % DNA  sequence  identity\* |
| Dinoroseobacter phage DFL12phi1 | KJ621082 | 75.0 | 49.3 | 86 | 0 | 100 |
| Dinoroseobacter phage vBDshPR2C | KJ803031 | 74.8 | 49.2 | 85 | 0 | 95.1 |

\* Determined using BLASTN

**Fig. 1.** Phylogenetic analysis of (A) large subunit terminase proteins, (B) major capsid proteins; and, (C) virion RNA polymerases. Proteins were aligned and the phylogenetic tree was constructed using MEGA5 [2]. The members of the *Dfl12virus* genus are boxed in red.

**A. Large terminase subunits**

****

**B. Major capsid proteins**

****

**C. virion RNA polymerases**

****

**Fig 2.** Synteny plot of the two isolates visualized with EasyFig [2]. The scale bar shows the level of nucleotide identity.

