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:** | ***2017.006B*** | | | | (to be completed by ICTV officers) |
| **Short title: To create one (1) new genus, *Doucettevirus*, including four (4) new species in the family *Siphoviridae*.** | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| 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:** | | | | | |
| 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) | | | **ICTV Bacterial and Archaeal Viruses Subcommittee** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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|  | | | | | |
| Date first submitted to ICTV: | | | | June 8, 2017 | |
| Date of this revision (if different to above): | | | |  | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2016.006B.N.v1.Doucettevirus** |

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

| additional material in support of this proposal |
| --- |
| **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:** | | |
| **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. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140. doi: 10.1186/1756-0500-6-140.  3. 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.  4. 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.  **B. This TaxoProp Specifically**  None | | |

**Species demarcation:** We have chosen 95% DNA 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 algorithm.

**Genus demarcation:** BLASTN (Table 1), progressiveMauve alignment (Fig. 2) [1] and phylogenetic analyses (Fig. 1) [3] all indicate that the proposed genus, *Doucettevirus*, is cohesive and distinct from other genera. On average the genomes of members of this genus are 37.8 kb in length (65.5 mol% G+C) and encode approximately 63 proteins and 0 tRNAs.

Some significant features of these phages: the temperate Propionibacterium phages Doucette and B22 were isolated in Los Angeles, CA (USA) on Propionibacterium freudenreichii TL110, whereas E6 and G4 were isolated in Rennes, France on P. freudenreichii LS2500 and Z435. The genome of Propionibacterium phage Doucette has defined ends with a 12bp 3' overlap (CAAACAAGTCAT), whereas those of G4 have a similar sequence (CCAACAAGTCAT). All of these belong to The Actinobacteriophage Database (<http://phagesdb.org/>) Cluster BW. Propionibacterium phage Doucette’s closest relative is Propionibacterium phage B3.

The type species *Propionibacterium virus Doucette* was chosen because it represents the second sequenced member of this genus.

The name of the new genus was based on that of its second sequenced member, since the name “B22virus” was not deemed sufficiently unique.

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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Propionibacterium phage | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNA | % DNA  sequence  identity\* |
| Doucette | KX620751 | 37.4 | 65.6 | 61 | 0 | 100 |
| B22 | KX620750 | 37.2 | 65.5 | 61 | 0 | 77 |
| E6 | KX620753 | 38.1 | 65.2 | 60 | 0 | 75 |
| G4 | KX620754 | 38.6 | 65.7 | 69 | 0 | 71 |
|  |  |  |  |  |  |  |

\* Determined using BLASTN

**Fig. 1.** Phylogenetic analysis of (A) large subunit terminase proteins, and (B) major capsid proteins major tail proteins of Propionibacterium phage Anatole-related viruses and variety of other phage proteins constructed using “one click” at phylogeny.fr [3]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative (Syst Biol. 2006;55(4):539-52.) for details".

**A. TerL proteins**

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**B. Major capsid proteins**

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**Fig. 2.** progressiveMauve 2.3.1 alignment [1] of the annotated genomes of members of the *Doucettevirus* genus from top to bottom: Propionibacterium phage G4, Propionibacterium phage E6, Propionibacterium phage B22, Propionibacterium phage Doucette. Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication).

