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:** | ***2017.028B*** | | | | (to be completed by ICTV officers) |
| **Short title:** To create three (3) new species in the genus *Lambdavirus* 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)  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:** | | | | | |
|  | | | | | |
|  | | | | | |
| 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:** |
|  |

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

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| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.028B.N.v1.Lambdavirus\_3sp** |

**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**  5. Casjens SR, Hendrix RW. Bacteriophage lambda: Early pioneer and still relevant. Virology. 2015;479-480:310-30  6. Juhala RJ, Ford ME, Duda RL, Youlton A, Hatfull GF, Hendrix RW. Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdoid bacteriophages. J Mol Biol. 2000;299(1):27-51.  7. Grose JH, Casjens SR. Understanding the enormous diversity of bacteriophages: the tailed phages that infect the bacterial family Enterobacteriaceae. Virology. 2014;468-470:421-43. | | |

**Introduction:**

Escherichia coli phage lambda (λ) was one of the first bacterial viruses classified by ICTV (1971 ICVN 1st Report). Currently, ICTV recognizes three species in the *Lambdavirus* genus: *Escherichia virus lambda* [1], *Escherichia virus HK022* [2], and *Escherichia virus HK97* [2]. This is unlike NCBI which recognizes 90 viruses as belonging to this genus or as “unclassified lambda-like viruses.” It is worthwhile distinguishing between lambdoid phages, which would include Salmonella phage P22, and members of the *Lambdavirus sensu strictu*. Figure 1 illustrates the total DNA and protein sequence identities of six lambdoid phages ascertained using BLAST (Fig. 1A) and CoreGenes3.5 (Fig. 1B, [2]). As can be readily appreciated from a taxonomic perspective these phages are only distantly related. This bears out the extensive study by Grose & Casjens [7] who showed that the genome of Escherichia phage Lambda is distinct from that of Escherichia phage HK022 and Escherichia phage HK97.

**Fig. 1.** Overall DNA (A) and total protein (B) sequence relatedness of a select group of lambdoid phages.



**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:** Gegenees BLASTN (Fig. 2), and phylogenetic analyses (Fig. 3) [3] all indicate that the proposed species belong to the genus *Lambdavirus.* On average the genomes of members of this genus are 46.4 kb in length (50.4 mol% G+C), and encode approximately 67 proteins and 0 tRNAs.

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

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Escherichia phage | RefSeq | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNA | % DNA  sequence  identity\* |
| Lambda | NC\_001416 | J02459 | 48.5 | 49.9 | [73](https://www.ncbi.nlm.nih.gov/genome/proteins/4416?genome_assembly_id=220781&gi=9626243) | 0 | 100 |
| DE3 |  | EU078592 | 42.9 | 51.9 | 56 | 0 | 74 |
| HK629 | NC\_019711 | JQ182735 | 47.3 | 49.6 | 69 | 0 | 68 |
| HK630 | NC\_019723 | JQ086376 | 47.1 | 50.1 | 69 | 0 | 82 |

\* Determined using BLASTN at NCBI

**Fig 2.** Gegenees BLASTN analysis of a group on lambdoid phage genomes using custom settings: window, 100 bp; slide, 50 bp.



**Fig. 3.** Phylogenetic analysis of the large subunit terminase proteins of Escherichia phage Lambda-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".

**TerL proteins**

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