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:** | ***2017.009B*** | | | | (to be completed by ICTV officers) |
| **Short title:** To create one (1) new subfamily, *Mccleskeyvirinae*, including two (2) new genera 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:** | | | | | |
|  | | | | | |
|  | | | | | |
| 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: 2017.009B.N.v1.Mccleskeyvirinae** |

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

**Part 3:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

|  |
| --- |
| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
| This subfamily is named in honour of Dr. Charles Shelton McCleskey (Louisiana State University, Baton Rouge) who carried out pioneering studies on *Leuconostoc* and its phages starting in 1947. |

**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: Kot W, Neve H, Heller KJ, Vogensen FK. Bacteriophages of leuconostoc, oenococcus, and weissella. Front Microbiol. 2014;5:186.  6: Kot W, Hansen LH, Neve H, Hammer K, Jacobsen S, Pedersen PD, Sørensen SJ, Heller KJ, Vogensen FK. Sequence and comparative analysis of Leuconostoc dairy bacteriophages. Int J Food Microbiol. 2014 ;176:29-37.  7: Ali Y, Kot W, Atamer Z, Hinrichs J, Vogensen FK, Heller KJ, Neve H. Classification of lytic bacteriophages attacking dairy Leuconostoc starter strains. Appl Environ Microbiol. 2013;79(12):3628-36. | | |

**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 [4] BLASTN (Fig. 2), CoreGenes [2], and phylogenetic analyses (Fig. 3) [3] all indicate that the proposed genera are cohesive and distinct from other genera.

*Una4virus*: On average, the genomes of members of this genus are 28.54 kb in length (36.1mol% G+C) and encode 44 proteins and 0 tRNAs.

*Lmd1virus*: On average, the genomes of members of this genus are 26.58 kb in length (36.6mol% G+C) and encode 39 proteins and 0 tRNAs.

**Subfamily demarcation:** These temperate phages can be clearly distinguished by DNA sequence identity, number of encoded proteins, and phylogeny.

The name of this subfamily recognizes the early work on Leuconostoc phages by Dr. Charles Shelton McCleskey (Louisiana State University, Baton Rouge (1947-1988). See: http://www.asmbranches.org/brscentral/history.htm; http://www.asmbranches.org/brscentral/awards.htm

**Table 1**. Properties of the phages belonging to the subfamily *Mccleskeyvirinae*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Leuconostoc phage | RefSeq No. | GenBank accession No. | Genome length (kb) | %G+C | # proteins | # tRNAs |
| ***A.     Una4virus*** |  |  |  |  |  |  |
| 1-A4 | NC\_027987 | GQ451696 | 29.51 | 36.1 | 50 | 0 |
| Ln-9 | NC\_027358 | KM262192 | 28.53 | 36.4 | 48 | 0 |
| Ln-8 | NC\_027377 | KM262191 | 28.92 | 36.1 | 45 | 0 |
| phiLN25 | NC\_024386 | KC013026 | 28.43 | 36.2 | 41 | 0 |
| phiLN34 | NC\_024388 | KC013027 | 28.02 | 36.0 | 41 | 0 |
| phiLNTR3 | NC\_024378 | KC013029 | 28.02 | 36.1 | 41 | 0 |
| phiLNTR2\* | NC\_024389 | KC013028 | 28.34 | 36.0 | 42 | 0 |
|  |  |  |  |  |  |  |
| ***B. Lmd1virus*** |  |  |  |  |  |  |
| P793 |  | KC013021 | 26.77 | 36.6 | 38 | 0 |
| phiLN12 |  | KC013025 | 28.19 | 36.6 | 41 | 0 |
| phiLN03 |  | KC013022 | 26.75 | 36.8 | 39 | 0 |
| phiLN04 |  | KC013023 | 25.86 | 36.6 | 39 | 0 |
| phiLN6B |  | KC013024 | 25.74 | 36.6 | 39 | 0 |
| Lmd1 |  | JQ659259 | 26.20 | 36.4 | 37 | 0 |

\* should be considered a strain of *Leuconostoc virus LNTR3* within this genus.

**Fig. 1.** Electron micrograph of negatively stained Leuconostoc phage PhiLN25 [modified from 7].



**Fig. 2.** Gegenees BLASTN heat plot [4] reveals two clusters and one orphan (phiMH1).



**Fig. 3.** CoreGenes 3.5 analysis of thepercentage of conserved proteins between pairs of viruses.



**Fig. 3.** Phylogenetic analysis of the DNA polymerases of Leuconostoc phages 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".

