Taxonomy proposal 2019 : Create one new subfamily (Tybeckvirinae) including four new genera in the family Siphoviridae

Kropinski, Andrew M.

International Committee on Taxonomy of Viruses (ICTV)
2020

Kropinski , A M , Adriaenssens , E & Poranen , M 2020 , Taxonomy proposal 2019 : Create one new subfamily (Tybeckvirinae) including four new genera in the family Siphoviridae . in ICTV Online: International Committee on Taxonomy of Viruses (ICTV) . International Committee on Taxonomy of Viruses (ICTV) . < https://talk.ictvonline.org/files/ictv_official_taxonomy_updates_since_the_8th_report/m/all-proposals/9600 >

http://hdl.handle.net/10138/319354

publishedVersion

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:	***2019.051B***

Short title: Create one new subfamily (*Tybeckvirinae*) including four new genera 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
Kropinski AM, Adriaenssens EM, Poranen M	Phage.Canada@gmail.com; Evelien.Adriaenssens@quadram.ac.uk; minna.poranen@helsinki.fi

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])
University of Guelph, Canada [AMK] Quadram Institute Bioscience, UK [EMA] University of Helsinki, Finland [MMP]

Corresponding author

Andrew M. Kropinski

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:

Authority to use the name of a living person:

Please provide the following information if you propose taxon name(s) which are derived from the name of a living person or persons. Please attach documents to verify that permission has been obtained.

Taxon name	Person from whom the name is derived	Permission obtained (Y/N)
Douglaswolinvirus	Julia Douglas	Y
Douglaswolinvirus	Meyer J. Wolin	Y

Date first submitted to ICTV:
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

Name of accompanying Excel module: 2019.051B.A.v1.Tybeckvirinae_1subfam4gen.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 criteria have 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.

additional material in support of this proposal

- 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.

References:

1: Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28.

2: Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71.

3: O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45.

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.

5: Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14.

6: 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.

7: Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147.

8: 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.

9: Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52.

Species demarcation criteria We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

Source of the name of the subfamily taxon: This subfamily is named in honour of Ethel Ingeborg Tybeck (1923 – 1982; who worked under the supervision of Artturi Ilmari Virtanen (Nobel Laureate in Chemistry) and then in a Finnish dairy manufacturer Valio to her death and who was one of the first scientists to study the phages of *Lactobacillus* (Ref. Kiuru, U. J. T., and E. Tybeck. 1955. Characteristics of bacteriophages active against lactic acid bacteria in Swiss cheese. Suom. Kemistilehti B 28:57-62.))

A. Proposal 1: To create a new genus, *Douglaswolinvirus*, consisting of a single species in this subfamily.

Source of the name of the taxon: This genus is named in honour of microbiologists L. Julia Douglas (b. 1944, retired from Division of Infection and Immunity, Faculty of Biomedical and Life Sciences, University of Glasgow, Scotland, UK) and Meyer J. Wolin (b. 1930, retired from Wadsworth Center for Laboratories and Research, New York State Department of Health, Albany, NY, USA) in whose laboratory at the University of Illinois, Lactobacillus phage ATCC 8014-B2 was isolated.

References:

Douglas LJ, Wolin MJ. Cell wall polymers and phage lysis of Lactobacillus plantarum. Biochemistry. 1971 Apr 27;10(9):1551-5.

Nes IF, Brendehaug J, von Husby KO. Characterization of the bacteriophage B2 of Lactobacillus plantarum ATCC 8014. Biochimie. 1988;70(3):423-7.

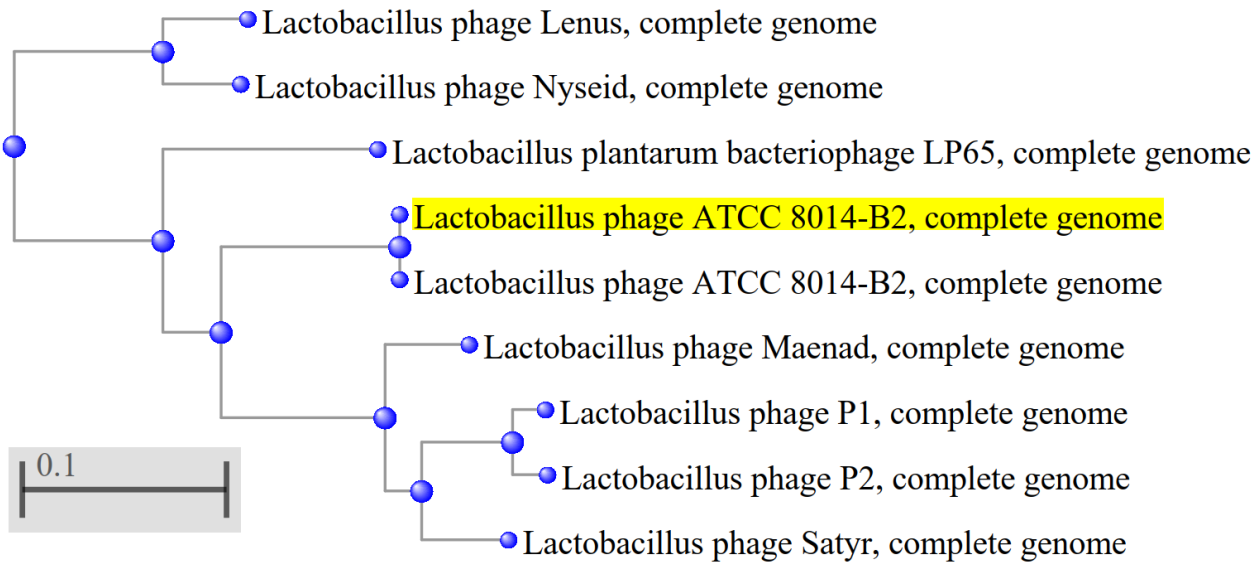
Briggiler Marcó M, Garneau JE, Tremblay D, Quiberoni A, Moineau S. Characterization of two virulent phages of Lactobacillus plantarum. Appl Environ Microbiol. 2012;78(24):8719-34.

History: Lactobacillus plantarum virulent siphophages ATCC 8014-B2 (B2), was isolated from anaerobic sewage sludge (Douglas & Wolin, 1971; Nes et al. 1988). “Phage B2 has an icosahedral capsid with a diameter of 74 nm and a tail of 240 nm in length and 10 nm in width.” (Briggiler Marcó et al. 2012).

GenBank Summary:

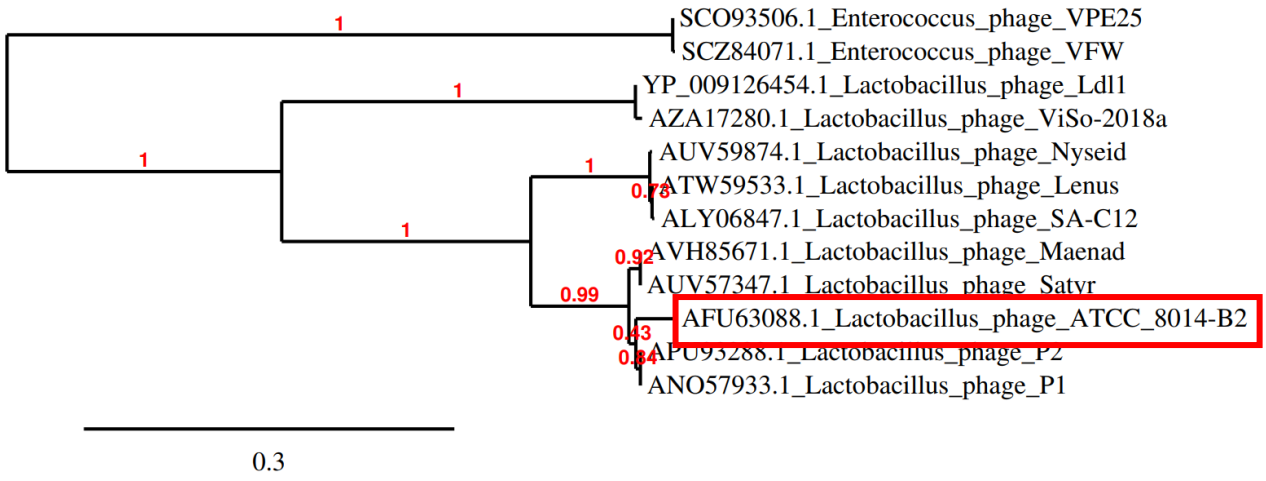
Phage name	RefSeq No.	INSDC	Size (Kb)	GC%	Protein	tRNA
Lactobacillus phage ATCC 8014-B2		JX486088.1	80.62	37.0	127	6

BLASTN homologs: The next most closely related phage is Lactobacillus phage Maenad which shares 58.2% identity with B2[1-3]. BLASTN tree: “BLAST computes a pairwise alignment between a query and the database sequences searched. It does not explicitly compute an alignment between the different database sequences (i.e., does not perform a multiple alignment). For purposes of this sequence tree presentation an implicit alignment between the database sequences is constructed, based upon the alignment of those (database) sequences to the query. It may often occur that two database sequences align to different parts of the query, so that they barely overlap each other or do not overlap at all. In that case it is not possible to calculate a distance between these two sequences and only the higher scoring sequence is included in the tree.”



Electron micrograph: None available

Phylogeny: The phylogenetic tree was constructed using the large subunit terminase protein homologs of B2 and related phages with phylogeny.fr in “one click” mode [8]. "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 [9] for details."



B. **Proposal 2:** To create a new genus, *Lidleunavirus*, consisting of two species in this subfamily.

Source of the name of the taxon: This genus is named after the first phage of this type Lactobacillus phage Ldl1.

Reference:

Casey E, Mahony J, Neve H, Noben JP, Dal Bello F, van Sinderen D. Novel phage group infecting Lactobacillus delbrueckii subsp. lactis, as revealed by genomic and proteomic analysis of bacteriophage Ldl1. Appl Environ Microbiol. 2015;81(4):1319-26.

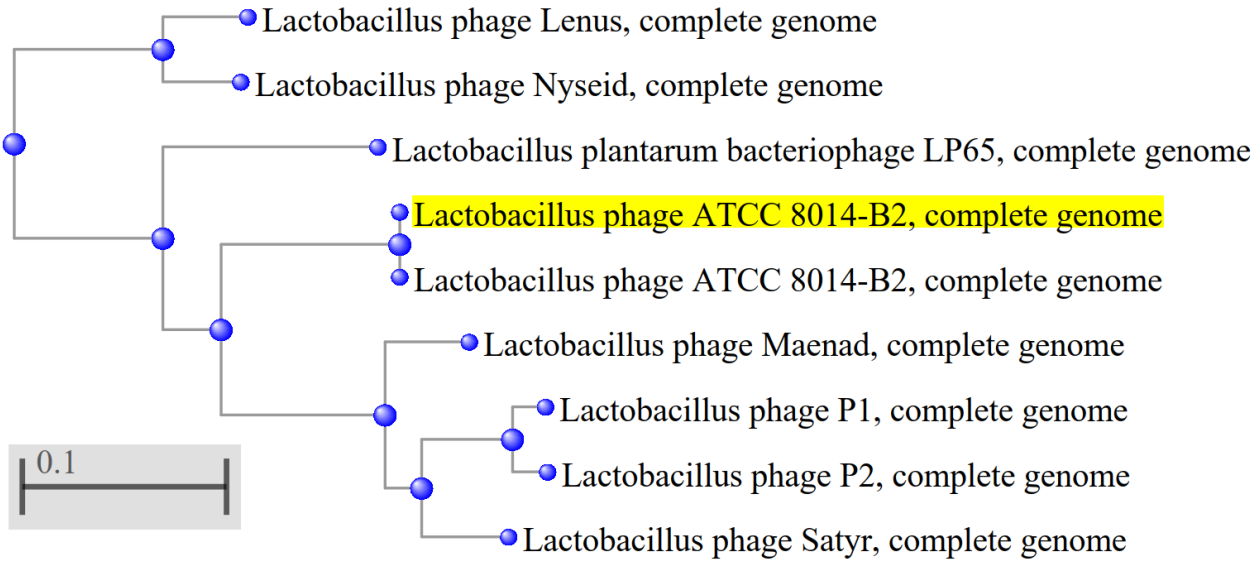
History: "Ldl1 is a virulent phage infecting the dairy starter Lactobacillus delbrueckii subsp. lactis LdlS. Electron microscopy analysis revealed that this phage exhibits a large head (73 nm) and a long (399 nm) tail." Lactobacillus phage ViSo-2018a was isolated from a natural whey culture from Gruyere cheese in Switzerland using Lactobacillus delbrueckii subsp. lactis isolate NWC_2_2 as the host bacterium.

GenBank Summary:

Phage name	RefSeq No.	INSDC	Size (Kb)	GC%	Protein	tRNA	Overall DNA sequence identity (**)	% common proteins (**)
Lactobacillus phage Ldl1	NC_026609.1	KM514685.1	74.81	37.8	79	1(*)	100	100
Lactobacillus phage ViSo-2018a		CP031026.1	72.36	37.4	87	1	87.2	84.8

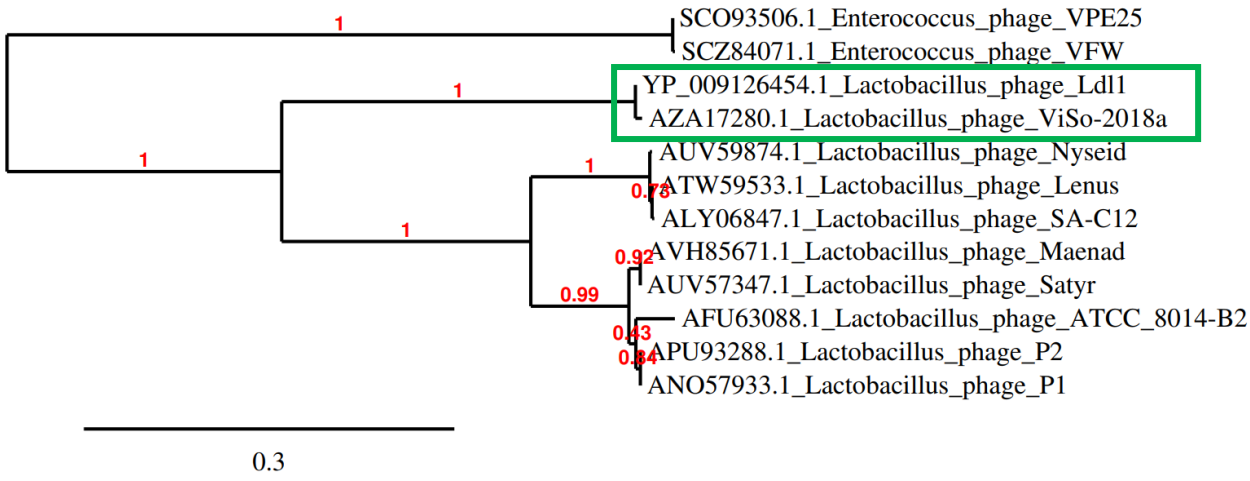
(*) None listed in the NCBI genome summary; discovered using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/ [5]
**** Determined using BLASTn at NCBI [1-3]**
***** Determined using CoreGenes 3.5 at http://binf.gmu.edu:8080/CoreGenes3.5/ [6]**

BLASTN homologs: The next most closely related phage is Lactobacillus phage P2 which shares 4.6% identity with Ldl12 [1-3]. BLASTN tree: "BLAST computes a pairwise alignment between a query and the database sequences searched. It does not explicitly compute an alignment between the different database sequences (i.e., does not perform a multiple alignment). For purposes of this sequence tree presentation an implicit alignment between the database sequences is constructed, based upon the alignment of those (database) sequences to the query. It may often occur that two database sequences align to different parts of the query, so that they barely overlap each other or do not overlap at all. In that case it is not possible to calculate a distance between these two sequences and only the higher scoring sequence is included in the tree."



Electron micrograph: None available

Phylogeny: The phylogenetic tree was constructed using the large subunit terminase protein homologs of B2 and related phages with phylogeny.fr in “one click” mode [8]. "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 [9] for details."



C. **Proposal 3:** To create a new genus, *Lenusvirus*, consisting of three species in this subfamily.

Source of the name of the taxon: This genus is named after one of the first phage of this type Lactobacillus phage Lenus.

Reference:
None

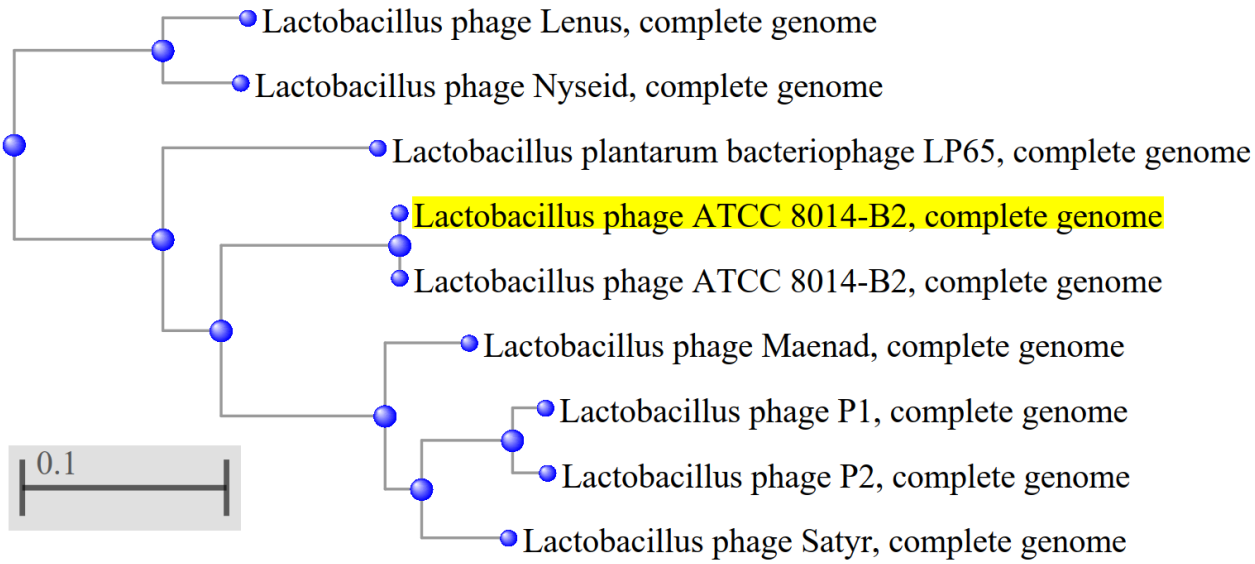
History: Both Lactobacillus phages Lenus and Nyseid were isolated in Denmark from organic waste runoff using Lactobacillus plantarum as a host. Lactobacillus phage SA-C12 was isolated from silage in Ireland using Lactobacillus brevis SA-C12 as the host strain.

GenBank Summary:

Phage name	RefSeq No.	INSDC	Size (Kb)	GC%	Protein	tRNA	Overall DNA sequence identity (**)	% common proteins (**)
Lactobacillus phage Lenus		MG252693.1	78.89	37.2	131	3	100	100
Lactobacillus phage Nyseid		MG765276.1	79.22	37.1	125	4	87.2	88.6
Lactobacillus phage SA-C12		KU052488.1	79.1	37.5	121	4(*)	78.6	72.5

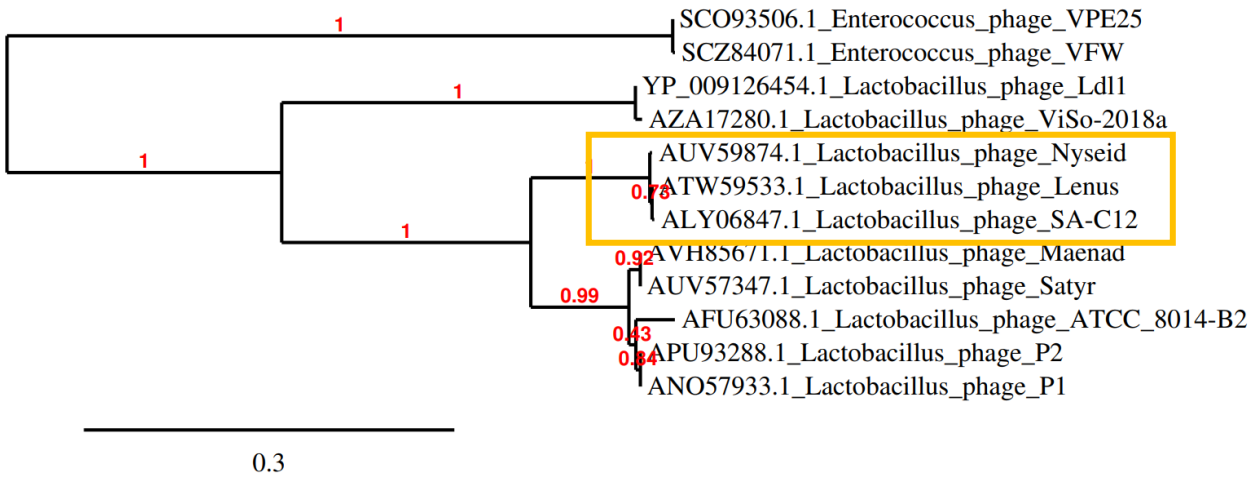
(*) None listed in the NCBI genome summary; discovered using tRNAscan-SE 2.0 at http://lowelab.ucsc.edu/tRNAscan-SE/ [5]
**** Determined using BLASTn at NCBI [1-3]**
***** Determined using CoreGenes 3.5 at http://binf.gmu.edu:8080/CoreGenes3.5/ [6]**

BLASTN homologs: The next most closely related phage is Lactobacillus phage ATCC 8014-B2 which shares 43.6% identity with Lenus [1-3]. BLASTN tree: "BLAST computes a pairwise alignment between a query and the database sequences searched. It does not explicitly compute an alignment between the different database sequences (i.e., does not perform a multiple alignment). For purposes of this sequence tree presentation an implicit alignment between the database sequences is constructed, based upon the alignment of those (database) sequences to the query. It may often occur that two database sequences align to different parts of the query, so that they barely overlap each other or do not overlap at all. In that case it is not possible to calculate a distance between these two sequences and only the higher scoring sequence is included in the tree."



Electron micrograph: None available

Phylogeny: The phylogenetic tree was constructed using the large subunit terminase protein homologs of B2 and related phages with phylogeny.fr in "one click" mode [8]. "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 [9] for details."



D. Proposal 4: To create a new genus, *Maenadvirus*, consisting of three species in this subfamily.

Source of the name of the taxon: This genus is named after one of the first phage of this type Lactobacillus phage Maenad.

Reference:
Chen X, Xi Y, Zhang H, Wang Z, Fan M, Liu Y, Wu W. Characterization and adsorption of Lactobacillus virulent phage P1. J Dairy Sci. 2016; 99(9):6995-7001.

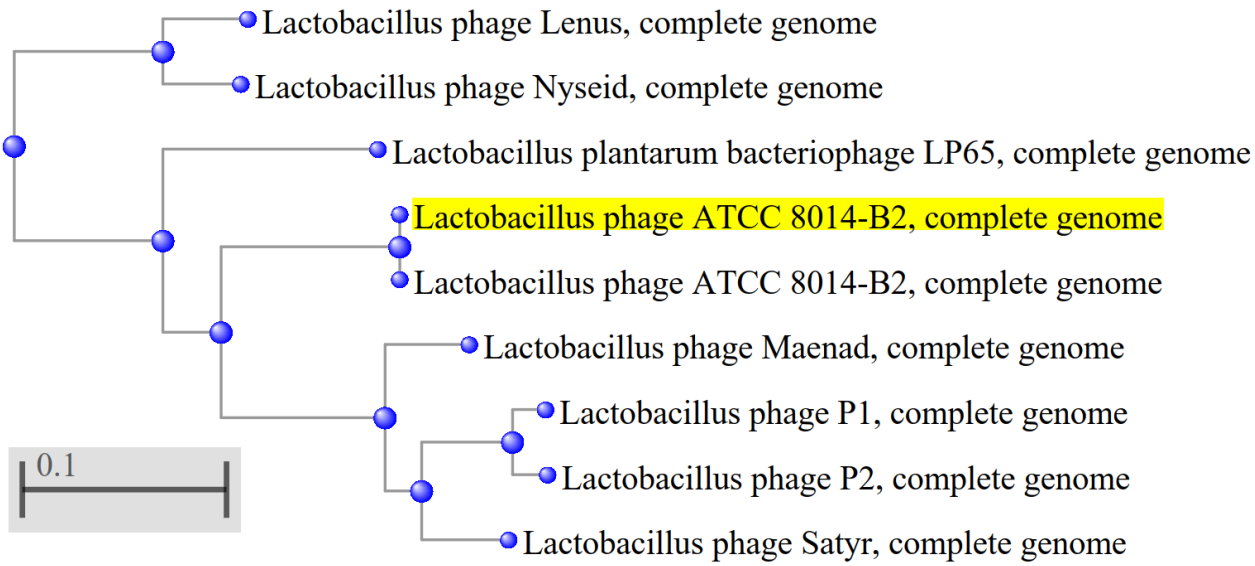
History: Lactobacillus phages Maenad and Satyr were isolated in Denmark from organic waste runoff using Lactobacillus plantarum as the host bacterium. Lactobacillus phage P1 was isolated in Inner Mongolia using fermentation broth from Lactobacillus plantarum IMAU10120. "The phage had an isometric capsid about 71.7 nm and a long noncontractile tail (about 272 nm long, 11.3 nm wide)."

GenBank Summary:

Phage name	RefSeq No.	INSDC	Size (Kb)	GC%	Protein	tRNA	Overall DNA sequence identity (**)	% common proteins (**)
Lactobacillus phage Maenad		MG765274.1	78.65	39.1	109	4	100	100
Lactobacillus phage Satyr		MG744354.1	81.08	39.4	111	4	89.2	96.3
Lactobacillus phage P1		KX223815.1	73.79	39.0	86(#)	2	77.7	65.1

Lactobacillus phage P2 should be considered a strain of P1
(#) the genome of this phage is underannotated
**** Determined using BLASTn at NCBI [1-3]**
***** Determined using CoreGenes 3.5 at http://binf.gmu.edu:8080/CoreGenes3.5/ [6]**

BLASTN homologs: The next most closely related phage is Lactobacillus phage ATCC 8014-B2 which shares 59.9% identity with Maenad [1-3]. BLASTN tree: "BLAST computes a pairwise alignment between a query and the database sequences searched. It does not explicitly compute an alignment between the different database sequences (i.e., does not perform a multiple alignment). For purposes of this sequence tree presentation an implicit alignment between the database sequences is constructed, based upon the alignment of those (database) sequences to the query. It may often occur that two database sequences align to different parts of the query, so that they barely overlap each other or do not overlap at all. In that case it is not possible to calculate a distance between these two sequences and only the higher scoring sequence is included in the tree."



Electron micrograph: None available

Phylogeny: The phylogenetic tree was constructed using the large subunit terminase protein homologs of Maenad and related phages with phylogeny.fr in “one click” mode [8]. "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 [9] for details."