This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2015.012a-eB***	(to be completed by ICTV officers)

Short title: In the family *Myoviridae*, subfamily *Spounavirinae*, create genus *P100virus* containing two species to be moved from the genus *Twortlikevirus*.
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☒	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☐	**10** ☒

Author(s):

Martin J. Loessner – ETH Zurich (Switzerland)
Jochen Klumpp – ETH Zurich (Switzerland)
Richard Calendar – University of California, Berkeley (USA)
Hans-Wolfgang Ackermann – Université Laval (Canada)
Martin Wiedmann – Cornell University (USA)
Thomas Denes – Cornell University (USA)
Hany Anany – University of Guelph (Canada)
Alexander Sulakvelidze – Intralytix (USA)
Andrew M. Kropinski – University of Guelph (Canada)
Evelien M. Adriaenssens – University of Pretoria (South Africa)

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Bacterial & Archaeal Virus Subcommittee

ICTV Study Group comments (if any) and response of the proposer:

Please note that we have chosen to refer to this new genus as *P100virus* rather than *P100likevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "*like*" and "*Phi*" from phage genus names.

Date first submitted to ICTV: May 2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2015.012aB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Spounavirinae***
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2015.012bB***	(assigned by ICTV officers)

To name the new genus: *P100virus*

Assigning the type species and other species to a new genus

Code	***2015.012cB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Listeria virus P100

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

BLASTN, CoreGenes (Table 1; 2), progressiveMauve alignment (Fig. 2; 1) and phylogenetic analyses (Fig. 3; 3) all indicate that the proposed genus, *P100virus*, is cohesive and distinct from the other genera of viruses.

Origin of the new genus name:

Named after the first phage of its type to be sequenced: *Listeria* phage P100

Reasons to justify the choice of type species:

First phage of its type to be sequenced

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these 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.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2015.012dB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Listeria phage P100 and *Listeria phage A511*

The present taxonomic position of these taxon/taxa:

Genus:	***Twortlikevirus***
Subfamily:	***Spounavirinae***
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Currently these phages are classified within the *Twortlikevirus* genus, but BLASTN, CoreGenes and phylogenetic analyses reveal that all the large lytic *Listeria* myoviruses are essentially identical and significantly different from *Staphylococcus* phage Twort. P100 and Twort only share 10% DNA sequence identity (BLASTN) and 39.7 % homologous proteins as shown by CoreGenes analysis (2). Furthermore, phylogenetic analysis (Fig. 2) of the major capsid and large subunit terminase proteins reveal that the proteins of phage Twort are significantly different from those of the large lytic *Listeria* myoviruses.

Part (b) re-assign to a higher taxon

Code	***2015.012eB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***P100virus*** **(new)**
Subfamily:	***Spounavirinae***
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Newly proposed genus (See Module 2)

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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.
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. Klumpp J, Dorscht J, Lurz R, Bielmann R, Wieland M, Zimmer M, Calendar R, Loessner MJ. The terminally redundant, nonpermuted genome of *Listeria* bacteriophage A511: a model for the SPO1-like myoviruses of gram-positive bacteria. J Bacteriol. 2008;190(17):5753-65.
5. Denes T, Vongkamjan K, Ackermann HW, Moreno Switt AI, Wiedmann M, den Bakker HC. Comparative genomic and morphological analyses of *Listeria* phages isolated from farm environments. Appl Environ Microbiol. 2014;80(15):4616-25.
6. Carlton RM, Noordman WH, Biswas B, de Meester ED, Loessner MJ. Bacteriophage P100 for control of *Listeria monocytogenes* in foods: genome sequence,bioinformatic analyses, oral toxicity study, and application. Regul ToxicolPharmacol. 2005;43(3):301-12.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1. Properties of the two phages belonging to the *P100virus* genus.

Phage	GenBank accession No.	Genome length (kb)	Genome (mol%G+C)	No. CDS	No. tRNAs
P100	DQ004855	131.4	36.0	174	18

* Determined using BLASTN; ** Determined using CoreGenes (2)

Table 2. Related phages

Phage	GenBank Accession Number
Listeria phage A511	DQ003638.2
Listeria phage vB_LmoM_AG20	JQ797329
Listeria phage LP-125	JX126918.2
Listeria phage LP-064	KJ094029
Listeria phage LP-083-2	KJ094030
Listeria phage LP-124	KJ094031
Listeria phage LP-048	KJ094033

Listeria phage List-36	KJ535721
Listeria phage LMSP-25	KJ535722
Listeria phage LMTA-94	KJ586795
Listeria phage LMTA-148	KJ591604
Listeria phage LMTA-57	KJ591605
Listeria phage WIL-1	KM373208

Fig. 1. Electron micrographs of negatively stained (uranyl acetate) *Listeria* phage P100

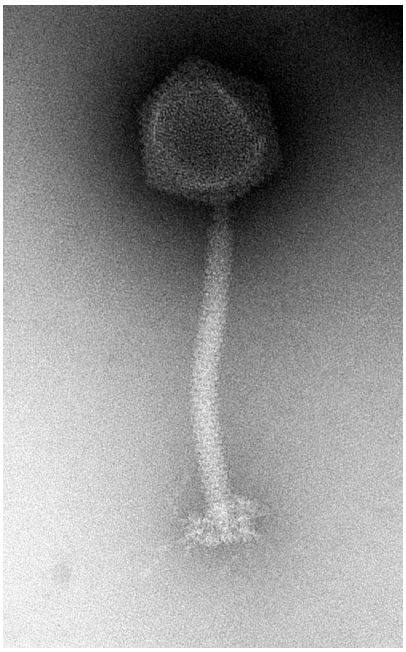

Fig. 2. Phylogenetic analysis of the large subunit terminase (top) and major capsid protein (bottom) of p100viruses and some related *Staphylococcus* phages constructed using "one click" at phylogeny.fr (3). "The "One Click mode" targets users that do not wish to deal with program and parameter selection. 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." Due to errors in the sequence of *Staphylococcus* phage Twort, the sequence of its terminase had to be reconstructed from the genome sequence.

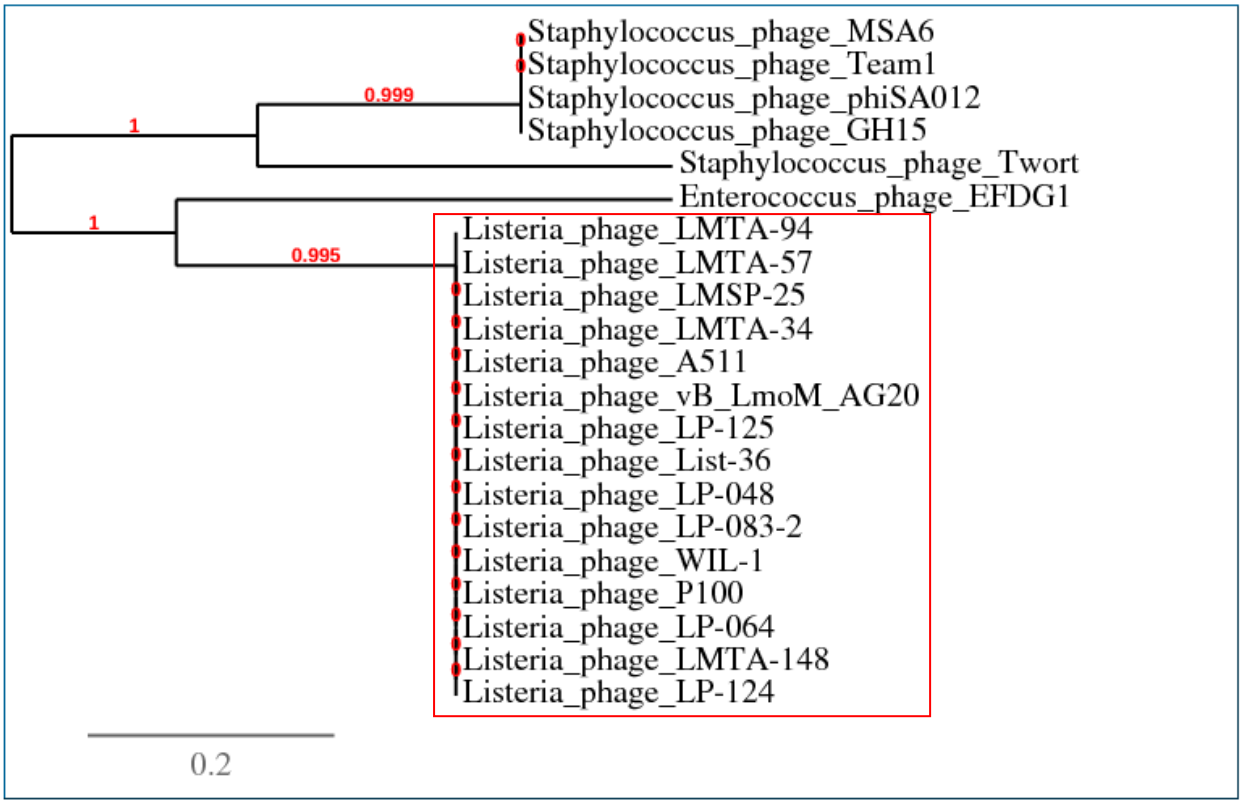

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*

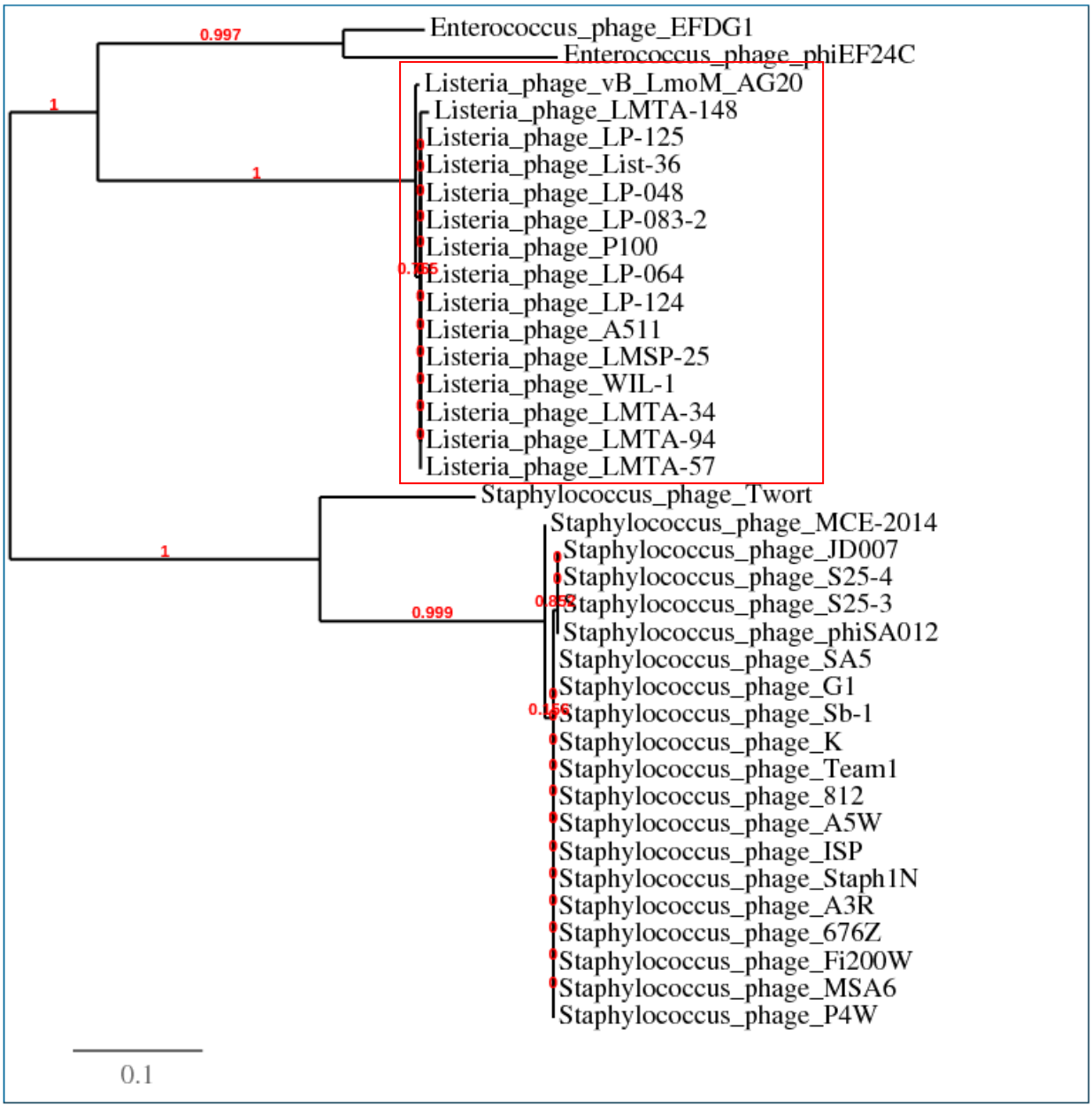

Figure 1: *Phylogenetic tree (the branch length is proportional to the number of substitutions per site).*