



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:	2015.041a-dB	(to be completed by ICTV officers)
Short title: Create the <i>Wphvirus</i> genus including 1 species within the family <i>Myoviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/> 2 <input type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input checked="" type="checkbox"/>	

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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 and Archaeal Virus Subcommittee

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

Date first submitted to ICTV:

June 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	2015.041aB	(assigned by ICTV officers)	
To create 1 new species within:			
Genus:	<i>Wphvirus</i>	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 genus is specified, enter “ unassigned ” in the genus box.	
Subfamily:			
Family:	<i>Myoviridae</i>		
Order:	<i>Caudovirales</i>		
Name of new species:	Representative isolate: (only 1 per species please)	GenBank sequence accession number(s)	
<i>Bacillus virus WPh</i>	Bacillus phage W.Ph.	HM144387	

Reasons to justify the creation and assignment of the new species:

- 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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

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 3: **NEW GENUS**

creating a new genus

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

Code	2015.041bB	(assigned by ICTV officers)
To create a new genus within:		
Subfamily:		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
Family:	Myoviridae	
Order:	Caudovirales	

naming a new genus

Code	2015.041cB	(assigned by ICTV officers)
To name the new genus: <i>Wphvirus</i>		

Assigning the type species and other species to a new genus

Code	2015.041dB	(assigned by ICTV officers)
To designate the following as the type species of the new genus		
<i>Bacillus virus WPh</i>		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		
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

“Phage W.Ph. was isolated by W. Beyer, University of Hohenheim, Germany in 2009 using a *Bacillus anthracis* strain isolated from a Zebra carcass (sample IDEB090416-01ZH) in Etosha National Park, Namibia (1, 2).” It infects *Bacillus anthracis*, *B. cereus* and *B. thuringiensis* strains (1). Morphologically this phage is indistinguishable from *Bacillus* phage Bastille but they only shares 23% overall DNA sequence identity. Phylogenetic analysis (6) of the major capsid (Fig. 3) and large subunit terminase (Fig. 4) reveal that phage W.Ph. is peripherally related to phages BPS13, Hakuna and Megatron; while analysis of the DNA polymerase (Fig. 5) suggests these phages form a clade. Whole genome BLASTN analysis reveals that BPS13, Hakuna and Megatron share approximately 70% overall DNA sequence identity with W.Ph., and possess a high mol%G+C and lack tRNA genes. At this time, we do not want to propose higher order relations.

The 157 kb genome (36.4 mol%G+C) encodes 274 proteins and 3 tRNAs.

Origin of the new genus name:

Bacillus phage W, Ph.

Reasons to justify the choice of type species:

The first fully sequenced member of this genus (1)

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 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Beyer, W., Bellan, S., Eberle, G., Ganz, H.H., Getz, W.M., Haumacher, R., Hilss, K.A., Kilian, W., Lazak, J., Turner, W.C., Turnbull, P.C., 2012. Distribution and molecular evolution of *Bacillus anthracis* genotypes in Namibia. PLoSNegl. Trop.Dis.6,e1534.
2. Klumpp J, Schmuki M, Sozhamannan S, Beyer W, Fouts DE, Bernbach V, Calendar R, Loessner MJ. The odd one out: *Bacillus* ACT bacteriophage CP-51 exhibits unusual properties compared to related *Spounavirinae* W.Ph. and Bastille. Virology. 2014;462-463:299-308.
3. Shin H, Lee JH, Park J, Heu S, Ryu S. Characterization and genome analysis of the *Bacillus cereus*-infecting bacteriophages BPS10C and BPS13. Arch Virol. 2014;159(8):2171-5.
4. Park J, Yun J, Lim JA, Kang DH, Ryu S. Characterization of an endolysin, LysBPS13, from a *Bacillus cereus* bacteriophage. FEMS Microbiol Lett. 2012;332(1):76-83.
5. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.
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. 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

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.

Fig. 1. Electron micrograph of phage W.Ph. (reproduced with permission of the publisher).

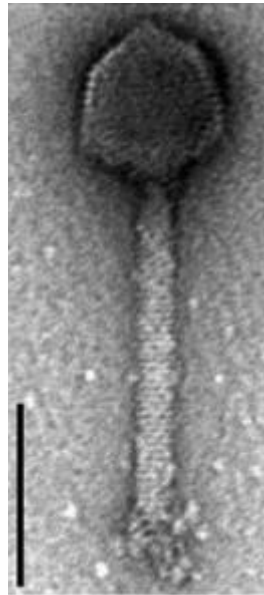


Table 1. Properties of the two phages belonging to the *Wphvirus*

Phage	GenBank Accession No.	Genome size (bp)	Genome (mol% G+C)	No. CDS	No. tRNAs	DNA (% sequence identity)*	% Homologous proteins **
W.Ph.	HM144387	156.9	36.4	274	3***	100	100

* Determined using BLASTN; ** Determined using CoreGenes (4); *** Not indicated in GenBank RefSeq record

Fig.2. Phylogenetic analysis of major capsid proteins of *Wphvirus* and variety of other *Bacillus* phage proteins constructed using “one click” at phylogeny.fr (5). N.B. The capsid gene of Hoody T contained a frameshift which was corrected prior to this analysis

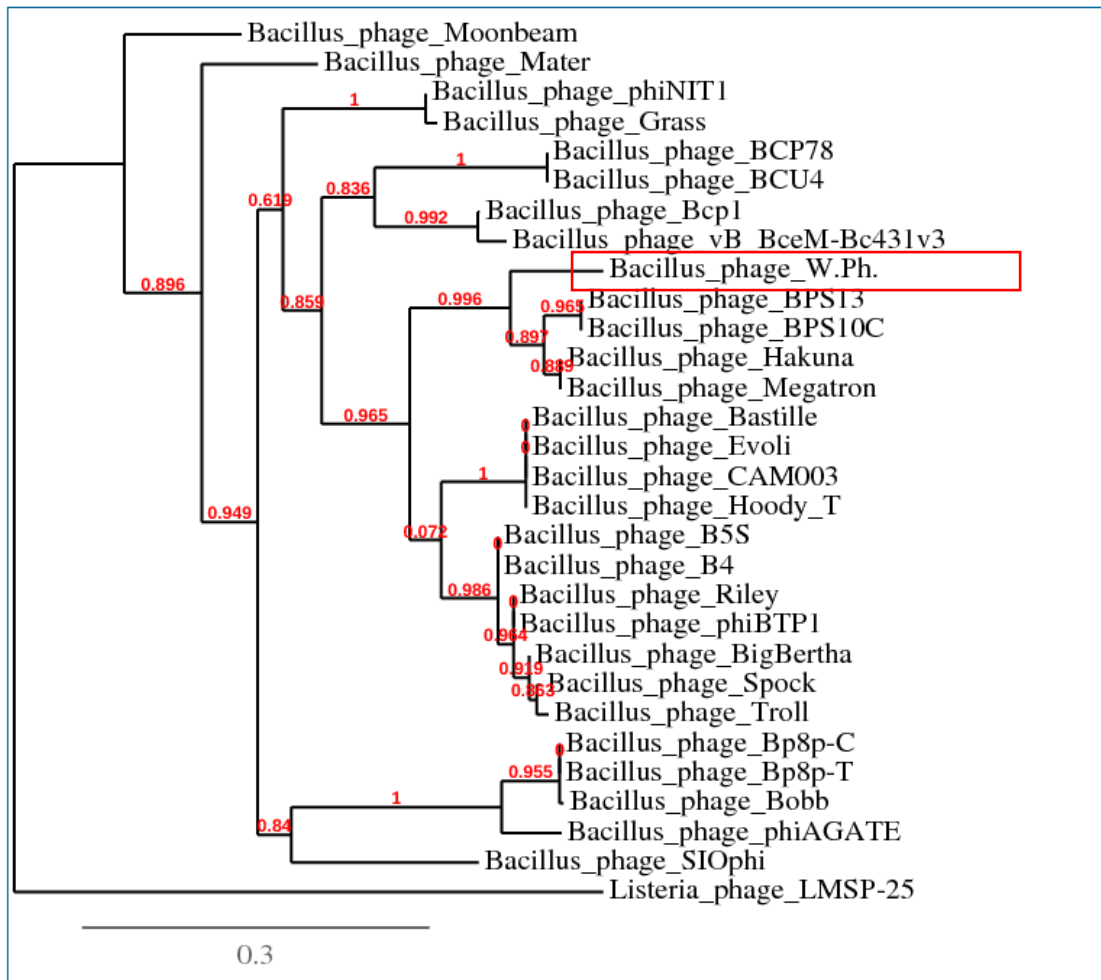


Figure 1: Phylogenetic tree (the branch length is proportional to the number of substitutions per site).

Fig. 3. Phylogenetic analysis of large subunit terminase proteins of *Wphvirus* and variety of other *Bacillus* phage proteins constructed using “one click” at phylogeny.fr (5).

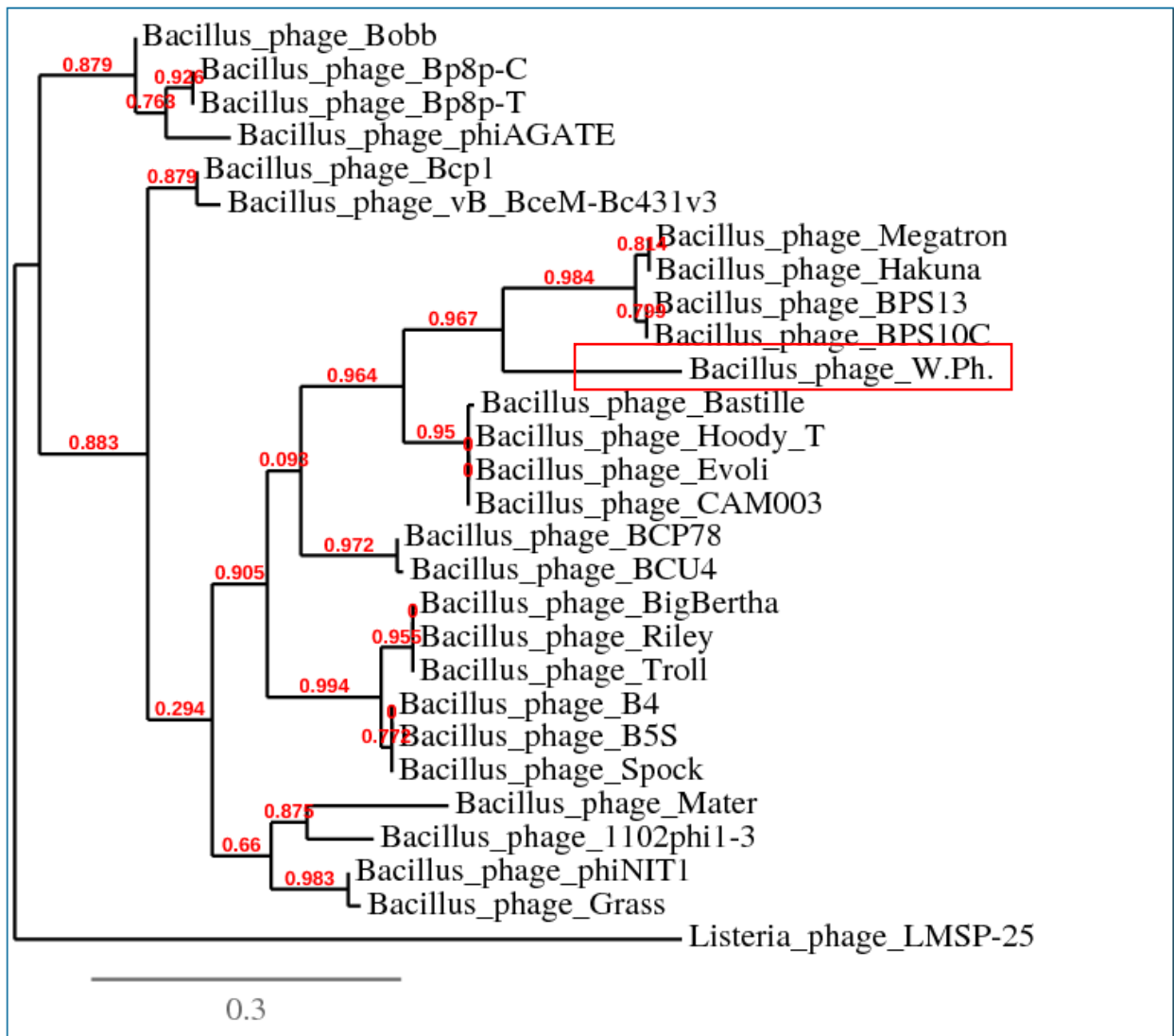


Figure 1: Phylogenetic tree (the branch length is proportional to the number of substitutions per site).

Fig. 4. Phylogenetic analysis of the metallophosphatases of *Wphvirus* and variety of other *Bacillus* phage proteins constructed using “one click” at phylogeny.fr (5).

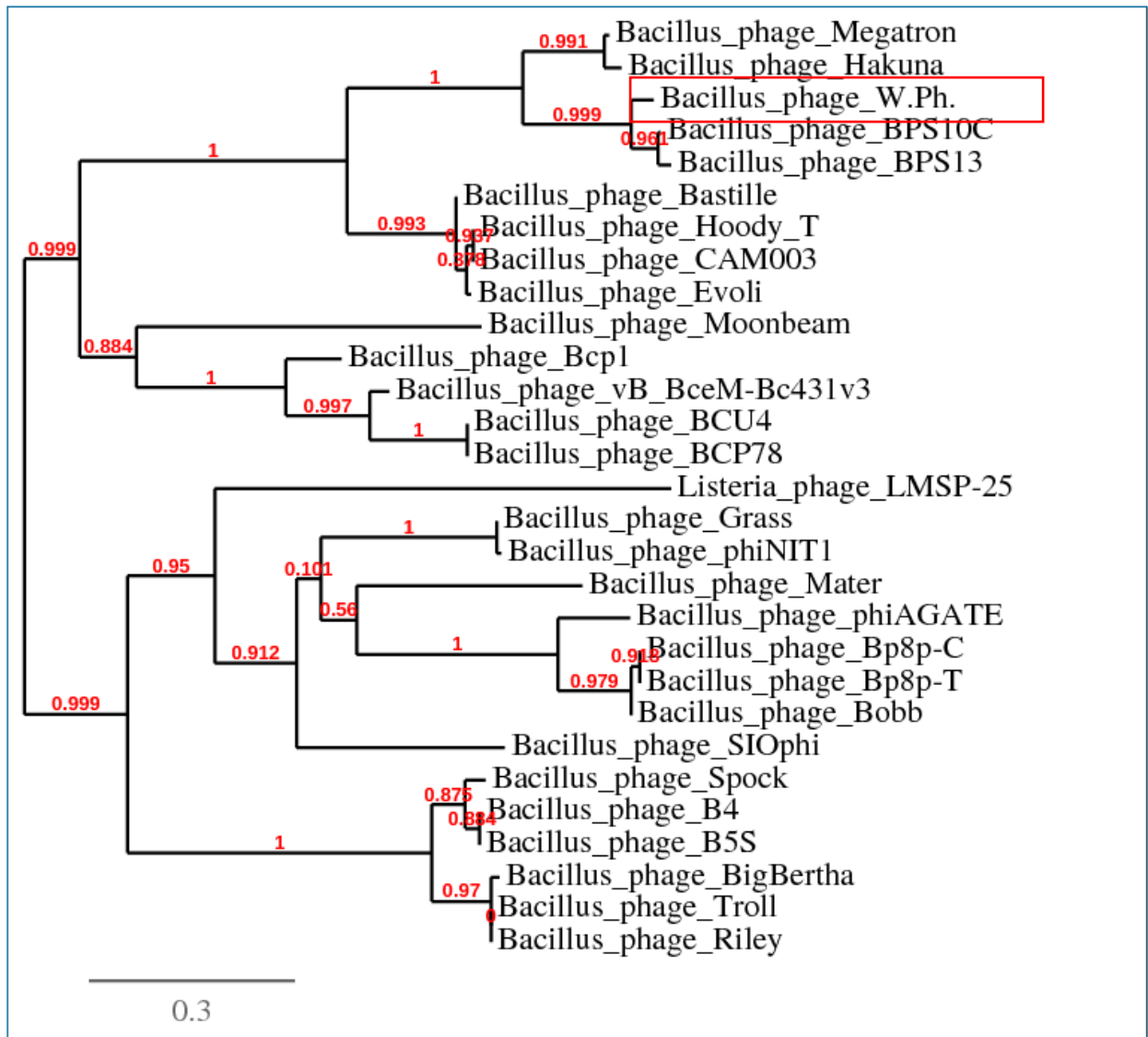


Figure 1: Phylogenetic tree (the branch length is proportional to the number of substitutions per site).