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: <u>**TITLE, AUTHORS, etc**</u>

Code assigned:	***2014.016aV***	(to be completed by ICTV officers)

Short title: Rename 12 picornavirus species
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

Nick Knowles (nick.knowles@pirbright.ac.uk) on behalf of the *Picornaviridae* Study Group

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)	*Picornaviridae* SG

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV: 07/07/2014
Date of this revision (if different to above):

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	*2014.016aV*	(assigned by ICTV officers)

Title of proposal: Renaming of 12 picornavirus species

Text of proposal:

In order to move towards a more consistent genus/species nomenclature (and in some cases to remove host species references) it is proposed to rename the species shown in Table 1. The virus common names, e.g. encephalomyocarditis virus would remain unchanged, thus helping to distinguish them from the species names. Possible renaming members of the *Aphthovirus* genus will be addressed in the future.

Table 1. Proposed new picornavirus species names.

Genus	Current species name	Proposed new species name	Virus common name*
Avihepatovirus	*Duck hepatitis A virus*	*Avihepatovirus A*	duck hepatitis A virus 1-3
Cardiovirus	*Encephalomyocarditis virus*	*Cardiovirus A*	encephalomyocarditis virus 1-2
Cardiovirus	*Theilovirus*	*Cardiovirus B*	Theiler's murine encephalomyelitis virus, Vilyuisk human encephalomyelitis virus, thera virus, Saffold virus 1-11
Erbovirus	*Equine rhinitis B virus*	*Erbovirus A*	equine rhinitis B virus 1-3
Hepatovirus	*Hepatitis A virus*	*Hepatovirus A*	hepatitis A virus 1
Parechovirus	*Human parechovirus*	*Parechovirus A*	human parechovirus 1-16
Parechovirus	*Ljungan virus*	*Parechovirus B*	Ljungan virus 1-4
Sapelovirus	*Porcine sapelovirus*	*Sapelovirus A*	porcine sapelovirus 1
Sapelovirus	*Simian sapelovirus*	*Sapelovirus B*	simian sapelovirus 1-3
Senecavirus	*Seneca Valley virus*	*Senecavirus A*	Seneca Valley virus 1
Teschovirus	*Porcine teschovirus*	*Teschovirus A*	porcine teschovirus 1-13
Tremovirus	*Avian encephalomyelitis virus*	*Tremovirus A*	avian encephalomyelitis virus 1

*, the virus common name would remain unchanged thus differentiating it from the species name.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

None.

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.

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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:	***2016.034a-dB***	(to be completed by ICTV officers)

Short title: To create one (1) new genus, *Pa6virus*, including fifty seven (57) new species in the family *Siphoviridae*.
(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):

Andrew M. Kropinski—University of Guelph (Canada)
Jens H. Kuhn—NIH/NIAID/IRF-Frederick, Maryland (USA)
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)	ICTV Bacterial and Archaeal Viruses Subcommittee

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

Date first submitted to ICTV:	June 2016
Date of this revision (if different to above):	

ICTV-EC comments and response of the proposer:

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	***2016.034aB***	(assigned by ICTV officers)

To create 57 new species within:

Genus:	***Pa6virus* (new)**
Subfamily:	
Family:	***Siphoviridae***
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 genus is specified, enter “**unassigned**” in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Propionibacterium virus ATCC29399BC	Propionibacterium phage ATCC29399B_C	JX262225.1
Propionibacterium virus ATCC29399BT	Propionibacterium phage ATCC29399B_T	JX262224.1
Propionibacterium virus Attacne	Propionibacterium phage Attacne	KR337651.1
Propionibacterium virus Keiki	Propionibacterium phage Keiki	KR337649.1
Propionibacterium virus Kubed	Propionibacterium phage Kubed	KR337645.1
Propionibacterium virus Lauchelly	Propionibacterium phage Lauchelly	KR337650.1
Propionibacterium virus MrAK	Propionibacterium phage MrAK	KR337643.1
Propionibacterium virus Ouroboros	Propionibacterium phage Ouroboros	KR337654.1
Propionibacterium virus P1.1	Propionibacterium phage P1.1	JX262223.1
Propionibacterium virus P1001	Propionibacterium phage P100_1	JX262222.1
Propionibacterium virus P100A	Propionibacterium phage P100_A	JX262221.1
Propionibacterium virus P100D	Propionibacterium phage P100D	JX262220.1
Propionibacterium virus P101A	Propionibacterium phage P101A	JX262217.1
Propionibacterium virus P104A	Propionibacterium phage P104A	JX262218.1
Propionibacterium virus P105	Propionibacterium phage P105	JX262219.1
Propionibacterium virus P144	Propionibacterium phage P14.4	JX262216.1
Propionibacterium virus P91	Propionibacterium phage P9.1	JX262215.1
Propionibacterium virus PA6	Propionibacterium phage PA6	DQ431235.1
Propionibacterium virus Pacnes201215	Propionibacterium phage Pacnes 2012-15	KJ722067.1
Propionibacterium virus PAD20	Propionibacterium phage PAD20	FJ706171.1
Propionibacterium virus PAS50	Propionibacterium phage PAS50	FJ706172.1
Propionibacterium virus PHL009M11	Propionibacterium phage PHL009M11	KJ578758.1
Propionibacterium virus PHL025M00	Propionibacterium phage PHL025M00	KJ578759.1
Propionibacterium virus PHL037M02	Propionibacterium phage PHL037M02	JX570706.1
Propionibacterium virus PHL041M10	Propionibacterium phage PHL041M10	KJ578761.1
Propionibacterium virus PHL060L00	Propionibacterium phage PHL060L00	JX570705.1
Propionibacterium virus PHL067M01	Propionibacterium phage PHL067M01	KJ578765.1
Propionibacterium virus PHL070N00	Propionibacterium phage PHL070N00	KJ578767.1
Propionibacterium virus PHL071N05	Propionibacterium phage PHL071N05	JX570710.1
Propionibacterium virus PHL082M03	Propionibacterium phage PHL082M03	KJ578770.1
Propionibacterium virus PHL092M00	Propionibacterium phage PHL092M00	KJ578773.1

Propionibacterium virus PHL095N00	Propionibacterium phage PHL095N00	KJ578774.1
Propionibacterium virus PHL111M01	Propionibacterium phage PHL111M01	JX570702.1
Propionibacterium virus PHL112N00	Propionibacterium phage PHL112N00	JX570714.1
Propionibacterium virus PHL113M01	Propionibacterium phage PHL113M01	JX570713.1
Propionibacterium virus PHL114L00	Propionibacterium phage PHL114L00	JX570712.1
Propionibacterium virus PHL116M00	Propionibacterium phage PHL116M00	KJ578776.1
Propionibacterium virus PHL117M00	Propionibacterium phage PHL117M00	KJ578778.1
Propionibacterium virus PHL117M01	Propionibacterium phage PHL117M01	KJ578779.1
Propionibacterium virus PHL132N00	Propionibacterium phage PHL132N00	KJ578780.1
Propionibacterium virus PHL141N00	Propionibacterium phage PHL141N00	KJ578781.1
Propionibacterium virus PHL151M00	Propionibacterium phage PHL151M00	KJ578783.1
Propionibacterium virus PHL151N00	Propionibacterium phage PHL151N00	KJ578784.1
Propionibacterium virus PHL152M00	Propionibacterium phage PHL152M00	KJ578785.1
Propionibacterium virus PHL163M00	Propionibacterium phage PHL163M00	KJ578786.1
Propionibacterium virus PHL171M01	Propionibacterium phage PHL171M01	KJ578787.1
Propionibacterium virus PHL179M00	Propionibacterium phage PHL179M00	KJ578788.1
Propionibacterium virus PHL194M00	Propionibacterium phage PHL194M00	KJ578789.1
Propionibacterium virus PHL199M00	Propionibacterium phage PHL199M00	KJ578790.1
Propionibacterium virus PHL301M00	Propionibacterium phage PHL301M00	KJ578791.1
Propionibacterium virus PHL308M00	Propionibacterium phage PHL308M00	KJ578792.1
Propionibacterium virus Pirate	Propionibacterium phage Pirate	KR337653.1
Propionibacterium virus Procrass1	Propionibacterium phage Procrass1	KR337644.1
Propionibacterium virus SKKY	Propionibacterium phage SKKY	KR337648.1
Propionibacterium virus Solid	Propionibacterium phage Solid	KR337647.1
Propionibacterium virus Stormborn	Propionibacterium phage Stormborn	KR337652.1
Propionibacterium virus Wizzo	Propionibacterium phage Wizzo	KR337646.1

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. 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.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2016.034bB***	(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:	***Siphoviridae***	
Order:	***Caudovirales***	

naming a new genus

Code	***2016.034cB***	(assigned by ICTV officers)

To name the new genus: *Pa6virus*

Assigning the type species and other species to a new genus

Code	***2016.034dB***	(assigned by ICTV officers)

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

Propionibacterium virus PA6	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:**

57

Reasons to justify the creation of a new genus:

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

Recently, large numbers of Propionibacterium phages have been isolated predominantly using *Propionibacterium acnes* ATCC 6919 as the host (http://phagesdb.org/clusters/BU/). Currently, 83 representatives are deposited in NCBI databases. Because of the time required to run individual BLASTN searches we have used the BLAST features of Gegenees [3] to group these viruses (Fig. 1 and Fig. 2). They all share ≥85% sequence identity to the type virus, Propionibacterium phage PA6 [2]; possessing ca. 29 kb genomes with a mol% G+C content of ca. 54 (somewhat less than the 60% present in the genomes of their host). All of these phages are virulent.

Origin of the new genus name:

Based upon the name of the first sequenced member of this genus.

Reasons to justify the choice of type species:

The first sequenced member of this genus.

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. 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.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. 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.
2. Farrar MD, Howson KM, Bojar RA, West D, Towler JC, Parry J, Pelton K, Holland KT. Genome sequence and analysis of a *Propionibacterium acnes* bacteriophage. J Bacteriol. 2007; 189(11):4161-7.
3. Agren J et al. (2012) Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One.;7(6):e39107

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 BLASTN analysis of all these viruses using Gegenees [3] with "custom" settings of fragmenting algorithm - size: 100 bp, shift 50 bp. The results were exported to Excel and the heatmap is colored according to percentage identity (>70% green, >80% yellow, >95% red). Strains belonging to the same proposed species are boxed in black.

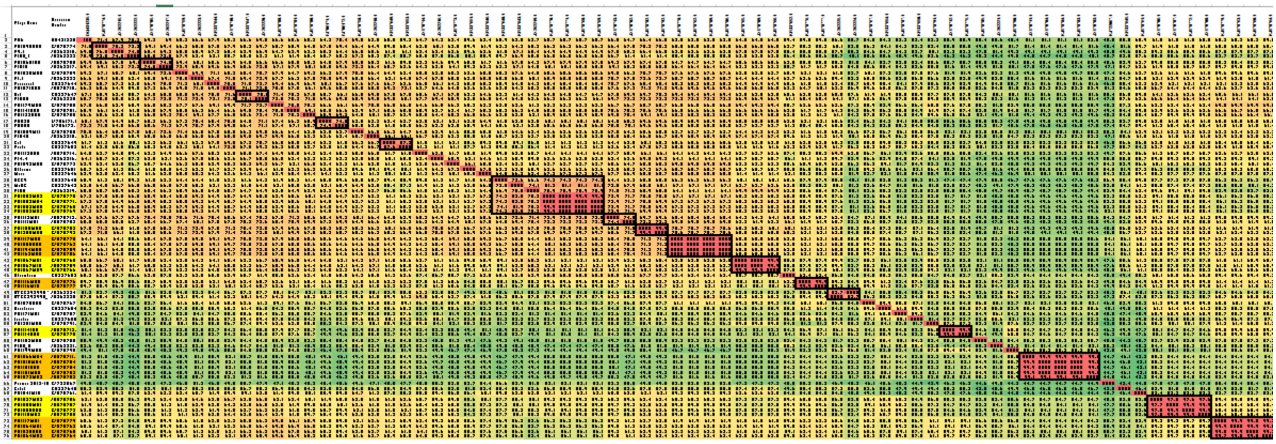


Fig. 2. TBLASTX analysis of all these viruses using Gegenees [3] with “custom” settings of fragmenting algorithm - size: 100 bp, shift 50 bp. The results were exported to Excel and the heatmap is colored according to percentage identity (>70% green, >80% yellow, >95% red). Strains belonging to the same proposed species are boxed in black.

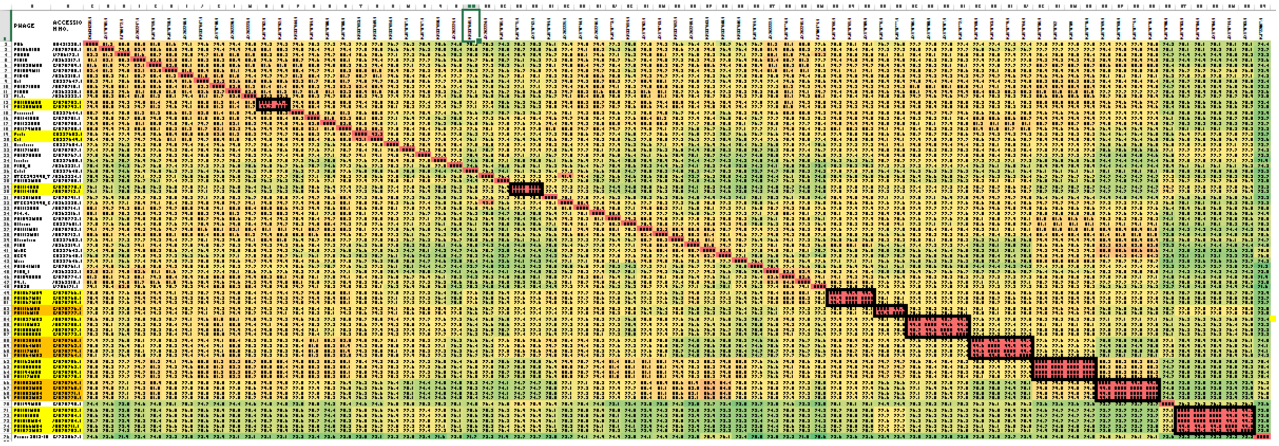


Fig. 3. Electron micrograph of negatively stained Propionibacterium phage Attacne (http://phagesdb.org/phages/Attacne/) - Limited permission was granted by The Actinobacteriophages Database, funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

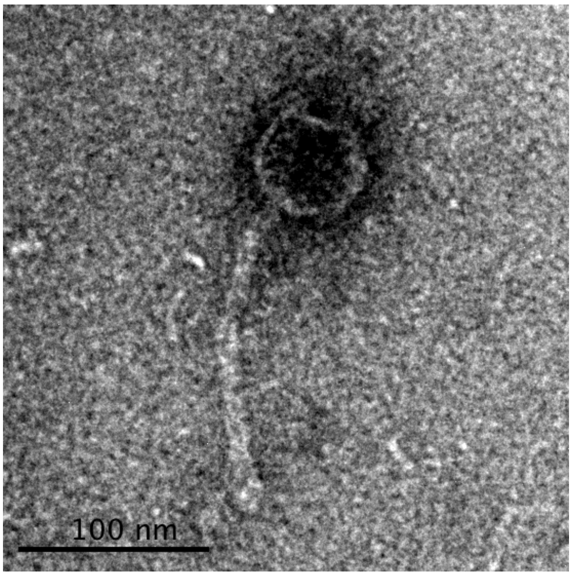


Table 1. Properties of phage PA6 and other viruses belonging to the genus *Pa6virus* based upon the data on 33 phages given in the Actinobacteriophage Database (http://phagesdb.org/clusters/BU/)

Name	**RefSeq**	**INSDC**	**Length (bp)**	**GC%**	**Protein**	**tRNA**
Propionibacterium	NC_009541.1	DQ431235.1	29,739	54.0	48	0

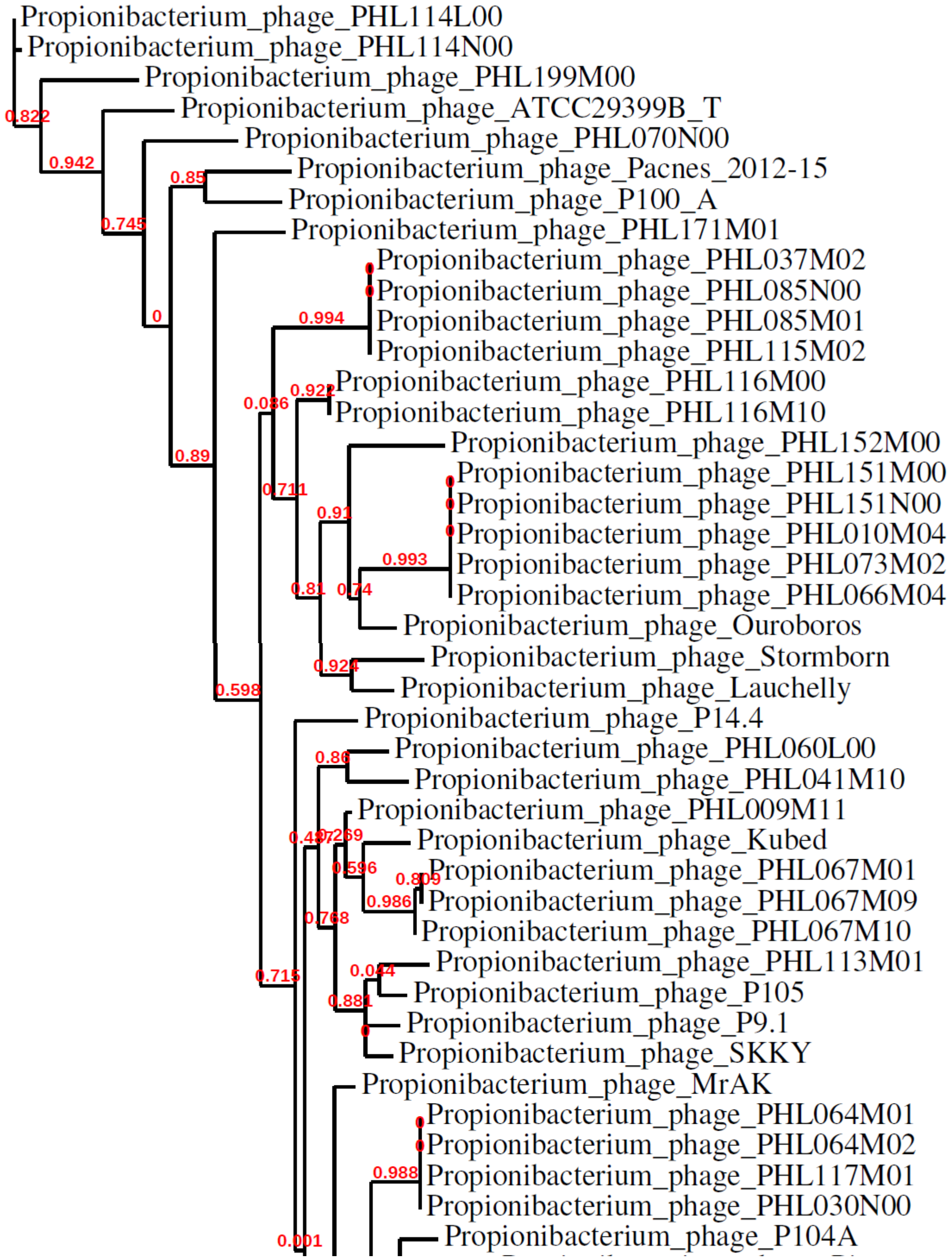
phage PA6						
(average)			29,397*	54.1	44.5	0

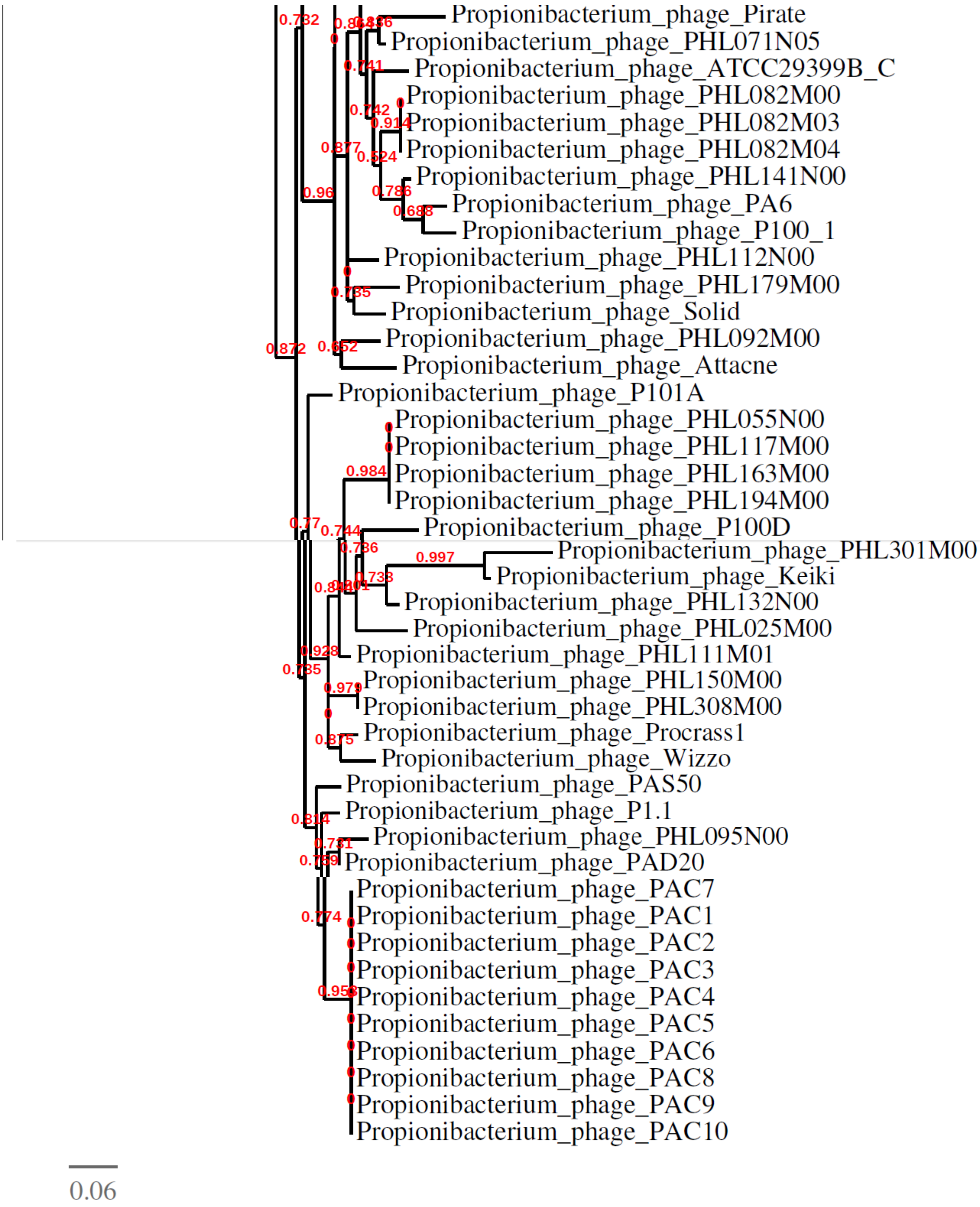
* 11-bp 3'cohesive overhang (TCGTACGGCTT)

Table 2. Phages which are considered strains of viruses within the *Pa6virus* genus.

Propionibacterium phage	**Accession No.**	**Strain of Propionibacterium phage**
Propionibacterium phage PHL082M04	KJ578771.1	PHL082M03
Propionibacterium phage PHL082M00	KJ578768.1	PHL082M03
Propionibacterium phage PHL082M02	KJ578769.1	PHL082M03
Propionibacterium phage PHL308M00	KJ578792.1	PHL151M00
Propionibacterium phage PHL055N00	KJ578762.1	PHL117M00
Propionibacterium phage PHL194M00	KJ578789.1	PHL117M00
Propionibacterium phage PHL163M00	KJ578786.1	PHL117M00
Propionibacterium phage PHL067M10	JX570709.1	PHL067M01
Propionibacterium phage PHL067M09	KJ578766.1	PHL067M01
Propionibacterium phage PHL116M10	KJ578777.1	PHL116M00
Propionibacterium phage PHL114N00	KJ578775.1	PHL114L00
Propionibacterium phage PHL010M04	JX570704.1	PHL151N00
Propionibacterium phage PHL066M04	JX570711.1	PHL151N00
Propionibacterium phage PHL073M02	JX570703.1	PHL151N00
Propionibacterium phage PHL085M01	JX570707.1	PHL037M02
Propionibacterium phage PHL085N00	KJ578772.1	PHL037M02
Propionibacterium phage PHL115M02	JX570708.1	PHL037M02
Propionibacterium phage PHL064M01	KJ578763.1	PHL117M01
Propionibacterium phage PHL030N00	KJ578760.1	PHL117M01
Propionibacterium phage PHL064M02	KJ578764.1	PHL117M01

Fig. 4. Phylogenetic analysis of large subunit terminase proteins of Propionibacterium phages constructed using “one click” at phylogeny.fr [1]. "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."




Propionibacterium_phage_Pirate
Propionibacterium_phage_PHL071N05
Propionibacterium_phage_ATCC29399B_C
Propionibacterium_phage_PHL082M00
Propionibacterium_phage_PHL082M03
Propionibacterium_phage_PHL082M04
Propionibacterium_phage_PHL141N00
Propionibacterium_phage_PA6
Propionibacterium_phage_P100_1
Propionibacterium_phage_PHL112N00
Propionibacterium_phage_PHL179M00
Propionibacterium_phage_Solid
Propionibacterium_phage_PHL092M00
Propionibacterium_phage_Attacne
Propionibacterium_phage_P101A
Propionibacterium_phage_PHL055N00
Propionibacterium_phage_PHL117M00
Propionibacterium_phage_PHL163M00
Propionibacterium_phage_PHL194M00
Propionibacterium_phage_P100D
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Propionibacterium_phage_PHL150M00
Propionibacterium_phage_PHL308M00
Propionibacterium_phage_Procrass1
Propionibacterium_phage_Wizzo
Propionibacterium_phage_PAS50
Propionibacterium_phage_P1.1
Propionibacterium_phage_PHL095N00
Propionibacterium_phage_PAD20
Propionibacterium_phage_PAC7
Propionibacterium_phage_PAC1
Propionibacterium_phage_PAC2
Propionibacterium_phage_PAC3
Propionibacterium_phage_PAC4
Propionibacterium_phage_PAC5
Propionibacterium_phage_PAC6
Propionibacterium_phage_PAC8
Propionibacterium_phage_PAC9
Propionibacterium_phage_PAC10
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0.96
0.786
0.688
0.735
0.872
0.652
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0.77
0.744
0.736
0.997
0.738
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0.735
0.979
0.875
0.814
0.781
0.789
0.774
0.958
0.06