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

<table>
<thead>
<tr>
<th>Code assigned:</th>
<th>2016.034a-dB (to be completed by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Short title:</strong></td>
<td>To create one (1) new genus, <em>Pa6virus</em>, including fifty seven (57) new species in the family <em>Siphoviridae</em>. (e.g. 6 new species in the genus <em>Zetavirus</em>)</td>
</tr>
<tr>
<td><strong>Modules attached</strong></td>
<td>1 2 3 4 5 6 7 8 9 10</td>
</tr>
<tr>
<td>(modules 1 and 10 are required)</td>
<td></td>
</tr>
</tbody>
</table>

**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:**

<table>
<thead>
<tr>
<th>ICTV Bacterial and Archaeal Viruses Subcommittee</th>
</tr>
</thead>
<tbody>
<tr>
<td>A list of study groups and contacts is provided at <a href="http://www.ictvonline.org/subcommittees.asp">http://www.ictvonline.org/subcommittees.asp</a>. If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)</td>
</tr>
</tbody>
</table>

**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:

<table>
<thead>
<tr>
<th>Genus:</th>
<th>Pa6virus (new)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Subfamily:</td>
<td></td>
</tr>
<tr>
<td>Family:</td>
<td>Siphoviridae</td>
</tr>
<tr>
<td>Order:</td>
<td>Caudovirales</td>
</tr>
</tbody>
</table>

### Name of new species:

- Propionibacterium virus ATCC29399BC
- Propionibacterium virus ATCC29399BT
- Propionibacterium virus Attacne
- Propionibacterium virus Keiki
- Propionibacterium virus Kubed
- Propionibacterium virus Lauchelly
- Propionibacterium virus MrAK
- Propionibacterium virus Ouroboros
- Propionibacterium virus P1.1
- Propionibacterium virus P1001
- Propionibacterium virus P100A
- Propionibacterium virus P100D
- Propionibacterium virus P101A
- Propionibacterium virus P104A
- Propionibacterium virus P105
- Propionibacterium virus P144
- Propionibacterium virus P91
- Propionibacterium virus PA6
- Propionibacterium virus Pacnes 2012-15
- Propionibacterium virus PAD20
- Propionibacterium virus PAS50
- Propionibacterium virus PHL009M11
- Propionibacterium virus PHL025M00
- Propionibacterium virus PHL037M02
- Propionibacterium virus PHL041M10
- Propionibacterium virus PHL060L00
- Propionibacterium virus PHL067M01
- Propionibacterium virus PHL070N00
- Propionibacterium virus PHL071N05
- Propionibacterium virus PHL082M03
- Propionibacterium virus PHL092M00

### Representative isolate: (only 1 per species please)

- Propionibacterium phage ATCC29399BC_C
- Propionibacterium phage ATCC29399B_T
- Propionibacterium phage Attacne
- Propionibacterium phage Keiki
- Propionibacterium phage Kubed
- Propionibacterium phage Lauchelly
- Propionibacterium phage MrAK
- Propionibacterium phage Ouroboros
- Propionibacterium phage P1.1
- Propionibacterium phage P100_1
- Propionibacterium phage P100_A
- Propionibacterium phage P100_D
- Propionibacterium phage P101_A
- Propionibacterium phage P104_A
- Propionibacterium phage P105
- Propionibacterium phage P144
- Propionibacterium phage P9.1
- Propionibacterium phage PA6
- Propionibacterium phage Pacnes 2012-15
- Propionibacterium phage PAD20
- Propionibacterium phage PAS50
- Propionibacterium phage PHL009M11
- Propionibacterium phage PHL025M00
- Propionibacterium phage PHL037M02
- Propionibacterium phage PHL041M10
- Propionibacterium phage PHL060L00
- Propionibacterium phage PHL067M01
- Propionibacterium phage PHL070N00
- Propionibacterium phage PHL071N05
- Propionibacterium phage PHL082M03
- Propionibacterium phage PHL092M00

### GenBank sequence accession number(s)

- JX262225.1
- JX262224.1
- KR337651.1
- KR337649.1
- KR337645.1
- KR337650.1
- KR337643.1
- KR337654.1
- JX262223.1
- JX262222.1
- JX262221.1
- JX262220.1
- JX262217.1
- JX262218.1
- JX262219.1
- JX262216.1
- JX262215.1
- JX262211.1
- KJ722067.1
- FJ706171.1
- FJ706172.1
- KJ578758.1
- KJ578759.1
- JX570706.1
- KJ578761.1
- JX570705.1
- KJ578765.1
- KJ578767.1
- KJ578767.1
- KJ578770.1
- KJ578773.1

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.
### 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.

<table>
<thead>
<tr>
<th>Code</th>
<th>2016.034bB</th>
<th>(assigned by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td>To create a new genus within:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Subfamily:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Family:</td>
<td>Siphoviridae</td>
<td></td>
</tr>
<tr>
<td>Order:</td>
<td>Caudovirales</td>
<td></td>
</tr>
</tbody>
</table>

name a new genus

<table>
<thead>
<tr>
<th>Code</th>
<th>2016.034cB</th>
<th>(assigned by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td>To name the new genus: Pa6virus</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Assigning the type species and other species to a new genus

<table>
<thead>
<tr>
<th>Code</th>
<th>2016.034dB</th>
<th>(assigned by ICTV officers)</th>
</tr>
</thead>
<tbody>
<tr>
<td>To designate the following as the type species of the new genus</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium virus PA6</td>
<td>Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered</td>
<td></td>
</tr>
</tbody>
</table>

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:


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 Pativirus based upon the data on 33 phages given in the Actinobacteriophage Database (http://phagesdb.org/clusters/BU/)

<table>
<thead>
<tr>
<th>Name</th>
<th>RefSeq</th>
<th>INSDC</th>
<th>Length (bp)</th>
<th>GC%</th>
<th>Protein</th>
<th>tRNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Propionibacterium</td>
<td>NC_009541.1</td>
<td>DQ431235.1</td>
<td>29,739</td>
<td>54.0</td>
<td>48</td>
<td>0</td>
</tr>
<tr>
<td>Propionibacterium phage</td>
<td>Accession No.</td>
<td>Strain of Propionibacterium phage</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>--------------------------------</td>
<td>---------------</td>
<td>-----------------------------------</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL082M04</td>
<td>KJ578771.1</td>
<td>PHL082M03</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL082M00</td>
<td>KJ578768.1</td>
<td>PHL082M03</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL082M02</td>
<td>KJ578769.1</td>
<td>PHL082M03</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL308M00</td>
<td>KJ578792.1</td>
<td>PHL151M00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL055N00</td>
<td>KJ578762.1</td>
<td>PHL117M00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL194M00</td>
<td>KJ578789.1</td>
<td>PHL117M00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL163M00</td>
<td>KJ578786.1</td>
<td>PHL117M00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL067M10</td>
<td>JX570709.1</td>
<td>PHL067M01</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL067M09</td>
<td>KJ578766.1</td>
<td>PHL067M01</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL116M10</td>
<td>KJ578777.1</td>
<td>PHL116M00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL114N00</td>
<td>KJ578775.1</td>
<td>PHL114L00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL010M04</td>
<td>JX570704.1</td>
<td>PHL151N00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL066M04</td>
<td>JX570711.1</td>
<td>PHL151N00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL073M02</td>
<td>JX570703.1</td>
<td>PHL151N00</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL085M01</td>
<td>JX570707.1</td>
<td>PHL037M02</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL085N00</td>
<td>KJ578772.1</td>
<td>PHL037M02</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL115M02</td>
<td>JX570708.1</td>
<td>PHL037M02</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL064M01</td>
<td>KJ578763.1</td>
<td>PHL117M01</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL030N00</td>
<td>KJ578760.1</td>
<td>PHL117M01</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Propionibacterium phage PHL064M02</td>
<td>KJ578764.1</td>
<td>PHL117M01</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* 11-bp 3’ cohesive overhang (TCGTACGCTT)

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