



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:	2015.030aB	(to be completed by ICTV officers)			
Short title: To amend the description of the <i>Pbunalikevirus</i> (proposed new name <i>Pbunavirus</i>); and, add five (5) new species (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)

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

Please note that 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:

June 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

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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	2015.030aB	(assigned by ICTV officers)
To create 5 new species within:		
Genus:	<i>Pbunalikevirus (to be renamed Pbunavirus)</i>	Fill in all that apply. <ul style="list-style-type: none"> • 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>Pseudomonas virus DL60</i>	Pseudomonas phage DL60	KR054030
<i>Pseudomonas virus DL68</i>	Pseudomonas phage DL68	KR054033
<i>Pseudomonas virus JG024</i>	Pseudomonas phage JG024	GU815091
<i>Pseudomonas virus KPP12</i>	Pseudomonas phage KPP12	AB560486
<i>Pseudomonas virus Ab28</i>	Pseudomonas phage vB_PaeM_C1-14_Ab28	LN610589

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

Several new PB1-like phage genomes have recently been deposited to GenBank. This proposal recognizes the fact that they are part of the *Pbunalikevirus* genus (new proposed name: *Pbunavirus*) (1,2,3,4).

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

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. Fukuda K, Ishida W, Uchiyama J, Rashel M, Kato S, Morita T, Muraoka A, Sumi T, Matsuzaki S, Daibata M, Fukushima A. *Pseudomonas aeruginosa* keratitis in mice: effects of topical bacteriophage KPP12 administration. PLoS One. 2012;7(10):e47742.
2. Garbe J, Wesche A, Bunk B, Kazmierczak M, Selezska K, Rohde C, Sikorski J, Rohde M, Jahn D, Schobert M. Characterization of JG024, a *Pseudomonas aeruginosa* PB1-like broad host range phage under simulated infection conditions. BMC Microbiol. 2010;10:301.
3. Neves PR, Cerdeira LT, Mitne-Neto M, Oliveira TG, McCulloch JA, Sampaio JL, Mamizuka EM, Levy CE, Sato MI, Lincopan N. Complete Genome Sequence of an F8-Like Lytic Myovirus (ϕ SPM-1) That Infects Metallo- β -Lactamase-Producing *Pseudomonas aeruginosa*. Genome Announc. 2014;2(2). pii: e00061-14.
4. Alemayehu D, Casey PG, McAuliffe O, Guinane CM, Martin JG, Shanahan F, Coffey A, Ross RP, Hill C. Bacteriophages ϕ MR299-2 and ϕ NH-4 can eliminate *Pseudomonas aeruginosa* in the murine lung and on cystic fibrosis lung airway cells. MBio. 2012;3(2):e00029-12.

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.

Note: Whole genome analysis using BLASTN reveals that these five phages are distinct, and clearly fall into the ICTV ratified genus *Pbunalikevirus* (new name *Pbunavirus*). Therefore, the only supplementary data that we will present is the DNA sequence identity (Table 1)

Table 1. Properties of the five phages belonging to the genus *Pbunavirus*

Phage	DNA (% sequence identity)*
PB1	100
DL60	93
DL68	86
JG024	85
KPP12	85
vB_PaeM_C1-14_Ab28	93

* Determined using BLASTN relative to PB1;

Table 2. Phages closely related to recognized PB1 species

Phage	GenBank accession number
Pseudomonas phage SPM-1	KF981875
Pseudomonas phage DL52	KR054028
Pseudomonas phage PhiNH-4	JN254800
Pseudomonas phage vB_PaeM_PA01_Ab29	LN610588
Pseudomonas phage vB_PaeM_PA01_Ab27	LN610579

Fig. 1. Electron micrograph of negatively stained *Pseudomonas* phage vB_PaeM_PA01_Ab27 (provided by Christine Pourcel).

