



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**

<b>Code assigned:</b>	<b>2015.046B</b>	(to be completed by ICTV officers)				
<b>Short title:</b> A proposal to streamline granting taxonomic status "not formally classified" or "no species status" viruses (e.g. 6 new species in the genus <i>Zetavirus</i> )						
<b>Modules attached</b> (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 Viruses 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:**

## MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

### References:

1. Fauquet CM, Fargette D. International Committee on Taxonomy of Viruses and the 3,142 unassigned species. Virol J. 2005 Aug 16;2:64.
2. Grose JH, Casjens SR. Understanding the enormous diversity of bacteriophages: the tailed phages that infect the bacterial family Enterobacteriaceae. Virology. 2014;468-470:421-43.

### 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.

In 2005, Fauquet and Fargette published an article entitled “International Committee on Taxonomy of Viruses and the 3,142 unassigned species” (1). On March 26 of this year Mike Adams provided us with an Excel spreadsheet of the 3508 ICTV approved viral RefSeqs in NCBI and the 2605 “not formally classified” or “no species status” viruses. Please note that this list only applied to RefSeq not to all viruses. There are 1905 complete siphoviral genomes currently in GenBank of which only 737 have RefSeq status and only 313 have been formally classified into genera. From my perspective in 10 years we haven’t made significant progress in eliminating the backlog.

An examination of the data on bacteriophages is particularly disturbing:

ICTV Approved Subfamily	Number	Illegal	Number
<i>Autographivirinae</i>	14	Autographivirinae	63
<i>Peduovirinae</i>	14	Peduovirinae	8
<i>Picovirinae</i>	8	Picovirinae	9
<i>Spounavirinae</i>	6	Spounavirinae	16
<i>Tevenvirinae</i>	10	Tevenvirinae	52
Total approved species	297	Unclassified	738

Though the Bacterial and Archaeal Virus Subcommittee has made huge progress in classifying phages at best we may classify 200-300 phages a year; yet 400-600 are deposited annually. The current process is cumbersome and problematic:

- a) it requires a substantial amount of work which is usually restricted to a limited number of people
- b) the TaxoProps subject to errors in spite of being proof-read by numerous talented individuals

- c) there is no incentive for regular virologists to submit TaxoProps; and if they do so they cannot easily re-use trees or figures already made and published due to copyright issues.
- d) I do not believe that most journals care about enforcing ICTV classifications/nomenclature.

Lamentably I have to question the relevance of ICTV to the average phage worker. We have already seen the grouping phages into “clusters” (2; and The Actinobacteriophage Database: <http://phagesdb.org/>) with no reference to ICTV taxa. Lastly, it is no secret that NCBI is working on development of an automated typing system based upon DNA sequence relatedness.

Therefore, since ICTV has already approved the criteria for assignment of phages to species/genera or subfamilies; I suggest that an alternative approach be taken to the approval of unclassified phages which clearly belong to one of these taxa – “taxonomic infilling.”

1. Every three (3) months the Subcommittee Chair will provide the Proposals Secretary with an Excel spreadsheet or Word document containing the names and Accession Numbers for phages which clearly fall into established taxa.  
1A. That this process will be initially restricted to those viruses labelled “not formally classified” on the aforementioned Excel spreadsheet.
  2. This document will be circulated to the EC members for email approval.
  3. Any potentially controversial suggestion would be automatically flagged and a decision delayed until the annual meeting.
  4. That after the initial trial period, an effort be made to position the “no species status” viruses into existing taxa.
  5. That the annual meeting be used for substantive issues including establishment of new genera and higher taxa.
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