



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>2015.040a-dB</b>   | (to be completed by ICTV officers)                                  |   |  |  |
| <b>Short title:</b> To create one (1) new genus, <i>Slashvirus</i> , including four (4) new species within the family <i>Siphoviridae</i><br>(e.g. 6 new species in the genus <i>Zetavirus</i> ) |   |   |   |  |  |
| <b>Modules attached</b><br>(modules 1 and 10 are required)   | 1 <input checked="" type="checkbox"/><br>6 <input type="checkbox"/> | 2 <input checked="" type="checkbox"/><br>7 <input type="checkbox"/> | 3 <input checked="" type="checkbox"/><br>8 <input type="checkbox"/> | 4 <input type="checkbox"/><br>9 <input type="checkbox"/> | 5 <input type="checkbox"/><br>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:**

Please note that we have chosen to refer to this new genus as *Slashvirus* rather than *Slashlikevirus* since the Bacterial and Archaeal Virus Subcommittee of ICTV has voted overwhelmingly in favour of eliminating "like" 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:**

|  |
|--|
|  |
|--|

## 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                                   | <b>2015.040aB</b>  | (assigned by ICTV officers)  |  |
| <b>To create 5 new species within:</b> |  |  |  |
| Genus:                                 | <i>Slashvirus (new)</i>  | Fill in all that apply.<br>• If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name.<br>• If no genus is specified, enter “ <b>unassigned</b> ” in the genus box. |  |
| Subfamily:                             |  |  |  |
| Family:                                | <i>Siphoviridae</i>  |  |  |
| Order:                                 | <i>Caudovirales</i>  |  |  |
| <b>Name of new species:</b>            | <b>Representative isolate:<br/>(only 1 per species please)</b> | <b>GenBank sequence accession number(s)</b>  |  |
| <i>Bacillus virus Slash</i>            | Bacillus phage Slash   | KF669661   |  |
| <i>Bacillus virus Staley</i>           | Bacillus phage Staley  | KF669663   |  |
| <i>Bacillus virus Stahl</i>            | Bacillus phage Stahl   | KP696447   |  |
| <i>Bacillus virus Stills</i>           | Bacillus phage Stills  | KP696448   |  |

### **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                                 | <b>2015.040bB</b>   | (assigned by ICTV officers)   |
| <b>To create a new genus within:</b> |                     |   |
| Subfamily:                           |                     | Fill in all that apply.<br>• If the higher taxon has yet to be created (in a later module, below) write “(new)” after its proposed name.<br>• If no family is specified, enter “unassigned” in the family box |
| Family:                              | <i>Siphoviridae</i> |   |
| Order:                               | <i>Caudovirales</i> |   |

naming a new genus

|   |                   |                             |
|---|-------------------|-----------------------------|
| Code  | <b>2015.040cB</b> | (assigned by ICTV officers) |
| <b>To name the new genus: <i>Slashvirus</i></b> |                   |                             |

Assigning the type species and other species to a new genus

|   |                   |   |
|---|-------------------|---|
| Code  | <b>2015.040dB</b> | (assigned by ICTV officers)   |
| <b>To designate the following as the type species of the new genus</b>  |                   |   |
| <i>Bacillus virus Slash</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 <b>TOTAL</b> number of species (including the type species) that the genus will contain: |                   |   |
| <b>4</b>  |                   |   |

### Reasons to justify the creation of a new genus:

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

These temperate viruses all infect *Bacillus megaterium*. An interesting feature of these temperate phages is that they encode a group of enzymes involved in DNA nucleotide metabolism including: thymidylate synthase, guanylate kinase (not annotated in Stahl), and ribonucleoside-diphosphate reductase subunit alpha. Phages in this newly proposed genus also encode a LysM/SCP-domain containing protein, a SleB homolog, and an Rha family regulatory protein.

BLASTN, CoreGenes (1) (Table 1), progressiveMauve alignment (2) (Fig. 2) and phylogenetic analyses (3) of terminase proteins (Fig. 3) all indicate that the proposed genus, *Slashvirus*, is cohesive and distinct from the other genera of viruses. The closest relative is *Bacillus cereus* phage Basilisk which can be distinguished on the basis of size, length of terminal repeats, mol%G+C and coding capacity. While these phages are clearly related, at this time we choose not to propose a subfamily until the Bacterial and Archaeal Viruses Subcommittee defines higher taxons at the molecular level.

*Bacillus* phage Slash has an icosahedral head (approximately 70 nm in diameter) with a flexible non-contractile tail (approximately 350 nm in length), indicating that it belongs to the family *Siphoviridae* (Fig. 1). The properties of 2 of the 4 phages that currently compose this newly proposed genus (Slash and Staley) have been described in Genome Announcements (4-5).

The *Slashvirus* members have the following average genome characteristics: size 80.7 kb (35.3 %G+C)

encoding 111 proteins and 0 tRNA. The genomes possess ca. 530 bp direct terminal repeats.

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.

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

**Origin of the new genus name:**

*Bacillus* phage Slash

**Reasons to justify the choice of type species:**

The first fully 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. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.

additional material in support of this proposal

## References:

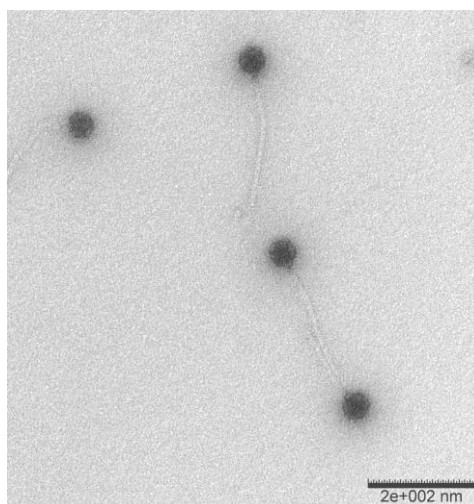
1. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013; 6:140.
2. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.
3. 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.
4. Decrescenzo AJ, Ritter MA, Chamakura KR, Kutty Everett GF. Complete Genome of *Bacillus megaterium* Siphophage Slash. Genome Announc. 2013;1(6). pii: e00862-13.
5. Hastings WJ, Ritter MA, Chamakura KR, Kutty Everett GF. Complete Genome of *Bacillus megaterium* Siphophage Staley. Genome Announc. 2013;1(6). pii: e00864-13.

## 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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**Fig. 1.** Electron micrograph of negatively stained phage Slash

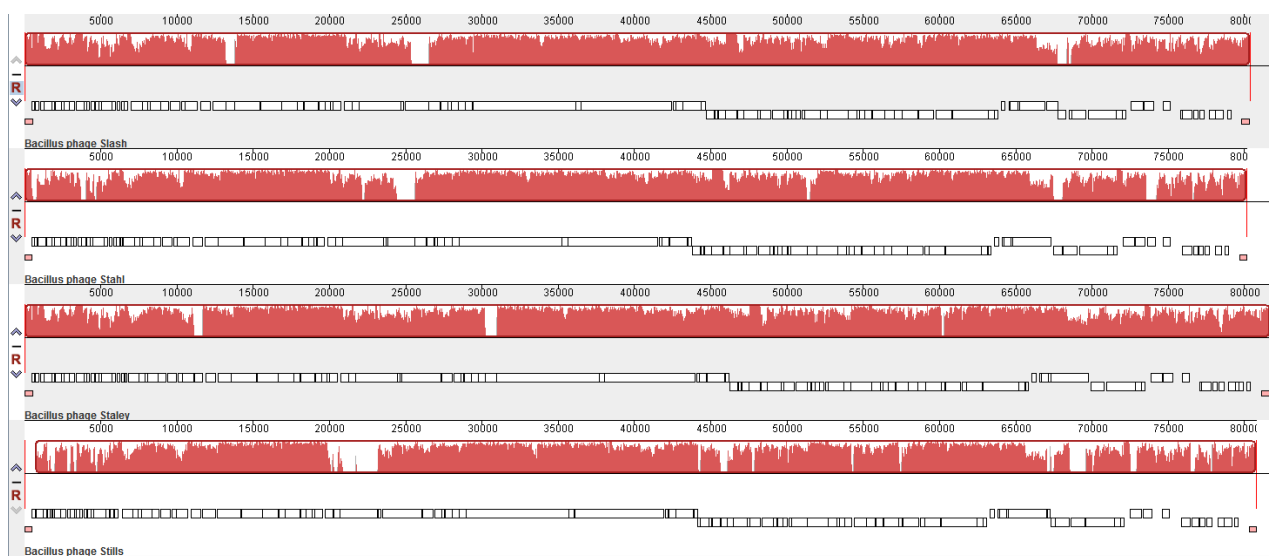


**Table 1.** Properties of the five phages belonging to the genus *Slashvirus* and closest relative *Bacillus cereus* phage Basilisk

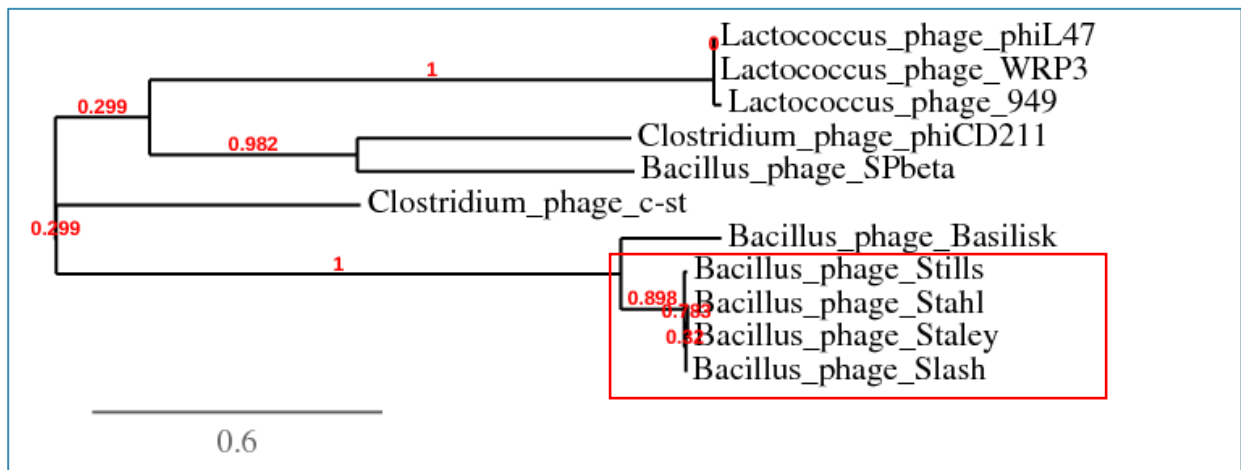
| Phage    | GenBank Accession No. | Genome length (kb) | Genome (mol% G+C) | No. CDS | Terminal Direct repeats (bp) | DNA (% sequence identity)* | % Homologous proteins ** |
|----------|-----------------------|--------------------|-------------------|---------|------------------------------|----------------------------|--------------------------|
| Slash    | KF669661              | 80.38              | 35.2              | 111     | 567                          | 100                        | 100                      |
| Staley   | KF669663              | 81.66              | 35.3              | 113     | 567                          | 92                         | 96.4                     |
| Stahl    | KP696447              | 80.15              | 35.3              | 110     | 497                          | 86                         | 91.0                     |
| Stills   | KP696448              | 80.80              | 35.5              | 110     | 491                          | 72                         | 84.7                     |
|          |                       |                    |                   |         |                              |                            |                          |
| Basilisk | KC595511              | 82.01              | 33.9              | 138     | 218                          | 9                          | 43.2                     |

\* Determined using BLASTN; \*\* Determined using CoreGenes (2).

**Fig. 2.** progressiveMauve alignment (1) of the annotated genomes of members of the *Slashvirus* genus (from top to bottom: Slash, Stahl, Staley and Stills). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity (Aaron Darling, personal communication).



**Fig. 3.** Phylogenetic analysis of large subunit terminase proteins of the slashviruses and variety of other related phage proteins constructed using "one click" at phylogeny.fr (3). "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."



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