



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

**Code(s) assigned:** **2008.076B** (to be completed by ICTV officers)

**Short title:** create species named Bacillus phage B103 within the genus "Phi29-like viruses" in the subfamily Picovirinae, family Podoviridae

(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

**Modules attached** | 1  2  3  4  5   
(please check all that apply): | 6  7

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

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



## MODULE 5: NEW SPECIES

Code	<b>2008.076B</b>	(assigned by ICTV officers)
<b>To create new species assigned as follows:</b>		
Genus:	<b>“Phi29-like viruses”</b>	Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put “unassigned” in the genus box)
Subfamily:	<b><i>Picovirinae</i></b>	
Family:	<b><i>Podoviridae</i></b>	
Order:	<b><i>Caudovirales</i></b>	

### Name(s) of proposed new species:

*Bacillus phage B103*

### Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

The genome of *Bacillus subtilis* bacteriophage B103 consists of double-stranded linear DNA 18,630 bp long ([NC\\_004165](#)). Its genome is related to phages Nf, phi29, PZA and phi15. Furthermore, It was shown that major promoters characterized in phi29 are retained in B103. Species demarcation criteria used were the absence of DNA homology throughout the genome and the presence of several unique genes.

### References:

\*\* Pecenková T, Benes V, Paces J, Vlcek C, Paces V. (1997) Bacteriophage B103: complete DNA sequence of its genome and relationship to other *Bacillus* phages. *Gene*. 15;199(1-2):157-63.

### Annexes:

Phage B103 has a 63% correlation score with phage  $\phi$ 29