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:	***2008.067B***	(to be completed by ICTV officers)

Short title: create species named Shigella phage Sf6 within the genus "P22-like viruses", family Podoviridae
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

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

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

MODULE 5: **NEW SPECIES**

Code	***2008.067B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	**"P22-like viruses"**
Subfamily:	
Family:	***Podoviridae***
Order:	***Caudovirales***

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)

Name(s) of proposed new species:

Shigella phage Sf6

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.

Shigella flexneri temperate bacteriophage Sf6 has a complete sequence of its 39,044 bp genome (NC_005344). It has chromosomal regions that encode proteins >80% identical with at least 15 different previously characterized P22-like & lambdoid phages, but 43% of the genome, including the virion assembly genes, is homologous to the genome of one phage, HK620. An analysis of the nucleotide differences between Sf6 and HK620 indicates that even these similar regions are highly variable.
By virtue of high degree of similarity in the encoding genes and their DNA target sites, we predict that the integrase, early transcription anti-terminator, CI and Cro repressors, and CII protein of Sf6 have DNA binding specificities very similar to the homologous proteins encoded by phages HK620, lambda, 434 and P22, respectively.
The Sf6 terminase genes are unusual. Analysis of in vivo initiation of the DNA packaging series showed that the Sf6 apparatus that recognizes DNA for packaging appears to cleave DNA for initiation of packaging series at many sites within a large region of about 1800 bp that includes a possible pac site. This is unlike previously characterized phage packaging mechanisms.

References:

** Casjens S, Winn-Stapley DA, Gilcrease EB, Morona R, Kühlewein C, Chua JE, Manning PA, Inwood W, Clark AJ. (2004) The chromosome of Shigella flexneri bacteriophage Sf6: complete nucleotide sequence, genetic mosaicism, and DNA packaging. J Mol Biol. 28;339(2):379-94.

Annexes:

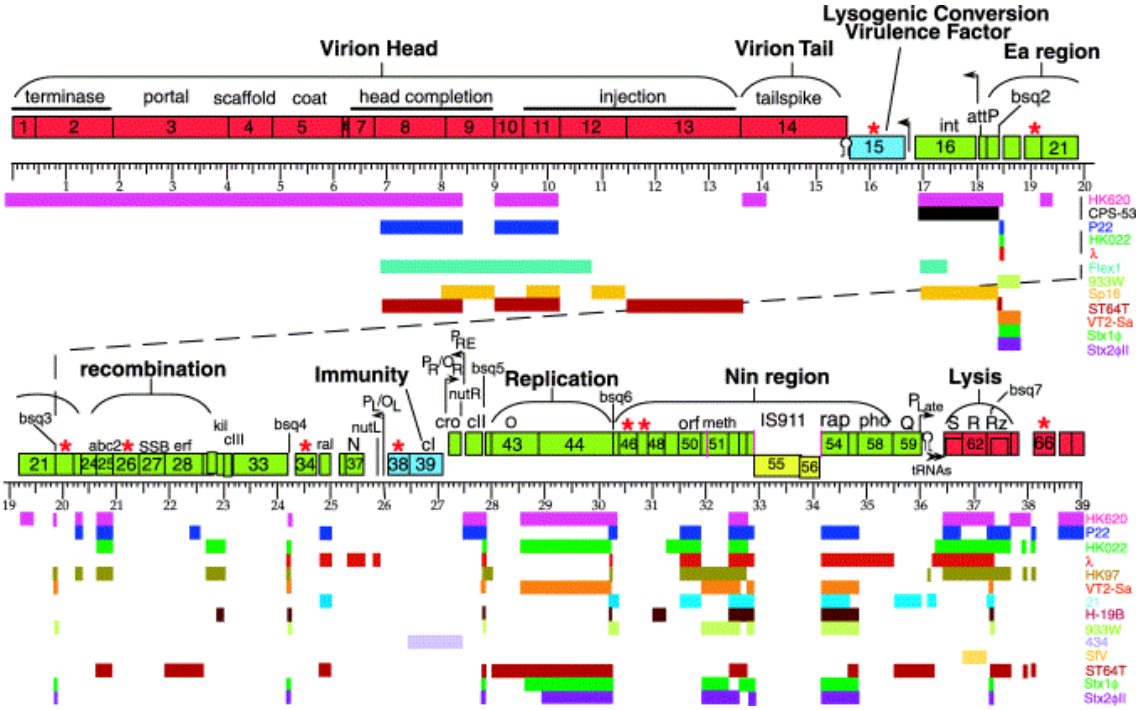

Figure 1. The bacteriophage Sf6 genome. The Sf6 chromosome is shown with a scale in kb. Boxes above the scale represent predicted genes, with those transcribed rightward at a higher position than those transcribed leftward. Selected gene names are shown within the boxes, and putative functions and names of homologous genes are given above. Black arrows, stem–loops, and vertical lines indicate predicted promoters, terminators and other DNA sites, respectively; vertical red lines indicate reading frame breaks compared to known homologues. Genes in the early and late operons are green and red, respectively, those expected to be expressed in the lysogen are blue, and genes in the IS911 sequence are yellow. Red asterisks identify genes without known phage-borne homologues. Below the scale, colored rectangles represent regions from other lambdoid phages that encode proteins that are >80% identical, or where there is no predicted gene, have >90% nucleotide sequence identity to Sf6; most of these are completely sequenced phages but 434, H-19B and 21 homologies were included because various aspects of these phages have been studied in some detail. The Sf6 nucleotide numbering is defined to begin at the first nucleotide of gene *1* so that its genetic map approximately parallels that of phages P22 and lambda.