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: *2008.070B* (to be completed by ICTV officers)

Short title: create species named Synechococcus phage syn5 to be unassigned within the subfamily Autographivirinae, 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	***2008.070B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	**unassigned**
Subfamily:	***Autographivirinae***
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:

Synechococcus phage syn5

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.

Syn5 is a short-tailed cyanophage isolated from the Sargasso Sea on Synechococcus strain WH8109. Syn5 has been grown in WH8109 to high titer in the laboratory and purified and concentrated retaining infectivity. Genome sequencing and annotation of Syn5 revealed that the linear genome is 46,214 bp with a 237 bp terminal direct repeat (NC_009531).

Based on genomic organization and sequence similarity to known protein sequences within GenBank, Syn5 shares features with "T7-like viruses", suggesting a correlation at the subfamily level. The presence of a putative integrase suggests access to a temperate life cycle.

Cryo-electron micrographs of purified Syn5 virions revealed that the capsid has a single "horn", a novel fibrous structure protruding from the opposing end of the capsid from the tail of the virion (Figure 1). The tail appendage displayed an apparent 3-fold rather than 6-fold symmetry. (Pope et al., 2007)

Establishment of a new species is based on the absence of genome-wide DNA homology (shown by either comparative genome analysis or blotting experiments), the presence of unique genes and differences in host range with existing species.

References:

**Pope WH, Weigele PR, Chang J, Pedulla ML, Ford ME, Houtz JM, Jiang W, Chiu W, Hatfull GF, Hendrix RW, King J. (2007) Genome sequence, structural proteins, and capsid organization of the cyanophage Syn5: a "horned" bacteriophage of marine synechococcus. J Mol Biol. 368(4):966-81.

Annexes:

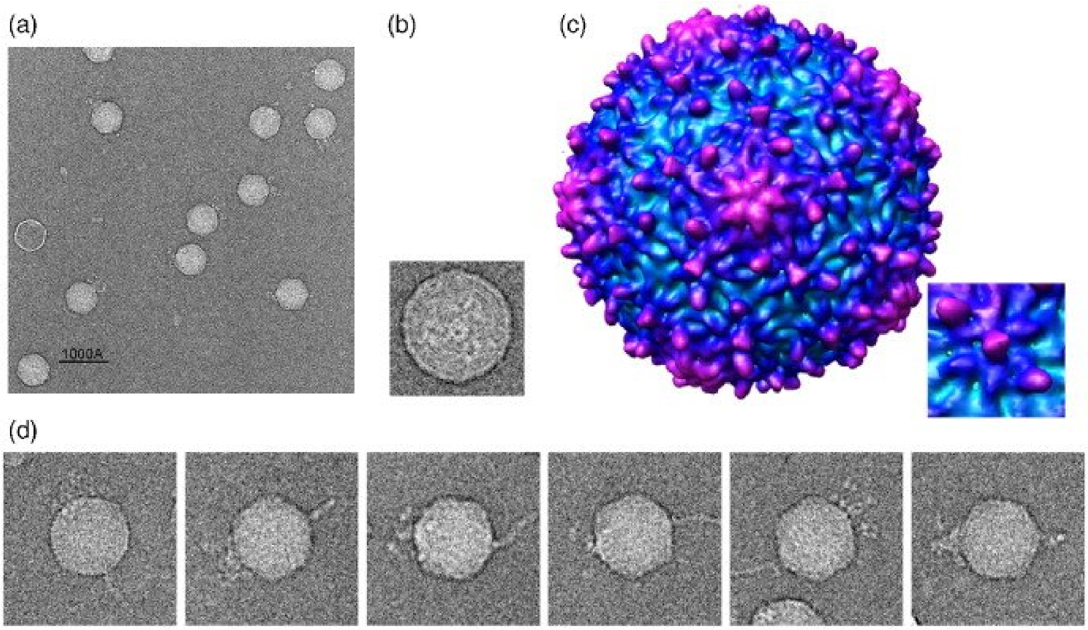

Figure 1. Cryo-electron micrographs of purified Syn5 particles and icosahedral 18 Å reconstruction of the capsid. Syn5 particles were flash-frozen and examined by cryo-electron microscopy. (a) Syn5 virions. The extended horn is seen directly opposite the three-pronged tail on the isometric capsid. The scale bar represents 100 nm. (b) End view of the Syn5 particle. The tail tube is surrounded by tail proteins with 3-fold symmetry. (c) An 18 Å reconstruction of the capsid with imposed icosahedral symmetry. The capsid is shown colored from cyan to purple with increasing radius. The map is in the T = 7L form, but the hand of the capsid has yet to be resolved. The three knobs on each hexon can be seen in the insert. (d) Gallery of single Syn5 particles with horn structures. The density map has been deposited in the European Bioinformatics Institute (www.ebi.ac.uk) with accession code EMD-1339.