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:	***2008.066B***	(to be completed by ICTV officers)

Short title: create species named Prochlorococcus phage P-SSP7 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	***2008.066B***	(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:

Prochlorococcus phage P-SSP7

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.

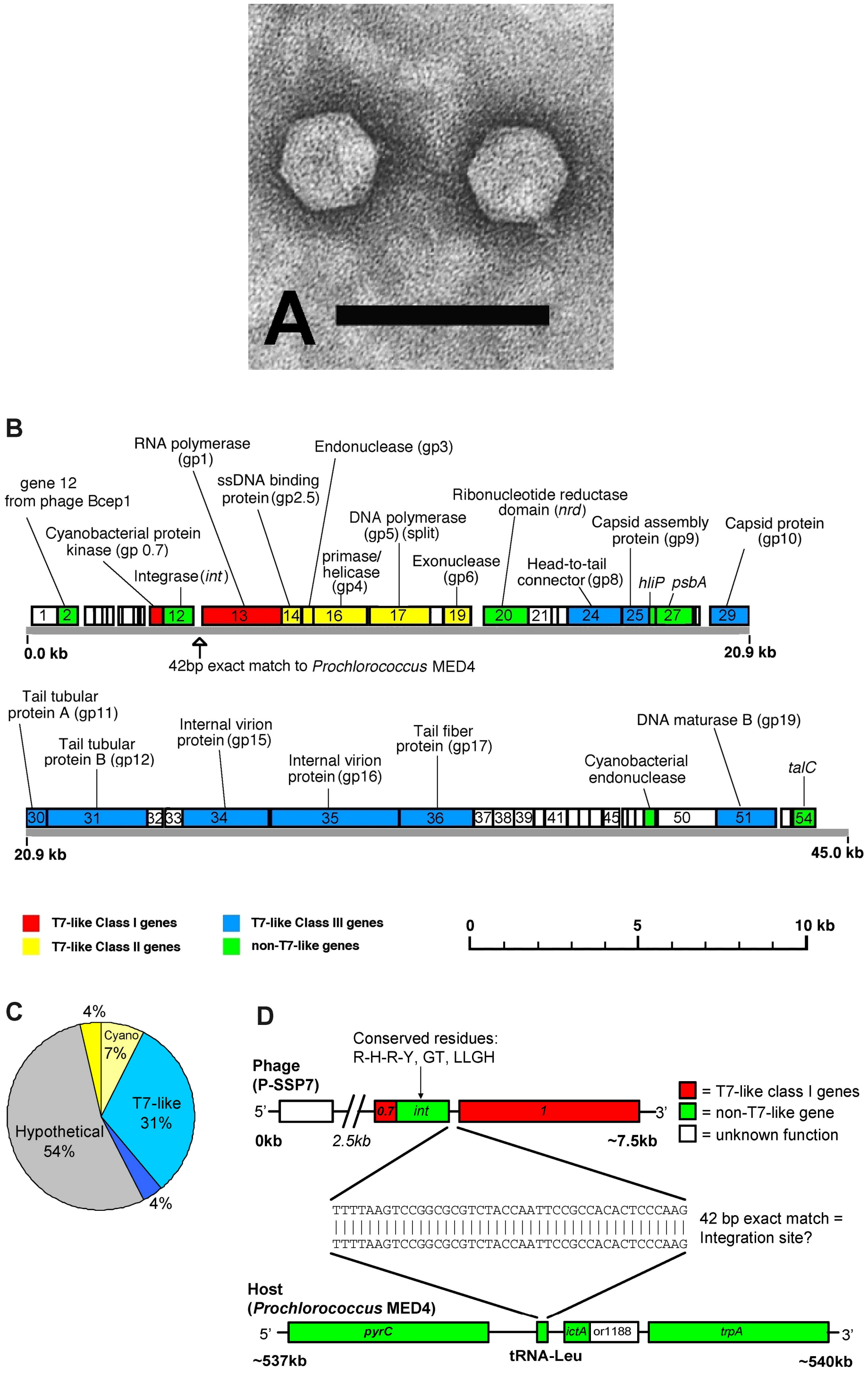
P-SSP7 is morphologically similar to the Podoviridae (tails are short and noncontractile; Figure 1A). It also includes a rectangular region of electron transparency (Figure 1A) that is similar to the gp14/gp15/gp16 core located at the unique portal vertex found in coliphage T7. Its genome contains 44,970 bp (54 open reading frames [ORFs]; 38.7% G+C content; Figure 1B) (NC_006882)

We found the podovirus contained 15 T7-like genes. The podovirus genome also contains an integrase gene (int) and other features that suggest it is capable of integrating into its host. If indeed it is, this would be unprecedented among cultured T7-related phages or marine cyanophages and would have significant evolutionary and ecological implications for phage and host (Sullivan et al., 2005). P-SSP7 was isolated from surface ocean waters at the end of summer stratification [8], when nutrients are extremely limiting. We have hypothesized [8] that the integrating phase of the temperate-phage life cycle may be selected for under these conditions; thus, finding the int gene in this particular phage is consistent with this hypothesis.

References:

** Sullivan MB, Coleman ML, Weigele P, Rohwer F, Chisholm SW. (2005) Three Prochlorococcus cyanophage genomes: signature features and ecological interpretations. PLoS Biol. 3(5):e144

Annexes:



(A) Electron micrograph of negative-stained podovirus P-SSP7. Note the distinct T7-like capsid and tail structure. Scale bar indicates 100 nm.

(B) Genome arrangement of Prochlorococcus podovirus P-SSP7. The ORFs are sequentially numbered within the boxes, and gene names are designated above the boxes. Gene designations use T7 nomenclature for T7-like genes [24] or microbial nomenclature for non-phage genes. Class I, II, and III genes refer to those in T7 [66] that belong to gene regions primarily involved in host transcription of phage genes (class I), DNA replication (class II),

and the formation of the virion structure (class III). The ORFs are designated by boxes, and in this genome, all ORFs are oriented in the same direction. Although the phage genome is one molecule of DNA, the representation is broken to fit on a single page. Note that the P-SSP7 genome is most similar to genomes of the T7-like phages.

(C) Taxonomy of best BLASTp hits for P-SSP7. Each predicted coding sequence from the phage genomes was used as a query against the nonredundant database to identify the taxon of the best hit (details in Materials and Methods). Blue slices indicate phage hits, while yellow slices indicate cellular hits.

(D) Diagrammatic representation of the genomic regions surrounding a putative phage and host integration site. This site consists of a 42-bp exact match between the podovirus P-SSP7 and its host Prochlorococcus MED4 located directly downstream of the phage integrase gene and the noncoding strand of a host tRNA gene.