



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: **2008.031B** (to be completed by ICTV officers)

Short title: create species named Streptococcus phage C1 within the genus "AHJD-like viruses" in the subfamily Picovirinae, family Podoviridae

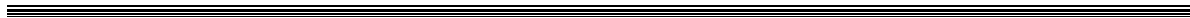
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

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

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

Rob Lavigne (rob.lavigne@biw.kuleuven.be)
Hans-W. Ackermann (Ackermann@mcBlaval.ca)
Andrew M. Kropinski (Andrew_Kropinski@phac-aspc.gc.ca)

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



MODULE 5: NEW SPECIES

Code	2008.031B	(assigned by ICTV officers)
To create new species assigned as follows:		
Genus:	“AHJD-like viruses”	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:	<i>Picovirinae</i>	
Family:	<i>Podoviridae</i>	
Order:	<i>Caudovirales</i>	

Name(s) of proposed new species:

Streptococcus phage C1

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.

C(1), a lytic bacteriophage infecting group C streptococci, is one of the earliest-isolated phages, and the method of bacterial classification known as phage typing was defined by using this bacteriophage. C(1) genome consists of a linear double-stranded DNA molecule of 16,687 nucleotides with 143-bp inverted terminal repeats ([NC_004814](#)). Examination of the C(1) DNA polymerase suggests that this phage utilizes a protein-primed mechanism of replication, which is prominent in the Picovirinae. Comparative genomics revealed 44AHJD as its closest evolutionary match.

References:

Nelson D, Schuch R, Zhu S, Tscherne DM, Fischetti VA. (2003) Genomic sequence of C1, the first streptococcal phage. J Bacteriol. 2003 Jun;185(11):3325-32.

Annexes:
