



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:** **2008.019B** (to be completed by ICTV officers)

**Short title:** create species named Endosymbiont phage APSE-1 unassigned within the 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	<input type="checkbox"/>	2	<input type="checkbox"/>	3	<input type="checkbox"/>	4	<input type="checkbox"/>	5	<input checked="" type="checkbox"/>
6	<input type="checkbox"/>	7	<input type="checkbox"/>						

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



**MODULE 5: NEW SPECIES**

Code	<b>2008.019B</b>	(assigned by ICTV officers)
<b>To create new species assigned as follows:</b>		
Genus:	<b>unassigned</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:	-	
Family:	<i>Podoviridae</i>	
Order:	<i>Caudovirales</i>	

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

Endosymbiont phage APSE-1

**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.

A bacteriophage infecting the secondary endosymbiont of the pea aphid *Acyrtosiphon pisum* was isolated and characterized. The phage was tentatively named bacteriophage APSE-1, for bacteriophage 1 of the *A. pisum* secondary endosymbiont. The genome consists of a circularly permuted and terminally redundant double-stranded DNA molecule of 36524 bp ([NC\\_000935](#)). Fifty-four open reading frames, putatively encoding proteins with molecular masses of more than 8 kDa, were distinguished. The virions of APSE-1.1 resemble P22 virions (appended figure), which is reflected by the structural protein homology, but APSE-1 differs the P22-like viruses in its metabolic genes, excluding this phage from this genus. Within a subfamily setting, APSE-1 and the P22-like phages would be related.

**References:**

\*\* van der Wilk F, Dullemans AM, Verbeek M, van den Heuvel JF. (1999) Isolation and characterization of APSE-1, a bacteriophage infecting the secondary endosymbiont of *Acyrtosiphon pisum*. *Virology*. 15;262(1):104-13.

**Annexes:**

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

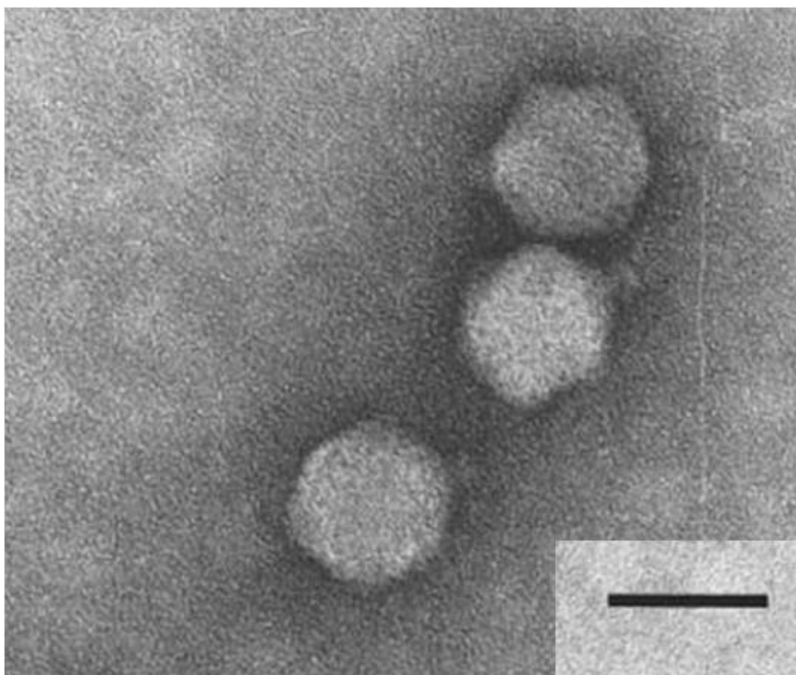


Figure 1: EM of APSE-1; phage particles were negatively stained with 2% uranyl acetate (Bar 50nm)

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