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:	***2008.082B***	(to be completed by ICTV officers)

Short title: create species named Enterobacteria phage K1E within the genus "SP6-like viruses", 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** ☐			

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

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

MODULE 5: **NEW SPECIES**

Code	***2008.082B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	**"SP6-like viruses"**
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:

Enterobacteria phage K1E

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.

Phage K1E was first described in 1977 as a phage specific for K1 capsulated strains of *Escherichia coli*. Morphologically, K1E belongs to the family *Podoviridae*. The phage codes for its own RNA polymerase and thus should be assigned to the subfamily *Autographivirinae.* The K1E genome contains 45251 bp (NC_007637). The promoter specificity of K1E RNA polymerase is different from that of SP6 and K1-5, and the terminal repeats - essential for DNA replication - are also different. A large self-splicing intron has invaded the essential large subunit of terminase, a feature unique to K1E. Of the 62 ORFs identified in K1E, 48 have counterparts in K1-5 with 58–98% amino acid identity. The host range of K1E partially overlaps that of K1-5, but K1E does not grow on K5-capsulated *Escherichia coli*. Hostrange is primarily determined by heaxameric sets of phage-coded tailspike enzymes with specificities for distinct polysaccharide capsules. In K1E, only one set of tailspikes is present.

References:

Gross, R. J., T. Cheasty, and B. Rowe. 1977. Isolation of bacteriophages specific for the Kl polysaccharide antigen of Eschenchia coli. J. Clin. Microbiol. 6:548-550.

Stummeyer, K., Schwarzer, D., Claus, H., Vogel, U., Gerardy-Schahn, R., and Muhlenhoff, M. (2006). Evolution of bacteriophages infecting encapsulated bacteria: lessons from Escherichia coli K1-specific phages. *Mol Microbiol*. **60**: 1123-35.

Annexes:

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