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: ***2008.065B*** (to be completed by ICTV officers)

Short title: create species named Escherichia phage phiV10 within the genus "Epsilon15-like viruses", 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	***2008.065B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	**“Epsilon15-like viruses”**
Subfamily:	
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:

Escherichia phage phiV10

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.

Bacteriophage phiV10 is a temperate phage, which specifically infects Escherichia coli O157:H7. The nucleotide sequence of the phiV10 genome is 39 104 bp long and contains 55 predicted genes and is circularly permuted, which is consistent with a headful-packaging mechanism (NC_007804). PhiV10 is closely related to two previously sequenced phages, the Salmonella enterica serovar Anatum (Group E1) phage epsilon15 and a prophage from *E. coli* APEC O1 (Figure 1). The attachment site of phiV10, like those of its two closest relatives, overlaps the 3' end of guaA in the host chromosome. phiV10 encodes an O-acetyltransferase, which modifies the O157 antigen. This modification is sufficient to block phiV10 superinfection, indicating that the O157 antigen is most likely the phiV10 receptor.

References:

** Kropinski AM, Kovalyova IV, Billington SJ, Patrick AN, Butts BD, Guichard JA, Pitcher TJ, Guthrie CC, Sydlaske AD, Barnhill LM, Havens KA, Day KR, Falk DR, McConnell MR. (2007) The genome of epsilon15, a serotype-converting, Group E1 *Salmonella* enterica-specific bacteriophage.
Virology. 369(2):234-44.

**Perry LL, SanMiguel P, Minocha U, Terekhov AI, Shroyer ML, Farris LA, Bright N, Reuhs BL, Applegate BM.
(2009) Sequence analysis of Escherichia coli O157:H7 bacteriophage PhiV10 and identification of a phage-encoded immunity protein that modifies the O157 antigen.
FEMS Microbiol Lett. 2009 Mar;292(2):182-6. Epub 2009 Feb 5.

Annexes:

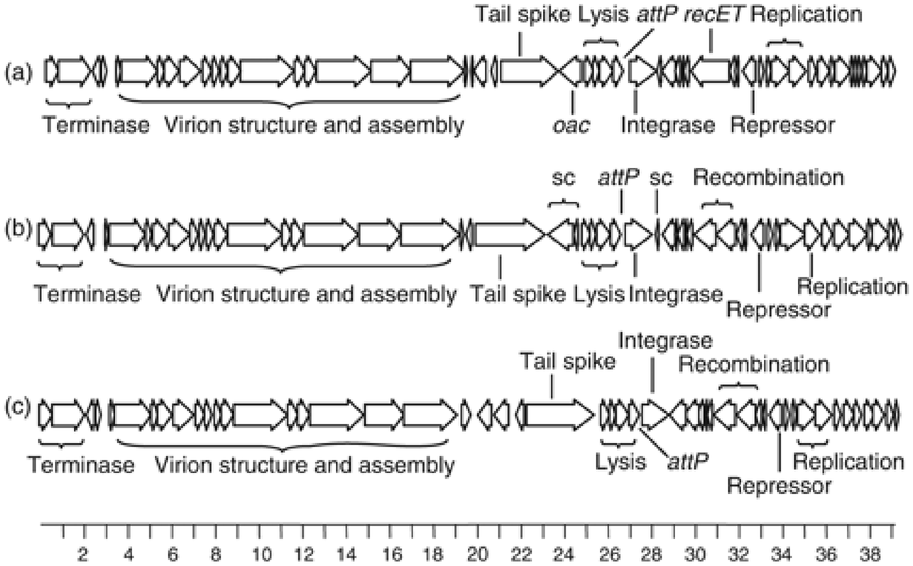

Figure 1: Genomes of phiV10 (a), epsilon15 (b), and prophage phiAP20 (c). The location of the phiV10 and phiAP20 termini were chosen to allow alignment of these genome maps with that of epsilon15, which is represented as published (Kropinski *et al.*, 2007). The ruler indicates length in kb. The abbreviation 'sc' denotes the three genes required for serotype conversion in epsilon15.