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:	***2008.001a-dB***	(to be completed by ICTV officers)

Short title: New genus "Phieco32-like viruses" in 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** ☐	**2** ☐	**3** ☐	**4** ☒	**5** ☒
	6 ☐	**7** ☐			

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

Ian J. Molineux molineux@mail.utexas.edu

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

MODULE 4: **NEW GENUS**

(if more than one genus is to be created, please complete additional copies of this section)

Code	***2008.001aB.U***	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	
Family:	***Podoviridae***
Order:	***Caudovirales***

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.

Code	***2008.001bB.U***	(assigned by ICTV officers)

To name the new genus: "Phieco32-like viruses"

Code	***2008.001cB.U***	(assigned by ICTV officers)

To assign the following as species in the new genus:
Enterobacteria phage Phieco32 **(new species)**

You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to 'REMOVE' it from that genus.

Code	***2008.001dB.U***	(assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:
Enterobacteria phage Phieco32

Argument to justify the creation of a new genus:

Analyses of the genome sequence, virion morphology, and host range all make PhiEco32 completely distinct from other members of the *Podoviridae.(*Figure 1*)* Phieco32 is a lytic virus for a natural isolate of *Escherichia coli*. The phage does not kill any of a variety of laboratory enteric bacteria; conversely, not one of a variety of laboratory enterobacteriophages kills the Eco32 PhiEco32 host. PhiEco32 virions have a C3 morphotype, which is rare among the *Caudovirales,* and no genus for C3 morphotype viruses yet exists. The DNA sequence of the PhiEco32 genome is 77,554 bp, significantly different from other coliphages (NC_010324). Only 43% of the predicted proteins have significant matches in the database. 18 of the 54 PhiEco32 proteins with meaningful matches are most closely related to the temperate *P. aeruginosa* phage PaP3, whose genome is only 60% the size of PhiEco32 and whose virion morphotype is C1 (isometric).

Origin of the new genus name:

Related to the name of the type species

Argument to justify the choice of type species:
Only characterized member of the genus. Two enterobacteriophages, 7-11 and Esc7-11, are related by virion morphology to PhiEco32 but there is inadequate information at present for those phages to be formally assigned members of the *Phieco32* genus

Species demarcation criteria in the genus:
If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

References:
Savalia, D., L. F., Westblade, M. Goel, L. Florens, P. Kemp, N. Akulenko, O. Pavlova, J. C. Padovan, B. T.Chait, M. P. Washburn, H-W. Ackermann, A. Mushegian, T. Gabisonia, I. Molineux, & K. Severinov. 2008. Genomic and proteomic analysis of phiEco32, a novel *Escherichia coli* phage. J. Mol. Biol. **377:**774-789.

Annexes:
Data supporting the creation of a new genus are provided with the description of the type species phi*Eco32*.

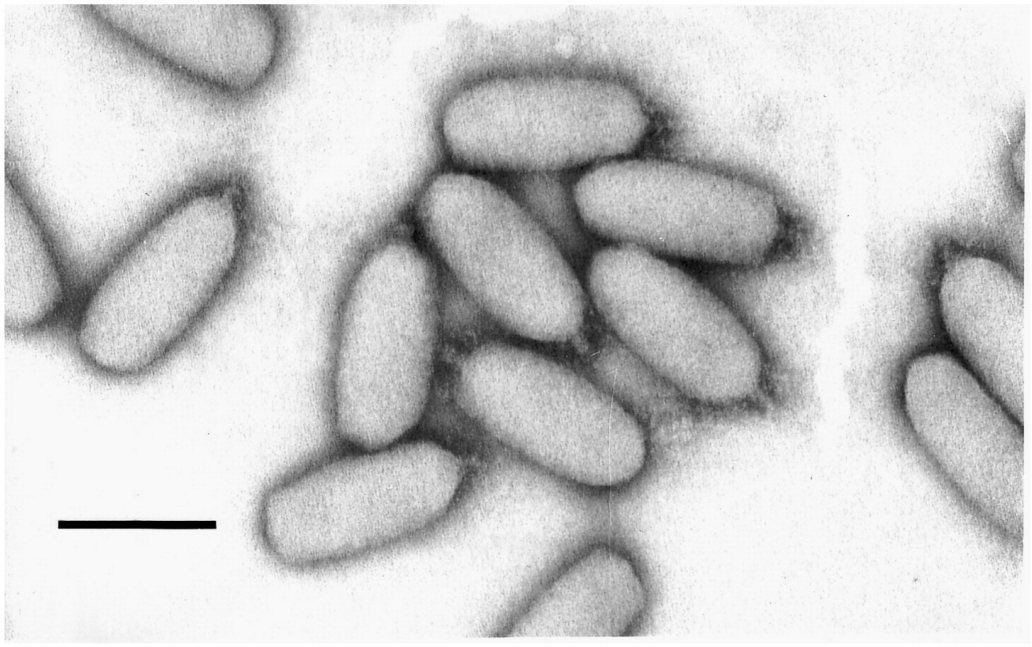

Fig. 1. Morphology of phiEco32 virions. Phage phiEco32 virions stained with phosphotungstate. Final magnification is 297,000×; the bar represents 100 nm. The virions appear oval due to flattening of the central part of the capsid.

MODULE 5: **NEW SPECIES**

Code	***2008.001eB.U***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	**"Phieco32-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:

Enterobacteria phage Eco32

Argument to justify the creation of the new species:

Eco32 (PhiEco32) is a lytic virus for a natural isolate of *Escherichia coli*. The phage does not kill any of a variety of laboratory enteric bacteria; conversely, not one of a variety of laboratory enterobacteriophages kills the Eco32 (PhiEco32) host. Eco32 (PhiEco32) virions have a C3 morphotype, which is rare. The DNA sequence of the Eco32 (PhiEco32) genome is 77554 bp, significantly different from other coliphages. The phage codes for an arginine tRNA and 128 proteins. Only 43% of the predicted proteins have significant matches in the database. 18 of the 54 Eco32 (PhiEco32) proteins with meaningful matches in the database are most closely related to the temperate *P. aeruginosa* phage PaP3, whose genome is only 60% the size of Eco32 (PhiEco32).

References:

Savalia, D., L. F., Westblade, M. Goel, L. Florens, P. Kemp, N. Akulenko, O. Pavlova, J. C. Padovan, B. T.Chait, M. P. Washburn, H-W. Ackermann, A. Mushegian, T. Gabisonia, I. Molineux, & K. Severinov. 2008. Genomic and proteomic analysis of phiEco32, a novel *Escherichia coli* phage. J. Mol. Biol. **377:**774-789.

Annexes:

QuickTime™ and a
TIFF (Uncompressed) decompressor
are needed to see this picture.

Phage phiEco32 virions stained with phosphotungstate. Final magnification is 297,000x; the bar represents 100 nm. The virions appear oval due to flattening of the central part of the capsid.

QuickTime™ and a
TIFF (Uncompressed) decompressor
are needed to see this picture.

Comparison of phiEco32 and PaP3 genomes. The phiEco32 and PaP3 genomes are drawn to scale with larger ORFs indicated as arrows, the direction of an arrow indicating the direction of transcription. Smaller ORFs have been reduced to bars. The ORFs in phiEco32 are colored according to functional predictions (blue: structural, DNA packaging; magenta: nucleotide metabolism; green: DNA replication/recombination). The light yellow bar in both genomes indicates the whole length of the genome. Black arrows (on top in PhiEco32 and below in PaP3) indicate the direction of transcription of the ORFs in that region.