Taxonomic proposal to the ICTV Executive Committee

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:	***2008.046B***	(to be completed by ICTV officers)

Short title: create species named Pseudomonas phage LUZ24 within the genus "LUZ24-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** ☐

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

MODULE 5: **NEW SPECIES**

Code	***2008.046B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	**"LUZ24-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:

Pseudomonas phage LUZ24

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 LUZ24 was isolated from hospital sewage using the clinical *P. aeruginosa* strain Li010 as enrichment host. Phage particle morphology clearly classifies LUZ24 within the *Podoviridae* family of short-tailed phages, consisting of an icosahedral head with a 63 nm diameter and a short tail of 12 × 8 nm. Some decoration proteins can be distinguished, protruding from the phage capsid.
Extensive host range screenings on environmental and clinical *P. aeruginosa* strains show that LUZ24 lyses 36 out of 123 (29%) strains, including multi-drug resistant *P. aeruginosa* strains Br642 and Br776. Surprisingly, only small and turbid plaques (1 mm) arise after infection of *P. aeruginosa* PAO1, although a slightly more efficient adsorption (91% in 5 min) and no significant difference in latent period or burst size could be noted. Despite the suspicion of lysogeny, all attempts to isolate stable lysogenic *P. aeruginosa* clones failed. DNA was extracted from phage-resistant *P. aeruginosa* clones isolated from turbid plaques and batch cultures. No phages could be induced, and no integrated LUZ24 DNA sequences could be demonstrated by PCR or restriction analysis.
The LUZ24 particle encapsulates a linear dsDNA molecule consisting of 45,625 bp (52% GC). The genome of bacteriophage LUZ24 is deposited at Genbank under accession number NC_010325 and displays an overall nucleotide identity of 71% to phage PaP3, suggesting these two phages can be considered as separate species. Phage LUZ24 encodes 68 proteins, 47 of which are arranged in rightward orientation while 21 aim leftward and is delineated by two 184 bp direct terminal repeats (DTR). It's DTRs at the genomic ends and lacks of genes or regulatory systems suggest no integration or lysogenic behavior in its host bacterium.

References:

** Ceyssens PJ, Hertveldt K, Ackermann HW, Noben JP, Demeke M, Volckaert G, Lavigne R. (2008) The intron-containing genome of the lytic *Pseudomonas* phage LUZ24 resembles the temperate phage PaP3. Virology. 1;377(2):233-8.

Annexes:

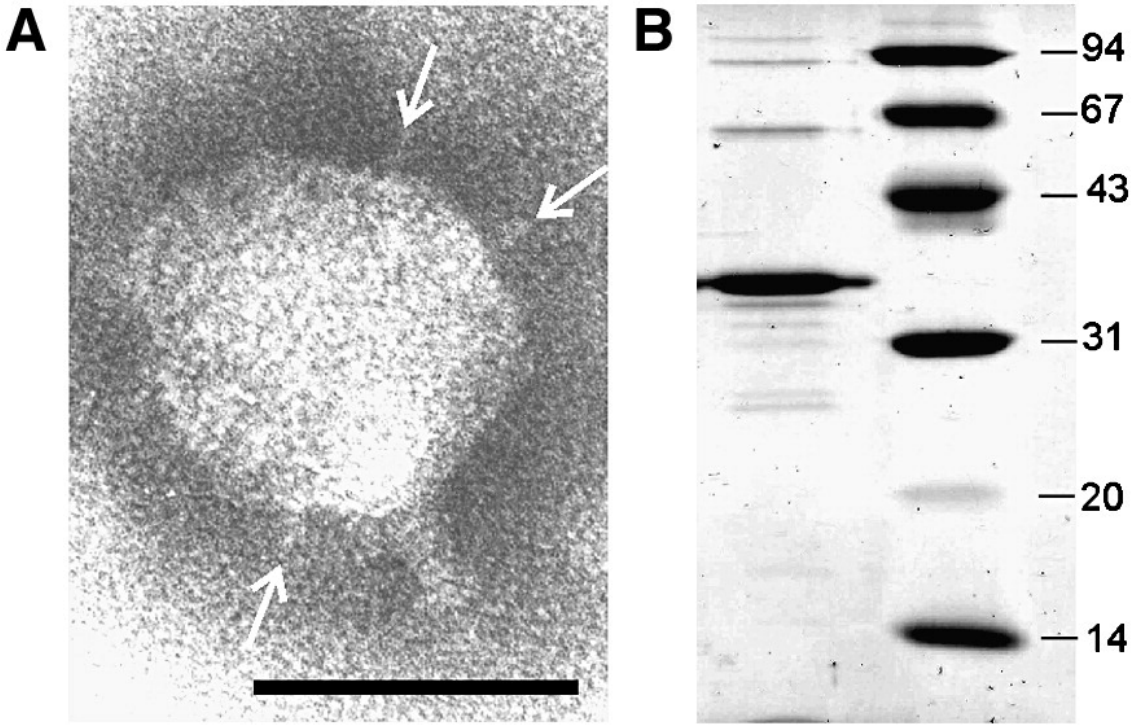

Fig. 1. A. Electron microscopic image of a negatively stained LUZ24 particle. Scale bar represents 50 nm, capsid decorations are marked by arrows. B. Phage particle proteins separated on a 12% SDS-PAGE gel, in parallel to a LMW-size ladder (kDa).