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:	***2008.058B***	(to be completed by ICTV officers)

Short title: create species named Pseudomonas phage PaP3 within the genus "LUZ24-like viruses"
(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	***2008.058B***	(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 PaP3

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.

The PaP3 genome contains 45 503 bp with GC content of 52.1% (NC_004466). A total of 256 open reading frames (ORFs) are found in the genome, and 71 ORFs are predicated as coding sequence (CDS). All 71 CDS are divided into the two opposite direction groups, and both groups meet at the bidirectional terminator site locating the near middle of the genome.
Analysis of integration site of PaP3 in the host bacterial genome confirmed that the core sequence of (GGTCGTAGGTTCGAATCCTAC-21mer) locates at tRNA(Pro) gene within the attP region and at tRNA(Lys) gene in the attB region. The results indicated that 3'-end of tRNA(Pro) gene of the PaP3 genome is involved in the integration reaction and 5'-end of tRNA(Lys) gene of host bacteria genome is hot spot of the integration.
However, in contrast to other tRNA-integrating phages like mycobacteriophage Ms6 and *Streptococcus* phage T12 , no site-specific recombinase is encoded upstream or downstream the PaP3 *attP* site. Although filamentous ssDNA phages like ctxφ exist which recruit host-encoded recombinases, underlying mechanisms differ profoundly and integration-associated proteins like RstB are encoded in the CTXφ genome. Furthermore, neither immunity nor reactivation of the integrated PaP3 DNA was demonstrated by Tan et al. (2007).These arguments call into question the temperate nature of PaP3.

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.

** Tan Y, Zhang K, Rao X, Jin X, Huang J, Zhu J, Chen Z, Hu X, Shen X, Wang L, Hu F. (2007) Whole genome sequencing of a novel temperate bacteriophage of *P. aeruginosa*: evidence of tRNA gene mediating integration of the phage genome into the host bacterial chromosome. Cell Microbiol. 9(2):479-91.

Annexes:

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

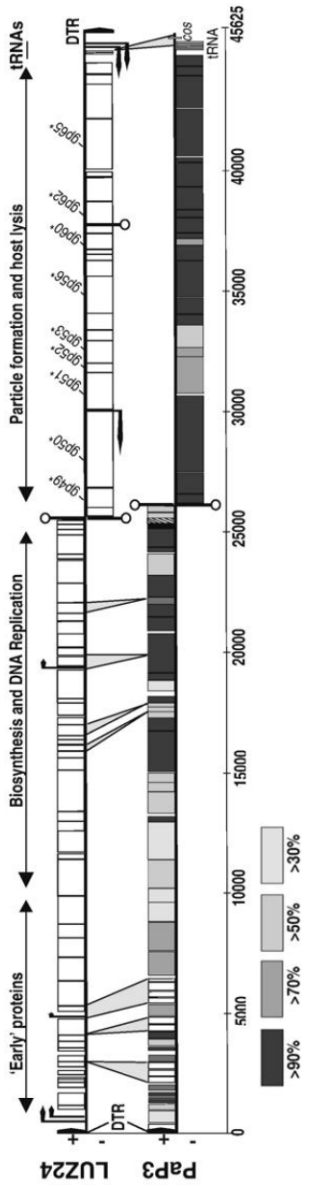

Figure 1: Comparison of the LUZ24 and PaP3 genomes, marking the amino acid identities of the corresponding ORFs in different shades of blue. Insertions and deletions are indicated, as are the experimentally identified σ70 promoters (arrows with length according to the promoter strength) and rho-independent terminators (open circles). One copy of the LUZ24 DTR (black arrow) is also present in the genome of PaP3. The identified structural proteins are marked with asterisks, and the newly annotated PaP3 gene is hatched.