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: ***2008.041B*** (to be completed by ICTV officers)

Short title: addition of an unassigned new species KSY1 within the Podoviridae family
(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	***2008.041B***	(assigned by ICTV officers)

To create new species assigned as follows:

Genus:	***Unassigned***
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:

Lactococcus phage KSY1

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 virulent lactococcal phage KSY1 possesses a large elongated capsid (223 nm long, 45 nm wide) and a short tail (32 nm). This phage of the *Podoviridae* group (C3 morphotype) has a linear 79,232-bp double-stranded DNA genome, which encodes 131 putative proteins and 3 tRNAs. This is the first description of the genome of a phage of this morphotype. KSY1 possesses a T7-like transcription system, including an RNA polymerase and a series of specific promoters, showing sequence homology to other known T7-like RNA polymerase promoters. Late stages of KSY1 multiplication are resistant to rifampicin. Otherwise, KSY1 shares limited similarity with other *Podoviridae* phages.(Chopin et al., 2007)

Despite the phage encoded RNA polymerase and T7-like transcription scheme, KSY1 is so different in overall morphology, genome size and proteome make-up, that a classification within the *Autographivirinae* subfamily would not be suitable at this time. Pending analyses of more closely related phages, this species is placed directly within the *Podoviridae* family.

References:

** Chopin A, Deveau H, Ehrlich SD, Moineau S, Chopin MC.

Annexes:

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