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:	***2008.006-009B***	(to be completed by ICTV officers)

Short title: Create the genus "AHJD-like viruses" in the subfamily Picovirinae, 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:

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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	***2008.006B***	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	***Picovirinae***
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	***2008.007B***	(assigned by ICTV officers)

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

Code	***2008.008B***	(assigned by ICTV officers)

To create the following species and assign to the new genus:

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.

Staphylococcus phage 44AHJD (new)
Streptococcus phage C1 (new)

Code	***2008.009B***	(assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:

Staphylococcus phage 44AHJD

Argument to justify the creation of a new genus:

The "AHJD-like viruses" in the CoreGenes analysis can be considered as very closely related (>85%) and include *Staphylococcus* phages 44AHJD (Vybriral et al., 2003), P68, SAP-2 and 66 (Kwan et al., 2005). Evidence which distinguishes them from φ29 group comes from their genome analysis which reveals that the 44AHJD and P68 lysis genes (amidases) are located within the morphogenesis genes rather than downstream, as is observed with φ29. Furthermore, these phages lack a classical holin-lysin cassette. Lastly, the gene for the major capsid protein (gp8) of φ29 and its close relatives is located in the left third of the genome, while the analogous genes in 44AHJD and P68 (gp20) are near the right end of the genome.

Origin of the new genus name:

After type species

Argument to justify the choice of type species:

Argument to justify the choice of type species:

First sequenced member of this 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.

No genome-wide DNA homology

References:

Kwan, T., Liu, J., DuBow, M., Gros, P. and Pelletier, J. (2005) The complete genomes and proteomes of 27 *Staphylococcus aureus* bacteriophages. Proceedings of the National Academy of Sciences of the United States of America 102, 5174-5179.

Vybiral, D., Takác, M., Loessner, M., Witte, A., von Ahsen, U. and Bläsi, U. (2003) Complete nucleotide sequence and molecular characterization of two lytic *Staphylococcus aureus* phages: 44AHJD and P68. FEMS Microbiology Letters 219, 275-283.

Annexes:

Staphylococcus phage P68 (NC_004679)
Staphylococcus phage 44AHJD (NC_004678)
Staphylococcus phage 66 (NC_007046)
Staphylococcus phage SAP-2(NC_009875)
Streptococcus phage C1 (NC_004814)