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:	***2008.020-023B***	(to be completed by ICTV officers)

Short title: create the subfamily Autographivirinae in the family Podoviridae, order Caudovirales
(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 3: NEW SUBFAMILY

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

Code	***2008.020B***	(assigned by ICTV officers)

To create a new Subfamily assigned as follows:

Family:	***Podoviridae***	If there is no Order, put "unassigned" here.
Order:	***Caudovirales***	

Code	***2008.021B***	(assigned by ICTV officers)

To name the new Subfamily: *Autographivirinae*

Code	***2008.022B***	(assigned by ICTV officers)

To assign the following genera to the new subfamily:

- **"T7-like viruses"**
- **"SP6-like viruses"**
- **"phiKMV-like viruses"**

Code	***2008.023B***	(assigned by ICTV officers)

To assign the following species to be unassigned in the new subfamily (i.e. within the subfamily but not assigned to any genus):

Synechococcus phage P60 (new)
Synechococcus phage syn5 (new)
Prochlorococcus phage P-SSP7 (new)

Argument to justify the creation of a new Subfamily:

Background (Lavigne et al., 2008):
The proposed taxonomic classification is based on available proteomic data. Using developed programs (CoreExtractor & CoreGenes) and careful review of available literature data, phages can be grouped. These programs parse-out/quantify the relationship between two phages into a single correlation score (= the relative number of homologous proteins between two sequenced phages).

Analysis and biological interpretation of the molecular correlations among all tailed phages (Caudovirales) with known genome sequence, shows this approach supports the current ICTV classification and proves that horizontal gene transfer does not mask the evolutionary relationship between phages.
Using a cut-off score of 40% homologous proteins between two phages, phages cluster

Argument to justify the creation of a new Subfamily:

correctly within existing genera.
In addition, we observe higher level relationships (20% correlation) that warrant the introduction of subfamilies. Subfamilies emphasize commonalities between related genera, prevent excessive subdivision during classification and solve classification difficulties with cross-family correlations.
Individual species demaraction is based on the absence of a genome-wide DNA homology between phages, differences in host range and the presence of unique genes.

The *Autographivirinae*

The T7, SP6 and φKMV-like viruses have long been recognized as being related and are often termed as members of a "supergroup." Since this description has no taxonomic status, we propose a subfamily designated as the *Autographivirinae*.
All genera within the *Autographivirinae* encode their own RNA polymerase and share a common general genome organization, with genes encoded solely on the Watson strand. This genomic correlation is reflected by the correlation score in the 20-39% range.

Within this subfamily, distinctive features warrant a separation in different genera. Phages SP6 and K1-5 have been considered an "estranged subgroup of the T7-like viruses" (Scholl et al., 2004). Also, the φKMV-like phages carry their single-subunit RNA polymerase gene adjacent to the structural protein region of the genome instead of in the early (host conversion) region, and they lack readily identifiable phage promoters. This suggests a different transcription scheme for ∀phiKMV-like viruses" compared to the "T7-like viruses" (Ceyssens et al., 2006).

It is possible that the cyanophages P60, Syn5 and P-SSP7 represent one or more additional genera in this subfamily, but since the genome of P60 contains numerous sequence errors an accurate analysis of relationships is impossible at this time. *Synechococcus* phage syn5 and *Prochlorococcus* phage P-SSP7, share a correlation to P60 (36% and 35% respectively) which could place them within a P60-like genus.

Bacteriophage SIO1 is related to this subfamily from an evolutionary perspective, but falls outside this subfamily because of the absence of a phage-encoded RNA polymerase and greater differences at the genome organization level (Figure 1). The same argument can be given for marine bacteriophage VpV262 infecting *Vibrio parahaemolyticus*. Genomic data indicates that an ancestral component of a T7 viral supergroup is conserved in the marine environment, but overall genomic differences and the lack of a phage encoded RNA polymerase places this virus outside this subfamily.

Phage KSY1 does contain a phage encoded RNA polymerase and T7-like transcription scheme, but its overall morphology, genome size and proteome make-up does not warrant a classification within this subfamily.

Origin of the new Subfamily name:

The origin of this name refers to the “auto-graphein” or “self-transcribing” phages which encode their own (single subunit) RNA polymerase, a common characteristic among the described phages of this subfamily.

References:

Ceyssens, P.J., Lavigne, R., Mattheus, W., Chibeu, A., Hertveldt, K., Mast, J., Robben, J. and Volckaert, G. (2006) Genomic analysis of *Pseudomonas aeruginosa* phages LKD16 and LKA1: establishment of the ϕKMV subgroup within the T7 supergroup. **Journal of Bacteriology 188, 6924-6931.

Lavigne, R., Seto, D., Mahadevan, P., Ackermann, H-W. en Kropinski, A.M. (2008) Use of BLASTP-tools to develop a rational classification system for the *Podoviridae*. **Research in Microbiology 159(5):406-414.

Scholl, D., Kieleczawa, J., Kemp, P., Rush, J., Richardson, C.C., Merril, C., Adhya, S. and Molineux, I.J. (2004) Genomic analysis of bacteriophages SP6 and K1-5, an estranged subgroup of the T7 supergroup. **Journal of Molecular Biology 335, 1151-1171.

Annexes:

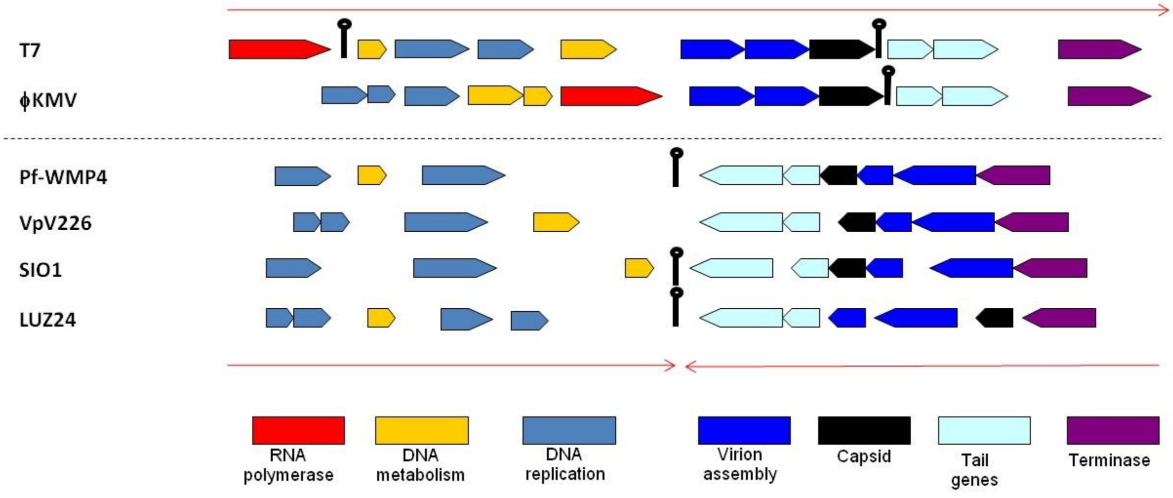
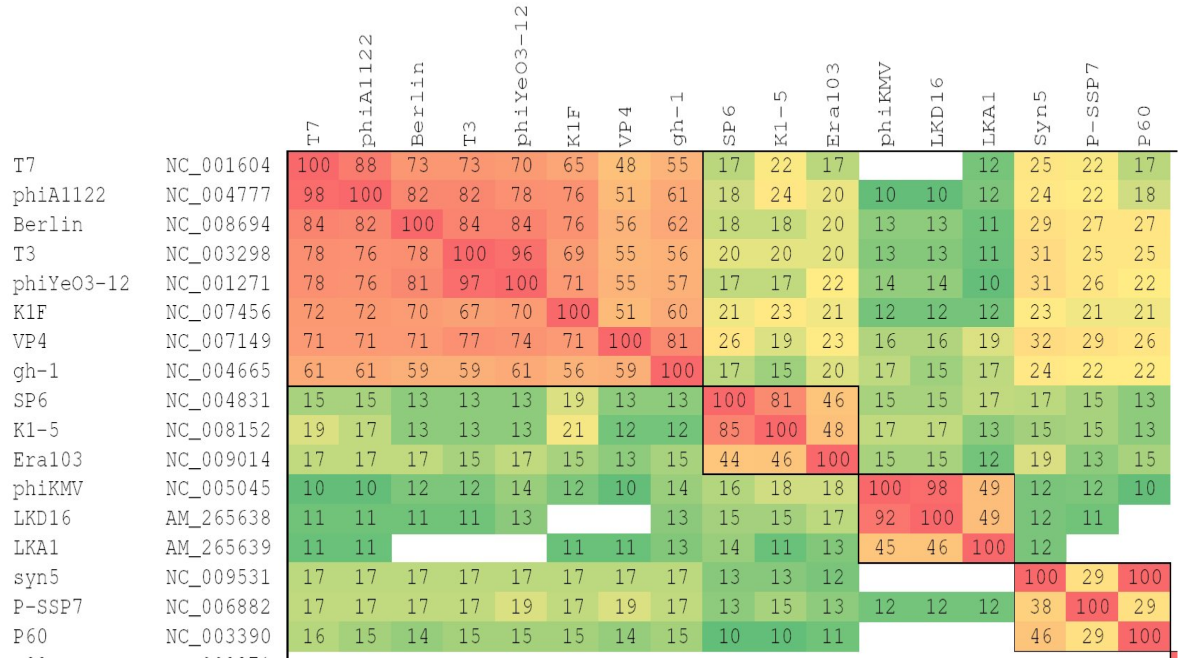


Figure 1: genomic organization (based on predicted protein function) of the *Autographivirinae* (represented by T7 and phiKMV) and other related phages.

A.



		T7	phiA1122	Berlin	T3	phiYeO3-12	K1F	VP4	gh-1	SP6	K1-5	Era103	phiKMV	LKD16	LKA1	Syn5	P-SSP7	P60
T7	NC_001604	100	88	73	73	70	65	48	55	17	22	17			12	25	22	17
phiA1122	NC_004777	98	100	82	82	78	76	51	61	18	24	20	10	10	12	24	22	18
Berlin	NC_008694	84	82	100	84	84	76	56	62	18	18	20	13	13	11	29	27	27
T3	NC_003298	78	76	78	100	96	69	55	56	20	20	20	13	13	11	31	25	25
phiYeO3-12	NC_001271	78	76	81	97	100	71	55	57	17	17	22	14	14	10	31	26	22
K1F	NC_007456	72	72	70	67	70	100	51	60	21	23	21	12	12	12	23	21	21
VP4	NC_007149	71	71	71	77	74	71	100	81	26	19	23	16	16	19	32	29	26
gh-1	NC_004665	61	61	59	59	61	56	59	100	17	15	20	17	15	17	24	22	22
SP6	NC_004831	15	15	13	13	13	19	13	13	100	81	46	15	15	17	17	15	13
K1-5	NC_008152	19	17	13	13	13	21	12	12	85	100	48	17	17	13	15	15	13
Era103	NC_009014	17	17	17	15	17	15	13	15	44	46	100	15	15	12	19	13	15
phiKMV	NC_005045	10	10	12	12	14	12	10	14	16	18	18	100	98	49	12	12	10
LKD16	AM_265638	11	11	11	11	13			13	15	15	17	92	100	49	12	11	
LKA1	AM_265639	11	11				11	11	13	14	11	13	45	46	100	12		
syn5	NC_009531	17	17	17	17	17	17	17	17	13	13	12				100	29	100
P-SSP7	NC_006882	17	17	17	17	19	17	19	17	13	15	13	12	12	12	38	100	29
P60	NC_003390	16	15	14	15	15	15	14	15	10	10	11				46	29	100

AUTOGRAPHIVIRINAE			
"T7-like viruses"			
Escherichia phage T7	NC_001604	100	100
Yersinia phage φA1122	NC_004777	98	78
Yersinia Berlin	NC_008694	84	58
Escherichia phage T3	NC_003298	78	67
Yersinia phage φYeO3-12	NC_001271	78	67
Escherichia phage K1F	NC_007456	72	55
Vibrio phage VP4	NC_007149	71	42
Pseudomonas phage gh-1	NC_004665	61	47
" SP6-like viruses"			
Salmonella phage SP6	NC_004831	100	100
Escherichia phage K1-5	NC_008152	85	82
Escherichia phage K1E	NC_007637	ND	75
Erwinia phage Era103	NC_009014	44	52

“ phiKMV-like viruses”			
Pseudomonas phage φKMV	NC_005045	100	100
Pseudomonas phage LKA1	AM_265639	45	54
(The P60-like phages)			
Synechococcus phage P60	NC_003390	100	100
Synechococcus phage syn5	NC_009531	ND	36
Prochlorococcus phage P-SSP7	NC_006882	29	35

Figure 2: A. Correlation score Graph for the *Autographivirinae*.
B. Table containing the Autographivirinae members, with their accession numbers, CoreExtractor scores and Coregenes score (from left to right).