Template for Taxonomic Proposal to the ICTV Executive Committee
To create a new Genus in an existing Family

Code†	**2007.115B**	To create a new genus in the family*	***Podoviridae***
Code†	**2007.116B**	To name the new genus*	**"SP6-like viruses"**
Code†	~~**2007.117B.02**~~	~~To remove from the list of tentative species in the genus "T7-like viruses"~~ ~~***Enterobacteria phage SP6***~~	
Code†	**2007.118B**	To create as type species in the new genus the species named*	***Enterobacteria phage SP6***
Code†	**2007.119B**	To designate the following as species of the new genus*:	***Enterobacteria phage SP6*** ***Enterobacteria phage K1E*** ***Enterobacteria phage K1-5*** ***Enterobacteria phage K5*** ***Erwinia amylovora phage Era103***
Code†		To designate the following as tentative species in the new genus*:	**None**

† Assigned by ICTV officers
* repeat these lines and the corresponding arguments for each genus created in the family

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Old Taxonomic Order

Order
Family
Genus
Type Species
Species in the Genus
Tentative Species in the Genus
Unassigned Species in the family

New Taxonomic Order

Order
Family

Genus	**SP6-like viruses**
Type Species	**Enterobacteria phage SP6**
Species in the Genus	**5**
Tentative Species in the Genus	**0**
Unassigned Species in the family	**0**

ICTV-EC comments and response of the SG

Accepted. Move to 02. Before next consideration need to amend proposal to create and name SP6 as a species in the newly created genus.

Argumentation to choose the type species in the genus

The defined host for SP6, *Salmonella enterica* serovar Typhimurium LT2, is genetically characterized, which simplifies genetic and physiological studies of the phage. A small number of mutants have also been isolated

Species demarcation criteria in the genus

Host range: including smooth and capsulated bacteria in different genera.

List of Species in the created genus

Enterobacteria phage SP6
Enterobacteria phage K1E
Enterobacteria phage K1-5
Enterobacteria phage K5
Erwinia amylovora phage Era103

List of Tentative Species in the created genus

None

Argumentation to create a new genus:

Larger genome and more genes (>10%) than most T7-like viruses. Apparent absence of several important proteins of T7-like viruses, including lysozyme, SSB, and homologs of gp18.5/18.7. DNA ligase unrelated to T7-like virus homologs. Tail spike enzymes vs. tail fibers in T7. Lack of complete synteny of essential genes in comparison to T7-like viruses. Protein similarity to comparable T7-like virus proteins variable, and often insignificant.

Origin of the proposed genus name

Salmonella enterica serovar Typhimurium phage SP6

References

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

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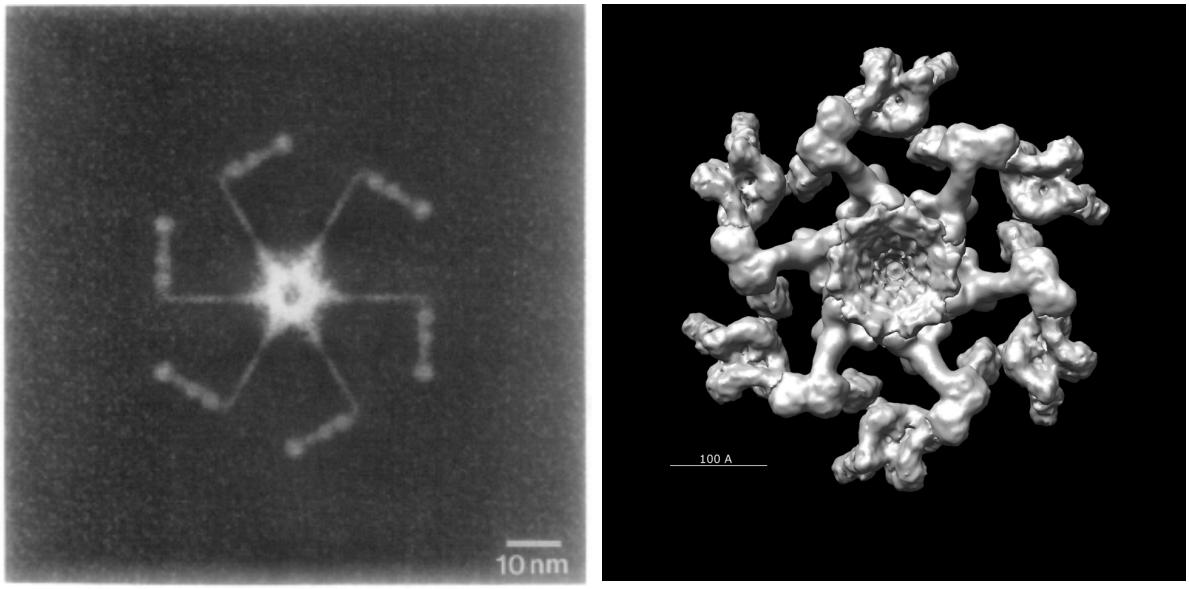
Annexes:

T7

Background

The present family ***Podoviridae*** of tailed phages has three genera. One of them is the genus "T7-like phages", which is characterized by virions with isometric heads, no base plate, and the presence of DNA and RNA polymerases.

During the last years, several phages with close affinities to T7 have been isolated and extensively characterized. The four phages proposed for the “SP6-like viruses” genus have diverged considerably from the T7 prototype. Among other properties, they adsorb to bacteria with complete O-antigens, and some have the capacity to degrade capsular polysaccharide. Degradation is due to the presence of tail spike enzymes, rather than the tail fibers of T7. The tail spikes are attached to the tail through an adapter protein not found in T7.



End on view of T7 (left) by electron microscopy (Steven and Trus, 1986), K1E (right) by cryoelectron microscopy (Leiman et al., 2007)

SP6-like phages generally have larger genomes than T7, potentially coding for more proteins, and their heads are also about 10% larger than T7. Although many proteins of the SP6-like viruses are clearly related to the T7-like viruses, several “essential” proteins of the latter genus have no obvious counterpart.

GENUS **SP6-LIKE VIRUSES**

Type Species *Salmonella enterica* serovar Typhimurium *phage SP6* (SP6)

Distinguishing Features

Podoviridae coding for an RNA polymerase and tailspike enzymes .

Virion Properties

Isometric head with internal core proteins. The head structural module is related that of the T7-like phages but the internal core proteins have diverged beyond all recognition other than size. The virion cell-wall degrading enzyme is fused to a different structural protein than in the T7-like viruses.

Genome Organization and Replication

The DNA replication machinery of SP6 shows clear homology to that of phages T3 and T7 except that there is not a separate helicase enzyme, no apparent SSB or transcription-regulatory lysozyme. DNA ligase has a bacterial origin and is unrelated to other phage ligases. The enzymes used to degrade the host chromosome have likewise diverged from T7, and genomic synteny with the T7-like viruses has been lost

Biological Properties

Phages infect enteric γ–proteobacteria.

List of Species Demarcation Criteria

Host range: including smooth and capsulated bacteria in different genera.

Official virus species names are in italics. Tentative virus species names, alternative names (), strains, or serotypes are not italicized. Virus names, genome sequence accession numbers [], and assigned abbreviations are:

SPECIES IN THE GENUS

Enterobacteria phage SP6
Enterobacteria phage K1E
Enterobacteria phage K1-5
Enterobacteria phage K5
Erwinia amylovora phage Era103

TENTATIVE SPECIES IN THE GENUS

None.

SUPPORTING MATERIAL

		Bp	**Genes**	**TR**	**G-C**	**DNAP**	**RNAP**	
E. coli	T7	39937	59	160	50	+	+	Dunn 83
	T3	38208	56	231	49.9	+	+	Pajunen 02
	SP6	43769	53	174	47.2	+	+	Dobbins, Scholl 04
	K1-5	44385	52	234	42.3	+	+	Scholl 04
	K1F	39704	43	179	49.8	+	+	Scholl 05
	K1E	45251	62	288	45.1	+	+	Stummeyer
Yersinia	ϕYeO3-12	39600	54	232	50.6	+	+	Pajunen 01
	ϕA1122	37555	49	148	48.3	+	+	Garcia
Pseudomonas	gh-1	37359	43?	216	57.4	+	+	Kovalyova
	ϕKMV	42519	48	414	62.3	+	+	Lavigne

Synechococcus	P60	47872	80			+	+	Chen
Roseobacter	SIO1	39906	30	?	46.2	+	---	Rohwer
Vibrio	VpV262	46012	58?	138		+	---	Hardies
Erwinia	Era103	45445	53	277	49.8	+	+	EF160123 (Genbank)

bp, base pairs; DNAP, DNA polymerase; RNAP, RNA polymerase; TR, direct terminal repeats

Common Properties in T7-Like Phages

1. One major and one minor head protein:
   T7, T3, K1F, øYeO3-12, øA1122. Not gh-1, øKMV, SP6, K1-5, K1E. Not known: P60, SIO1, VpV262.

2. Two tubular tail proteins:
   Not identified in SIO1, VpV262

3. Internal proteins in capsid (2-4):
   Not identified in P60, SIO1, VpV262

4. Frameshifting within major capsid protein:
   Found in T3, T7, ϕYeO3-12, K1F; not gh-1, SP6, K1-5, K1E and ϕKMV

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