This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2009.012a-qB***	(to be completed by ICTV officers)

Short title: Create the new subfamily *Peduovirinae*, containing the new genus *Hp1likevirus*, in the family *Myoviridae*, order *Caudovirales*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☐
	6 ☐	**7** ☒	**8** ☐	**9** ☒	

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Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	**Yes**

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:
Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.
If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.012aB***	(assigned by ICTV officers)

To create 12 new species with the name(s):

Enterobacteria phage Wphi
Yersinia phage L-413C
Enterobacteria phage 186
Enterobacteria phage PsP3
Salmonella Fels-2
Salmonella SopEphi
Burkholderia phage phiE202
Mannheimia phage phiMhaA1-PHL101
Pseudomonas phage phiCTX
Burkholderia phage phi52237
Ralstonia phage RSA1
Burkholderia phage phiE12-2

Part (b) assigning new species to higher taxa
All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.012bB***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***P2likevirus*** (proposed new name for "P2-like viruses")
Subfamily:	***Peduovirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.
- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Phages of this genus infect different types of bacterial species. Apart from their differences in host specificity, available genome seuqence data for these phages suggest the absence of genome-wide DNA homology between the phages. Furthermore, although these phages share a similar genome organisation, each phage encodes gene products unique to that phage, which is reflected in the dissimilarity cluster given in Module 9 (Figure 1). A list of Genbank accession numbers for these phages is given in module 9.

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	***2009.012cB***	(assigned by ICTV officers)

To create 6 new species with the name(s):

Haemophilus phage HP1
Haemophilus phage HP2
Pasteurella phage F108
Vibrio phage K139
Vibrio phage Kappa
Aeromonas phage phiO18P

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	***2009.012dB***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	***HP1likevirus* (new)**
Subfamily:	***Peduovirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Phages of this genus infect different types of bacterial species. Apart from their differences in host specificity, available genome seuqence data for these phages suggest the absence of genome-wide DNA homology between the phages. Furthermore, although these phages share a similar genome organisation, each phage encodes gene products unique to that phage, which is reflected in the dissimilarity cluster given in Module 9 (Figure 1). A list of Genbank accession numbers for these phages is given in module 9.

MODULE 3: **NEW GENUS**

creating and naming a new genus

Code	***2009.012eB***	(assigned by ICTV officers)

To create a new genus to contain the species listed below

Code	***2009.012fB***	(assigned by ICTV officers)

To name the new genus: *HP1likevirus*

assigning a new genus to higher taxa

Code	***2009.012gB***	(assigned by ICTV officers)

To assign the new genus as follows: Ideally, a genus should be placed within a higher taxon, but if not, write "**unassigned**" in the box below.

Subfamily:	***Peduovirinae*** (new)
Family:	***Myoviridae***
Order:	***Caudovirales***

If any of these taxa has yet to be created (in module 4, 5 or 6) please write "**(new)**" after its proposed name.

assigning type species and other species to a new genus

Code	***2009.012hB***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Haemophilus phage HP1

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

Code	***2009.012iB***	(assigned by ICTV officers)

To assign the following as additional species of the new genus:

Haemophilus phage HP2
Pasteurella phage F108
Vibrio phage K139
Vibrio phage Kappa
Aeromonas phage phiO18P

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

The genus *HP1likevirus* comprise a group of viruses sharing ≥50% proteins in common. Proteome based dissimilarity (Module 9 Figure 1) clearly segregates this proposed genus from "P1-like viruses".

Origin of the new genus name:

After type species

Reasons to justify the choice of type species:

This is the first sequenced phage of this genus

Species demarcation criteria in the new 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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences of new species

MODULE 4: **NEW SUBFAMILY**

creating and naming a new subfamily

Code	***2009.012jB***	(assigned by ICTV officers)

To create a new subfamily containing the genera listed below

Code	***2009.012kB***	(assigned by ICTV officers)

To name the new subfamily: *Peduovirinae*

assigning a new subfamily to a family

Code	***2009.012lB***	(assigned by ICTV officers)

To assign the new subfamily as follows:

Peduovirinae (new)

Family:	***Myoviridae***
Order:	***Caudovirales***

If the family has yet to be created (in Module 5) please write "**(new)**" after the proposed name.
If there is no Order, write "**unassigned**" here.

genera and species assigned to the new subfamily

Code	***2009.012mB***	(assigned by ICTV officers)

genera assigned to the new subfamily

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family

P2likevirus (proposed new name for "P2-like viruses")

HP1likevirus (new)

Code		(assigned by ICTV officers)

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

You may list several species here. For each species, please state whether it is new or existing. If the species is new, it must be created in Module 2

Reasons to justify the creation of the new subfamily:

Additional material in support of this proposal may be presented in the Appendix, Module 9

See module 9 and information presented above. Phages are typical Myoviridae and morphologically identical. Heads are icosahedra of about 60 nm in diameter and 72 capsomers (60 hexamers and 12 pentamers, T=7). Tails measure 135 x 18 nm and have a collar and six short kinked fibers. Upon contraction, the tail sheath becomes loose and slides along the tail core. Phages P2 and HP1 and their relatives fall into two different, but related genomic groups. Specific genomic integration of the viral DNA after infection separates this subfamily from Mu and Mu-related phages.

Origin of the new subfamily name:
Named after the best-studied of these phages, coliphage P2.

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2009.012nB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Haemophilus phage HP1

The present taxonomic position of these taxon/taxa:

Genus:	***P2likevirus*** (proposed new name for "P2-like viruses")
Subfamily:	
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right	

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Part (b) re-assign to a higher taxon

Code	***2009.012oB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	***HP1likevirus***
Subfamily:	***Peduovirinae***
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Cfr modules 3 & 9

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2009.012pB***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Genus *P2likevirus* (proposed new name for "P2-like viruses")

The present taxonomic position of these taxon/taxa:

Genus:	--
Subfamily:	**unassigned**
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

Part (b) re-assign to a higher taxon

Code	***2009.012qB***	(assigned by ICTV officers)

To re-assign the taxon (or taxa) listed in Part (a) as follows:

Genus:	--
Subfamily:	***Peduovirinae***
Family:	***Myoviridae***
Order:	***Caudovirales***

Fill in all that apply.

- If the higher taxon has yet to be created write "**(new)**" after its proposed name and complete relevant module to create it.

If no genus is specified, enter "**unassigned**" in the genus box.

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Cfr. Modules 4 & 9

-

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Reference List

1. Bertani, L. E. 1951. Studies in lysogenesis. I. The mode of phage liberation by lysogenic Escherichia coli. Journal of Bacteriology 62:293-300.
2. Bertani, L. E. and G. Bertani. 1971. Genetics of P2 and related phages. Advances in Genetics 16:199-237.:199-237.
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4. Esposito, D., W. P. Fitzmaurice, R. C. Benjamin, S. D. Goodman, and J. J. Scocca. 1996. The complete nucleotide sequence of bacteriophage HP1 DNA. Nucleic Acids Research 24:2360-2368.
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6. Kropinski, A. M., M. Borodovsky, T. J. Carver, A. M. Cerdeno-Tarraga, A. Darling, A. Lomsadze, P. Mahadevan, P. Stothard, D. Seto, D. G. Van, and D. S. Wishart. 2009. In silico identification of genes in bacteriophage DNA. Methods in Molecular Biology 502:57-89.:57-89.
7. Lavigne, R., P. Darius, E. J. Summer, D. Seto, P. Mahadevan, A. S. Nilsson, H.-W. Ackermann, and A. M. Kropinski. 2009. Classification of Myoviridae bacteriophages using protein sequence similarity (in press). BMC Microbiology.
8. Nilsson, A. S. and E. Haggård-Ljungquist. 2006. The P2-like bacteriophages, p. 365-390. In: R. Calendar (ed.), The Bacteriophages. Second ed. Oxford University Press, New York.
9. Portelli, R., I. B. Dodd, Q. Xue, and J. B. Egan. 1998. The late-expressed region of the temperate coliphage 186 genome. Virology 248:117-130.
10. Zafar, N., R. Mazumder, and D. Seto. 2002. CoreGenes: a computational tool for identifying and cataloging "core" genes in a set of small genomes. BMC Bioinformatics 3:12.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders.
The use of Figures and Tables is strongly recommended.

The ICTV currently lists only 2 sequenced viruses as members of the P2 phage genus**,** namely enterobacterial phage P2, and *Haemophilus* phage HP1. Several others including Enterobacteria phage 186, Enterobacteria phage Wϕ, *Haemophilus* phage HP2, *Pseudomonas* phage ϕCTX, *Salmonella* phage Fels-2, and *Vibrio* phage K139 are listed as tentative members. Based on the

Myoviridae cluster dendrogram (Fig. 1), the current ICTV genus "P2 viruses" should be subdivided into two genera, thus necessitating the creation of a subfamily, the *Peduovirinae*, named after the best-studied of these phages, coliphage P2.

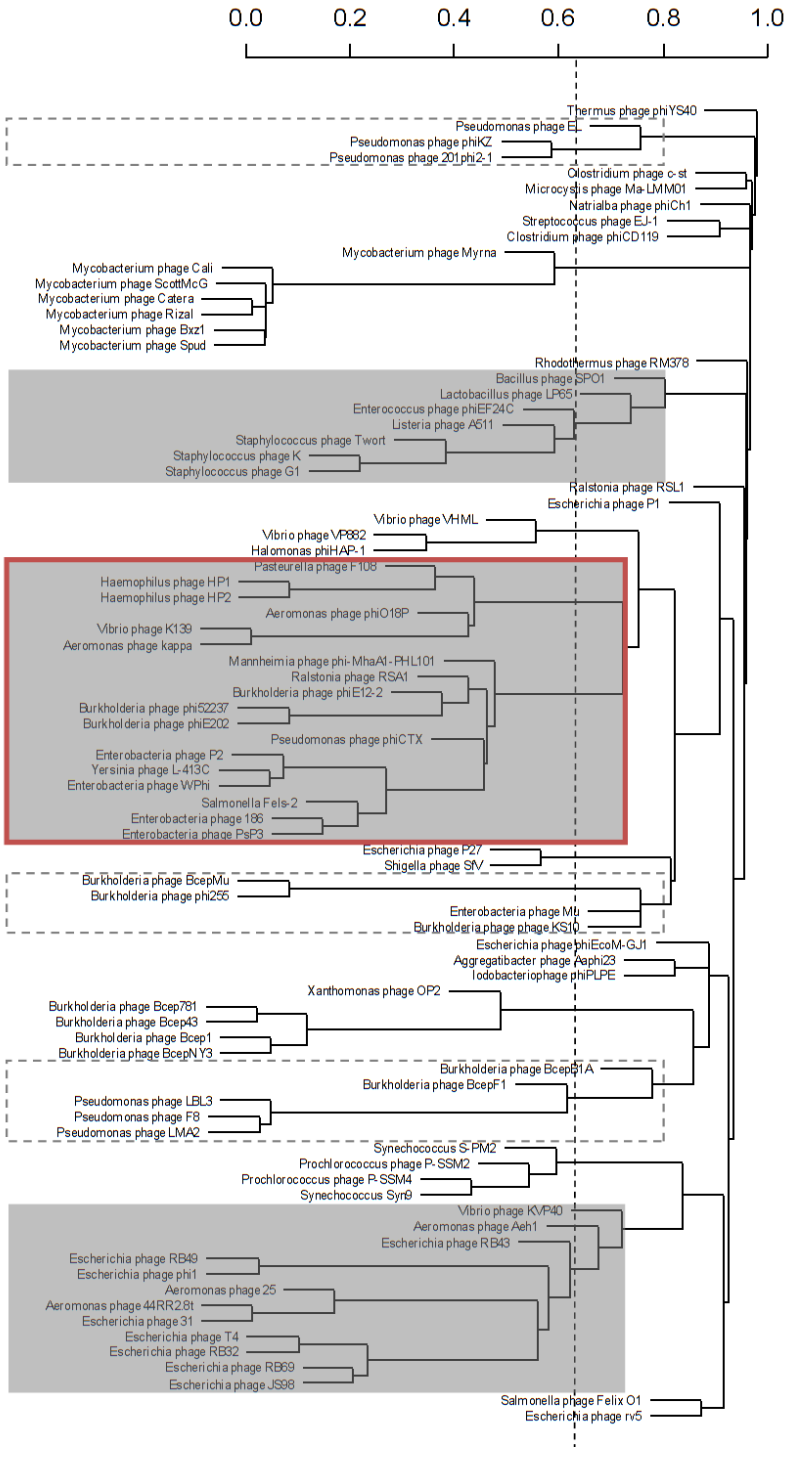

Figure 1: Hierarchical cluster dendrogram of the *Myoviridae*
The relative dissimilarity between the phage proteomes (between 0.0 and 1.0) forms the basis for the proposed groupings. The dotted lines reflects the cut-off value used for the establishement of genera, used consistently for all *Myoviridae* and the previously defined *Podoviridae* (Lavigne et al., 2008). Subfamily and tentative subfamily groupings are indicated in the grey and dotted boxes, respectively. The *Peduovirinae* is marked in red.

An analysis of eleven temperate P2-like bacteriophages from -proteobacteria shows that the evolution of all but a few genes in these phages is vertical (Nilsson, submitted; Figure 2). All genomes contained genes that showed no similarity to genes in the other genomes, but many of these genes are probably homologous although it is impossible to show due to evolutionary differentiation. P2-like phages seem to carry only a few nonessential genes, and could not be regarded as mosaics. A phylogenetic tree of P2-related phage resembles the tree of their hosts, which implies that P2-like phages evolve, and are closely associated, with their hosts. In addition, these trees are not inconsistent with the proposed subdivision in this subfamily.

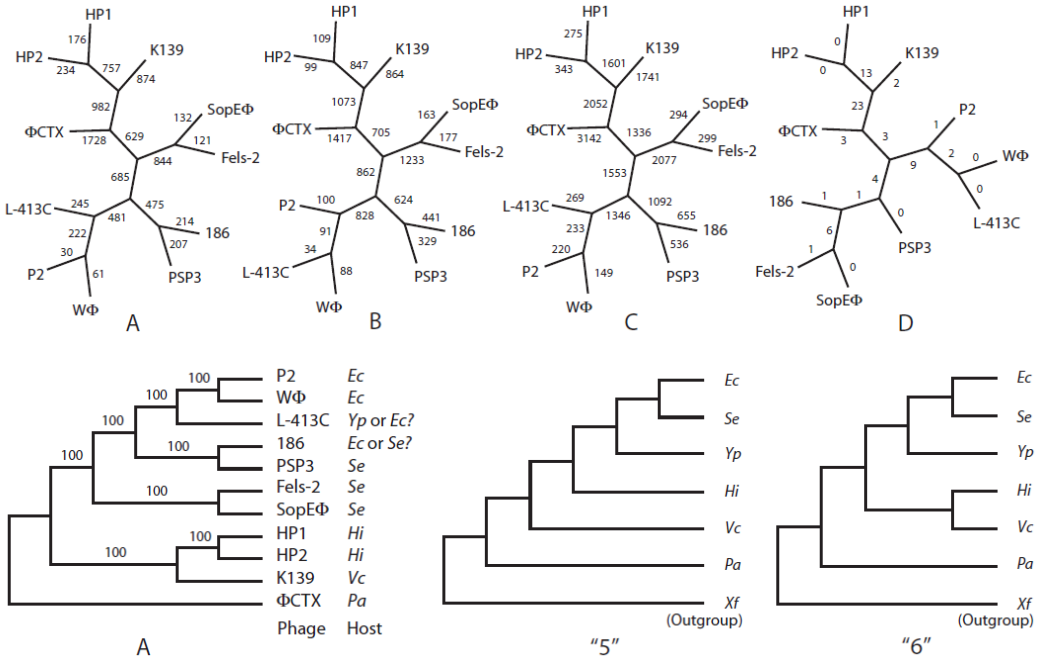

Figure 2:

a) Unrooted maximum parsimony phylogenetic trees based on different data from the genomes of eleven P2-related phages. Branch lengths (the number of character steps) are marked beside each branch. (A). Relationship of the genes present in all phages. (B). Relationship of the genes present in at least 4 and at most 10 phages. (C). A joint tree constructed from the concatenated datasets A and B reflecting the relationship of all shared proteins. (D). Relationship utilizing the genome gene content as informational characters. The tree is based on the homologous genes in 2 – 9 genomes. All trees were the shortest tree found in exhaustive searches, using PAUP, version 4.0b10.

b) Rooted maximum parsimony phylogenetic trees of P2-like phages and γ-proteobacteria. (A). The joint tree constructed from the concatenated datasets A and B (top figure a) rooted by ΦCTX from *P. aeruginosa.* ("5" and "6"). Subtrees including taxa relevant for the evolution of phages in this paper derived from tree "5" and "6" from a study on the phylogenetic relationships of γ-proteobacteria (35). Tree "5" is slightly better supported by the bacterial core genes than tree "6". The phage tree (A) mirrors the evolutionary relationships in tree "6". The trees were generated by PAUP, version 4.0b10.

1. "P2-like viruses" (proposed new name: *P2likevirus*)

This genus includes P2 itself and its extensively studied relative, coliphage 186. Both originate from the Pasteur Institute in Paris, France. Phage P2 is one of three phages (P1, P2, P3) isolated by G. Bertani in the beginning of the 1950´s from the "Li" (Lisbonne and Carrère) strain of *E. coli* (1). Later on, F. Jacob and E. Wollman isolated

phage 186 and many other viruses from enterobacteria collected by L. Le Minor (5). The reason for the early interest in these phages was that P2 and 186 are temperate. The analysis of the genetic control of these two modes was the starting point for ongoing fertile research on phage biology and molecular biology in general.

The genomes of phage P2 and 186 were the first P2 genomes to be fully sequenced and analyzed. Almost all P2 and 186 genes have been assigned a function (2,8,9). Coliphages WΦ and L-413C are very similar to P2 in both gene content and gene order. They are closely related to each other, sharing all but one protein in common. The only genes of these phages that differ from P2 are the lysogeny related genes, which may have been horizontally acquired and are totally different but inserted at the same locations in all genomes. There is however one exception to this; Phage P2 has a 786 bp orf (orf30) with unknown function inserted between the *S* and *V* genes. There is no such insertion in WΦ and L-413C, but *Pseudomonas* phage ΦCTX (see below) has another uncharacterized orf located at this position. Enterobacterial phages 186, PSP3, Fels-2, and SopEΦ also share most of their gene order and many genes with P2 but the genes are more differentiated. Unlike P2, these phages are UV-inducible due to the presence of the *tum* gene. In addition, they have a different lysis-lysogeny switch region. P2 phages seem to have either of two different proteins for repression of the lytic cycle. P2, WΦ and L-413C have the repressor gene *C* whereas 186, PSP3, Fels-2, SopEΦ, HP1, HP2, and K139 (below) instead have the sequence-unrelated genes *CI* and *CII* which are also needed for establishing lysogeny.

Mannheimia phage Φ-MhaA1-PHL101, *Pseudomonas* phage ΦCTX, and *Ralstonia* phage RSA1 have many P2 genes and a gene order of structural genes that is P2-like, although interspersed with some uncharacterized genes. Their presumed regulatory gene regions include additional putative and uncharacterized orfs. Phage ΦCTX has only the P2 regulatory gene *ogr* (transcriptional activator of the late genes) and the recombination enzyme *int* (integrase), Φ-MhaA1-PHL101 has repressor (CI) and antirepressor (Cro) equivalents which are most closely related to the regulatory proteins of the P22-like Enterobacteria phage ST104 than to P2.

Phage RSA1 seem not to have any P2 regulatory genes. The *ogr* gene in ΦCTX and RSA1 encodes integrases that are more similar to the P2-like *Burkholderia* phages (ΦE202, Φ52237, and ΦE12-2).

Table 1. Properties of "P2-like viruses" (proposed new name: *P2likevirus*)

Phage	Host	GenBank accession No.	Genome Mass (bp)	ORFs	Mol%GC
P2	Enterobacteria	AF063097	33,593	43	50
Wφ	Enterobacteria	AY135739	32,684	43	52
L-413C	*Yersinia*	AY251033	30,728	40	52
186	Enterobacteria	U32222	30,624	45	53
PsP3	Enterobacteria	AY135486	30,636	42	52
Fels-2	*Salmonella*	NC_003197	33,693	47	52
SopEφ	*Salmonella*	AY319521	35,155	69	51
φE202	*Burkholderia*	CP000623	35,741	48	65
φ-MhaA1-PHL101	*Mannheimia*	DQ426904	34,525	49	41
φCTX	*Pseudomonas*	AB008550	35,580	47	62
φ52237	*Burkholderia*	DQ087285	37,639	47	64
RSA1	*Ralstonia*	AB276040	38,760	51	65

φE12-2	*Burkholderia*	CP000624	36,690	50	64

2. Genus *Hp1likevirus*

The genome architecture of HP1 (4) and its close relative, HP2, resembles that of P2 although their *cos* sites, as with *Pseudomonas* ΦCTX, are located next to *attP* rather than downstream of the portal protein-encoding gene as it is in P2. The P2 gene order is also conserved in *Vibrio* phages K139 and κ and the *Pasteurella* phage F108. As in P2, the genomes can be divided into blocks of structural and regulatory genes. The structural genes are more similar in HP1 and HP2 than the regulatory genes. The six genes coding for capsid proteins are arranged in the same order in HP1 phages and many P2 phages. The other structural genes, coding mainly for tail components, show generally no similarity to those of P2 phages. Only some of the regulatory genes are similar in both HP1 and P2 phages, e.g., *int*, *CI*, and *rep* (*A*). Regulatory genes in general are more conserved within the HP1 group.

Aeromonas phage ΦO18P is included in the HP1 phages. It contains slightly more genes related to HP1 than to P2, although, when looking at individual proteins it sometimes appears to have an intermediate position. Its Rep protein is very similar to the DNA replication protein of *Salmonella* PSP3 and the A protein of phages K139, F108, WΦ, and P2 homologs. The ΦO18P major capsid protein is similar to the capsid proteins of phages K139**,** ΦCTX, 186, and the *Burkholderia* phages.

Table 2. Properties of the Hp1-like viruses

Phage	Host	GenBank accession No.	Genome Mass (bp)	ORFs	Mol%GC
HP1	*Haemophilus*	U24159	32,355	42	40
HP2	*Haemophilus*	AY027935	31,508	37	39
F108	*Pasteurella*	DQ114220	30,505	44	42
K139	*Vibrio*	AF125163	33,106	44	48
κ	*Vibrio*	AB374228	33,134	45	48
ΦO18P	*Aeromonas*	DQ674738	33,985	45	61