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:	***2013.004a-kB***	(to be completed by ICTV officers)

Short title: create two genera (*Cp220likevirus* and *Cp8unalikevirus*) within a new subfamily (*Eucampyvirinae*) in the family *Myoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

Andrew M. Kropinski	akropins@uoguelph.ca
Rob Lavigne	Rob.Lavigne@biw.kuleuven.be
Hans-Wolfgang Ackermann	ackermann@mcb.ulaval.ca
Christine Szymanski	cszymans@ualberta.ca
M. Afzal Javed	majaved@ualberta.ca
Ian Connerton	Ian.Connerton@nottingham.ac.uk
Andrew Timms	andrew.timms@nottingham.ac.uk
Joana Azeredo	jazeredo@deb.uminho.pt
Carla M. Carvalho	carlacarvalho@deb.uminho.pt
Stefan Hertwig	stefan.hertwig@bfr.bund.de
Jens Andre Hammerl	jens-andre.hammerl@bfr.bund.de

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at http://www.ictvonline.org/subcommittees.asp . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	

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

Date first submitted to ICTV: June 2013
Date of this revision (if different to above): July 2014

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.004aB***	(assigned by ICTV officers)

To create 4 new species within: *Cp220likevirus (new)*

Genus:	***Cp220likevirus*** (new)
Subfamily:	***Eucampyvirinae*** (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Campylobacter phage CP220	FN667788
Campylobacter phage CPt10	FN667789
Campylobacter phage IBB35	HM246720- HM246724
Campylobacter phage CP21	HE815464

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

We have chosen 95% DNA sequence identity to *Campylobacter* phage CP220 genome as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the EMBOSS Stretcher algorithm.

MODULE 2: **NEW SPECIES 2**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2013.004bB***	(assigned by ICTV officers)

To create 3 new species within: *Cp8unalikevirus (new)*

Genus:	***Cp8unalikevirus*** (new)
Subfamily:	***Eucampyvirinae*** (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Campylobacter phage CP81	FR823450
Campylobacter phage CPX	JN132397
Campylobacter phage NCTC12673	GU296433

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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

We have chosen 95% DNA sequence identity to *Campylobacter* phage CP81 as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the EMBOSS Stretcher algorithm.

.MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.004cB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Eucampyvirinae*** (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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.004dB***	(assigned by ICTV officers)

To name the new genus: *Cp220likevirus*

Assigning the type species and other species to a new genus

Code	***2013.004eB***	(assigned by ICTV officers)

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

Campylobacter phage CP220

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

4

Reasons to justify the creation of a new genus:

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

It was pointed out by Petrov et al. (2010) that *Campylobacter* phages CP220 and CPt10 were part of the T4 "superfamily." Subsequent to this publication five other *Campylobacter* phages have been isolated all of which share the T4 core proteome. Phylogenetic studies clearly indicate that the *Campylobacter* phages fall into two related yet distinct clades.

Origin of the new genus name:

Named after the first bacteriophage of its type to be fully sequenced

Reasons to justify the choice of type species:

The first phage of its type to be sequenced

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.

The phages belonging to this genus have long been referred to as the Group II *Campylobacter* myoviruses. Phages belonging to this genus share a comparable genome size (172 – 183 kb), and a comparable GC content (27%). Members of this genus also have a comparable morphology, with an icosahedral head, necks, but no collars and no apparent base plates. Tail fibers are short and thin (Figure 1).

The gene specifying the large subunit of terminase is contiguous unlike the case with the *Cp8unalikevirus*.

This group shows considerable DNA sequence homology (Figure 3) but little with the *Cp8unalikevirus*.

Phylogenetic analysis of the major capsid proteins and the DNA polymerase proteins indicate two clearly distinct clades (Figure 5/Figure 6).

We have proposed a shared protein content of at least 40% (as analyzed by CoreGenes 3.5) as indicative of membership in the same genus.   These phages share 76-89% homologs.

MODULE 3: NEW GENUS 2

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2013.004fB***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Eucampyvirinae*** (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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.004gB***	(assigned by ICTV officers)

To name the new genus: *Cp8unalikevirus*

Assigning the type species and other species to a new genus

Code	***2013.004hB***	(assigned by ICTV officers)

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

Campylobacter phage CP81

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

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

3

Reasons to justify the creation of a new genus:

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

It was pointed out by Petrov et al. (2010) that *Campylobacter* phages CP220 and CPt10 were part of the T4 “superfamily.” Subsequent to this publication five other *Campylobacter* phages have been isolated all of which share the T4 core proteome. Phylogenetic studies clearly indicate that the *Campylobacter* phages fall into two related clades.

Origin of the new genus name:

Named after the first bacteriophage of its type to be fully sequenced

Reasons to justify the choice of type species:

The first phage of its type to be sequenced

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.

The phages belonging to this genus have long been referred to as the Group III *Campylobacter* myoviruses. The heads are icosahedral, with contractile tails somewhat shorter than the *Cp220likevirus* (Figure 1).

The gene specifying the large subunit terminase is discontinuous and in opposite orientations, i.e., homology to the *N*-terminal portion of the protein was found approximately 22 kb away from the region showing homology to the *C*-terminus.

This group shows considerable DNA sequence homology (Figure 4) but little with the *Cp220likevirus*.

Phylogenetic analysis of the major capsid proteins and the DNA polymerase proteins indicate two clearly distinct clades (Figure 5/Figure 6).

We have proposed a shared protein content of at least 40% (as analyzed by CoreGenes 3.5) as indicative of membership in the same genus. These phages share 79-86% homologs.

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MODULE 4: **NEW SUBFAMILY**

creating a new subfamily

A subfamily can only be created within a family.

Code	*2013.004iB*	(assigned by ICTV officers)

To create a new subfamily within:

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.

naming a new subfamily

Code	*2013.004jB*	(assigned by ICTV officers)

To name the new subfamily: *Eucampyvirinae*

genera and species assigned to the new subfamily

Code	*2013.004kB*	(assigned by ICTV officers)

To assign the following genera 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

Cp220likevirus

Cp8unalikevirus

The new subfamily will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the subfamily will contain (those NOT within any of the genera listed above):**

0

Reasons to justify the creation of the new subfamily:

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

The morphological, genomic and proteomic similarities reveal that these two genera are part of a subfamily. They share, based upon CoreGenes analysis 34-36% proteins in common.

Origin of the new subfamily name:

The name derives from the host of all these viruses Campylobacter

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Petrov VM, Ratnayaka S, Nolan JM, Miller ES, Karam JD. Genomes of the T4-related bacteriophages as windows on microbial genome evolution. Virol J. 2010 7:292.

Hammerl JA, Jackel C, Reetz J, Beck S, Alter T, Lurz R, Barretto C, Brüssow H, Hertwig S: *Campylobacter jejuni* group III phage CP81 contains many T4-like genes without belonging to the T4-type phage group: implications for the evolution of T4 phages. Journal of Virology 2011, 85:8597-8605.

Hammerl JA, Jackel C, Reetz J, Hertwig S: The complete genome sequence of bacteriophage CP21 reveals modular shuffling in *Campylobacter* group II phages. Journal of Virology 2012, 86:8896.

Carvalho CM, Kropinski AM, Lingohr EJ, Santos SB, King J, Azeredo J: The genome and proteome of a *Campylobacter coli* bacteriophage vB_CcoM-IBB_35 reveal unusual features. Virology Journal 2012, 9:35.

Kropinski AM, Arutyunov D, Foss M, Cunningham A, Ding W, Singh A, Pavlov AR, Henry M, Evoy S, Kelly J, Szymanski CM: Genome and proteome of *Campylobacter jejuni* bacteriophage NCTC 12673. Applied & Environmental Microbiology 2011, 77:8265-8271.

Timms AR, Cambray-Young J, Scott AE, Petty NK, Connerton PL, Clarke L, Seeger K, Quail M, Cummings N, Maskell DJ, Thomson NR, Connerton IF: Evidence for a lineage of virulent bacteriophages that target *Campylobacter*. BMC Genomics 2010, 11:214.

Javed MA, Ackermann HW, Azeredo J, Carvalho CM, Connerton I, Evoy S, Hammerl JA, Hertwig S, Lavigne R, Singh A, Szymanski CM, Timms A, Kropinski AM. A suggested classification for two groups of Campylobacter myoviruses. Arch Virol. 2014; 159(1):181-90.

Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010; 5(6):e11147.

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 but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

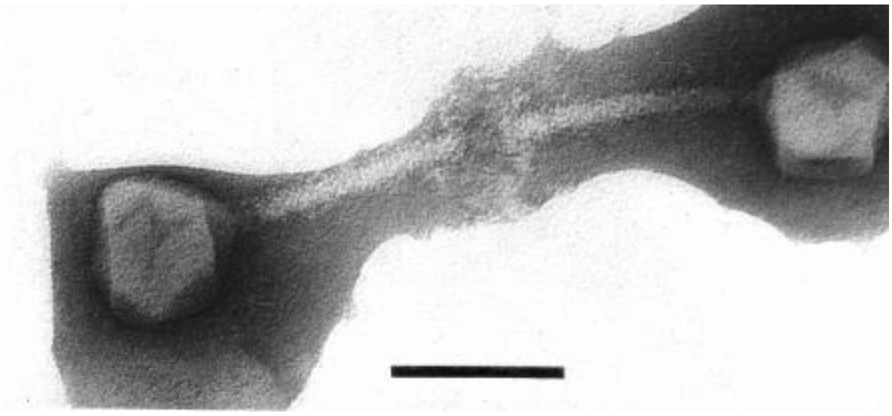

Figure 1. Phage CP220 stained with 2% ammonium molybdate

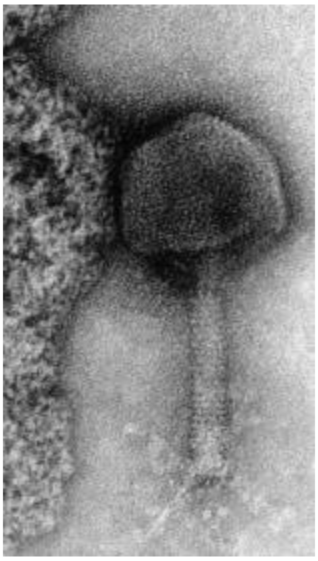

Figure 2. Phage CP81 stained with 2% ammonium molybdate

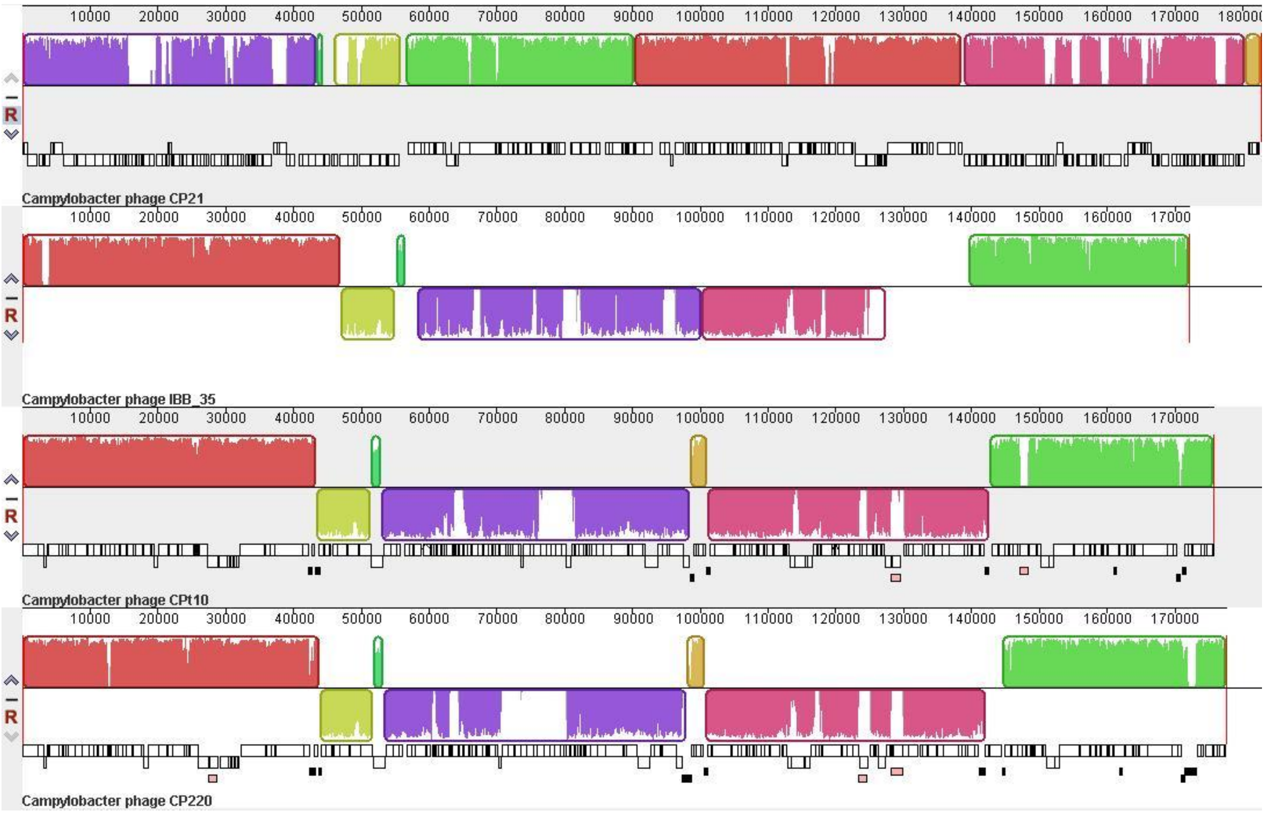

Figure 3. progressiveMauve alignment (Darling et al. 2010) of the genomes of the proposed genus *Cp220likevirus* (full genome represented by its annotated ORFs in white blocks) (7). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

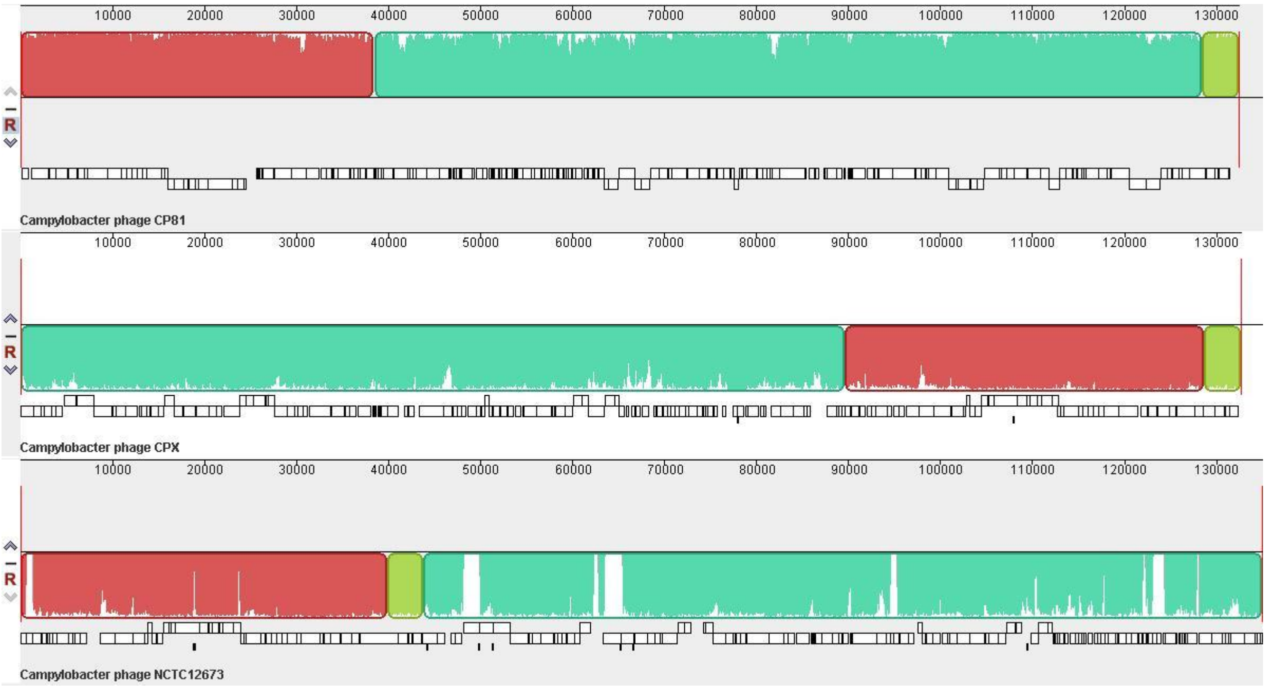

Figure 4. progressiveMauve alignment (Darling et al. 2010) of the genomes of the proposed genus *Cp8unalikevirus* (full genome represented by its annotated ORFs in white blocks) (7). Colored blocks indicate the regions of 1 to 1 best alignment with rearrangement breakpoints in a different random color. The degree of sequence similarity between regions is given by a similarity plot within the colored blocks with the height of the plot proportional to the average nucleotide identity.

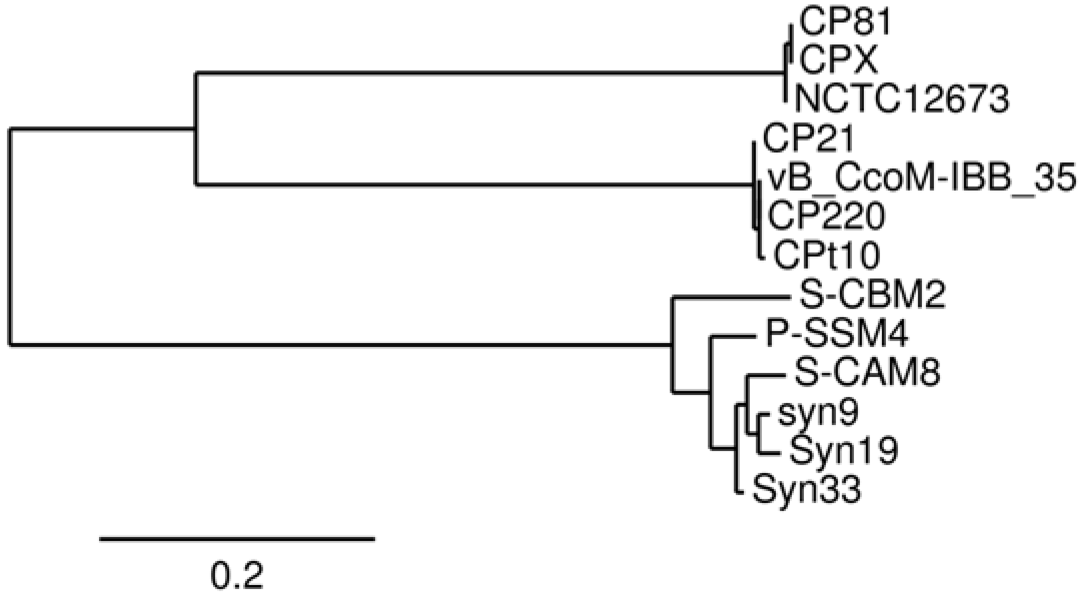

Figure 5. Phylogenetic analysis of gp23 (major capsid protein) homologs of *Campylobacter* and *Synechococcus* phages (S-CBM2 to Syn33) using one click phylogeny at phylogeny.fr, clearly indicates two clades. All other phages are too distant to present a reasonably phylogenetic tree.

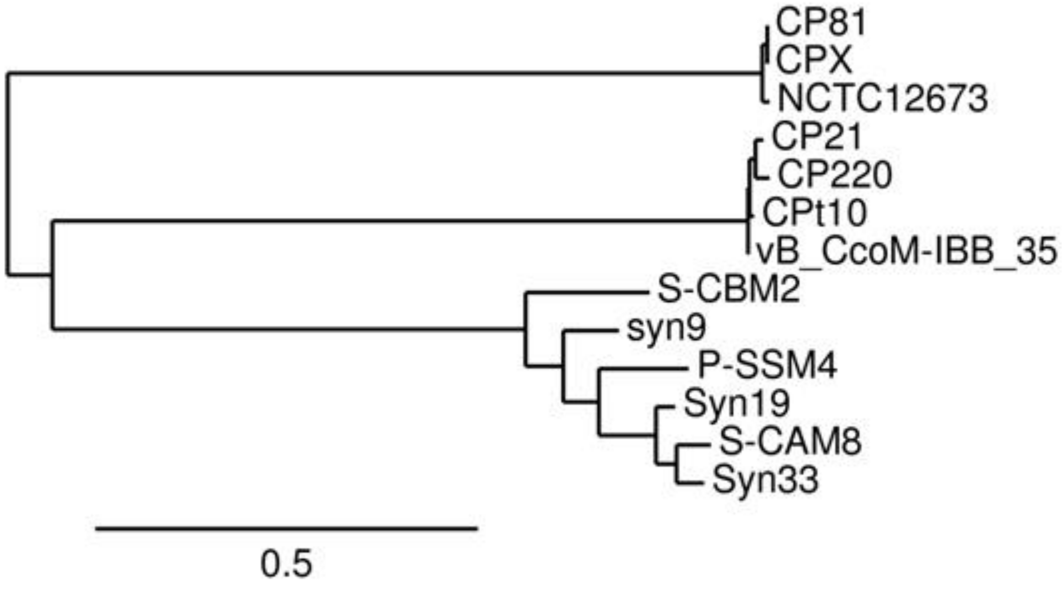

Figure 6. Phylogenetic analysis of gp43 (DNA polymerase) homologs of *Campylobacter* and *Synechococcus* phages clearly indicates two clades. All other phages are too distant to present a reasonably phylogenetic tree.