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:	***2012.006aB***	(to be completed by ICTV officers)

Short title: create two new species in the genus "PhiKMV-like viruses"
(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** ☒	

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

Rob Lavigne (rob.lavigne@biw.kuleuven.be)
Evelien Adriaenssens (evelien.adriaenssens@biw.kuleuven.be)

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:

Use lower case in species names.

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

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	***2012.006aB***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	**"PhiKMV-like viruses"***
Subfamily:	***Autographivirinae***
Family:	***Podoviridae***
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:**
Pantoea phage Limelight *Pantoea phage Limezero*	FR687252 FR751545

*proposed new name *Phikmvlikevirus* (see <2011.010aB.A.v2.Caudovirales_genus-ren>)

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

Phages of the *Autographivirinae* (Lavigne et al. 2008) share a common genome organization and make use of both the host RNA polymerase and a phage-encoded RNA polymerase. A typical characteristic of the genus "phiKMV-like viruses" is that the early and middle region of the genome ends with the DNA-dependent RNA polymerase and encompasses the host conversion and DNA replication genes. The late region comprises the genes coding for structural and lysis proteins. This organization is clearly visible in the newly proposed phage species *Pantoea phage Limelight* en *Pantoea phage Limezero* (Figures 1 and 2). Phylogenetic analysis also corroborates the classification of these phages (Figures 3, 4 and 5).

LIMElight and LIMEzero share less than 50% DNA homology with each other and the other known species and have a difference in host range (Adriaenssens et al. 2011), making them two different species.

A more detailed description of *Pantoea phage Limelight* and *Pantoea phage Limezero* can be found in Adriaenssens et al. (2011)

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adriaenssens EM, Ceyssens P-J, Dunon V, Ackermann H-W, Van Vaerenbergh J, Maes M., De Proft M, and Lavigne R (2011) Bacteriophages LIMElight and LIMEzero of *Pantoea agglomerans*, belonging to the 'phiKMV-like viruses' Appl. Env. Microbiol. 77:3443-3450

Lavigne R., D. Seto, P. Mahadevan, H-W. Ackermann, and A. M. Kropinski. (2008) Unifying classical and molecular taxonomic classification: analysis of the *Podoviridae* using BLASTP-based tools. Res. Microbiol. 159:406-414.

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.

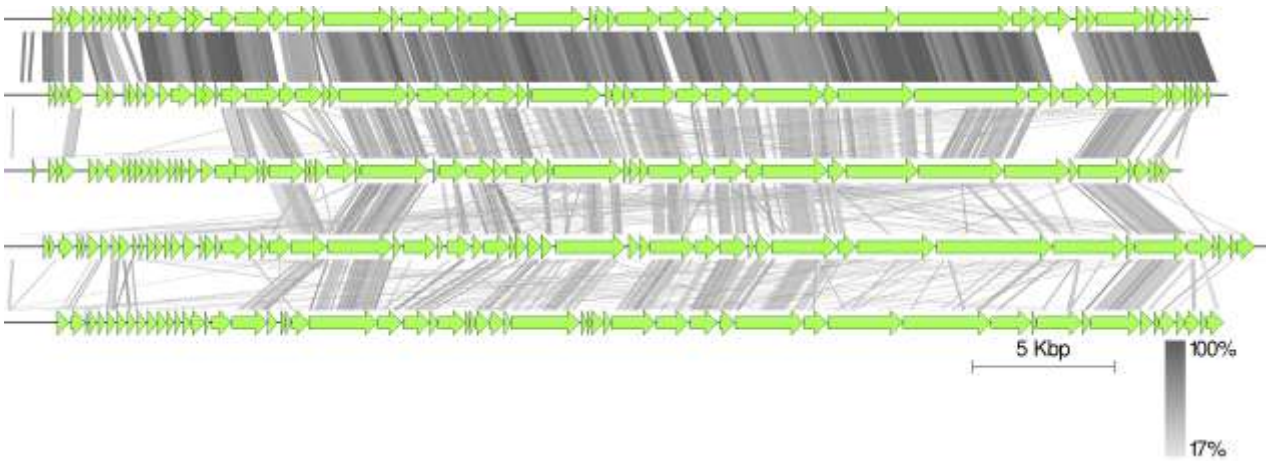

Figure 1: Tblastx comparison of (from top to bottom) phages φKMV, LKD16, LKA1, LIMElight and LIMEzero, each phage compared with its neighbor on the figure. ORFs are indicated with arrows.

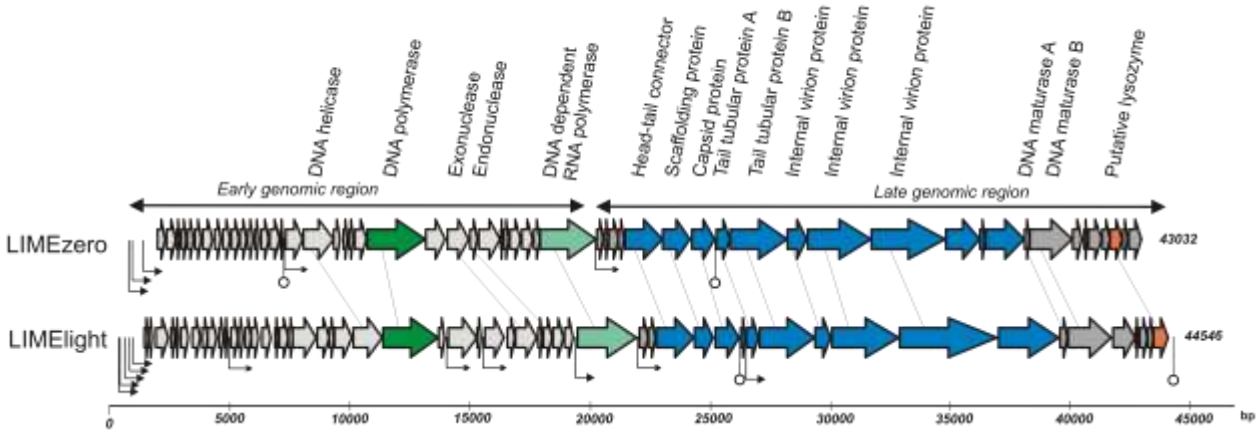

Figure 2: Schematic representation of the genomes of phages LIMEzero and LIMElight. The polymerases are shown in green, structural proteins in blue and the putative lysozyme in orange. Triangular arrows indicate host promotors, small arrows phage specific promotors and hairpins indicate factor-independent terminators.

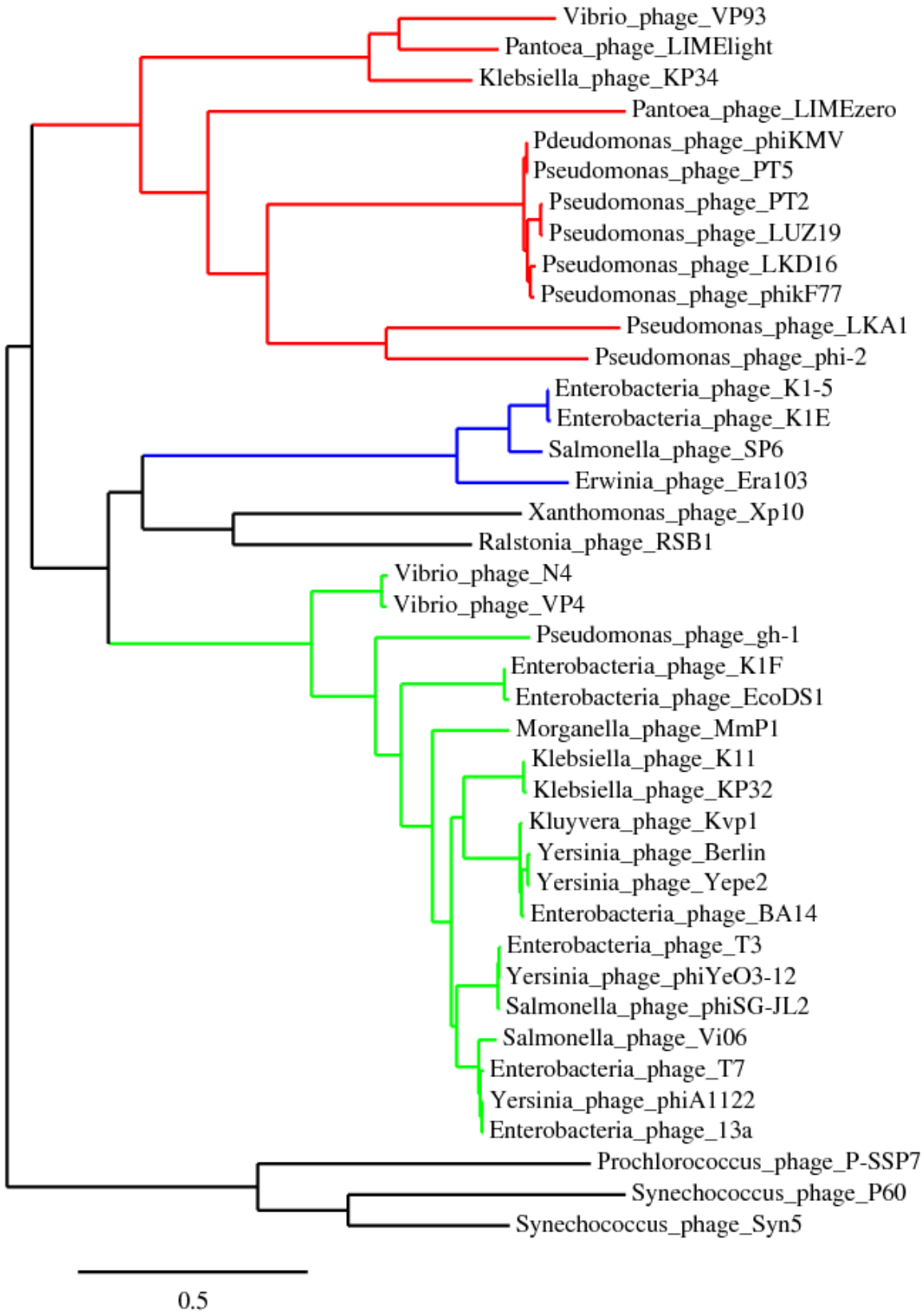

Figure 3: PhyML phylogenetic tree of the RNA polymerases of a representative number of phages of the *Autographivirinae*. Red lines indicate the clade of "phiKMV-like viruses"; blue lines, the "SP6-like viruses"; and green lines, the "T7-like viruses." The unassigned *Autographivirinae* are indicated by black lines, as are Siphovirus phage Xp10 and *Ralstonia* phage RSB1, which do not cluster in any of the previous groups.

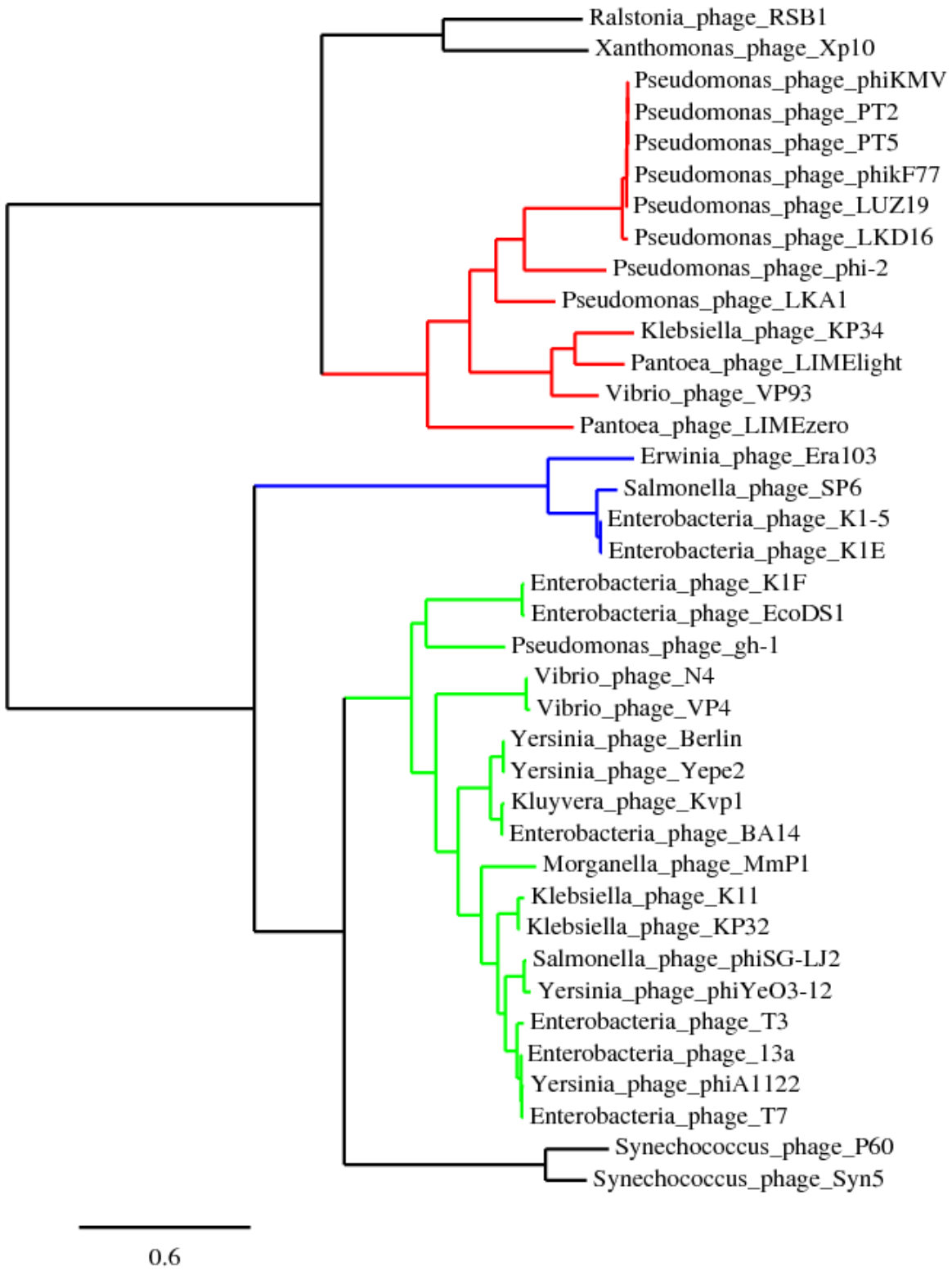

Figure 4: PhyML phylogenetic tree of the DNA polymerases of a representative number of phages of the *Autographivirinae*. Red lines indicate the clade of "phiKMV-like viruses"; blue lines, the "SP6-like viruses"; and green lines, the "T7-like viruses." The unassigned *Autographivirinae* are indicated by black lines, as are Siphovirus phage Xp10 and *Ralstonia* phage RSB1, which do not cluster in any of the previous groups.

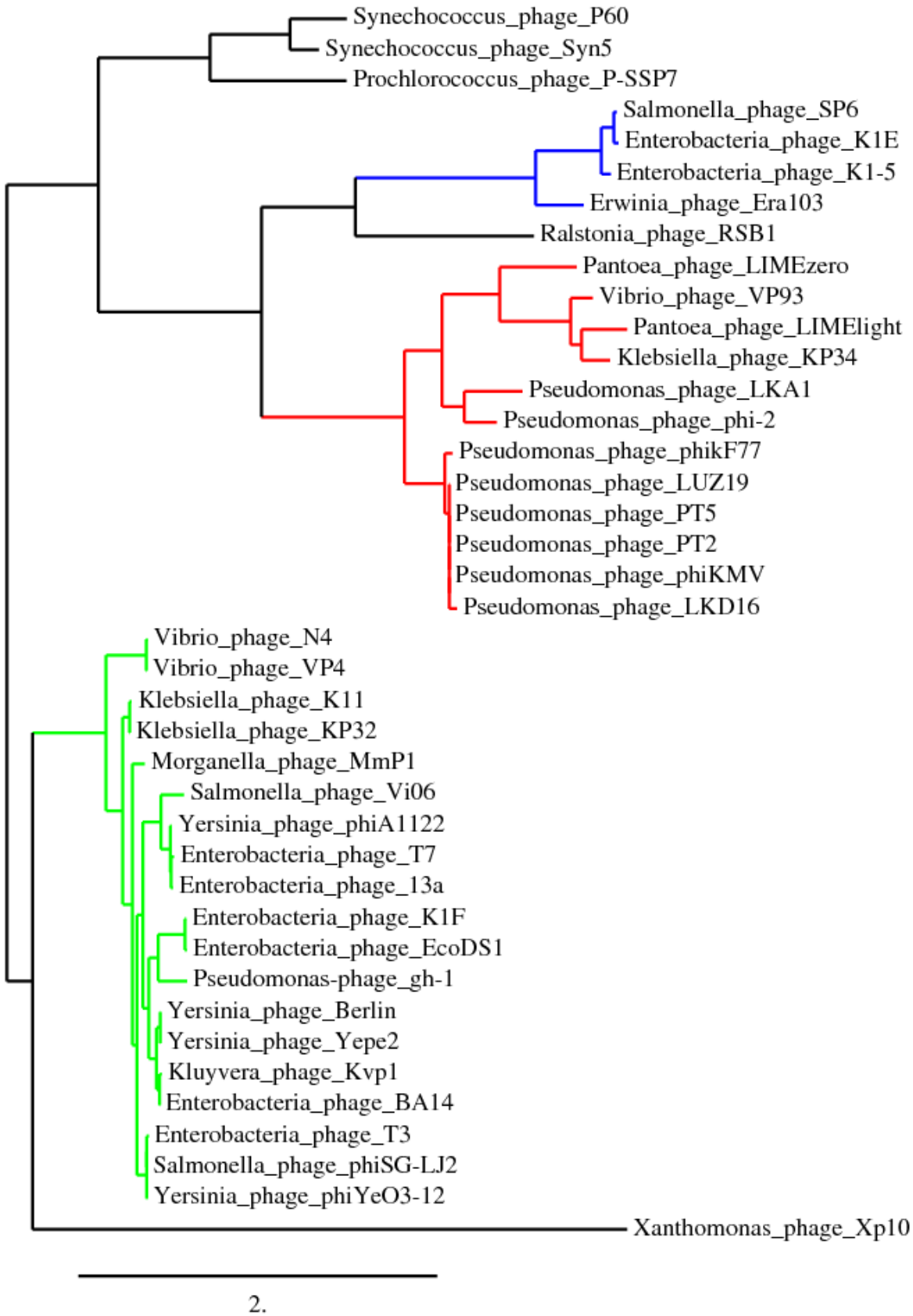

Figure 5: PhyML phylogenetic tree of the major capsid proteins of a representative number of phages of the *Autographivirinae*. Red lines indicate the clade of "phiKMV-like viruses"; blue lines, the "SP6-like viruses"; and green lines, the "T7-like viruses." The unassigned *Autographivirinae* are indicated by black lines, as are Siphovirus phage Xp10 and *Ralstonia* phage RSB1, which do not cluster in any of the previous groups.