This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | ***2019.070B*** |  |
| **Short title:** Create ten new genera including thirteen new species in the family *Myoviridae* |
|  |
| **Author(s) and email address(es):**  |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | Provide email address for each author in a single line separated by semi-colons |
| Kropinski AM, Adriaenssens EM | Phage.Canada@gmail.com;evelien.adriaenssens@quadram.ac.uk |
| **Author(s) institutional address(es) (optional):**

|  |
| --- |
| Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) |
| University of Guelph, Canada [AMK]Quadram Institute Bioscience, UK [EMA] |

 |
| **Corresponding author** |
| Andrew M. Kropinski |
| **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 (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | **Bacterial and Archaeal Viruses Subcommittee** **Caudovirales Study Group** |
|

|  |
| --- |
| **Authority to use the name of a living person:**Please provide the following information if you propose taxon name(s) which are derived from the name of a living person or persons*.* Please attach documents to verify that permission has been obtained.  |
| **Taxon name** | **Person from whom the name is derived** | **Permission obtained (Y/N)** |
| *Salmondvirus* | George Salmond | Y |
|  |  |  |
|  |  |  |
|  |

**ICTV Study Group comments (if any) and response of the proposer:** |
|       |
|  |
| Date first submitted to ICTV: |       |
| Date of this revision (if different to above): |       |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|       |

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
| --- |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.070B.A.v1.Myoviridae\_10gen13sp.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:* **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing.
* **Higher taxa**:
	+ There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.
	+ Please indicate the **origin of names** assigned to new taxa at genus level and above.
	+ For each new genus a **type species** must be designated to represent it. Please explain your choice.
* **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).

Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

| **References:** |
| --- |
| 1: Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. 2: Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. 3: O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45.4: Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6):e39107. 5: Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. 6: Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. 7: Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147.8: Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. 9: Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52.  |

**Species demarcation criteria:** We have chosen 95% DNA sequence identity 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 BLASTN algorithm.

**Proposal A:** To create a new genus, *Heilongjiangvirus*

**Source of the name of this taxon:** The name of this genus is directly derived from Heilongjiang, China's northernmost province. It was here at College of Veterinary Medicine, Northeast Agricultural University that the type phage was isolated.

**History:** This temperate phage was isolated from pickle using Lactobacillus brevis ATCC 367 as the host bacterium.

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Lactobacillus phage Lb | [MG020111.1](https://www.ncbi.nlm.nih.gov/nuccore/MG020111.1) | 43.42 | 41.7 | 61 | 0 |

**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the Terminase large subunit protein homologs of Lb and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal B:** To create a new genus, *Anamdongvirus*

**Source of the name of this taxon:** The name of this genus is derived from Anam-dong a neighbourhood of Seongbuk-gu in Seoul, South Korea. It was here at the College of Life Sciences and Biotechnology,

Korea University that the type phage was isolated.

**History:** This temperate phage was induced from Lactobacillus brevis. “Bacteriophage LBR48 was found to have an isometric head of 60 nm in diameter and a long contractile tail of 280 nm in length and 18 nm in width.”

**Reference:** Jang SH, Yoon BH, Chang HI. Complete nucleotide sequence of the temperate

bacteriophage LBR48, a new member of the family Myoviridae. Arch Virol. 2011;156(2):319-22.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Lactobacillus phage LBR48 | [NC\_027990.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_027990.1) | [GU967410.1](https://www.ncbi.nlm.nih.gov/nuccore/GU967410.1) | 48.21 | 45.9 | 86 | 0 |

**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the major capsid protein homologs of LBR48 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**Major capsid protein**



**Proposal C:** To create a new genus, *Baikalvirus*

**Source of the name of this taxon:** The name of this genus is derived from the source: “The novel giant Pseudomonas aeruginosa bacteriophage PaBG was isolated from a water sample of the ultrafreshwater Lake Baikal.”

**History:** This lytic phage was isolated on Pseudomonas aeruginosa strain PAO1. “Negative staining transmission electron microscopy revealed that bacteriophage PaBG belongs to the A1 morphotype of the *Myoviridae* family. The phage particles are composed of a large icosahedral head that is ~136 nm in diameter and a ~220-nm-long contractile tail.”

**Reference:** Sykilinda NN, Bondar AA, Gorshkova AS, Kurochkina LP, Kulikov EE, Shneider MM,

Kadykov VA, Solovjeva NV, Kabilov MR, Mesyanzhinov VV, Vlassov VV, Drukker VV,

Miroshnikov KA. Complete Genome Sequence of the Novel Giant Pseudomonas Phage

PaBG. Genome Announc. 2014 Jan 9;2(1). pii: e00929-13..

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Pseudomonas phage PaBG | [NC\_022096.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_022096.1) | [KF147891.1](https://www.ncbi.nlm.nih.gov/nuccore/KF147891.1) | 258.14 | 55.8 | 308 | 4(\*) |

**(\*) None indicated in GenBank genomic record; discovered using tRNAscan-SE 2.0 at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[5]**

**BLASTN homologs:** Genomic orphan [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of PaBG and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal D:** To create a new genus, *Loughboroughvirus*

**Source of the name of this taxon:** The name of this genus is derived from Loughborough, a town in the Charnwood borough of Leicestershire, England, where the Division of Microbiology, Brewing & Biotechnology, School of Biosciences, University of Nottingham is located. It is at this institution that the type phage was sequenced. It was isolated in Egypt using *Salmonella enterica* subsp. *enterica* serovar

Enteritidis WT as the host.

**History:** This lytic phage

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Salmonella phage ZCSE2 |  | [MK673511.1](https://www.ncbi.nlm.nih.gov/nuccore/MK673511.1) | 53.97 | 45.8 | 78 | 0 |

**BLASTN homologs:** The next most related phage is Salmonella phage vB\_SenM\_PA13076 which shows 67.3% sequence identity to ZCSE2 [1-3]. While this is sufficient to suggest a subfamily, we do not propose one at this time.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of ZCSE2 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal E:** To create a new genus, *Rosemountvirus*

**Source of the name of this taxon:** The name of this genus is derived from the address Rosemount Ave. of Biophage Pharma Inc. (now Phagelux Canada) who isolated this virus.

**History:** This lytic phage was isolated from sewage against Salmonella enterica Infantis.

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Salmonella phage BP63 | [NC\_031250.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031250.1) | [KM366099.1](https://www.ncbi.nlm.nih.gov/nuccore/KM366099.1) | 52.44 | 46.0 | 76 | 0 |

**N.B. Salmonella phage vB\_SenM\_PA13076, Salmonella phage UPF\_BP2 and Salmonella phage LSE7621 should be considered strains of BP63**

**BLASTN homologs:** The next most related phage is Salmonella phage ZCSE2 which shows 67.7% sequence identity to Bp63 [1-3]. While this is sufficient to suggest a subfamily, we do not propose one at this time.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of BP63 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal F:** To create a new genus, *Yoloswagvirus*

**Source of the name of this taxon:** The name of this genus is derived from the name of the first isolate of this type Erwinia phage vB\_EamM\_Yoloswag.

**History:** This lytic phage was isolated from Guernsey Orchard, Pleasant Grove, UT, USA using *Erwinia amylovora* as the host bacterium.

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Erwinia phage vB\_EamM\_Yoloswag |  | [KY448244.1](https://www.ncbi.nlm.nih.gov/nuccore/KY448244.1) | 259.7 | 46.9 | 333 | 0 |

**BLASTN homologs:** Genomic orphan [1-3]. The next most related phage is Erwinia phage vB\_EamM\_Y3.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Yoloswag and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal G:** To create a new genus, *Alexandravirus* with two species.

**Source of the name of this taxon:** The name of this genus is derived from the name of the first isolate of this type Erwinia phage vB\_EamM\_Alexandra.

**History:** This lytic phage was isolated from Provo, Utah, USA using *Erwinia amylovora* strain phiEa100 ATCC 29780 as the host bacterium.

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Erwinia phage vB\_EamM\_Alexandra | [MH248138.1](https://www.ncbi.nlm.nih.gov/nuccore/MH248138.1) | 266.53 | 50.1 | 345 | 100 | 100 |
| Dickeya phage vB\_DsoM\_AD1 | [MH460463.1](https://www.ncbi.nlm.nih.gov/nuccore/MH460463.1) | 261.66 | 49.4 | 330 | 67.7 | 89.3 |

****

**BLASTN homologs:** Genomic orphan [1-3]. The next most related phage is Dickeya phage vB\_DsoM\_AD1 which exhibits 67.0% DNA sequence identity with Alexandra. While this is sufficient to propose a relationship at the subfamily level, we do not propose one at this time.

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Alexandra and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal H:** To create a new genus, *Sasquatchvirus* containing a single species.

**Source of the name of this taxon:** The name of this genus is derived from the fact that the authors describe this phage as being a “hairy Myoviridae.” “The word Sasquatch is believed to be an Anglicization of the Salish word Sasq’ets, meaning “wild man” or “hairy man.” J.W. Burns coined the term in the 1930s. Burns was an Indian agent assigned to the Chehalis Band, now known as the Sts’ailes First Nation.” (<https://www.thecanadianencyclopedia.ca/en/article/sasquatch>)

**History:** This lytic phage was isolated using *Erwinia amylovora* strain phiEa100 ATCC 29780 as the host bacterium.

**Reference:** Buttimer C, Born Y, Lucid A, Loessner MJ, Fieseler L, Coffey A. Erwinia amylovora phage vB\_EamM\_Y3 represents another lineage of hairy Myoviridae. Res Microbiol. 2018;169(9):505-514.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC  | Size (Kb) | GC%  | Protein  | tRNA |
| Erwinia phage vB\_EamM\_Y3 |  | [KY984068.1](https://www.ncbi.nlm.nih.gov/nuccore/KY984068.1) | 261.37 | 47.2 | 333 | 0 |

**BLASTN homologs:** The next most related phage is Dickeya phage vB\_DsoM\_AD1 which exhibits 53.8% DNA sequence identity with Y3. While this might be sufficient to propose a relationship at the subfamily level, we do not intend to create one at this time[1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Y3 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal I:** To create a new genus, *Salmondvirus* containing two species.

**Source of the name of this taxon:** This taxon is named in honour of Professor George P. C. Salmond (Department of Biochemistry, University of Cambridge, UK) who isolated these viruses.

**History:** These lytic phage was isolated using Dickeya solani as the host bacterium. “These phages possess an icosahedral head with a diameter of around 90 nm, a contractile tail around 110 nm in length and structures at the base of the tail that have been described as “stars” or “prongs” and have been identified as tail spikes.”

**Reference:** Day A, Ahn J, Salmond GPC. Jumbo Bacteriophages Are Represented Within an

Increasing Diversity of Environmental Viruses Infecting the Emerging Phytopathogen, Dickeya solani. Front Microbiol. 2018;9:2169.

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | tRNA | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Dickeya phage vB\_DsoM\_JA11 | [MH389777.1](https://www.ncbi.nlm.nih.gov/nuccore/MH389777.1) | 255.36 | 44.5 | 321 | 0 | 100 | 100 |
| Dickeya phage vB\_DsoM\_JA29 | [MH460461.1](https://www.ncbi.nlm.nih.gov/nuccore/MH460461.1) | 253.32 | 43.8 | 318 | 0 | 87.6 | 96.6 |

**N.B. Dickeya phage vB\_DsoM\_JA33 and Dickeya phage vB\_DsoM\_JA13 should be considered strains of JA11.**

****

**BLASTN homologs:** JA11 is peripherally related to Erwinia phage vB\_EamM\_Y3 [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of JA11 and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**



**Proposal J:** To create a new genus, *Carpasinavirus* containing two species.

**Source of the name of this taxon:** This taxon is named after Xanthomonas phage Carpasina.

**History:** These lytic phages were isolated using *Xanthomonas campestris* as the host bacterium. “These phages possess an icosahedral head with a diameter of around 90 nm, a contractile tail around 110 nm in Carpasina was isolated in Denmark and XcP1 in Brazil.

**Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC  | Size (Kb) | GC%  | Protein  | tRNA | Overall DNA sequence identity (\*\*) | % common proteins (\*\*) |
| Xanthomonas phage Carpasina | [MH059633.1](https://www.ncbi.nlm.nih.gov/nuccore/MH059633.1) | 61.94 | 52.4 | 86 | 0 | 100 | 100 |
| Xanthomonas virus XcP1 | [MH191395.1](https://www.ncbi.nlm.nih.gov/nuccore/MH191395.1) | 61.83 | 52.5 | 81 | 0 | 91.2 | 87.2 |

****

**BLASTN homologs:** JA11 is peripherally related to Pseudomonas phage E79 [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homologs of Carpasina and related phages with phylogeny.fr in “one click” mode [8]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [9] for details."

**TerL protein**

