

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

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| **Code assigned:** | **2021.082B** |  |
| **Short title:** Create two new families (*Kyanoviridae* and *Straboviridae*) (*Caudoviricetes*) | | |
|  | | |

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**List the ICTV Study Group(s) that have seen this proposal**

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**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

|  |  |
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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2021 |
| Date of this revision (if different to above) |  |

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

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| Acceptance of proposal 2021.001B.abolish\_Caudovirales by EC53 results in removal of the order *Caudovirales* and families *Myoviridae*, *Podoviridae* and *Siphoviridae*. All underlying taxa are to be assigned directly to the class *Caudoviricetes*. The Excel module of this proposal has been altered to reflect the future changes; however, the Word module has been unaltered while awaiting the ratification vote. |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2021.082B.R.Tevens\_new\_families |

**Abstract**

|  |
| --- |
| This proposal creates two new families, the *Kyanoviridae* and *Straboviridae* from the T4-like phages. Eighteen new genera are created within the family *Kyanoviridae* and 11 new genera in the class *Caudoviricetes*. |

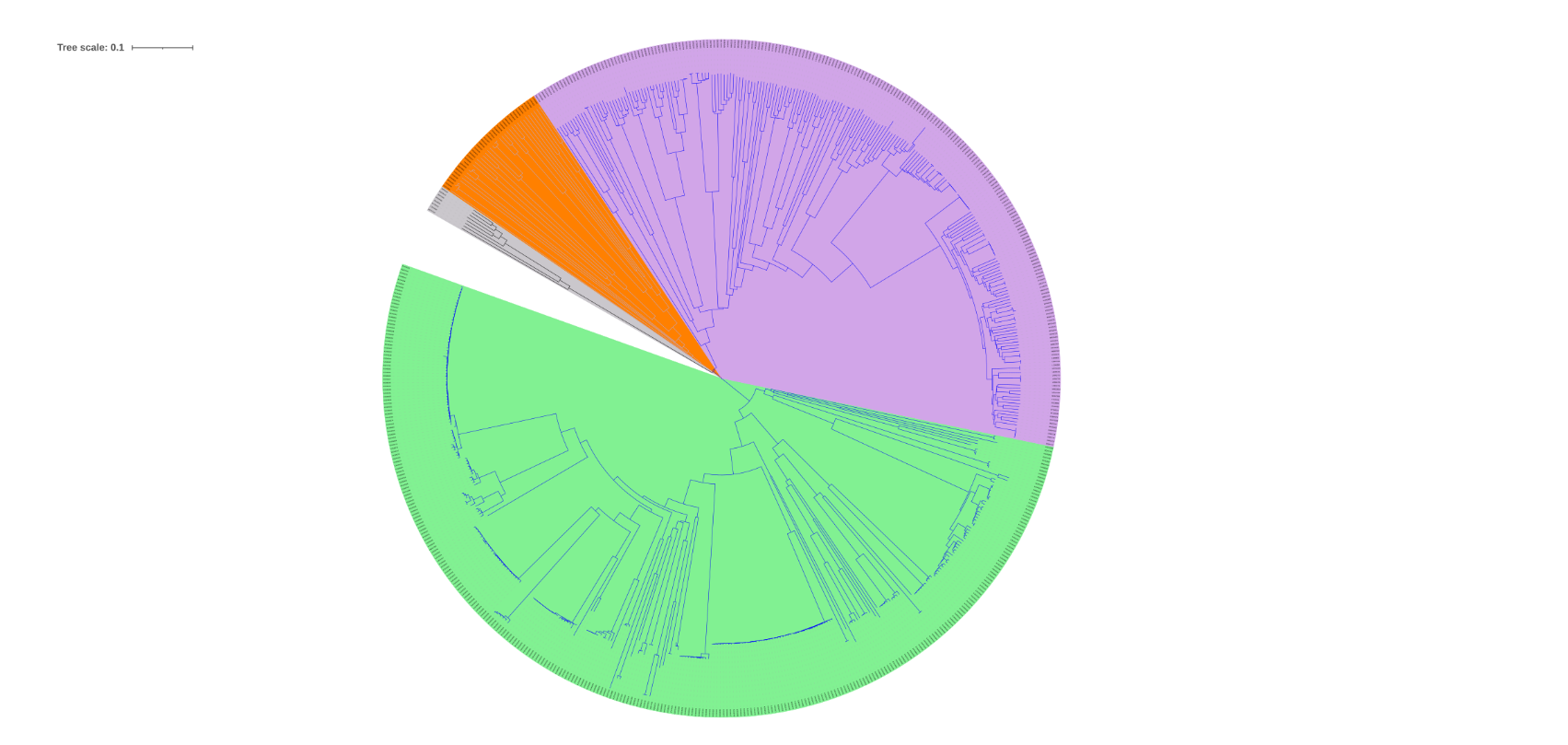
**Text of proposal**

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| --- | --- |
| |  | | --- | | With the planned abolishment of the family *Myoviridae* [1], we propose the creation of two new families from phage that have previously been referred to as T4-like phages.  **Proposal 1: Creation of the family *Straboviridae***  This family includes all T4-like phages that infect histotrophic bacteria, including the existing subfamilies *Tevenvirinae, Emmerichvirinae* and *Twarogvirinae*. Within this family 11 new genera are created.  The subfamily *Tevenvirinae* is no longer monophyletic and we propose moving the genera: *Schizotequatrovirus, Slopekvirus, Pseudotevenvirus, Krischvirus* out of the sub-family as floating genera within the new family. In addition, we have created the following genera *Tegunavirus, Kagamiyamavirus, Winklevirus, Mosugukvirus, Kanagawavirus, Roskildevirus* in the subfamily *Tevenvirinae*.  **Proposal 2: Creation of the family *Kyanoviridae***  Previously many cyanophages that are T4-like have not been formally classified. We propose the creation of the family *Kyanoviridae*, that will encompass T4like cyanophages.  Within the family *Kyanoviridae* we propose the creation of 20 new genera, and the inclusion of 26 existing genera.  **Proposal 3: Renaming of taxa within the *Straboviridae* and *Kyanoviridae* to binomial form.**  **Species demarcation criteria**: We have chosen 95% DNA sequence identity as the criterion for demarcation of species across all genera, as recommended [1]. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed via VIRIDIC analysis [2].  **Genus demarcation criteria**: As a starting point we have chosen 70% nucleotide identity over the genome length as the demarcation of genera. This has been combined with phylogenetic placement for border line cases [1].    **Subfamily demarcation criteria:** The subfamily *Tevenvirinae* was based on roughly equivalent branch lengths that were observed for the recently created genera of *Emmerichvirinae* and *Twarogvirinae*.  **Family demarcation criteria:** A monophyletic group based on the use of ViPTree analysis and vContact2 analysis based on phylogenetic analysis of shared genes. | |

**Supporting evidence**

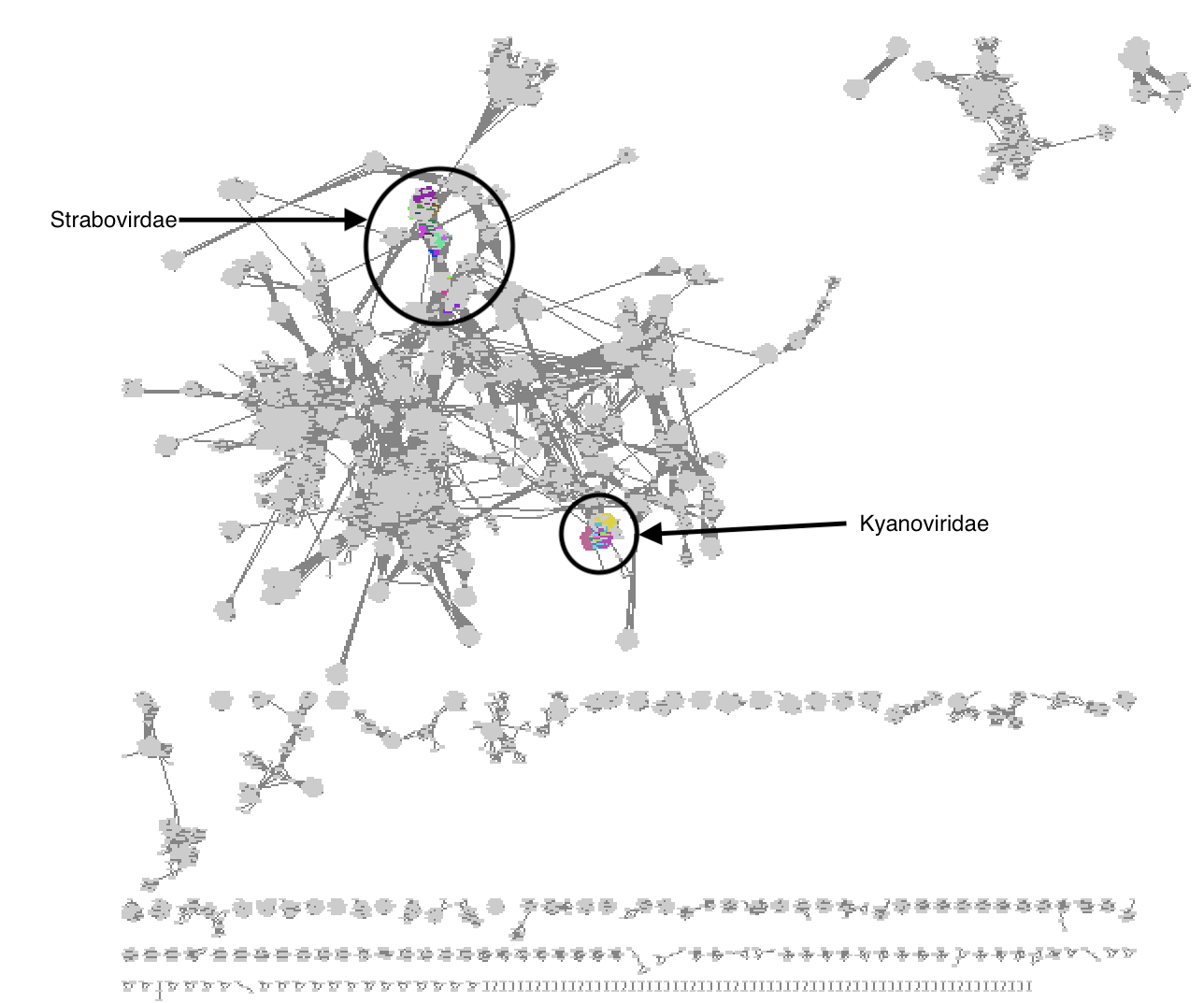
Creation of the Families *Straboviridae and Kyanoviridae*

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [3] is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [4]. The familiy *Herelleviridae* iq marked in orange and *Ackermanviridae* in grey, as references. The families *Straboviridae* and *Kyanoviridae* are coloured in mauve and green, respectively (“VIPTree\_NEW\_FAMILIES.pdf).



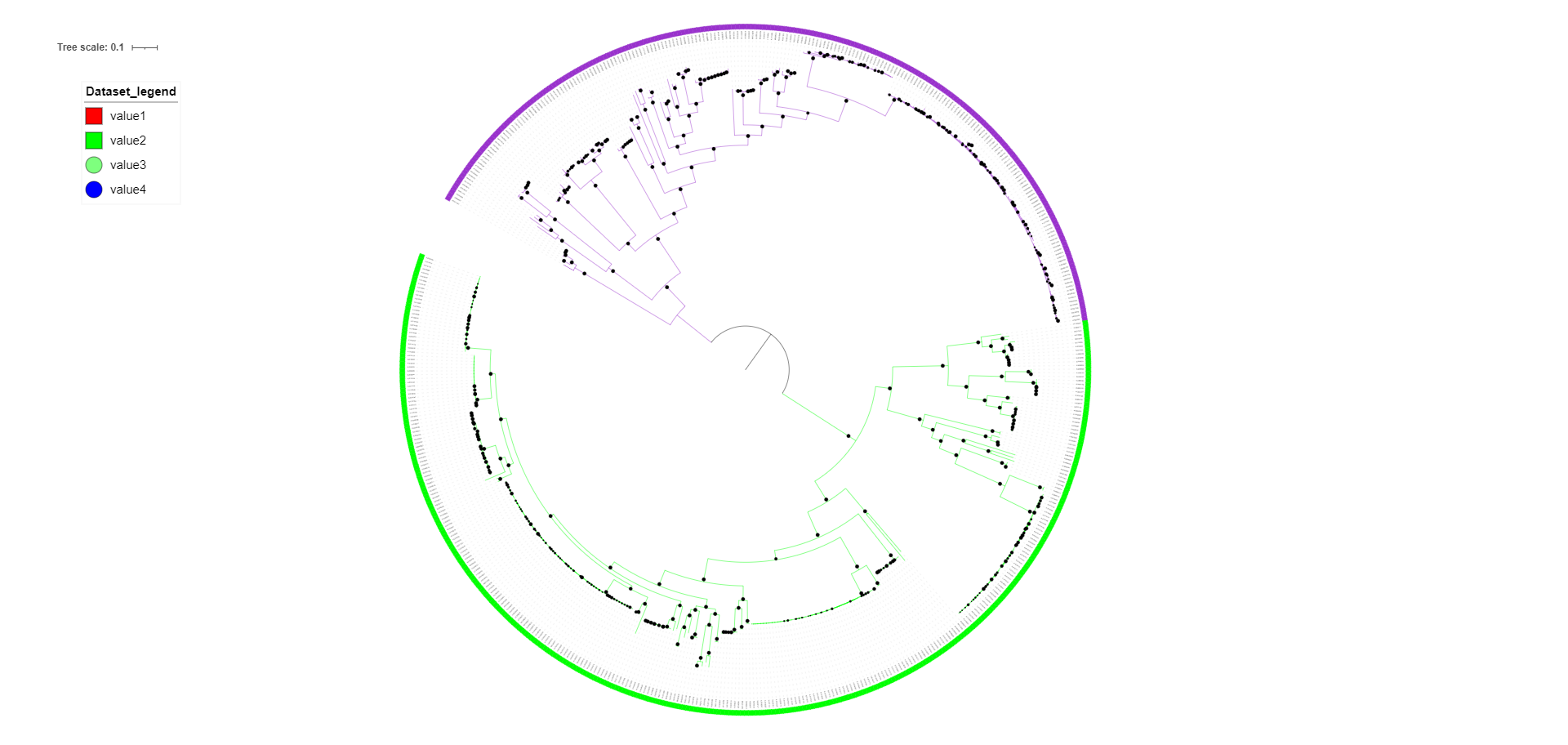
Phylogenetic analysis highlights a deep branching between the proposed families *Straboviridae* and *Kyanoviridae*

Further analysis using vContact2[5] confirms the distant separation of the two proposed families that form two distinct clusters in a network graph



vContact2 analysis of all genomes available as of Jan2020. The proposed families *Straboviridae and Kyanoviriade* form two distinct clusters. vContact2 was run with default settings.

The T4like phages have previously had a core-gene set identified that is conserved across both phages infecting heterotrophic and phototrophic (cyanobacteria) organisms [6–8]. Using this as starting point 14 core genes were used to construct a phylogeny of all T4like phages.



Phylogenetic analysis was carried out for both families based on a set of 14 conserved core genes. The list of genes used to construct the phylogeny is listed below, with the gene names identified by their designation in phage T4

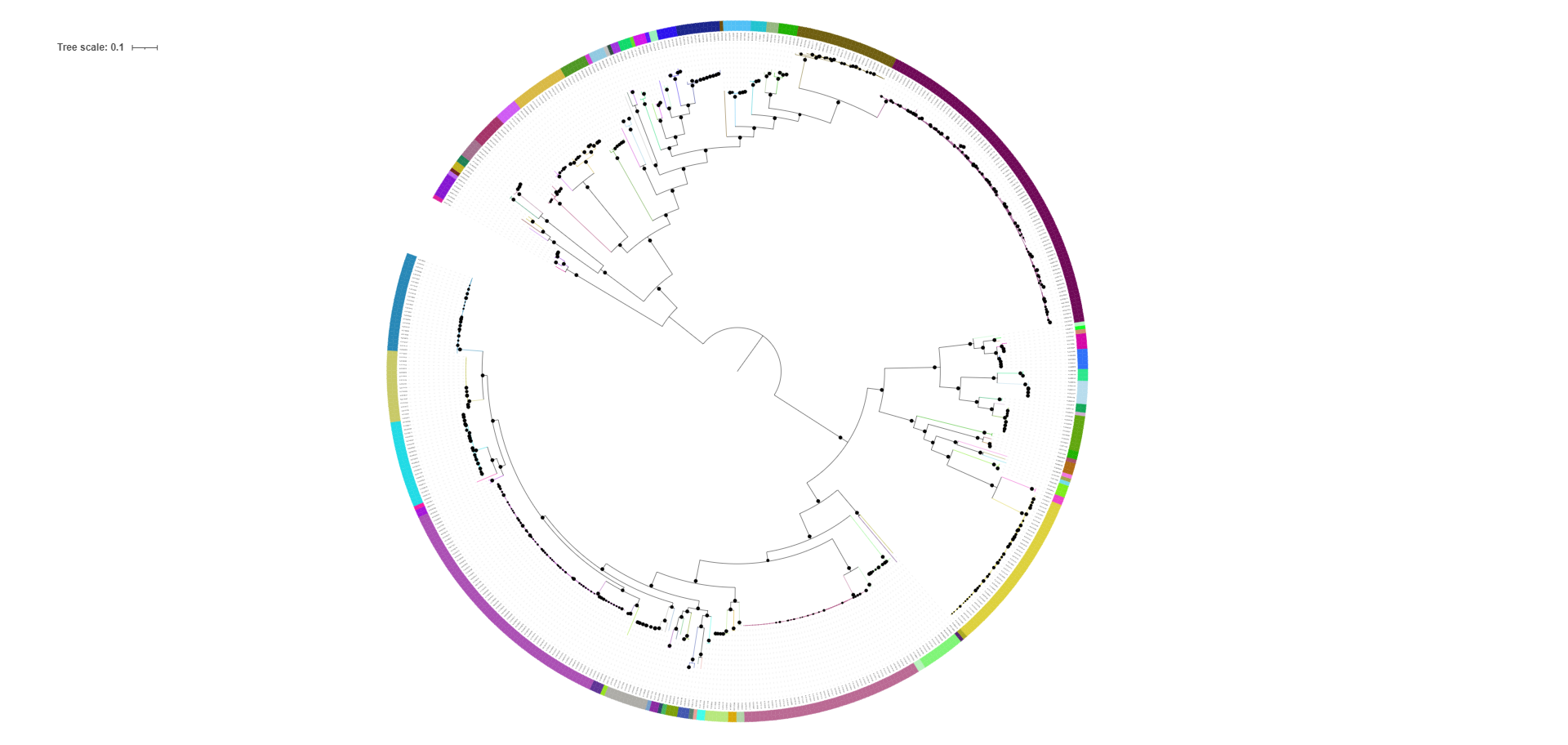
|  |  |
| --- | --- |
| **T4 gene name** | **Product** |
| Gp14 | Neck protein |
| Gp17 | Terminase subunit |
| Gp18 | Tail sheath protein |
| Gp19 | Tail tube protein |
| Gp22 | Capsid assembly protein |
| Gp23 | Major capsid protein |
| Gp41 | Helicase |
| Gp44 | Sliding clamp loader protein |
| Gp46 | Exonuclease subunit |
| Gp55 | Sigma factor |
| Gp47 | Exonuclease subunit |
| Gp61 | primase |
| RegA | Translational regulatory protein |
| Uvsw | Helicase |

Genes were aligned in MAFFT [9], prior to concatenation. Phylogenetic analysis was carried out in IQ-TREE with the following settings “iqtree -m GTR20 -bb 1000”. [10] (Two\_families.pdf for a high-resolution tree)

The phylogenetic analysis highlights the clear separation of the *Straboviridae* from the *Kyanoviridae*. The *Straboviridae* are marked in purple and the *Kyanoviriade* marked in green.

This tree formed the basis of all further classifications of genera along with VIRIDIC analysis, provided as individual attachments of PDFs.

Genera are differentiated by colored rings around the edge of the tree. Each genus will be detailed below.



A high definition tree is included that contains both accession numbers and proposed genus names. This is included as a PDF (tree3.pdf) and an SVG (Tree3.svg)

**Family**: *Straboviridae*

The family is named after the Greek philosopher Strabo.

Creation of the following genera: *Kagamiyamavirus, Angelvirus, Bragavirus, Mosugukvirus, Mylasvirus, Roskildevirus, Jiangsuvirus, Chrysonvirus, Cinqassovirus, Gaultarvirus, Carettavirus*

Across the entire family species were demarcated at 95% ANI as calculated by VIRIDIC. Genera were split based on phylogeny and 70% nucleotide identity across the genome as a starting point.

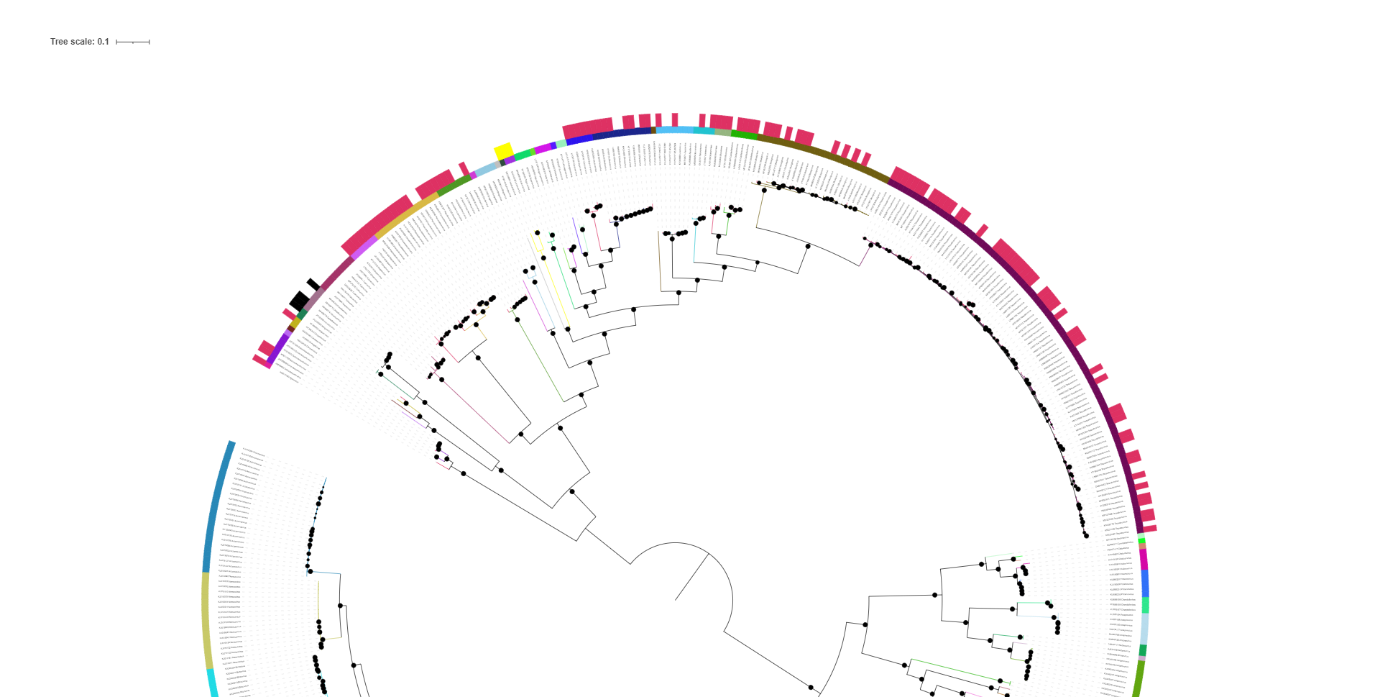
**Removal of genera from the Subfamily** *Tevenvirinae*

Currently there are three sub-families *Tevenvirinae*, *Emmerichvirinae* and *Twarogvirinae* that contain current genera that will be moved to the new family *Straboviridae*.

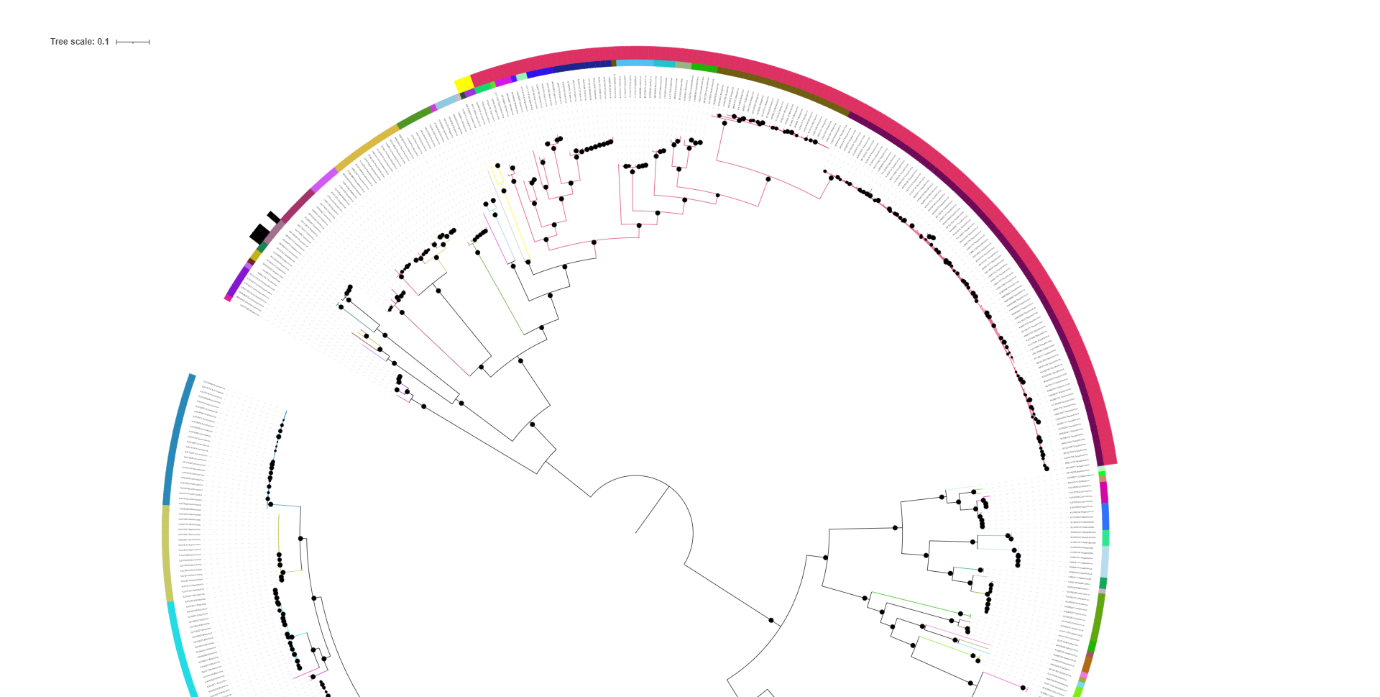
The subfamily *Emmerichvirinae* and *Twarogvirinae* are deep branching within the proposed new family (marked by black and yellow arrows on the image below) (see Subfamilies.svg for high resolution image).

The subfamily *Tevenvirinae* is no longer monophyletic and we propose moving the genera: *Schizotequatrovirus*, *Slopekvirus*, *Pseudotevenvirus, Krischvirus* out of the sub-family.

With the inclusion of the following genera *Tegunavirus, Kagamiyamavirus*, *Winklevirus*, *Mosugukvirus*, *Kanagawavirus*, *Roskildevirus* in the subfamily *Tevenvirinae.*



Phylogeny with current sub-families of *Tevenvirinae*, *Twarogvirinae* and *Emmerichvirinae* marked by the colours; pink, black and yellow respectively on the outer ring.



Removal of the genera *Schizotequatrovirus*, *Slopekvirus*, *Pseudotevenvirus*, *Krischvirus* from the sub-family *Tevenvirinae*. With the inclusion of the following genera *Tegunavirus, Kagamiyamavirus, Winklevirus, Mosugukvirus, Kanagawavirus , Roskildevirus* to make single monophyletic subfamily.

**Genus*: Carettavirus***

Create the genus *Carettavirus*, named after location of institute of isolation.

Create a single species *Carettavirus e142* within the genus

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Carettavirus* | *Carettavirus e142* | KU255730 | Escherichia phage phiE142 | 121442 |

Escherichia phage phiE142 [11]

**Genus: *Tequatrovirus***

To be consistent across both proposed families, species were demarcated at 95% identity as calculated by VIRIDIC. The output of this is attached in the file “Tequatrovirus\_VIRIDIC.pdf”.

All species names were updated to a binomial format

Table of new species in the genus Tequatrovirus

|  |  |  |  |
| --- | --- | --- | --- |
| Species | Accession Number | Exemplar virus name | Length |
| *Tequatrovirus kit03* | AP018932 | Escherichia phage KIT03 | 166848 |
| *Tequatrovirus RB51* | FJ839693 | Enterobacteria phage RB51 | 168394 |
| *Tequatrovirus vtec* | HM997020 | Escherichia phage wV7 | 166452 |
| *Tequatrovirus ecomufv133* | KU867876 | Escherichia phage vB\_EcoM-UFV13 | 165772 |
| *Tequatrovirus kpn1* | KX452694 | Escherichia phage KNP1 | 165831 |
| *Tequatrovirus knp5* | KX452698 | Shigella phage KNP5 | 193624 |
| *Tequatrovirus slur04* | LN881729 | Tequatrovirus slur04 | 167298 |
| *Tequatrovirus slur07* | LN881732 | Escherichia phage slur07 | 167124 |
| *Tequatrovirus fps90* | LR215723 | Yersinia phage fPS90 | 167132 |
| *Tequatrovirus ecomim339* | MH051915 | Enterobacteria phage EcoMIME339 | 164366 |
| *Tequatrovirus mlf4* | MH992121 | Escherichia MLF4 | 167379 |
| *Tequatrovirus fps65* | LR215724 | Yersinia phage fPS-65 | 167058 |

**Genus: *Roskildevirus***

Creation of one new species within the genus *Roskildevirus*.

Genus named after Roskilde, Denmark, where Erwinia phage Cronus was isolated at Aarhus University.

Table of new species in the genus Rosklidivirus

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession Number | Exemplar virus Name | Length |
| *Rosklidevirus* | *Roskildevirus cronus* | MH059636 | Erwinia phage Cronus | 175774 |

(No publication for exemplar phage)

**Genus: *Chrysonvirus***

Chyrsonvirus\_VIRIDIC.pdf

Move the species Aeromonas phage phiAS5 out of the subfamily *Tevenvirinae* and rename to a binomial.

Genus named after Chryson, a Greek sea spirit.

Table of new species in the genus *Chrysonvirus*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Chrysonvirus* | *Chrysonvirus as5* | HM452126 | Aeromonas phage phiAS5 | 225268 |

The exemplar virus Aeromonas phage phiAS5 was isolated in Nanjing, China. [12]

**Genus: *Angelvirus***

Create the new genus *Angelvirus* with a single species, based on VIRIDIC and phylogenetic analysis (Angelvirus\_VIRIDIC.pdf).

Rename current species to a binomial.

Genus named after Los Angeles, the city where Aeromonas phage PX29 was isolated, at Tulane University.

Table of new species in the genus *Angelvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Angelvirus* | *Angelvirus px29* | GU396103 | Aeromonas phage PX29 | 222006 |

Exemplar Aeromonas phage PX29 [13]

**Genus: *Schizotequatrovirus***

Move the genus *Schizotequatovirus* out of the subfamily *Tevenvirinae*.

Rename the existing species to binomials.

Table of new species in the *Schizotequatrovirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Schizotequatrovirus* | *Schizotequatrovirus* vh7d | KC131129 | Vibrio phage VH7D | 246964 |

Vibrio phage VH7D [14]

**Genus: *Mylasvirus***

Move phage Vibriophage nt1 (HQ317393) into a new genus *Mylasvirus*. Based on VIRIDIC (Mylasvirus\_VIRIDIC.pdf) analysis and phylogenetic analysis, it forms a separate group from the phages of the genus *Schizotequatrovirus*.

Renaming of the species to a bionomial.

Genus named after Mylas, a greek water spirit.

Table of new species in the genus *Mylasvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Mylavirus* | *Mylasvirus persius* | HQ317393 | Vibrio phage nt-1 | 247511 |

Vibrio phage nt-1 [15]

**Genus: *Cinqassovirus***

Based on phylogenetic analysis (above) move the phages into the new genus *Cinqassovirus* and rename to a binomial. Also supported by VIRIDIC analysis (Cinqassovirus\_VIRIDIC.pdf). Named cinq, as it was the 5th new genera to be identified within the new family

Table of new species in the genus *Cinqassovirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Cinqassovirus* | *Cinqassovirus ah1* | MG250483 | Aeromonas phage Ah1 | 221116 |
| *Cinqassovirus* | *Cinqassovirus aeh1* | AY266303 | Aeromonas virus Aeh1 | 233234 |

Aeromonas phage Ah1

Aeromonas virus Aeh1 [16]

**Genus*: Ishigurovirus***

Renaming of species to a binomial.

**Genus: *Ceceduovirus***

Renaming of species to a binomial.

**Genus: *Tulanevirus***

Creation of two new species based on VIRIDIC analysis (Tulanevirus\_VIRIDIC.pdf).

Renaming of species to a binomial.

Table of new species in the genus *Tulanevirus*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Tulanevirus* | *Tulanevirus 50ahydr13pp* | MH179476 | Aeromonas phage 50AhydR13PP | 164983 |
| *Tulanevirus* | *Tulanevirus 60ahydrpp* | MH179477 | Aeromonas phage 60AhydR15PP | 165795 |

Exemplar phages Aeromonas phage 50AhydR13PP and Aeromonas phage 60AhydR15PP [17].

**Genus: *Slopekvirus***

Create one new species within the genus *Slopekvirus*.

Table of new species in the genus *Slopekvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Slopekvirus* | *Slopekvirus pht4A* | KX130727 | Escherichia phage phT4A | 171598 |

Removal of the species Klebsiella phage Miro as > 95% similar to Klebsiella phage Matisse.

Removal of species Klebsiella phage PMBT1 as > 95% > Enterobacter phage phiEap-3.

Confirmed by VIRIDIC analysis Slopkevirus\_VIRIDIC.pdf

Escherichia phage phT4A [18]

**Genus: *Pseudotevenvirus***

Rename species to binomials.

**Genus: *Krischvirus***

Create one new species *Krischvirus kfsec.*

Based on VIRIDIC analysis (Krischviridic\_VIRIDIC.pdf).

Table of new species in the genus *Krischvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Krischvirus* | *Krischvirus kfsec* | MH560358 | Escherichia virus KFS-EC | 164715 |

Escherichia virus KFS-EC [24]

**Genus: *Gualtarvirus***

Create the new genus *Gualtarvirus,* named after Gualtar, taken form the address where the institute of isolation is situated.

One new species *Gualtarvirus mp1* with the exemplar phage vB\_MmoM\_MP1 , isolated from wastewater [2]

Table of new species in the genus *Gualtarvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Gualtarvirus* | *Gualtarvirus mp1* | KX078569 | Morganella phage vB\_MmoM\_MP1 | 164018 |

**Genus: *Bragavirus***

Genus named after Braga, where the institute of isolation of Proteus phage vB\_PmiM\_Pm5461, University of Minho, is situated.

Creation of the new genus *Bragavirus*, and 4 new species within this genus. Species were confirmed by VIRIDIC analysis (Bragavirus\_VIRIDIC.pdf)

Table of new species in the genus Bragavirus

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Bragavirus* | *Bragavirus pm5461* | KP890823 | Proteus phage vB\_PmiM\_Pm5461 | 161989 |
| *Bragavirus* | *Bragavirus pm2* | MF001355 | Proteus phage PM2 | 163469 |
| *Bragavirus* | *Bragavirus p43* | MG696114 | Proteus phage phiP4-3 | 167849 |

Exemplar phages:

Proteus phage vB\_PmiM\_Pm5461 (No publication)

Proteus phage PM2: (No publication)

Proteus phage phiP4-3 (No publication)

**Genus: *Hadassahvirus***

Renaming of two species to binomial.

**Genus: *Jiangsuvirus***

Creation of the genus *Jiangsuvirus* named after the location of the institute where the phage was isolated.

Create a single species *Jiangsuvirus pspyzu05* from the exemplar virus Pseudomonas phage PspYZU05 (No publication available)

Table of new species in the genus *Jiangsuvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Jiangsuvirus* | *Jiangsuvirus pspyzu05* | KP890823 | Pseudomonas phage PspYZU05 | 166442 |

**Genus: *Lazarusvirus***

Rename two species to binomials.

**Genus: *Tegunavirus***

Create one new species *Tegunavirus fheyen901*.

Rename binomials

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Tegunavirus* | *Tegunavirus fheyen901* | KY593455 | Yersinia phage fHe-Yen9-01 | 167773 |

Creation of a new species in the genus *Tegunavirus,* species *Tegunavirus* *fheyen90* (Tegunavirus\_VIRIDIC.pdf)

Yersinia phage fHe-Yen9-01 [25]

**Genus: *Kagamiyamavirus***

Creation of the genus *Kagamiyamavirus* with one new species, *Kagamiyamavirus ecs1* isolated from sewage samples [27]. Genus is named after the address of the institute of isolation (Kagamiyamvirus\_VIRIDIC.pdf)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Kagamiyamavirus* | *Kagamiyamavirus ecs1* | LC371242 | Escherichia phage EcS1 | 167773 |

**Genus*: Winklervirus***

Create one new species in this genus: *Winklervirus xtwenty.* (Winklevirus.VIRIDIC.pdf)

Rename current species to binomials

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Winklervirus* | *Winklervirus xtwenty* | MF036692 | Serratia phage X20 | 172450 |

Exemplar phage Serratia phage X20 [28].

**Genus:** ***Mosugukvirus***

Create the genus *Mosugukvirus* with one species *Mosugukvirus pm2*. Genus named after the ancient tribal name of Mosu- guk that later became Suwon, the area in Korea where the institute of isolation is located.

The exemplar phage Pectobacterium bacteriophage PM2 was isolated against Pectobacterium[4] (*Mosuguk*virus\_VIRIDIC.pdf)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Mosugukvirus* | *Mosugukvirus pm2* | |  | | --- | | KF835987 | | Pectobacterium bacteriophage PM2 | 170286 |

Pectobacterium bacteriophage PM2[29]

**Genus: *Kanagawavirus***

Rename species to binomials.

**Genus: *Gaprivervirus***

Rename species to binomials.

**Genus: *Dhakavirus***

Creation of four new species. See Dhakavirus\_VIRIDIC.pdf

Renamed current species to binomial

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Dhakavirus* | *Dhakavirus ime281* | MH051913 | Enterobacteria phage vB\_EcoM\_IME281 | 170531 |
| *Dhakavirus* | *Dhakavirus ime348* | MH051917 | Enterobacteria phage vB\_EcoM\_IME341 | 172379 |
| *Dhakavirus* | *Dhakavirus anyang* | MK234886 | Escherichia phage AnYang | 169215 |
| *Dhakavirus* | *Dhakavirus ecom005* | MK295203 | Escherichia phage vB\_EcoM\_005 | 155101 |

Enterobacteria phage vB\_EcoM\_IME281 [30]

Enterobacteria phage vB\_EcoM\_IME341 [30]

Escherichia phage AnYang (Not published)

Escherichia phage vB\_EcoM\_005 (not published)

**Genus: *Jiaodavirus***

Creation of four new species from VIRIDIC analysis (Jiadovirus\_VIRIDIC.pdf)

Rename to binomials

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Jiaodavirus* | *Jiaodavirus kpv477* | KX258185 | Klebsiella phage vB\_KpnM\_KpV477 | 168272 |
| *Jiaodavirus* | *Jiaodavirus kppv15* | KY000080 | Klebsiella phage KPV15 | 167034 |
| *Jiaodavirus* | *Jiaodavirus mineola* | MH333064 | Klebsiella phage Mineola | 166130 |
| *Jiaodavirus* | *Jiaodavirus s kp179* | MH729874 | Klebsiella phage KP179 | 162630 |

Klebsiella phage vB\_KpnM\_KpV477[31]

Klebsiella phage KPV15 [32]

Klebsiella phage Mineola [33]

Klebsiella phage KP179 No publication available

**Genus: *Karamvirus***

Creation of two new species and renaming to binomials (Karamvirus\_VIRIDIC.pdf).

The species *Karamvirus petcm34 and Karamvirus mypsh1140*.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Karamvirus* | *Karamvirus petcm34* | LT614807 | Cronobacter phage Pet-CM3-4 | 171975 |
| *Karamvirus* | *Karamvirus mypsh1140* | MG999954 | Enterobacter phage myPSH1140 | 172614 |

Cronobacter phage Pet-CM3-4: No publications associated with this phage

Enterobacter phage myPSH1140 [34]

**Genus*: Moonvirus***

Rename species to binomials.

**Genus: *Gelderlandvirus***

Create one new species *Gelderlandvirus cgg41* ((Gelderlandvirus\_VIRIDIC.pdf) with the exemplar phage Salmonella phage vB\_SnwM\_CGG4-1 [35].

Table of species within the genus Gelderlandvirus

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Gelderlandvirus* | *Gelderlandvirus cgg41* | KU867307 | Salmonella phage vB\_SnwM\_CGG4-1 | 159878 |

**Genus: *Mosigvirus***

***Abolish 2 species***

*Escherichia virus O157tp6 (*KP869104*) and Escherichia virus O157tp3* are >95% similar

Escherichia virus STO ( *MF044457)* >95% similar to Escherichia virus vB\_EcoM\_JS09 ( KF582788 )

Create five new species within the genus (Mosigvirus\_VIRIDIC.pdf)

Table of species within the genus *Mosigvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Mosigvirus* | *Mosigvirus atk47* | KT184309 | Enterobacteria phage ATK47 | 170020 |
| *Mosigvirus* | *Mosigvirus c120* | KY703222 | Escherichia phage phiC120 | 186570 |
| *Mosigvirus* | *Mosigvirus 25307* | MG589383 | Shigella phage phi25-307 | 167544 |
| *Mosigvirus* | *Mosigvirus sf* | MH359124 | Escherichia phage SF | 168695 |
| *Mosigvirus* | *Mosigvirus p000v* | MK047717 | Escherichia phage p000v | 167803 |

Enterobacteria phage ATK47 (No associated publication)

Escherichia phage phiC120 [36]

Shigella phage phi25-307 (No associated publication)

Escherichia phage SF (No associated publication)

Escherichia phage p000v [37]

**Family: *Kyanoviridae***

**Creation of the following genera**

*Alisovirus Sokavirus Bristolvirus Sedonavirus Ormenosvirus Chalconvirus Shandvirus Neritesvirus Makelovirus Emcearvirus Galenevirus Macariavirus Gibbetvirus Glaucusvirus Greenvirus Haifavirus Lowelvirus Lipsvirus*

Across the entire family species were demarcated at 95% ANI as calculated by VIRIDIC. Genera were split based on phylogeny and 70% nucleotide identity across the genome as recommended guidelines [1]

**Genus: *Sedonavirus***

Creation of one new species within the new genus *Sedonavirus* (Sedonavirus\_VIRIDIC.pdf). Genus named after city of Sedona.

Table of species within the genus *Sedonavirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Sedonavirus* | *Sedonavirus tusconh* | KF156338 | Synechococcus phage ACG-2014h | 189311 |

Synechococcus phage ACG-2014h [38]

**Genus: *Gibbetvirus***

New genus, *Gibbetvirus*, named after Gibbet Hill, Coventry, where Synechococcus phage S-RSM4 was isolated. Creation of one new species Gibbetvirus rms4 (Gibbetvirus\_VIRIDIC.pdf)

Table of species within the genus *Gibbetvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Gibbetvirus* | *Gibbetvirus rsm4* | FM207411 | Synechococcus phage S-RSM4 | 194454 |

Synechococcus phage S-RSM4[6]

**Genus: *Chalconvirus***

Creation of two new species within the new genus *Chalconvirus*. Genus named after Chalcon, a Greek water spirit.

Table of species within the genus *Chalconvirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Chalconvirus* | *Chalconvirus acg2014e* | KJ019054 | Synechococcus phage ACG-2014e | 189418 |
| *Chalconvirus* | *Chalconvirus acg2014i* | KJ019082 | Synechococcus phage ACG-2014i | 190768 |

Synechococcus phage ACG-2014e [38]

Synechococcus phage ACG-2014i [38]

**Genus: *Potamoivirus***

Create 2 new species within the genus *Potamoivirus.*

Table of species within the genus *Potamoivirus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Potamoivirus* | *Potamoivirus tusconj* | KJ019089 | Synechococcus phage ACG-2014j | 192108 |
| *Potamoivirus* | *Potamoivirus cam4* | KU686200 | Synechococcus phage S-CAM4 | 191937 |

Synechococcus phage ACG-2014j [38]

Synechococcus phage S-CAM4 [39]

**Genus: *Charybdisvirus***

Species renamed as binomial.

**Genus: *Nodenvirus***

Species renamed as binomial.

**Genus: *Bristolvirus***

Create single new species, *Bristolvirus rhodeisland* (Bristolvirus\_VIRIDIC.pdf)

Creation of new genus, *Bristolvirus*, named after Bristol, the city of isolation.

Table of species within the genus Bristolvirus

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Bristolvirus* | *Bristolvirus rhodeisland* | KU594606 | Cyanophage S-RIM32 | 194437 |

Cyanophage S-RIM32 [39]:

**Genus: *Vellamovirus***

Species renamed to binomials.

**Genus:*Lipsvirus***

Create new genus *Lipsvirus,* derived from the Greek god of the southwest wind

Create single new species *Liptusvirus ssm7*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Lipsvirus* | *Lipsvirus ssm7* | GU071098 | Synechococcus phage S-SSM7 | 232878 |

Synechococcus phage S-SSM7 [8]

**Genus: *Makelovirus***

Create new genus *Makelovirus*, named after Greek sea spirit.

Create single new species *Makelovirus prm1* [40]

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Makelovirus* | *Makelovirus prm1* | MH629685 | Synechococcus virus S-PRM1 | 144311 |

**Genus*:Kanaloavirus***

Rename species to binomial only

**Genus:*Haifavirus***

Creation of a new genus *Haifavirus* with a single new species.

Genus named after Haifa, city in Israel where the institute of isolation is located.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Haifavirus* | *Haifavirus tim68* | KM359505 | Prochlorococcus phage P-TIM68 | 197361 |

Exemplar phage Prochlorococcus phage P-TIM68 [41]

**Genus: *Bellamyvirus***

Rename species to binomial only.

**Genus:*Nilusvirus***

Creation of a new genus *Nilusvirus* with a single new species.

Genus named after the God of the River Nile of Greek mythology.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Nilusvirus* | *Nilusvirus ssm2* | GU071095 | Synechococcus phage S-SM2 | 190789 |

Synechococcus phage S-SM2 [8]

**Genus:*Atlauavirus***

Create three new species

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Atlauavirus* | *Atlauavirus synus* | KJ019085 | Synechococcus phage AC2014fSyn7803C8 | 222326 |
| *Atlauavirus* | *Atlauavirus zona* | KJ019086 | Synechococcus phage ACG-2014f isolate Syn7803US17 | 226849 |
| *Atlauavirus* | *Atlauavirus ari* | KJ019146 | Synechococcus phage ACG-2014f isolate Syn7803C16 | 225418 |

**Genus: *Sokavirus***

Creation of a new genus *Sokavirus* with a single new species.

Genus named after Soka University of America, the institute of isolation.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Sokavirus* | *Sokavirus swam1* | KU686210 | Synechococcus phage S-WAM1 | 185102 |

Synechococcus phage S-WAM1 [39]

**Genus:*Libanvirus***

Rename phage species to binomial

**Genus: *Glaucusvirus***

Create new genus *Glaucusvirus*, named after Glaucus, ancient Greek sea god.

Creation of the genus *Glaucusvirus* with one new species *Glaucusvirus ssm5*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Glaucusvirus* | *Glaucusvirus ssm5* | GU071097 | Synechococcus phage S-SSM5 | 176184 |

Synechococcus phage S-SSM5 [8]

**Genus: *Greenvirus***

*Creation of the genus Greenvirus with one new species Synechococcus phage S-SSM4.* Named after the colour green associated with colour of seawater

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Greenvirus* | *Greenvirus ssm4* | HQ316583 | Synechococcus phage S-SSM4 | 182368 |

Synechococcus phage S-SSM4 [42]

**Genus: *Leucotheavirus***

Rename to bionomials

**Genus: *Lowelvirus***

Creation of the genus *Lowelvirus*, named after location of University of isolation, with one new species *Lowelvirus tuscon4d*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Lowelvirus* | *Lowelvirus tuscon4d* | KJ019028 | Synechococcus phage ACG-2014d | 179116 |

Synechococcus phage ACG-2014d [43]

**Genus: *Macariavirus***

Creation of the genus *Macariavirus*, named after the Greek god Macaria, with one new species *Macariavirus tuscon14g*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Macariavirus* | *Macariavirus tuscon14g* | KJ019071 | Synechococcus phage ACG-2014g | 174885 |

Synechococcus phage ACG-2014g [38]

**Genus: *Mazuvirus***

Rename as binomial only

**Genus: *Namakavirus***

Rename Species as binomial only.

**Genus: *Neptunevirus***

Rename as binomial only

**Genus*: Nereusvirus***

Rename as binomial only

**Genus*: Neritesvirus***

Creation of the genus *Neritesvirus*, named after the ancient Greek sea spirit Nerites, and creation of one new species *Neritesvirus scam8*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Neritesvirus* | *Neritesvirus scam8* | HQ634178 | Synechococcus phage S-CAM8 | 171407 |

**Genus: *Nerrivikvirus***

Rename as bionomial

**Genus: *Nodensvirus***

Rename species to Binomial only.

**Genus: *Ormenosvirus***

Create a new genus *Ormenosvirus*, named after the ancient Greek sea spirit Ormenos. Create one new species *Ormenosvirus syn9.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Ormenosvirus* | *Ormenosvirus syn9* | DQ149023 | Synechococcus phage syn9 | 177300 |

Synechococcus phage syn9 [46]

**Genus: *Palaemonvirus***

Rename species to binomial only.

**Genus: *Pontusvirus***

Rename species to binomial only.

**Genus: *Salacisavirus***

Rename species as binomial only.

**Genus: *Ronodorvirus***

Rename species as binomial only.

**Genus: *Shandvirus***

Create two new species into the genus *Shandvirus.*

Genus is an abbreviation of the state they were isolated in.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Shandvirus* | *Shandvirus sh35* | KY945241 | Synechococcus phage S-H35 | 174231 |
| *Shandvirus* | *Shandvirus sb64* | MH107246 | Synechococcus phage S-B64 | 151867 |

S-H35: no reference for this phage

S-B64 [47]

**Genus: Tefnutvirus**

Rename species as binomial only.

**Genus: *Thaumasvirus***

Rename species as binomial only.

**Genus: *Thetisvirus***

Rename species as binomial only.

**Genus: *Acionnavirus***

Rename species as binomial only.

**Genus: *Ahtivirus***

Rename species as binomial only.

**Genus: *Alisovirus***

Create genus *Alisovirus*, named based on address of University of isolation.

Creates single new species Alisovirus socal22

Table of species of Alisovirus

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Alisovirus* | *Alisovirus socal22* | KU686207 | Synechococcus phage S-CAM22 | 172230 |

Synechococcus phage S-CAM22 [39]

**Genus: *Anaposvirus***

Rename species as binomial only.

**Genus: *Brizovirus***

Rename as binomials

Remove the species *Cyanophage S-RIM12 isolate W1\_08\_0910 ( KX349323)* as it > 95% similar based on VIRIDIC to Cyanophage S-RIM12 isolate RW\_06\_0310 (KX349313 ) (Brizovirus\_VIRIDIC.pdf)

**Genus: *Cymopoleiavirus***

Rename species as binomial only.

**Genus: *Emcearvirus***

Create genus *Emcearvirus*

Create a single species *Emcearvirus gerard.*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Emcearvirus* | *Emcearvirus gerard* | HQ634175 | Cyanophage P-RSM1 | 177211 |

**Genus: *Galenevirus***

Create new genus *Galenevirus*, named after the ancient Greek sea deity Galen.

Create and single new species, *Galenevirus mbcm1*, in the genus.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genus | Species | Accession | Exemplar virus name | Length |
| *Galenevirus* | *Galenevirus mbcm1* | JN371769 | Synechococcus phage metaG-MbCM1 | 172879 |

List of all updated species is attached as “species list.xls”

**References**

1. Turner D, Kropinski AM (2021) A Roadmap for Genome-Based Phage Taxonomy. 1–10

2. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC — A Novel Tool to Calculate the Intergenomic Similarities of. Viruses 12:1268

3. Nishimura Y, Yoshida T, Kuronishi M, et al (2017) ViPTree: The viral proteomic tree server. Bioinformatics. https://doi.org/10.1093/bioinformatics/btx157

4. Rohwer F, Edwards R (2002) The phage proteomic tree: A genome-based taxonomy for phage. J Bacteriol. https://doi.org/10.1128/JB.184.16.4529-4535.2002

5. Bin Jang H, Bolduc B, Zablocki O, et al (2019) Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. Nat Biotechnol. https://doi.org/10.1038/s41587-019-0100-8

6. Millard AD, Zwirglmaier K, Downey MJ, et al (2009) Comparative genomics of marine cyanomyoviruses reveals the widespread occurrence of *Synechococcus* host genes localized to a hyperplastic region: Implications for mechanisms of cyanophage evolution. Environ Microbiol 11:2370–2387. https://doi.org/10.1111/j.1462-2920.2009.01966.x

7. Ignacio-Espinoza JC, Sullivan MB (2012) Phylogenomics of T4 cyanophages: Lateral gene transfer in the “core” and origins of host genes. Environ Microbiol 14:2113–2126. https://doi.org/10.1111/j.1462-2920.2012.02704.x

8. Sullivan MB, Huang KH, Ignacio-Espinoza JC, et al (2010) Genomic analysis of oceanic cyanobacterial myoviruses compared with T4-like myoviruses from diverse hosts and environments. Environ Microbiol 12:3035–3056. https://doi.org/10.1111/j.1462-2920.2010.02280.x

9. Katoh K, Standley DM (2013) MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Mol Biol Evol 30:772–780. https://doi.org/10.1093/molbev/mst010

10. Nguyen L, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol 32:268–274. https://doi.org/10.1093/molbev/msu300

11. Amarillas L, Chaidez C, González-Robles A, León-Félix J (2016) Complete genome sequence of new bacteriophage phiE142, which causes simultaneously lysis of multidrug-resistant *Escherichia coli O157:H7* and *Salmonella enterica*. Stand Genomic Sci 11:89. https://doi.org/10.1186/s40793-016-0211-5

12. Liu J, Gao S, Dong Y, et al (2020) Isolation and characterization of bacteriophages against virulent Aeromonas hydrophila. BMC Microbiol 20:. https://doi.org/10.1186/s12866-020-01811-w

13. Petrov VM, Ratnayaka S, Nolan JM, et al (2010) Genomes of the T4-related bacteriophages as windows on microbial genome evolution. Virol. J. 7

14. Luo ZH, Yu YP, Jost G, et al (2015) Complete genome sequence of a giant Vibrio bacteriophage VH7D. Mar Genomics 24:. https://doi.org/10.1016/j.margen.2015.10.005

15. Comeau AM, Arbiol C, Krisch HM (2014) Composite conserved promoter-terminator motifs (PeSLs) that mediate modular shuffling in the diverse T4-like myoviruses. Genome Biol Evol 6:. https://doi.org/10.1093/gbe/evu129

16. Tetart F, Desplats C, Kutateladze M, et al (2001) Phylogeny of the major head and tail genes of the wide-ranging T4-type bacteriophages. J Bacteriol 183:. https://doi.org/10.1128/JB.183.1.358-366.2001

17. Kazimierczak J, Wójcik EA, Witaszewska J, et al (2019) Complete genome sequences of Aeromonas and Pseudomonas phages as a supportive tool for development of antibacterial treatment in aquaculture. Virol J 16:. https://doi.org/10.1186/s12985-018-1113-5

18. Pereira C, Moreirinha C, Lewicka M, et al (2017) Characterization and in vitro evaluation of new bacteriophages for the biocontrol of Escherichia coli. Virus Res 227:. https://doi.org/10.1016/j.virusres.2016.09.019

19. Abbasifar R, Kropinski AM, Sabour PM, et al (2012) Complete Genome Sequence of Cronobacter sakazakii Bacteriophage vB\_CsaM\_GAP161. J Virol 86:. https://doi.org/10.1128/jvi.02546-12

20. Kushkina AI, Tovkach FI, Comeau AM, et al (2013) Complete genome sequence of Escherichia phage Lw1, a new member of the RB43 group of pseudo T-even bacteriophages. Genome Announc 1:. https://doi.org/10.1128/genomeA.00743-13

21. Hwang K, Luna AJ, Hernandez AC, Kuty Everett GF (2015) Complete genome sequence of Citrobacter freundii myophage Miller. Genome Announc 3:. https://doi.org/10.1128/genomeA.01425-14

22. Oliveira H, Pinto G, Oliveira A, et al (2017) Characterization and genomic analyses of two newly isolated Morganella phages define distant members among Tevenvirinae and Autographivirinae subfamilies. Sci Rep 7:. https://doi.org/10.1038/srep46157

23. Endersen L, Buttimer C, Nevin E, et al (2017) Investigating the biocontrol and anti-biofilm potential of a three phage cocktail against Cronobacter sakazakii in different brands of infant formula. Int J Food Microbiol 253:. https://doi.org/10.1016/j.ijfoodmicro.2017.04.009

24. Lee C, Choi IY, Park DH, Park M-K (2020) Isolation and characterization of a novel Escherichia coli O157:H7-specific phage as a biocontrol agent. J Environ Heal Sci Eng 18:. https://doi.org/10.1007/s40201-020-00452-5

25. Jun JW, Park SC, Wicklund A, Skurnik M (2018) Bacteriophages reduce Yersinia enterocolitica contamination of food and kitchenware. Int J Food Microbiol 271:. https://doi.org/10.1016/j.ijfoodmicro.2018.02.007

26. Leon-Velarde CG, Happonen L, Pajunen M, et al (2016) Yersinia enterocolitica-specific infection by bacteriophages TG1 and φR1-RT is dependent on temperature-regulated expression of the phage host receptor OmpF. Appl Environ Microbiol 82:. https://doi.org/10.1128/AEM.01594-16

27. Saad AM, Askora A, Kawasaki T, et al (2018) Full genome sequence of a polyvalent bacteriophage infecting strains of Shigella, Salmonella, and Escherichia. Arch Virol 163:. https://doi.org/10.1007/s00705-018-3971-y

28. Chen B, Akusobi C, Fang X, Salmond GPC (2017) Environmental T4-family bacteriophages evolve to escape abortive infection via multiple routes in a bacterial host employing “altruistic suicide” through type III toxin-antitoxin systems. Front Microbiol 8:. https://doi.org/10.3389/fmicb.2017.01006

29. Lim JA, Lee DH, Heu S (2015) Isolation and genomic characterization of the T4-Like Bacteriophage PM2 Infecting Pectobacterium carotovorum subsp. carotovorum. Plant Pathol J 31:. https://doi.org/10.5423/PPJ.NT.09.2014.0099

30. Li P, Lin H, Mi Z, et al (2019) Screening of Polyvalent Phage-Resistant Escherichia coli Strains Based on Phage Receptor Analysis. Front Microbiol 10:1–14. https://doi.org/10.3389/fmicb.2019.00850

31. Komisarova E V., Kislichkina AA, Krasilnikova VM, et al (2017) Complete nucleotide sequence of Klebsiella pneumoniae bacteriophage vB\_KpnM\_KpV477. Genome Announc 5:. https://doi.org/10.1128/genomeA.00694-17

32. Aleshkin A, Ershova O, Volozhantsev N, et al (2016) Phagebiotics in treatment and prophylaxis of healthcareassociated infections. In: Bacteriophages: An Overview and Synthesis of a Re-Emerging Field

33. Boeckman JX, Lessor L, Gill JJ, Liu M (2019) Complete Genome Sequence of Klebsiella pneumoniae Myophage Mineola. Microbiol Resour Announc 8:. https://doi.org/10.1128/mra.00257-19

34. Manohar P, Tamhankar AJ, Lundborg CS, Nachimuthu R (2019) Therapeutic characterization and efficacy of bacteriophage cocktails infecting Escherichia coli, klebsiella pneumoniae, and enterobacter species. Front Microbiol 10:. https://doi.org/10.3389/fmicb.2019.00574

35. El-Dougdoug NK, Cucic S, Abdelhamid AG, et al (2019) Control of Salmonella Newport on cherry tomato using a cocktail of lytic bacteriophages. Int J Food Microbiol 293:. https://doi.org/10.1016/j.ijfoodmicro.2019.01.003

36. Amarillas L, Villicaña C, Lightbourn-Rojas L, et al (2021) The complete genome and comparative analysis of the phage phiC120 infecting multidrug-resistant Escherichia coli and Salmonella strains. G3 Genes, Genomes, Genet 11:. https://doi.org/10.1093/g3journal/jkab014

37. Howard-Varona C, Vik DR, Solonenko NE, et al (2018) Whole-Genome Sequences of Phages p000v and p000y, Which Infect the Bacterial Pathogen Shiga-Toxigenic Escherichia coli. Microbiol Resour Announc 7:. https://doi.org/10.1128/mra.01400-18

38. Deng L, Ignacio-Espinoza JC, Gregory AC, et al (2014) Viral tagging reveals discrete populations in Synechococcus viral genome sequence space. Nature 513:242–5. https://doi.org/10.1038/nature13459

39. Crummett LT, Puxty RJ, Weihe C, et al (2016) The genomic content and context of auxiliary metabolic genes in marine cyanomyoviruses. Virology 499:219–229. https://doi.org/10.1016/j.virol.2016.09.016

40. Chénard C, Kolundžija S, Lauro FM (2018) Complete genome sequence of the cyanophage S-PRM1 isolated from Singapore coastal waters. Mar Genomics 10–12. https://doi.org/10.1016/J.MARGEN.2018.08.005

41. Fridman S, Flores-Uribe J, Larom S, et al (2017) A myovirus encoding both photosystem I and II proteins enhances cyclic electron flow in infected Prochlorococcus cells. Nat Microbiol. https://doi.org/10.1038/s41564-017-0002-9

42. Kelly L, Ding H, Huang KH, et al (2013) Genetic diversity in cultured and wild marine cyanomyoviruses reveals phosphorus stress as a strong selective agent. ISME J 7:. https://doi.org/10.1038/ismej.2013.58

43. Gregory AC, Solonenko SA, Ignacio-Espinoza JC, et al (2016) Genomic differentiation among wild cyanophages despite widespread horizontal gene transfer. BMC Genomics 17:. https://doi.org/10.1186/s12864-016-3286-x

44. Marston MF, Pierciey FJ, Shepard A, et al (2012) Rapid diversification of coevolving marine Synechococcus and a virus. Proc Natl Acad Sci U S A 109:. https://doi.org/10.1073/pnas.1120310109

45. Marston MF, Martiny JBH (2016) Genomic diversification of marine cyanophages into stable ecotypes. Environ Microbiol 18:4240–4253. https://doi.org/10.1111/1462-2920.13556

46. Weigele PR, Pope WH, Pedulla ML, et al (2007) Genomic and structural analysis of Syn9, a cyanophage infecting marine Prochlorococcus and Synechococcus. Environ Microbiol 9:. https://doi.org/10.1111/j.1462-2920.2007.01285.x

47. You S, Wang M, Jiang Y, et al (2019) The Genome Sequence of a Novel Cyanophage S-B64 from the Yellow Sea, China. Curr Microbiol 76:. https://doi.org/10.1007/s00284-019-01680-1

48. Avrani S, Wurtzel O, Sharon I, et al (2011) Genomic island variability facilitates Prochlorococcus-virus coexistence. Nature 474:604–8. https://doi.org/10.1038/nature10172