This Word module should be used for all taxoSd1nomic 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:** | ***2019.100B*** |  |
| **Short title:** Create one new family (*Drexlerviridae*), three new subfamilies, and 12 new genera - an *in silico* taxonomic reassessment of the T1-like viruses |
|  |
| **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, Sullivan MB, Bishop-Lilly KA; Lueder MR, Bin Jang H, Adriaenssens EM | Phage.Canada@gmail.com; sullivan.948@osu.edu;kimberly.a.bishop-lilly.civ@mail.mil;matthew.r.lueder.ctr@mail.mil;jang.377@osu.edu; 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]Department of Microbiology, Ohio State University, Columbus, OH, USA [MBS, HBJ]Naval Medical Research Center-Frederick, USA [MRL, KAB-L] |

 |
| (The views expressed in this article reflect the results of research conducted by the author and do not necessarily reflect the official policy or position of the Department of the Navy, Department of Defense, nor the United States Government. This work was supported/funded by work unit number A1417.). This applies to MRL and KAB-L.**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)** |
| *Drexlerviridae* | Henry Drexler | Y |
| *Braunvirinae* | Volkmar Braun | 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:** 2019.100B.A.v2.Drexlerviridae\_1newfam.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. <https://ftp.ncbi.nlm.nih.gov/genomes/Viruses/FamilyPhylogeneticTree/>
2. Meier-Kolthoff JP, Göker M. VICTOR: genome-based phylogeny and classification

of prokaryotic viruses. Bioinformatics. 2017;33(21):3396-3404. <https://victor.dsmz.de> 1. Jang, H.B., Bolduc, B., Zablocki, O., Kuhn, J., Roux, S., Adriaenssens, E.M., Brister, J. R., Kropinski, A. M., Krupovic, M., Lavigne, R., Turner, D., Sullivan, M.B. 2019. Gene sharing networks to automate genome-based prokaryotic viral taxonomy. Nature Biotechnology. In Press.
2. Aiewsakun P, Simmonds P. The genomic underpinnings of eukaryotic virus

taxonomy: creating a sequence-based framework for family-level virusclassification. Microbiome. 2018;6(1):38.1. Aiewsakun P, Adriaenssens EM, Lavigne R, Kropinski AM, Simmonds P. Evaluation

of the genomic diversity of viruses infecting bacteria, archaea and eukaryotesusing a common bioinformatic platform: steps towards a unified taxonomy. J GenVirol. 2018;99(9):1331-1343.1. Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. Basic local alignment

search tool. J Mol Biol. 1990; 215(3):403-10.1. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment

of multiple genomes for determining phylogenomic distances and genetic signaturesunique for specified target groups. PLoS One. 2012; 7(6):e39107.1. Adriaenssens EM, Edwards R, Nash JHE, Mahadevan P, Seto D, Ackermann HW,

Lavigne R, Kropinski AM. Integration of genomic and proteomic analyses in theclassification of the *Siphoviridae* family. Virology. 2015; 477:144-154. 1. 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. BMCRes Notes. 2013; 6:140. 1. Lavigne R, Darius P, Summer EJ, Seto D, Mahadevan P, Nilsson AS, Ackermann HW, Kropinski AM. Classification of *Myoviridae* bacteriophages using protein sequence similarity. BMC Microbiol. 2009; 9:224.
2. Lavigne R, Seto D, Mahadevan P, Ackermann HW, Kropinski AM. Unifying classical and molecular taxonomic classification: analysis of the *Podoviridae* using

BLASTP-based tools. Res Microbiol. 2008; 159(5):406-14.  |

When originally proposed in 1996 the “T1-like phages” contained a single species *Enterobacteria phage T1*. Since that time numerous taxonomic changes have been introduced with the genus name changing to *T1likevirus* to *Tunalikevirus* to *T1virus* ultimately to *Tunavirus*. In 2015, the subfamily *Tunavirinae* was introduced consisting of five genera: *Kp36virus, Rogue1virus, Rtpvirus, T1virus* and *Tlsvirus.* In 2018, this subfamily contained an additional three genera: *Eclunavirus, Hanrivervirus* and *Sertoctavirus* and the *Rogue1virus, T1virus* and *Kp36virus* being renamed *Rogunavirus, Tunavirus* and *Webervirus*, respectively. In total 31 species have been classified. GenBank now contains the genomes of 84 T1-like phages rendering it imperative that their relationship be re-examined. “Hundreds of thousands of metagenome-derived viral genomes and large genome fragments (more than 700,000 at IMG/VR23) dwarf the 34,091 prokaryotic virus genomes present in the National Center for Biotechnology Information (NCBI)

GenBank database [In 2018: 1787 new caudoviral genomes were deposited; so far in 2019, 594 have appeared]. … evaluation of approaches to establish a scalable, genome-based viral taxonomy is needed to enable a universal classification framework.” [3] The number of complete phage genomes being deposited each year in GenBank has reached a point where the traditional taxonomic approaches employed by ICTV simply cannot keep up.

A number of automated system based predominantly on protein homology have been devised for automated viral classification. These include NCBI [1], DSMZ’s VICTOR [2], vConTACT2 [3], and GRAViTy [4,5]. For the past dozen years bacterial viruses have been grouped based upon overall DNA sequence homology determined using BLASTn at NCBI [6] or using Gegenees [7]. Overall protein homology was determined using tBLASTx in Gegenees of BLASTp using CoreGenes 3.5 [8-11]. From these studies, and associated TaxoProps we have noted phages which share ≥70% DNA sequence identity are members of the same genus. Overall protein similarity can be used to define higher taxa. The combination of total genome and total proteome analyses preclude the relevance of phylogenetic trees based upon single proteins.

BLASTn analysis currently lacks the scalability for analysis of large numbers of viral sequences. This has been overcome by Mathew Lueder who has developed a new approach. BLASTn was used with an e-value cut-off of 0.001 to create pairwise alignments between each pair of genomes in the taxon. The BLAST results were parsed and for each pairwise comparison, high-scoring segment pairs (HSPs) were split at locations of overlaps with other HSPs. This results in a larger set of HSPs which either do not overlap with any other HSP, or overlap with another HSP(s) for 100% of their length. After this, the set of non-overlapping HSPs which maximizes the number of total identities was determined. Percent identity is calculated by dividing the sum of identities in this set by the length of the larger genome in the pairwise comparison and multiplying the result by 100. The BLASTn analysis of the T1-like phages identified in GenBank is shown in Appendix A.

“vConTACT v.2.0, is a network-based application utilizing whole genome gene-sharing profiles for virus taxonomy that integrates distance-based hierarchical clustering and confidence scores for all taxonomic predictions. We report near-identical (96%) replication of existing genus-level

viral taxonomy assignments from the International Committee on Taxonomy of Viruses for National Center for Biotechnology Information virus RefSeq.” [3]

In this TaxoProp we have applied the new BLASTn approach of Lueder, and the protein clustering approach of Jang et al. [3] to a reanalysis of the T1-like phages which are currently clustered in the subfamily, *Tunavirinae*. This has resulted in this proposal to create a new family *Drexlerviridae*, named in honour of American phage T1 pioneering researcher Henry Drexler (b. 1927, r. 1991, Wake Forest University Medical Center, Winston-Salem, USA)

1. **Addition of new species to existing genera**

**Proposal 1:** To add eight new species to the *Tlsvirus* genus.

**vConTACT Cluster 1** – composed of two VCs (10\_0 and 10\_1). VC 10\_0 members: Citrobacter phages CF1 DK-2017, Stevie, & Sazh, Escherichia phages TLS & LL5; and Salmonella phages FSL SP-126, phSE-5 GJL01, YSP2, vB\_SenS\_PHB07, 36 and phSE-2.

VC 10\_1 consists of Escherichia phages vB\_Eco\_mar001J1, vB\_Eco\_mar001J1 strain vB\_Eco\_mar002J2, vB\_Eco\_swan01, SECphi27, vB\_EcoS-95, and Shigella phage pSf-1. BLASTn analysis reveals that the genome of the latter phage is sufficiently different from the others to remain the single representative of the *Hanrivervirus*.

In conformity with our state policy on “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.

**Table 1.** Properties of new phages belonging to the genus *Tlsvirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| TLS (type phage) | [NC\_009540.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_009540.1) | [AY308796.1](https://www.ncbi.nlm.nih.gov/nuccore/AY308796.1) | 49.90 | 42.7 | 87 |
| **NEW SPECIES** |  |  |  |  |  |
| Salmonella phage 36 [1] |  | KR296690.1 | 41.10 | 43.5 | 91 |
| Salmonella phage FSL SP-126 [2] |  | [KC139513.1](https://www.ncbi.nlm.nih.gov/nuccore/KC139513.1) | 51.09 | 42.9 | 83 |
| Salmonella phage vB\_ SenS\_ PHB07 |  | [MH102284.1](https://www.ncbi.nlm.nih.gov/nuccore/MH102284.1) | 51.82 | 43.4 | 87 |
| Salmonella phage YSP2 |  | [MG241338.1](https://www.ncbi.nlm.nih.gov/nuccore/MG241338.1) | 50.32 | 42.9 | 87 |
| Escherichia phage LL5 |  | [MH491968.1](https://www.ncbi.nlm.nih.gov/nuccore/MH491968.1) | 49.79 | 42.5 | 88 |
| Citrobacter phage CF1 DK-2017 |  | [KY694971.1](https://www.ncbi.nlm.nih.gov/nuccore/KY694971.1) | 50.34 | 42.6 | 87 |
| Salmonella phage phSE-2 | [NC\_031026.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031026.1) | [KX015770.1](https://www.ncbi.nlm.nih.gov/nuccore/KX015770.1) | 49.17 | 42.9 | 83 |
| Citrobacter phage Sazh |  | [MH729819.1](https://www.ncbi.nlm.nih.gov/nuccore/MH729819.1) | 49.67 | 42.8 | 87 |

1: Karpe YA, Kanade GD, Pingale KD, Arankalle VA, Banerjee K. Genomic characterization of Salmonella bacteriophages isolated from India. Virus Genes. 2016;52(1):117-26.

2: Moreno Switt AI, Orsi RH, den Bakker HC, Vongkamjan K, Altier C, Wiedmann M. Genomic characterization provides new insight into Salmonella phage diversity. BMC Genomics. 2013;14:481.

**Proposal 2:** To create eight new species in the genus *Tunavirus.*

**vConTACT** **Cluster 2:** represented by VC 11\_0 consists of Escherichia phages ADB-2, T1, JMPW2, JMPW1, vB\_EcoS\_SH2, vB\_EcoS\_IME18, vB\_EcoS\_IME167, and Eco\_BIFF; and, Shigella phage SH6, vB\_SsoS-ISF002, Sfin-1, vB\_SflS-ISF001, phi2457T, vB\_SsoS\_008, pSf-2 and Shfl1. BLASTn analysis clearly reveal this as a single genus: *Tunavirus.*

**Table 2.** Properties of new phages belonging to the genus *Tunavirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| T1 (type phage) | NC\_005833.1 |  AY216660.1 | 48.84 | 45.5 | 78 |
| **NEW SPECIES** |  |  |  |  |  |
| Shigella phage SH6 |  | [KX828710.1](https://www.ncbi.nlm.nih.gov/nuccore/KX828710.1) | 50.55 | 45.8 | 82 |
| Escherichia phage Eco\_BIFF |  | [MH285980.1](https://www.ncbi.nlm.nih.gov/nuccore/MH285980.1) | 49.37 | 45.3 | 76 |
| Shigella phage vB\_SsoS-ISF002 [1] |  | [MF093736.1](https://www.ncbi.nlm.nih.gov/nuccore/MF093736.1) | 50.56 | 45.5 | 76 |
| Shigella phage vB\_SflS-ISF001 |  | [MG049919.1](https://www.ncbi.nlm.nih.gov/nuccore/MG049919.1) | 50.55 | 45.6 | 78 |
| Shigella phage vB\_SsoS\_008 |  | [MK335533.1](https://www.ncbi.nlm.nih.gov/nuccore/MK335533.1) | 50.41 | 45.7 | 83 |
| Shigella phage Sfin-1 |  | [MF468274.1](https://www.ncbi.nlm.nih.gov/nuccore/MF468274.1) | 50.4 | 45.2 | 81 |
| Enterobacteria phage vB\_EcoS\_IME18 |  | [MH051911.1](https://www.ncbi.nlm.nih.gov/nuccore/MH051911.1) | 50.35 | 45.6 | 82 |
| Escherichia phage vB\_EcoS\_SH2 |  | [KY985004.1](https://www.ncbi.nlm.nih.gov/nuccore/KY985004.1) | 49.09 | 45.5 | 80 |

1: Shahin K, Bouzari M, Wang R. Isolation, characterization and genomic analysis of a novel lytic bacteriophage vB\_SsoS-ISF002 infecting Shigella sonnei and Shigella flexneri. J Med Microbiol. 2018;67(3):376-386.

**Proposal 3:** To create twelve new species in the genus *Webervirus.*

**vConTACT** **Cluster 3:** represented by VC 12\_0 consists of Enterobacter phage F20; and, Klebsiella phages 1513, KLPN1, KP36, PKP126, Sushi, vB\_KpnS\_KpV522, KOX1, KPN N141, MezzoGao, GML-KpCol1, JY917, NJS1, TAH8, NJS2, NJS3, NJR15, TSK1, GH-K3, and KpKT21phi1. These are all members of the *Webervirus* genus.

**Table 3.** Properties of new phages belonging to the genus *Webervirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| KP36 (type phage) | NC\_029099.1 |  JF501022.1 | 49.8 | 50.7 | 79 |
| **NEW SPECIES** |  |  |  |  |  |
| Klebsiella phage vB\_KpnS\_KpV522 |  | [KX237515.1](https://www.ncbi.nlm.nih.gov/nuccore/KX237515.1) | 51.1 | 50.8 | 79 |
| Klebsiella phage KOX1 |  | [KY780482.1](https://www.ncbi.nlm.nih.gov/nuccore/KY780482.1) | 50.53 | 51.2 | 81 |
| Klebsiella phage TSK1 |  | [MH688453.1](https://www.ncbi.nlm.nih.gov/nuccore/MH688453.1) | 49.86 | 50.5 | 74 |
| Klebsiella phage NJS1 |  | [MH445453.1](https://www.ncbi.nlm.nih.gov/nuccore/MH445453.1) | 49.29 | 50.7 | 71 |
| Klebsiella phage NJS2 |  | [MH633485.1](https://www.ncbi.nlm.nih.gov/nuccore/MH633485.1) | 50.13 | 50.8 | 79 |
| Klebsiella phage TAH8 |  | [MH633484.1](https://www.ncbi.nlm.nih.gov/nuccore/MH633484.1) | 49.34 | 51.1 | 76 |
| Klebsiella phage NJR15 |  | [MH633487.1](https://www.ncbi.nlm.nih.gov/nuccore/MH633487.1) | 49.47 | 51.0 | 75 |
| Klebsiella phage MezzoGao |  | [MF612072.1](https://www.ncbi.nlm.nih.gov/nuccore/MF612072.1) | 49.81 | 51.0 | 76 |
| Klebsiella virus GML-KpCol1 |  | [MG552615.1](https://www.ncbi.nlm.nih.gov/nuccore/MG552615.1) | 50.25 | 51.0 | 78 |
| Klebsiella phage KPN N141 |  | [MF415412.1](https://www.ncbi.nlm.nih.gov/nuccore/MF415412.1) | 49.09 | 51.0 | 76 |
| Klebsiella phage KpKT21phi1 |  | [MK278861.1](https://www.ncbi.nlm.nih.gov/nuccore/MK278861.1) | 49.11 | 50.9 | 76 |
| Klebsiella phage GH-K3 |  | [MH844531.1](https://www.ncbi.nlm.nih.gov/nuccore/MH844531.1) | 49.43 | 50.2 | 77 |

**Proposal 4:** To add one new species to the genus *Rogunavirus*

*Rogunavirus* – consists currently of Escherichia phages e4/1c, vB\_EcoS\_AHS24, vB\_EcoS\_AHP24, vB\_EcoS\_AKS96, vB\_EcoS\_AHP42, phiJLA23, C119, phiKP26, vB\_EcoS\_Rogue1 and Jk06.

**Table 4.** Properties of a new phage belonging to the genus *Rogunavirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| vB\_EcoS\_Rogue1 (type phage) | [NC\_019718.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019718.1) | [JQ182736.1](https://www.ncbi.nlm.nih.gov/nuccore/JQ182736.1) | 45.81 | 44.2 | 74 | 1 |
| **NEW SPECIES** |  |  |  |  |  |  |
| Enterobacteria phage phiJLA23 |  | [KC333879.1](https://www.ncbi.nlm.nih.gov/nuccore/KC333879.1) | 43.02 | 44.5 | 65 | 1\* |

**\* Not indicated in GenBank file; found using tRNAscan-SE 2.0**

**Proposal 5:** To add a new phage species to the genus *Rtpvirus*.

*Rtpvirus* – only consists currently of Escherichia phages RTP and vB\_EcoS-IME253.

**Table 5.** Properties of two phages which belong to the genus *Rtpvirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| RTP (type phage) | [NC\_007603.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_007603.1) | [AM156909.1](https://www.ncbi.nlm.nih.gov/nuccore/AM156909.1) | 46.22 | 44.3 | 75 |
| **NEW SPECIES** |  |  |  |  |  |
| Enterobacteria phage vB\_EcoS-IME253 |  | [MK372342.1](https://www.ncbi.nlm.nih.gov/nuccore/MK372342.1) | 46.55 | 43.6 | 71 |

**B. To create new genera of T1-like phages based upon overall DNA and protein relatedness**

**Proposal 6:** To create a new genus containing five species with the name *Warwickvirus*. This genus is named in honour of the UK University where the first representative was isolated.

**Table 6.** Properties of phages belonging to the genus Warwickvirus

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| Escherichia phage vB\_Eco\_swan01 |  | [LT841304.1](https://www.ncbi.nlm.nih.gov/nuccore/LT841304.1) | 50.87 | 44.7 | 83 |
| Escherichia phage vB\_EcoS-95 |  | [MF564201.1](https://www.ncbi.nlm.nih.gov/nuccore/MF564201.1) | 50.91 | 44.8 | 89 |
| Escherichia phage SECphi27 |  | [LT961732.1](https://www.ncbi.nlm.nih.gov/nuccore/LT961732.1) | 51.81 | 44.7 | Not annotated |
| Escherichia virus vB\_Eco\_mar001J1 |  | LR027388 | 50.34 | 44.4 | 78 |
| Escherichia virus vB\_Eco\_mar001J1 strain vB\_Eco\_mar002J2 |  |  LR027385 | 50.34 | 44.4 | 79 |

**Proposal 7:** To create a new genus containing five species with the name *Loudonvirus*

*Loudonvirus* – contains a single species Escherichia phage DTL and is named after the town in Tennessee (USA) where this virus was first identified by DuPont Tate & Lyle BioProducts.

**Table 7.** Properties of the single phage which belongs to the genus *Loudonvirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| Escherichia phage DTL |  | [MG050172.1](https://www.ncbi.nlm.nih.gov/nuccore/MG050172.1) | 45.81 | 44.3 | 60 |

**Proposal 8:** To create a new genus containing five species with the name *Christensenvirus*

*Christensenvirus* – contains Escherichia phage vB\_EcoS\_IME542 and is named in honour of James Roger Christensen (b. 1925, d. 2014; Past Chair of Microbiology and Immunology, University of Rochester, NY, USA) who was Henry Drexler’s PhD supervisor.

**Table 8.** Properties of the single phage which belongs to the genus *Christensenvirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| Escherichia phage vB\_EcoS\_IME542 |  | [MK372342.1](https://www.ncbi.nlm.nih.gov/nuccore/MK372342.1) | 46.55 | 43.6 | 71 |

**Proposal 9:** To create a new genus containing five species with the name *Guelphvirus*

*Guelphvirus* – consists of Escherichia phages vB\_EcoS\_ACG-M12 and vB\_Ecos\_CEB\_EC3a and named after the city in Canada where this virus was isolated.

**Table 9.** Properties of the two phages belonging to the genus *Guelphvirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Escherichia phage vB\_EcoS\_ACG-M12 | [NC\_019404.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019404.1) | [JN986845.1](https://www.ncbi.nlm.nih.gov/nuccore/JN986845.1) | 46.05 | 43.5 | 78 | 1 |
| Escherichia phage vB\_Ecos\_CEB\_EC3a |  | [KY398841.1](https://www.ncbi.nlm.nih.gov/nuccore/KY398841.1) | 44.23 | 44.2 | 70 | 1 |

**Proposal 10:** To create a new genus containing five species with the name *Eastlansingvirus*

*Eastlansingvirus –* consists of Shigella phage Sf12, and named after the city in Michigan (USA) where this virus was isolated.

**Table 10.** Properties of the single phage which belongs to the genus *Eastlansingvirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Shigella phage Sf12 |  | [MF158039.1](https://www.ncbi.nlm.nih.gov/nuccore/MF158039.1) | 47.65 | 44.3 | 74 | 1 |

**Proposal 11:** To create a new genus containing five species with the name *Wilsonroadvirus*

*Wilsonroadvirus* – consists of Shigella phage Sd1, named after the location of the Biochemistry and Molecular Biology Department, Michigan State University, where this virus was first isolated.

**Table 11.** Properties of the single phage which belongs to the genus *Wilsonroadvirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Shigella phage Sd1 |  | [MF158042.1](https://www.ncbi.nlm.nih.gov/nuccore/MF158042.1) | 48.26 | 44.5 | 73 | 2 |

**Proposal 12:** To create a new genus containing five species with the name *Lindendrivevirus*

*Lindendrivevirus* – consisting of Escherichia phage phiEB49 and named after the street which houses the Department of Medical Microbiology and Immunology, University of Wisconsin where this virus was isolated.

**Table 12.** Properties on phages belonging to the genus *Lindendrivevirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Escherichia phage phiEB49 [1] | [NC\_023743.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023743.1) | [JF770475.1](https://www.ncbi.nlm.nih.gov/nuccore/JF770475.1) | 47.18 | 44.0 | 74 | 2 |

1: Battaglioli EJ, Baisa GA, Weeks AE, Schroll RA, Hryckowian AJ, Welch RA. Isolation of generalized transducing bacteriophages for uropathogenic strains of Escherichia coli. Appl Environ Microbiol. 2011; 77(18):6630-5.

**Proposal 13:** To create a new genus, *Badaguanvirus*, containing a single species.

*Badaguanvirus* – consisting of Escherichia phage vB\_EcoS\_IME347 and named after the district where College of Food Science and Engineering, Ocean University of China is located and where this virus was isolated.

**Table 13.** Properties on phages belonging to the genus *Badaguanvirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Escherichia phage vB\_EcoS\_IME347 |  | [MH051918.1](https://www.ncbi.nlm.nih.gov/nuccore/MH051918.1) | 50.05 | 49.7 | 87 | 0 |

**Proposal 14:** To create a new genus containing five species with the name *Gyeonggidovirus*

To create a new genus *Gyeonggidovirus* to contain two Cronobacter phages (ESP2949-1 & CS01). The genus is named after the province in South Korea where Cronobacter phage ESP2949-1 was isolated. **vConTACT** **Cluster 5:** represented by VC Outlier Unrepresented cluster

**Table 14.** Properties on phages belonging to the genus *Gyeonggidovirus*

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins |
| Cronobacter phage ESP2949-1 [2] | [NC\_019509.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_019509.1) | [JF912400.1](https://www.ncbi.nlm.nih.gov/nuccore/JF912400.1) | 49.12 | 50.1 | 45 |
| Cronobacter phage PhiCS01 [1] |  | [MH845412.1](https://www.ncbi.nlm.nih.gov/nuccore/MH845412.1) | 48.2 | 50.1 | 75 |

1: Kim GH, Kim J, Kim KH, Lee JS, Lee NG, Lim TH, Yoon SS. Characterization and Genomic Analysis of Novel Bacteriophage ΦCS01 Targeting Cronobacter sakazakii. J Microbiol Biotechnol. 2019 Apr 12. doi: 10.4014/jmb.1812.12054.

2: Lee YD, Kim JY, Park JH, Chang H. Genomic analysis of bacteriophage ESP2949-1, which is virulent for Cronobacter sakazakii. Arch Virol. 2012;157(1):199-202.

**Proposal 15:** To create a new genus, *Vilniusvirus*, containing a single species.

*Vilniusvirus* – consisting of Escherichia phage vB\_EcoS\_NBD2 and named after the capital of Lithuania where it was isolated in the Department of Molecular Microbiology and Biotechnology, Institute of Biochemistry, Vilnius University, Lithuania.

**Table 15.** Properties on phages belonging to the genus *Vilniusvirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Escherichia phage vB\_EcoS\_NBD2 | [NC\_031050.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031050.1) | [KX130668.1](https://www.ncbi.nlm.nih.gov/nuccore/KX130668.1) | 51.8 | 49.8 | 87 | 1 |

**Proposal 16:** To create a new genus, *Nouzillyvirus*, containing a single species.

*Nouzillyvirus* – consisting of Escherichia phage vB\_EcoS\_ESCO41 and named after the city in France where it was isolated at the Université Francois Rabelais de Tours.

**Table 16.** Properties on phages belonging to the genus *Nouzillyvirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Escherichia phage vB\_EcoS\_ESCO41 |  | [KY619305.1](https://www.ncbi.nlm.nih.gov/nuccore/KY619305.1) | 50.8 | 46.1 | 79 | 1 |

**Proposal 17:** To create a new genus, *S**auletekiovirus*, containing a single species.

*Sauletekiovirus* – consisting of Pantoea phage vB\_PagS\_AAS23 and named after the street in Vilnius, Lithuania, where the Department of Molecular Microbiology and Biotechnology, Vilnius University, Life Sciences Centre, Institute of Biochemistry is located and where this virus was isolated.

**Table 17.** Properties on phages belonging to the genus S*auletekiovirus*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. Proteins | tRNA |
| Pantoea phage vB\_PagS\_AAS23 |  | [MK095606.1](https://www.ncbi.nlm.nih.gov/nuccore/MK095606.1) | 51.17 | 47.6 | 92 | 0 |

1. **To redefine membership in the *Tunavirinae*

Proposal 18:** On the basis of DNA sequence similarity the subfamily *Tunavirinae* to include only three genera: *Tunavirus, Badaguanvirus* and *Seroctavirus*

**D. To create a new subfamily of T1-like phages, *Tempevirinae*.

Proposal 19:** On the basis of shared proteins and DNA sequence similarity to create a new subfamily, *Tempevirinae*, consisting of *Tlsvirus, Hanrivervirus* and *Warwickvirus.* This subfamily was named in honour of The University of Arizona Tempe Campus where Rajeev Misra first isolated phage TLS.

**vConTACT** **Cluster 4:** represented by VC 9\_0 consists of Escherichia phages Jk06, vB\_EcoS\_Rogue1, e4/1c, EB49, vB\_Eco\_ACG-M12, vB\_EcoS\_AHP42, vB\_EcoS\_AHS24, vB\_EcoS\_AHP24, C119, vB\_EcoS-IME253, RTP, vB\_Ecos\_CEB\_EC3a, vB\_EcoS\_IME542 and Shigella phages Sf12, Sd1, and

DTL. Based upon BLASTn analysis we now recognize eight genera:

1. **To create a new subfamily of T1-like phages, *Rogunavirinae*.**

**Proposal 20:** On the basis of DNA sequence similarity the subfamily *Rogunavirinae* consists of the genera *Rogunavirus, Eastlansingvirus, Wilsonroadvirus* and *Lindendrivevirus*.

1. **To create a new subfamily of T1-like phages, *Braunvirinae*.**

**Proposal 21:** On the basis of DNA sequence similarity the subfamily *Braunvirinae* consists of the genera *Rtpvirus, Shandongvirus, Loudonvirus* and *Guelphvirus.* This genus is named in honour of Prof. Dr. Volkmar Braun (1938 -) - Professor for Microbiology at the University of Tuebingen, and Max Planck Institute for Developmental Biology; in whose laboratory phage RTP was isolated.

**Appendix A.** BLASTn analysis of the T1-like phages identified in GenBank.

**Appendix B.** vConTACT 2.0 analysis of the T1-like phages.