

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

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| **Code assigned:** | **2020.133B** |  |
| **Short title:** Create one new subfamily (*Rhodovirinae*) including seven genera (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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

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| N4-like phages Study Group, Bacterial and Archaeal Viruses Subcommittee |

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

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

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

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| --- | --- |
| Date first submitted to SC Chair | July 2020 |
| Date of this revision (if different to above) |  |

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

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

**Name of accompanying Excel module**

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| 2020.146B.R.Schitoviridae.xlsx |

**Abstract**

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| Here, we propose the creation of the new subfamily *Rhodovirinae* including the existing genus *Baltimorevirus* and six new genera *Plymouthvirus* (1 species), *Sanyabayvirus* (1 species), *Pomeroyivirus* (1 species), *Aoqinvirus* (1 species), *Raunefjordenvirus* (1 species) and *Aorunvirus* (2 species), based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analysises of terminase and vRNA polymerase protein sequences. All of those bacteriophages infect members of the *Rhodobacteraceae*. |

**Text of proposal**

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| --- | --- |
| |  | | --- | | **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 | |

**Supporting evidence**

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [1]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [2]. The *Herelleviridae* root marked with **red arrowhead**; other arrowheads indicate subfamilies to be created.





**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>) computes pairwise intergenomic distances/similarities amongst phage genomes. The black box delineates strains. Column 2 - (P) partial genome. The colour codes in columns 3 and 4 indicate the boundaries of the proposed subfamilies and genera. The subfamily *Rhodovirinae* is indicated in black (col3).



**Phylogenetic analysis** using the (A) terminase and (B) vRNA polymerase protein sequences of N4-like phages. The amino acid sequences were compared using MUSCLE with MEGA7 [4]. The tree was constructed using the maximum likelihood algorithm. The percentages of replicate trees were assessed with the bootstrap test (100).

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B

A

**Proposal 1: To include the genus *Baltimorevirus***

**History:** Currently the genus *Baltimorevirus* contains a single species *Dinoroseobacter virus DFL12* and was created through TaxoProp 2018.007B.

**Specific Reference:** NA

**GenBank Summary:** NA

**Proposal 2: To create a new genus, *Plymouthvirus,* with one species**

**Source of the name of this taxon:** This genus is named after Roseovarius Plymouth Podovirus 1

**History: “**Two lytic phages RLP1 and RPP1, infecting two strains of Roseovarius were isolated from seawater collected from Langstone Harbour, Hampshire, UK and from water collected from station L4 in the English Channel, respectively. The phages were named using the nomenclature suggested by Kropinski et al. (2009); vB\_Rsv217\_RLP1 (RLP1, Roseovarius Langstone Podovirus) which infects Roseovarius (Rsv.) 217 and vB\_RsvN\_RPP1 (RPP1, Roseovarius Plymouth Podovirus) which infects Rsv. nubinhibens. RLP1 and RPP1 had capsid head sizes of 72.4 ± 2 and 77.4 ± 5 nm respectively.” [Chan JZ et al. 2014]. Both phage genomes are described as partial.

**Specific Reference:** Chan JZ, Millard AD, Mann NH, Schäfer H. Comparative genomics defines the core genome of the growing N4-like phage genus and identifies N4-like Roseophage specific genes. Front Microbiol. 2014;5:506. Published 2014 Oct 10. doi:10.3389/fmicb.2014.00506

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Roseovarius Plymouth Podovirus 1 | [FR719956.1](https://www.ncbi.nlm.nih.gov/nuccore/FR719956.1) | 74.7 | 49.1 | [91](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/84641/697051|Roseovarius Plymouth podovirus 1/viral segment/) | 3 |

**N.B. Roseovarius sp. 217 phage 1 should be considered a strain in this genus**

**Electron micrograph:** None available

**Proposal 3: To create a new genus, *Sanyabayvirus,* with one species**

**Source of the name of this taxon:** This genus is named after Sanya Bay, northern South China Sea where the first virus of this type was isolated.

**History: “**Bacteriophages RD-1410Ws-07, and DS-1410Ws-06 were isolated from the surface water of Sanya Bay, northern South China Sea, on two marine bacteria type strains of the Roseobacter lineage. These phages have an isometric head and a short tail, morphologically belonging to the *Podoviridae* family.” [Li B et al. 2016]

**Specific Reference:** Li B, Zhang S, Long L, Huang S. Characterization and Complete Genome Sequences of Three N4-Like Roseobacter Phages Isolated from the South China Sea. Curr Microbiol. 2016;73(3):409-418. doi:10.1007/s00284-016-1071-3

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Dinoroseobacter phage DS-1410Ws-06 | [KU885988.1](https://www.ncbi.nlm.nih.gov/nuccore/KU885988.1) | 76.47 | 50.0 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71768/399635|Dinoroseobacter phage DS-1410Ws-06/viral segment/) | 0 |

**N.B. Roseobacter phage RD-1410Ws-07 is a strain in this genus**

**Electron micrograph:** None available

**Proposal 4: To create a new genus, *Pomeroyivirus,* with one species**

**Source of the name of this taxon:** This genus is named after the host bacterium

**History:** This lytic phage was isolated from water from Baltimore inner harbour using Ruegeria pomeroyi DSS-3 as the host bacterium.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Ruegeria phage vB\_RpoP-V13 | [MH015256.1](https://www.ncbi.nlm.nih.gov/nuccore/MH015256.1) | 74.83 | 50.8 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70933/388840|Ruegeria phage vB_RpoP-V13/viral segment/) | 4(\*) |

**(\*) None indicated in the Replicon Info. These found u****sing tRNAscan-SE at http://lowelab.ucsc.edu/tRNAscan-SE/ [6]**

**Electron micrograph:** None available

**Proposal 5: To create a new genus, *Aoqinvirus,* with one species**

**Source of the name of this taxon:** This genus is named after Ao Qin, the Dragon King of the Southern Sea.

**History: Lytic** bacteriophage RD-1410W1-01 was isolated from the surface water of Sanya Bay, northern South China Sea, on marine Roseobacter denitrificans OCh114. This phage has an isometric head (63.2 ± 1.6 nm) and a short tail (40 ± 3.7 nm), morphologically belonging to the Podoviridae family. [Li B et al. 2016]

**Specific Reference:** Li B, Zhang S, Long L, Huang S. Characterization and Complete Genome Sequences of Three N4-Like Roseobacter Phages Isolated from the South China Sea. Curr Microbiol. 2016;73(3):409-418. doi:10.1007/s00284-016-1071-3

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Roseobacter phage RD-1410W1-01 | [KU885989.1](https://www.ncbi.nlm.nih.gov/nuccore/KU885989.1) | 72.67 | 49.5 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71771/399638|Roseobacter phage RD-1410W1-01/viral segment/) | 0 |

**Electron micrograph:** None available

**Proposal 6: To create a new genus, *Raunefjordenvirus,* with one species**

**Source of the name of this taxon:** This genus is named after Raunefjorden, Norway where the first virus of its type was isolated.

**History:** Lytic phage ΦCB2047-B was isolated from a mesocosm study in Raunefjorden, Norway, using standard virus enrichment and plaque assay techniques. “Unlike other N4-like phages, ΦCB2047-B contains a deoxycytidine triphosphate (dCTP) deaminase instead of a deoxycytidine monophosphate deaminase, indicating a preference for an alternative route for the generation of dUMP for thymidine biosynthesis.” [Ankrah NY et al. 2014]

**Specific Reference:** Ankrah NY, Budinoff CR, Wilson WH, Wilhelm SW, Buchan A. Genome Sequence of the Sulfitobacter sp. Strain 2047-Infecting Lytic Phage {Phi}CB2047-B. Genome Announc. 2014;2(1):e00945-13. Published 2014 Jan 16. doi:10.1128/genomeA.00945-13

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Sulfitobacter phage phiCB2047-B | [NC\_020862.2](https://www.ncbi.nlm.nih.gov/nuccore/NC_020862.2) | [HQ317387.2](https://www.ncbi.nlm.nih.gov/nuccore/HQ317387.2) | 74.49 | 43.0 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/3875/455847|Sulfitobacter phage phiCB2047-B/viral segment Unknown/) | 15 |

**Electron micrograph:** None available

**Proposal 7: To create a new genus, *Aorunvirus,* with two species**

**Source of the name of this taxon:** This genus is named after Ao Run, the Dragon King of the Western Sea.

**History:** Two lytic bacteriophages, DSS3Phi2 and EE36Phi1, which infect marine roseobacters Silicibacter pomeroyi DSS-3 and Sulfitobacter sp. EE-36, respectively, were isolated from Baltimore Inner Harbor water.[Zhao Y et al.2009] The other phages were isolated from the same source on Ruegeria pomeroyi DSS-3.

**Specific Reference:** Zhao Y, Wang K, Jiao N, Chen F. Genome sequences of two novel phages infecting marine roseobacters. Environ Microbiol. 2009;11(8):2055-2064. doi:10.1111/j.1462-2920.2009.01927.x

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | % DNA sequence identity (\*\*) | % Common proteins (\*\*\*) |
| Sulfitobacter phage EE36phi1 (=Roseophage EE36P1) | [NC\_012696.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_012696.1) | [FJ591094.1](https://www.ncbi.nlm.nih.gov/nuccore/FJ591094.1) | 73.33 | 47.0 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/6468/459147|Sulfitobacter phage EE36phi1/viral segment Unknown/) | 3(\*) | 100 | 100 |
| Ruegeria phage vB\_RpoP-V12 |  | [MH015250.1](https://www.ncbi.nlm.nih.gov/nuccore/MH015250.1) | 74.68 | 47.9 | [85](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/70927/388834|Ruegeria phage vB_RpoP-V12/viral segment/) | 3 | 83.4 | 83.5 |

**(\*) No indicated in Replicon Info. These discovered using tRNAscan-SE at http://lowelab.ucsc.edu/tRNAscan-SE/ [6]**

**(\*\*) Determined from VIRIDIC heat map [3]**

**(\*\*\*) Determined using CoreGenes 3.5 at** [**http://binf.gmu.edu:8080/CoreGenes3.5/**](http://binf.gmu.edu:8080/CoreGenes3.5/) **[5]**

**N.B. Ruegeria phage vB\_RpoP-V21, Ruegeria phage vB\_RpoP-V14, Roseophage DSS3P2, and**

**Ruegeria phage vB\_RpoP-V17 should be considered strains in this genus.**

**Electron micrograph:** None available

**Proposal 8: To create a new subfamily, *Rhodovirinae,* with these seven genera.**

**Source of the name of this taxon:** This subfamily’s name is based upon the fact that all the hosts are members of the family *Rhodobacteraceae*.

**Strain table**

|  |  |  |
| --- | --- | --- |
| **Phage** | **Accession** | **Belongs to species** |
| Ruegeria phage vB\_RpoP-V21 | MH015253 | *Ruegeria virus V12* |
| Ruegeria phage vB\_RpoP-V14 | MH015250 | *Ruegeria virus V12* |
| Roseophage DSS3P2 (=Silicibacter phage DSS3phi2) | FJ591093 | *Ruegeria virus V12* |
| Ruegeria phage vB\_RpoP-V17 | MH015259 | *Ruegeria virus V12* |

**References**

1. Nishimura Y, Yoshida T, Kuronishi M, Uehara H, Ogata H, Goto S. ViPTree: the viral proteomic tree server. Bioinformatics. 2017; 33(15):2379-2380. doi:10.1093/bioinformatics/btx157. PubMed PMID: 28379287.
2. Rohwer F, Edwards R. The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol. 2002 Aug;184(16):4529-35. DOI: 10.1128/jb.184.16.4529-4535.2002 PMID: 12142423
3. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv doi: 10.1101/2020.07.05.188268. http://kronos.icbm.uni-oldenburg.de/viridic/
4. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol. Biol. Evol. 2016,33, 1870–4, doi:10.1093/molbev/msw054 PMID: 27004904.
5. 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. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
6. Lowe, T.M. and Chan, P.P. (2016) tRNAscan-SE On-line: Search and Contextual Analysis of Transfer RNA Genes. Nucl. Acids Res. 44:W54-57. doi: 10.1093/nar/gkw413 PMID: 27174935.