

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

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| **Code assigned:** | **2020.139B** |  |
| **Short title:** Create one new subfamily (*Rothmandenesvirinae*) including four genera (*Caudovirales*: *Schitoviridae*) | | |
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**Author(s) and email address(es)**

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| --- |
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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)** |
| *Rothmandenesvirinae* | Lucia Rothman-Denes | Y |
| *Pourcelvirus* | Christine Pourcel | Y |
|  |  |  |

**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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| We have created a new subfamily, *Rothmandenesvirinae,* named in honour the eminent N4-research scientists Dr Lucia Rothman-Denes, to encompass predominantly Achromobacter podoviruses. |

**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/](about:blank); [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.

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**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [3]; [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)) 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.



**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 create a new genus *Pourcelvirus* with two species**

**Source of the name of this taxon:** This genus is named in honour of Dr. Christine Pourcel (b. 1952; Ph.D. Université Paris-VII (1982); scientist with L’Institut Pasteur (Paris) until 2003 when she joined Institute for Integrative Biology of the Cell at L’Université Paris-Saclay. Since 2009 she has concentrated on bacteriophage isolates many which are found in this subfamily.

**History:** These two lytic phages were isolated in 2017 from Côte d'Ivoire using *Achromobacter xylosoxidans* I2BC as the host bacterium. Their genomes possess 404 bp direct terminal repeats.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Achromobacter phage vB\_AxyP\_19-32\_Axy10 | [MK962629.1](about:blank) | 73.9 | 54.3 | [83](about:blank#!/proteins/82548/609616|Achromobacter phage vB_AxyP_19-32_Axy10/viral segment/) | 1 | 100 | 100 |
| Achromobacter phage vB\_AxyP\_19-32\_Axy11 | [MK962630.1](about:blank) | 73.41 | 54.3 | [81](about:blank#!/proteins/82549/609617|Achromobacter phage vB_AxyP_19-32_Axy11/viral segment/) | 1 | 92.5 | 96.4 |

**N.B.**

**(\*) Determined using VIRIDIC [3]**

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

**Electron micrograph:** None available

**Proposal 2: To create a new genus, *Inbricusvirus*, containing a single species**

**Source of the name of this taxon:** This name of this genus is directly derived from that of the type species Pseudomonas phage inbricus.

**History:** Lytic phage inbricus was isolated in Denmark against Pseudomonas syringae pv. avii

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Pseudomonas phage inbricus | [MG018928.1](about:blank) | 70.21 | 55.9 | [76](about:blank#!/proteins/68269/369416|Pseudomonas phage inbricus/viral segment/) | 2 |

**N.B. Achromobacter phage vB\_AxyP\_19-32\_Axy13 should be considered a strain in this genus**

**Electron micrograph:** None available

**Proposal 3: To create a new genus, *Dongdastvirus* contains four species**

**Source of the name of this taxon:** This genus name is derived from the address (Dongda Street, Fengtai District, Beijing, China) where in the Department of Infectious Disease Control, Institute of Disease Control and Prevention, the first virus of its type, Achromobacter phage phiAxp-3, was isolated.

**History:** These lytic phages were enriched on *Achromobacter xylosoxidans*. Achromobacter phage phiAxp-3 was isolated in China while the others came from Cote d'Ivoire. Achromobacter phage vB\_AxyP\_19-32\_Axy04 has 419 bp direct terminal repeats, while those of Achromobacter phage phiAxp-3 are 416 bp.

Achromobacter phage phiAxp-3 in the species *Achromobacter virus Axp3* was previously assigned to the genus *Jwalphavirus*, however, with only 59% nucleotide identity with the type species, it is now moved into its own genus.

**Specific Reference:** None

**GenBank Summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs | Overall DNA sequence identity (\*) | % common proteins (\*\*) |
| Achromobacter phage phiAxp-3 | [NC\_028908.2](about:blank) | [KT321317.2](about:blank) | 72.83 | 55.2 | [80](about:blank#!/proteins/42598/462162|Achromobacter phage phiAxp-3/viral segment Unknown/) | 1(\*\*\*) | 100 | 100 |
| Achromobacter phage vB\_AxyP\_19-32\_Axy04 |  | [MK962626.1](about:blank) | 73.83 | 54.9 | [80](about:blank#!/proteins/82545/609613|Achromobacter phage vB_AxyP_19-32_Axy04/viral segment/) | 1 | 90.3 | 93.7 |
| Achromobacter phage vB\_AxyP\_19-32\_Axy12 |  | [MK962631.1](about:blank) | 74.1 | 55.0 | [82](about:blank#!/proteins/82550/609618|Achromobacter phage vB_AxyP_19-32_Axy12/viral segment/) | 1 | 89.9 | 95.0 |
| Achromobacter phage vB\_AxyP\_19-32\_Axy24 |  | [MK962641.1](about:blank) | 74.74 | 54.9 | [82](about:blank#!/proteins/82560/609628|Achromobacter phage vB_AxyP_19-32_Axy24/viral segment/) | 1 | 89.8 | 95.0 |

**(\*) Determined using VIRIDIC [3]**

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

**(\*\*\*) None indicated in GenBank Replicon Info. This one discovered using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](about:blank) **[6]**

**Electron micrograph:** None available

**Proposal 4: To create a new subfamily for these viruses, named *Rothmandenesvirinae***

**Source of the name of this taxon:** This subfamily is named in honour of Professor Lucia B. Rothman-Denes (b. 1943; is an Argentinian American microbiologist who is the A. J. Carlson Professor in the Department of Molecular Genetics at the University of Chicago. She is known for studying the regulation of transcription and host interactions that occur during bacterial virus infection, particular in coliphage N4. She has been a member National Academy of Sciences, USA since 2014).

**Proposal 5: To move *Jwalphavirus* to this subfamily**

**History:** see 2017.022B

**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. PubMed PMID: 12142423
3. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. [http://rhea.icbm.uni-oldenburg.de/VIRIDIC/](about:blank)
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.
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.