

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

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| **Code assigned:** | **2020.146B** |  |
| **Short title:** Create one new family (*Schitoviridae*) including eight existing subfamilies and 40 existing genera (*Caudovirales*) | | |
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**Author(s) and email address(es)**

|  |  |
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| Adriaenssens EM, Tolstoy I, Kropinski AM, Moraru C, Wittmann J | evelien.adriaenssens@quadram.ac.uk;  tolstoy@ncbi.nlm.nih.gov;  Phage.Canada@gmail.com; liliana.cristina.moraru@uol.de; jow12@dsmz.de |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of Guelph, Canada [AMK]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  DSMZ, Germany [JW] |

**Corresponding author**

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| --- |
| Johannes Wittmann |

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

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| *Caudovirales* 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**

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| *Schitoviridae* | Gian Carlo Schito | Y |
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**Submission dates**

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| --- | --- |
| Date first submitted to SC Chair | 6 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 to create a new family, *Schitoviridae*, in the order *Caudovirales* including 119 isolates, 75 species, 41 genera and 8 subfamilies based on genome comparisons and phylogenetic analysis of terL protein sequences. |

**Text of proposal**

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| |  | | --- | | **Demarcation criteria:**  **Species:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.  **Genus:** 70% DNA sequence identity was the criterion for creation of new genera and monophyly in the terL gene tree.  **Family:** Members of the new family also reveal a gene for a large virion RNA polymerase and genome sizes between 59 and 79kb.  Members of the family *Schitoviridae* are bacterial viruses that infect proteobacteria. Host genera include several members of the alpha-, beta- and gammaproteobacteria, e.g. *Roseobacter*, *Achromobacter*, *Escherichia* and *Pseudomonas*. The virions reveal characteristic features of podovirus morphology, i.e. short tail structures and an icosahedral head. The genomes of schitoviruses consist of linear dsDNA with terminal repeats of ~300-2000bp (Ohmori, 1988 [1]; Wittmann, 2014 [2]; Fouts, 2013 [3]). Most genomes sizes range from 59-79 kb. Members of the *Alteavirus* reveal larger genome sizes of about 104kb, and were considered related, but not members of the family. tRNAs were identified for some members. | |

**Table 1. *Schitoviridae.*** Characteristic features of members of the family *Schitoviridae*

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| **Characteristic** | **Description** |
| Typical member | Escherichia phage N4 (EF056009), first isolate of this family, species *Escherichia virus N4* genus *Enquatrovirus* |
| Virion | Head-tail with short tails, heads generally isometric with diameters of 50–70 nm |
| Genome | Linear, terminally redundant, non-permuted dsDNA of 59-104 kb |
| Replication | Phage-encoded DNA polymerase |
| Transcription | 2 RNA polymerase genes in cluster for early genes, 1 large virion-associated RNA polymerase |
| Translation | Bacterial translation |
| Host range | Bacteria of the phylum Proteobacteria |
| Taxonomy | Order *Caudovirales*, 8 subfamilies, 40 genera and 74 species |

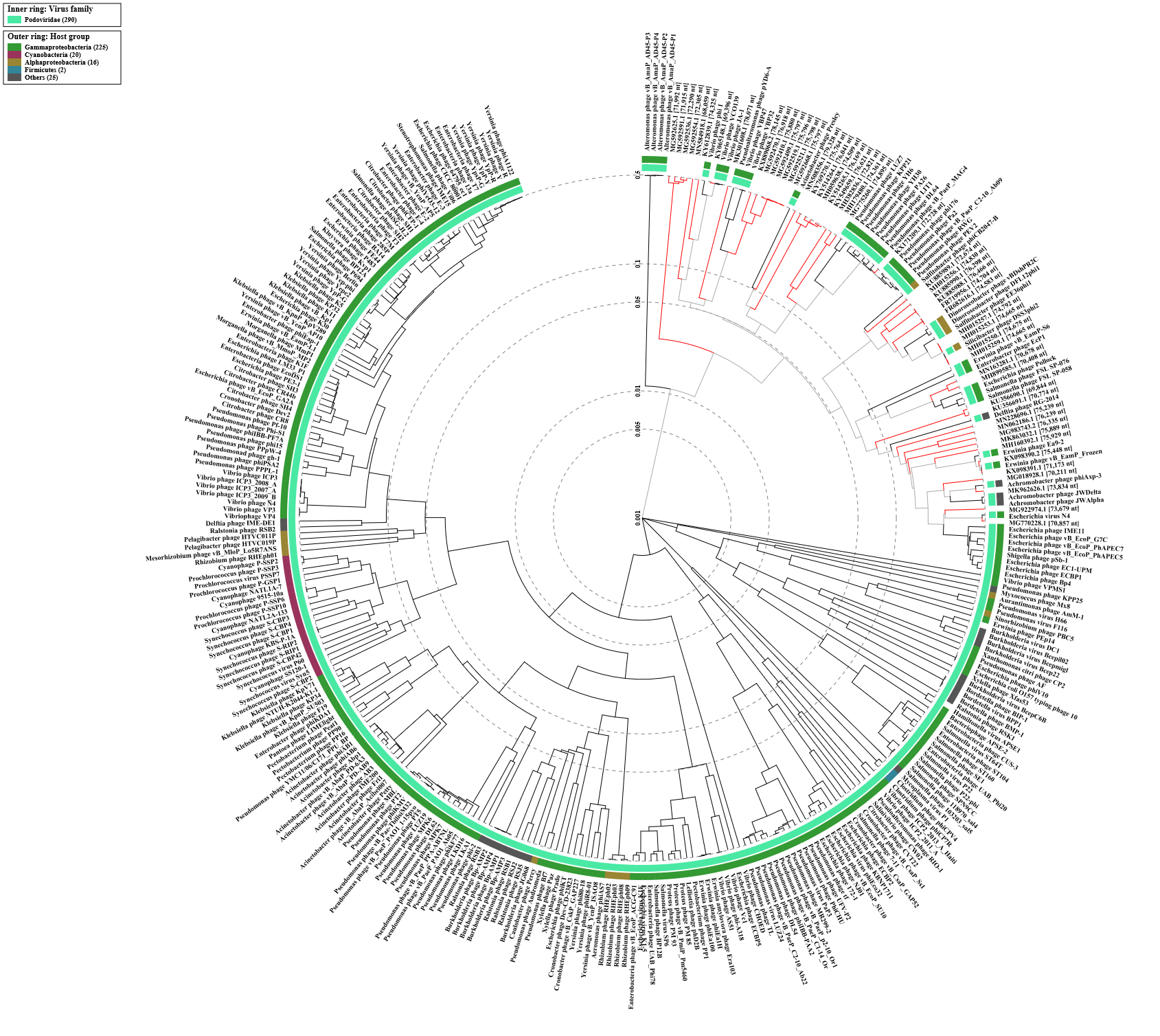
**Virion morphology**

Virions have isometric, icosahedral heads of 50–72 nm in diameter and short tails with a length of 10-40 nm. (Figure 1. Schito*viridae*).

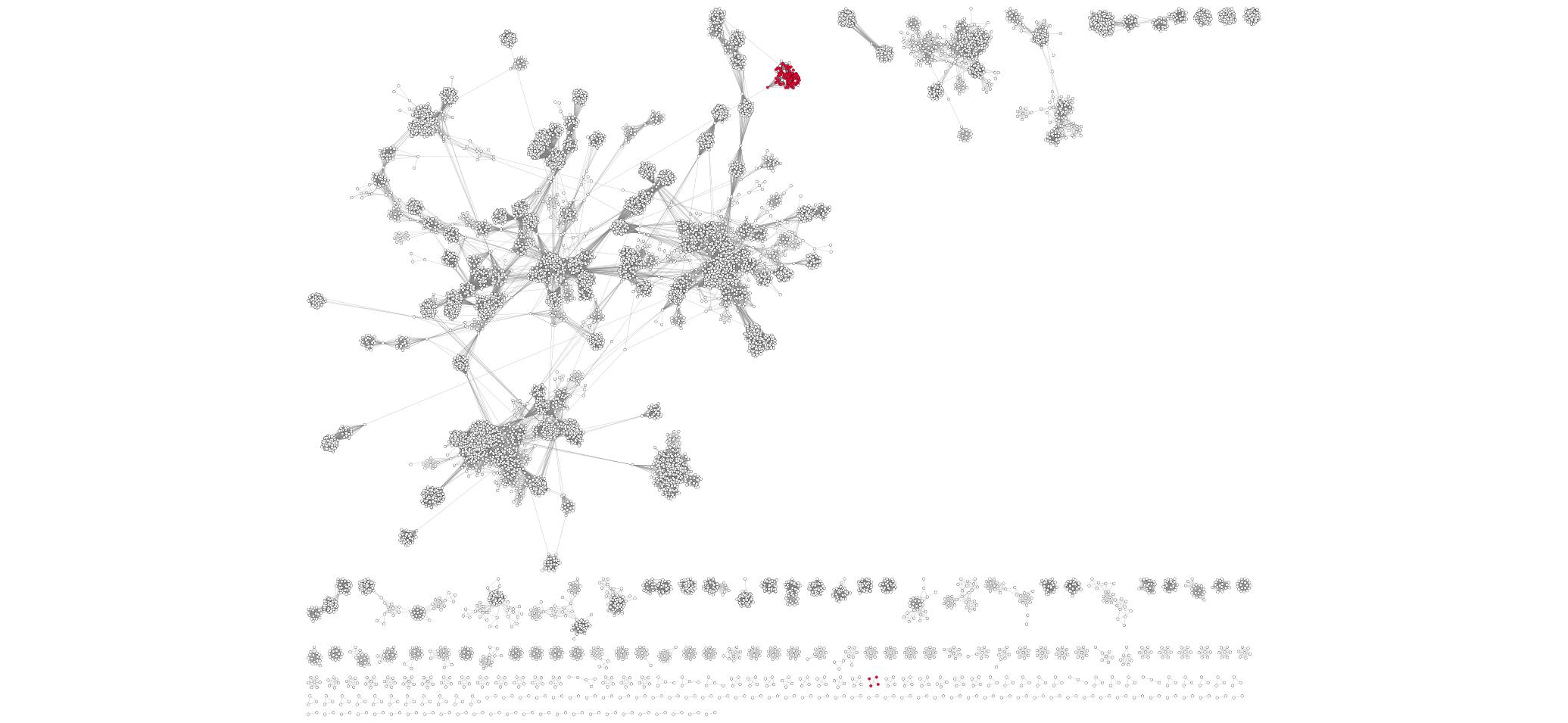
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| **Figure 1.*Schitoviridae*.** Transmission electron micrograph of Achromobacter phage Jwalpha, a member of the family *Schitoviridae* (subfamily *Rothmandenesvirinae*). Virions were stained with 2% uranyl acetate. |

**Supporting evidence**

**ViPTree analysis:** ViPTree analysis (<https://www.genome.jp/viptree/>; [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. Members of the new family are framed in blue.

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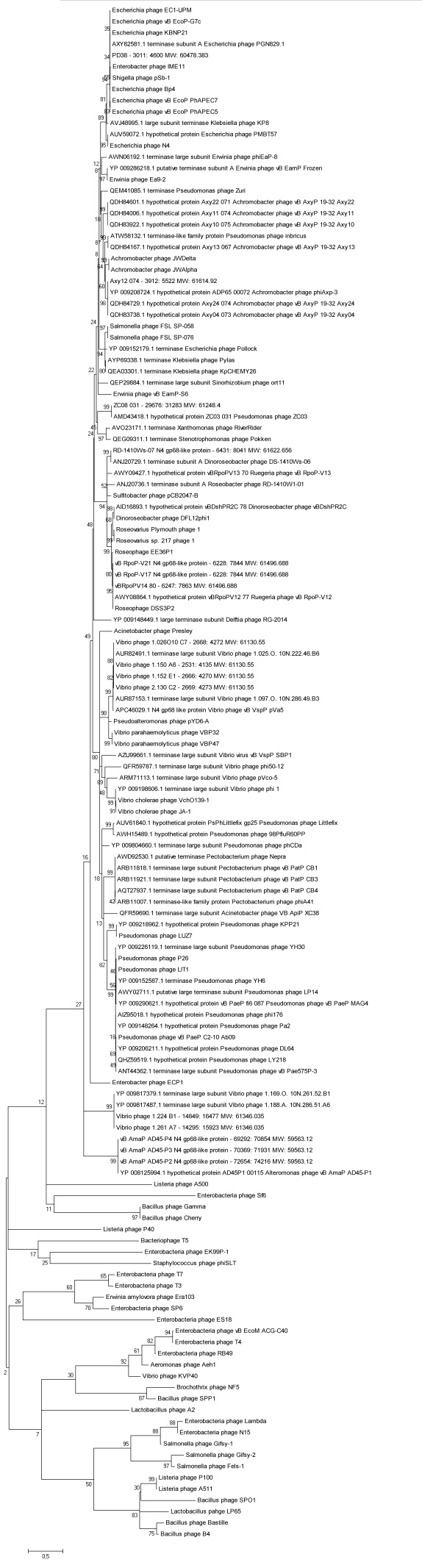
**Vcontact2 network** with the *Schitoviridae* family and the Alteavirus coloured in red.



**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; [6]; <http://rhea.icbm.uni-oldenburg.de/VIRIDIC/>) computes pairwise intergenomic distances/similarities amongst phage genomes. Columns 3 and 4 indicate the boundaries of the proposed subfamilies and genera.



**Phylogenetic analysis** using the terminase (A) and virion RNA polymerase (B) protein sequences of N4-like phages. The amino acid sequences were compared using MUSCLE with MEGA7 [7]. 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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A

B

**Source of the name of this taxon:**

This taxon is named in honour of Professor Gian Carlo Schito (b. 1935. San Remo, Italy; MD University of Genoa Medical School (1960); Libera docenza in Virology (1964); Full professor of Clinical Microbiology and Director of the Institute of Microbiology at the University of Genoa Medical School; retired 2000. He isolated Escherichia phage N4, which for a long time was a genomic orphan.



**Member taxa**

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| **subfamily** | **genera** |
| *Migulavirinae* | *Litunavirus, Luzseptimavirus* |
| *Enquatrovirinae* | *Enquatrovirus, Gamaleyavirus, Kaypoctavirus* |
| *Rothmandenesvirinae* | *Dongdastvirus, Inbricusvirus, Jwalphavirus, Pourcelvirus, Yonginvirus* |
| *Erskinevirinae* | *Johnsonvirus, Yonginvirus* |
| *Rhodovirinae* | *Aoqinvirus, Aorunvirus, Baltimorevirus, Plymouthvirus, Pomeroyivirus, Raunefjordvirus, Sanyabayvirus* |
| *Fuhrmanvirinae* | *Mazuvirus, Stoningtonvirus* |
| *Pontosvirinae* | *Dorisvirus, Galateavirus, Nahantvirus* |
| *Humphriesvirinae* | *Ithacavirus, Pollockvirus, Pylasvirus* |
|  | *Cbunavirus, Dendoorenvirus, Eceepunavirus, Huelvavirus, Littlefixvirus, Mukerjeevirus, Pacinivirus, Pokkenvirus, Presleyvirus, Riverridervirus, Shizishanvirus, Waedenswilsvirus, Zicotriavirus, Zurivirus* |

**References**

1. Ohmori H, Haynes LL, Rothman-Denes LB (1988) Structure of the ends of the coliphage N4 genome. J Mol Biol 202:1–10 PMID: 3172206 DOI: 10.1016/0022-2836(88)90512-8
2. Wittmann J, Dreiseikelmann B, Rohde M, Meier-Kolthoff JP, Bunk B et al (2014) First genome sequences of Achromobacter phages reveal new members of the N4 family. Virol J 11:14. PMID: 24468270 PMCID: PMC3915230 DOI: 10.1186/1743-422X-11-14
3. Fouts DE, Klumpp J, Bishop-Lilly KA, Rajavel M, Willner KM et al (2013) Whole genome sequencing and comparative genomic analyses of two Vibrio cholerae O139 Bengal-specific Podoviruses to other N4-like phages reveal extensive genetic diversity. Virol J 10:165. PMID: 23714204 PMCID: PMC3670811 DOI: 10.1186/1743-422X-10-165
4. 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.
5. 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
6. 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/
7. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol Biol Evol. 2016 Jul; 33(7):1870-4. doi:10.1093/molbev/msw054 PMID: 27004904.