

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

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| **Code assigned:** | **2020.054B** |  |
| **Short title:** Create one subfamily (*Enquatrovirinae*) including three new 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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| *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)** |
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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 ”Enquatrovirinae” including three genera, *Gamaleyavirus, Enquatrovirus* and *Kaypoctavirus*, based on genome-based comparisons, proteomic analysis using ViPTree and phylogenetic analyses of terminase and vRNA polymerase protein sequences. |

**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**

**Proposal A: Create a new genus, *Kaypoctavirus*, including one new species**

**Proposal B: Create a new subfamily, *Enquatrovirinae*, grouping the genera *Enquatrovirus, Gamaleyavirus* and *Kaypoctavirus***

**Proposal A: Create a new genus, *Kaypoctavirus*, including one new species**

**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 [1-3].

**Source of the name of this taxon:** The name is derived from the name of the isolated phage of this type, Klebsiella phage KP8

**History:** Phage KP8 is a member of the *Podoviridae* family and the superfamily of N4-like viruses that infect *K. pneumoniae*. Bacteriophage KP8 was isolated from a wastewater sample from the Novosibirsk infectious hospital №1[4].

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA |
| KP8 |  | MG922974 | 73.68 | 44.2 | 94 | 3 |

**BLASTN homologs:** The next closest relative is *Enterobacter* phage IME11,[JX880034.1] which shares 46.67% DNA sequence identity with KP8 [1-3].

**Electron micrograph:** None available

**Phylogeny:** The phylogenetic tree was constructed with VICTOR [5], using whole genome sequences of N4-like phages at the nucleotide level.

A picture containing drawing

Description automatically generated

**Proposal B: Create a new subfamily, *Enquatrovirinae*, grouping the genera *Enquatrovirus, Gamaleyavirus* and *Kaypoctavirus***

**Source of the name of this taxon:** This subfamily contains the first isolated phage with characteristic virion-associated RNA polymerase, *Escherichia* phage N4.

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [1]) is based upon Rohwer and Edwards (2002) Phage Proteomic Tree [2]. The *Herelleviridae* root distance as a reference is marked with a **red arrowhead**; the **purple arrowhead** indicates the subfamily 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 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 [6]. 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

**References**

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