

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

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| **Code assigned:** | ***2022.028B*** |  |
| **Short title:** Create a new subfamily of Gordonia phages (*Deeyouvirinae*) with two genera (*Caudoviricetes*) | | |
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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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| Bacterial Viruses Subcommittee, Caudoviricetes Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| --- | --- | --- | --- |
| **Study Group** | **Number of members** | | |
| **Votes support** | **Votes against** | **No vote** |
|  |  |  |  |
|  |  |  |  |

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

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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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 | May 2022 |
| Date of this revision (if different to above) |  |

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

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| --- |
| 2022.028B.N.v1.Deeyouvirinae\_nsf.xlsx |

**Abstract**

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| Based on overall protein and DNA sequence similarity, and phylogeny we propose to create a new subfamily (*Deeyouvirinae*) containing two genera. On average the genomes of the genus *Nevillevirus* possess the following properties: 76.19 kb (58.8 mol%G+C) encoding 130 proteins and 7 tRNA. On average the genomes of the genus *Octobienvirus* possess the following properties: 76.19 kb (58.6 mol%G+C) encoding 138 proteins and 6 tRNA. Phages Neville and Octobien14 share 26.0% DNA sequence identity and 51.9% proteins. |

**Text of proposal**

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| |  | | --- | | **Species demarcation criteria:** Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates.  These values can be calculated by a number of tools, such as BLASTn [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  **Genus demarcation criteria:** In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, the Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [8]  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny. [8] | |

**Supporting evidence**

**Proposal A. To create a new genus, *Octobienvirus*, with four species**

**Proposal B. To create a new genus, *Nevillevirus*, with three species**

**Proposal C: To create a new subfamily, *Deeyouvirinae* with these two genera**

**General data:**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes.

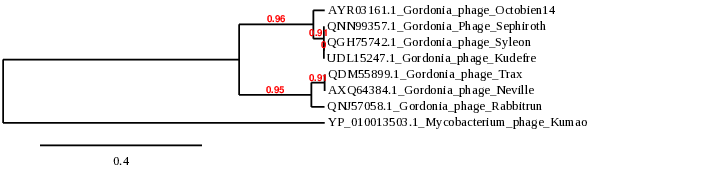
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**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [3]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [4]. The phages of interest are indicated with **red stars**.





**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from these and related phages with phylogeny.fr in “one click” mode [6]. "The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences." It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. "The usual bootstrapping procedure is replaced by a new confidence index that is much faster to compute. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [7] for details." The members of this subfamily are indicated with a **blue rectangle**.

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**Proposal A. To create a new genus, *Octobienvirus*, with four species**

**Origin of the name of this taxon:** This taxon is named after Gordonia phage Octobien14

**Historical aspects:** Temperate siphovirus Octobien14 was isolated in 2017 by Bienfaiteur Mugisha (Durham Technical Community College, NC, USA) from soil using Gordonia terrae NRRL B-16283 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Its genome contains 11 nt 3’-cohesive termini (ATCTGCGCCCC). The Actinobacteriophage Database classifies this phage to Cluster DU. Our results suggest that this cluster should be divided up.

**Electron micrograph:** NA

**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage Octobien14 | [MH976515.1](https://www.ncbi.nlm.nih.gov/nuccore/MH976515.1) | 76.36 | 58.7 | [143](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/73815/418513|Gordonia phage Octobien14/viral segment/) | 6 | 100 | 100 |
| Gordonia Phage Sephiroth | [MT684599.1](https://www.ncbi.nlm.nih.gov/nuccore/MT684599.1) | 76.06 | 58.6 | [131](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94597/986815|Gordonia Phage Sephiroth/viral segment/) | 6 | 71.1 | 80.4 |
| Gordonia phage Kudefre | [OK040786.1](https://www.ncbi.nlm.nih.gov/nuccore/OK040786.1) | 76.73 | 58.6 | [140](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/107505/1731376|Gordonia phage Kudefre/viral segment/) | 6 | 71.6 | 83.2 |
| Gordonia phage Syleon | [MN444870.1](https://www.ncbi.nlm.nih.gov/nuccore/MN444870.1) | 75.61 | 58.7 | [138](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85548/743707|Gordonia phage Syleon/viral segment/) | 6 | 70.4 | 80.4 |

**(\*) determined using VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**On average the genomes of *Octobienvirus* possess the following properties: 76.19 kb (58.6 mol%G+C) encoding 138 proteins and 6 tRNA**

**Proposal B. To create a new genus, *Nevillevirus*, with three species**

**Origin of the name of this taxon:** This taxon is named after Gordonia phage Neville

**Historical aspects:** Temperate phage Neville was isolated in 2017 by Lauren Andrews and Emma Bragdon (University of Maine, ME, USA) from soil sample taken from a garden/pumpkin patch using Gordonia terrae 3612 as the host bacterium. This was part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. Its genome contains 11 nt 3’-cohesive termini (ATCTGCCCCAC). The Actinobacteriophage Database classifies this phage to Cluster DU.

**Electron micrograph:** Electron micrographs of negatively stained Gordonia phage Neville (<https://phagesdb.org/phages/Neville/>). Limited permission was granted by The Actinobacteriophages Database (<https://phagesdb.org/>), funded by the Howard Hughes Medical Institute, to use this electron micrograph for this taxonomy proposal; it cannot be reused without permission of The Actinobacteriophages Database.

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**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Gordonia phage Neville | [MH651182.1](https://www.ncbi.nlm.nih.gov/nuccore/MH651182.1) | 75.81 | 58.8 | [129](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72150/400286|Gordonia phage Neville/viral segment/) | 7 | 100 | 100 |
| Gordonia phage Trax | [MK967378.1](https://www.ncbi.nlm.nih.gov/nuccore/MK967378.1) | 75.94 | 58.7 | [128](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82909/624782|Gordonia phage Trax/viral segment/) | 7 | 88.3 | 90.7 |
| Gordonia phage Rabbitrun | [MT658805.1](https://www.ncbi.nlm.nih.gov/nuccore/MT658805.1) | 76.82 | 58.8 | [132](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/94268/980545|Gordonia phage Rabbitrun/viral segment/) | 6 | 74.3 | 86.8 |

**(\*) determined using VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**On average the genomes of *Nevillevirus* possess the following properties: 76.19 kb (58.8 mol%G+C) encoding 130 proteins and 7 tRNA**

**Proposal C: To create a new subfamily, *Deeyouvirinae* with these two genera**

**Origin of the name of this taxon:** The name of this taxon is derived from the Actinobacteriophage Database Cluster DU to which these phages belong.

**Date:** Our proteomic and genomic data, coupled with the assessment of the Actinobacteriophage Database confirm that members of the DU cluster are closely related.

**References**

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