

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

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| **Code assigned:** | ***2023.016B*** |  |
| **Short title:** To create a new genus, *Commandariavirus* in the family *Zierdtviridae* [*Caudoviricetes*] | | |
|  | | |

**Author(s) and email address(es)**

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| --- | --- |
| Kurtböke I, Turner D, Moraru C, Tolstoy I, Kropinski AM | IKurtbok@usc.edu.au; Dann2.Turner@uwe.ac.uk; liliana.cristina.moraru@uol.de; tolstoy@ncbi.nlm.nih.gov; Phage.Canada@gmail.com |

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

|  |
| --- |
| University of the Sunshine Coast, Queensland, Australia [IK]  University of the West of England, Bristol, UK [DT]  Carl von Ossietzky Universität Oldenburg, Germany [CM]  National Center for Biotechnology Information, MD, USA [IT]  University of Guelph, Ontario, Canada [AMK] |

**Corresponding author**

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| Andrew M. Kropinski |

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

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

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

|  |  |  |
| --- | --- | --- |
| **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 2023 |
| 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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| 2023.016B.N.v1.Commandariavirus\_ng.xlsx |

**Abstract**

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| In this proposal we have recognized a new genus, *Commandariavirus*, in the subfamily *Emilbogenvirinae*, family *Zierdtviridae*. |

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| **Text of proposal**   |  | | --- | | **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 [1,2] – usually calculated using intergenomic distance calculator VIRIDIC [3].  **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 [10]. | |

**Supporting evidence**

**Proposal Data:**

1. **Create a new genus, *Commandariavirus*, containing a single species**

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**Figure 1. VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [3]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. Data values which are bordered in black correspond to strains. Abbreviations: phg = phage; Gord = Gordonia.

![A close-up of a graph

Description automatically generated with low confidence]()

A screenshot of a computer

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**Figure 2. ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank); [4]) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree [5]. The phages of interest are indicated with **red lines and stars**.

**Taxonomic Proposals:**

1. **Create a new genus, *Commandariavirus*, containing a single species**

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of one of the first virus of its type Gordonia phage Commandaria

**Historical aspects:** This lytic siphophage was isolated from Unity (ME, USA) soil against Gordonia terrae 3612 by Andreas Stephanou and Sam Weafer (University of Maine, USA) as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome has 10 nt 3’-cohesive termini (CGCCGCGTAC). The Actinobacteriophage Database considers this phage to be part of Cluster CR/Subcluster CR2. We have split their cluster into several genera. Commandaria is most closely related species of the genus *Foxborovirus.*

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**Electron micrograph:** Electron micrographs of negatively stained Gordonia phage Commandaria (<https://phagesdb.org/phages/Commandaria/>). 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.

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) |
| Gordonia phage Commandaria | [OQ709208.1](https://www.ncbi.nlm.nih.gov/nuccore/OQ709208.1) | 68.06 | 66.2 | [94](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/127528/2174204|Gordonia phage Commandaria/viral segment/) | 0 | 100 |

**Conclusion:** A genus comprised of a single species is proposed based on DNA (Fig. 1) and protein (Fig. 2) similarity.

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