

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

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| **Code assigned:** | ***2023.026B*** |  |
| **Short title:** To create eleven (11) new species in the genus *Gordonvirus* [*Caudoviricetes*] | | |
|  | | |

**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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| Actinophages Study Group |

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

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**ICTV Study Group votes on proposal**

|  |  |  |  |
| --- | --- | --- | --- |
| **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 |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

|  |  |
| --- | --- |
| 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**

|  |
| --- |
| 2023.026B.N.v1.Gordonvirus\_11ns.xlsx |

**Abstract**

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| We propose to add 11 new species to the genus *Gordonvirus*. |

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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**

**Proposals Data:**

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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. The names in white boxes are strains, while those in gold boxes are existing species. Abbreviations: phg = phage; Arth = Arthrobacter.



**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 a **blue bar**.

**Taxonomic Proposals:**

1. **Create 11 new species in the genus *Gordonvirus***

**Origin of the name of this taxon:** N/A

**Historical aspects:** This taxon was established through Taxonomy Proposal 2016.070a-dB.A.v1.Gordonvirus with two species: *Gordonvirus captnmurica* and *Gordonvirus gordon.*  All of the viruses listed below conform to the criteria with which we define species [10].

**Genome summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Gordon | [KU160646.1](https://www.ncbi.nlm.nih.gov/nuccore/KU160646.1) | 58.28 | 49.8 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63536/466156|Arthrobacter phage Gordon/viral segment/) | 100 | 100 |
| Arthrobacter phage Teacup | [MF140432.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140432.1) | 58.24 | 49.8 | [88](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63717/466338|Arthrobacter phage Teacup/viral segment/) | 81.82 | 89.9 |
| Arthrobacter phage Niktson | [MF038790.1](https://www.ncbi.nlm.nih.gov/nuccore/MF038790.1) | 58.41 | 49.9 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63647/466268|Arthrobacter phage Niktson/viral segment/) | 83.07 | 91.0 |
| Arthrobacter phage Nightmare | [MF140423.1](https://www.ncbi.nlm.nih.gov/nuccore/MF140423.1) | 58.84 | 49.9 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/63710/466331|Arthrobacter phage Nightmare/viral segment/) | 82.93 | 88.8 |
| Arthrobacter phage Breylor17 | [MH450115.1](https://www.ncbi.nlm.nih.gov/nuccore/MH450115.1) | 57.82 | 49.9 | [84](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71866/399738|Arthrobacter phage Breylor17/viral segment/) | 86.13 | 86.5 |
| Arthrobacter phage Synepsis | [MH479926.1](https://www.ncbi.nlm.nih.gov/nuccore/MH479926.1) | 57.54 | 49.9 | [84](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71899/399771|Arthrobacter phage Synepsis/viral segment/) | 86.88 | 87.6 |
| Arthrobacter phage CastorTray | [MZ274309.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ274309.1) | 58.38 | 50.0 | [93](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/104883/1671042|Arthrobacter phage CastorTray/viral segment/) | 87.06 | 91.0 |
| Arthrobacter phage Tatanka | [MH399789.1](https://www.ncbi.nlm.nih.gov/nuccore/MH399789.1) | 58.12 | 50.0 | [85](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71226/391002|Arthrobacter phage Tatanka/viral segment/) | 84.43 | 84.3 |
| Arthrobacter phage Trustiboi | [ON456335.1](https://www.ncbi.nlm.nih.gov/nuccore/ON456335.1) | 58.24 | 50.0 | [90](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/116333/1897097|Arthrobacter phage Trustiboi/viral segment/) | 87.71 | 91.0 |
| Arthrobacter phage Darby | [ON456340.1](https://www.ncbi.nlm.nih.gov/nuccore/ON456340.1) | 57.76 | 50.1 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/116332/1897096|Arthrobacter phage Darby/viral segment/) | 87.73 | 91.0 |
| Arthrobacter phage DevitoJr | [MZ209303.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ209303.1) | 58.04 | 50.0 | [92](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/106944/1720663|Arthrobacter phage DevitoJr/viral segment/) | 86.95 | 91.0 |
| Arthrobacter phage ScienceWizSam | [ON645338.1](https://www.ncbi.nlm.nih.gov/nuccore/ON645338.1) | 58.22 | 50.0 | [96](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/117016/1910175|Arthrobacter phage ScienceWizSam/viral segment/) | 86.01 | 91.0 |

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

**(\*\*) determined using CoreGenes 3.5 [6]**

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