

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

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| **Code assigned:** | **2020.073B** |  |
| **Short title:** Create one new genus (*Hnatkovirus*) including one new species (*Caudovirales*: *Siphoviridae*) | | |
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**Author(s) and email address(es)**

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| Andrew Kropinski |

**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 | June 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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| 2020.073B.R.Hnatkovirus.xlsx |

**Abstract**

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| The Actinobacteriophage Database classifies *Mycobacterium phage DS6A* as a singleton. We have chosen to honour a pioneering mycobacteriophage scientist by naming this genus after him. |

**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**

**Source of the name of this taxon:** The genus is named in honour of Canadian clinical microbiologist, and University of Alberta Professor Emeritus Dr. Stephen I. Hnatko (1924 – 2017) who in the early 1950’s was among the first to study the bacteriophages of *Mycobacterium*. The names of the genera in this subfamily are all directly related to the names of the phages. Photograph provided by his son, Dr. Gary Hnatko, Assoc Adjunct Prof/Ped Psych Faculty of Medicine & Dentistry - Pediatrics Dept, University of Alberta, Canada)



**History:** Phage DS6A was isolated in 1960 by W. B. Redmond (University of Pittsburgh) from stockyard soil using *Mycobacterium tuberculosis* H37Rv as the host bacterium.The linear genome of this virus has 12 bp (CGAGGCCGACAT) 3’-cohesive termini, and is classified by The Actinobacteriophage Database as a singleton. BLASTN analysis at NCBI confirm this [1-3].

**Electron micrograph:** Electron micrograph of negatively stained *Mycobacterium* phage DS6A (<https://phagesdb.org/phages/DS6A/>) - Limited permission was granted by The Actinobacteriophages Database, 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.



**Reference:** W.B. Redmond and J.C. Cater "A bacteriophage specific for *Mycobacterium tuberculosis*, varieties hominis and bovis" Amer. Rev. Resp. Dis. 82:781-786 (1960).

**GenBank Summary:**

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| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA**(\*)** |
| DS6A | [NC\_023744.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_023744.1) | [JN698994.1](https://www.ncbi.nlm.nih.gov/nuccore/JN698994.1) | 60.59 | 68.4 | [97](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/31673/460625|Mycobacterium phage DS6A/viral segment Unknown/) | 2 |

**(\*) None indicated in the GenBank Replicon Info. Two found using tRNAScan-SE [5]**

**Phylogeny:** The phylogenetic tree was constructed using the terminase large subunit protein homolog of DS6A and related *Mycobacterium* phages with phylogeny.fr in “one click” mode [8]. "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 [9] for details."



**References**

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