

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

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| **Code assigned:** | ***2022.069B*** |  |
| **Short title:** Create a new, single species, genus (*Quivirus*) (*Caudoviricetes*) | | |
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**Author(s) and email address(es)**

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**Corresponding author**

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| Andrew M. Kropinski |

**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** |
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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 |

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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) | September 2022 |

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

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| ICTV-EC: The evidence for the creation of a new family is not convincing enough. Please provide more data.  Proposer: We have reassessed our data and realized we need to perform more analyses. Instead of proposing a new family, we have reworked the proposal to just propose the new genus in the family. |

**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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| 2022.069B.Uc.v2.Quivirus\_ng.xlsx |

**Abstract**

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| Arthrobacter phage Qui is a unique siphovirus which the Actinobacteriophage Database, vCLUSTER analyses and phylogenetic analyses reveal are distinct from other Arthrobacter phages. The distinguishing characteristics are an elongated capsid (length:width ratio 62:40 nm) and a large genome of 113 kb. Interestingly, the characteristics of its genome shares some sequence similarity to members of the *Mudcatvirus* but the genome size (59 kb) and capsid morphology (L:W, 63:21 nm) plus its placement by the Actinobacteriophage Database render it sufficient different to be consider unique. We have chosen to create a new genus, *Quivirus,* for viruses of is type. |

**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] | |

**Supporting evidence**

**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. The black box delineates strains. While VIRIDIC analysis suggests a distant relationship between Qui and *Mudcatvirus* members, their genomes differ widely in size.

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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 **blue arrowhead**. These results indicate that phage Qui is related to the phages indicated with **red stars** but we have chosen not to define a higher taxon at this time.

  


**Phylogeny:** The phylogenetic tree was constructed using the TerL proteins from Qui and related phages with phylogeny.fr in “one click” mode [6]. It also includes the use of Gblocks to eliminate poorly aligned positions and divergent regions. See: Anisimova M., Gascuel O. Approximate likelihood ratio test for branches: A fast, accurate and powerful alternative [7] for details." The members of the *Quivirus* are indicated with a **blue rectangle**. These results indicate that phage Qui is related to the phages Arcadia, Dynamite, Nason etc. but we have chosen not to define a higher taxon at this time.

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**Proposals:**

**A. Create a new genus *Quivirus*, with a single species**

**Origin of the name of this taxon:** This taxon is named after Arthrobacter phage Qui

**Historical aspects:** This lytic siphophage was isolated in 2018 by Quiana Walton (University of Wisconsin-River Falls, WI, USA) against Arthrobacter globiformis NRRL B-2979 from a river bank as part of the Science Education Alliance-Phage Hunters Advancing Genomics and Evolutionary Science program. The genome possesses a 9 nt 3’-cohesive terminus (CGCCGCCCT) The Actinobacteriophage Database classified Qui to Cluster FK.

**Electron micrograph:** Electron micrographs of negatively stained Gordonia phage Pons (<https://phagesdb.org/phages/Qui/>). 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 | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Arthrobacter phage Qui | [MN183282.1](https://www.ncbi.nlm.nih.gov/nuccore/MN183282.1) | 113.68 | 47.6 | [247](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83588/658571|Arthrobacter phage Qui/viral segment/) | 100 | 100 |

**(\*) determined using BLASTn [1] or VIRIDIC [2]**

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

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