

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

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| **Code assigned:** | ***2023.078B*** |  |
| **Short title:** Create a new genus (*Xajduovirus*) with a single species (*Caudoviricetes*) | | |
|  | | |

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

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| Andrew M. Kropinski |

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

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| *Caudoviricetes* Study Group |

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

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| No comments |

**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 | April 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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| --- |
| 2023.078B.N.v1.Xajduovirus\_ng.xlsx |

**Abstract**

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| In this proposal, we suggest the creation of one new genus containing one new species.  This new genus probably will form part of a new family containing siphoviruses infecting a wide variety of gamma proteobacteria. |

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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**

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Description automatically generated**

**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; Para = Paracoccus; Sphi = Sphingomonas; Xant = Xanthomonas; Esch = Escherichia

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Description automatically generated]()**

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Description automatically generated with medium confidence]()**

**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**.

**A black screen with red numbers

Description automatically generated with low confidence**

**Figure 3. Phylogeny:** The phylogenetic tree was constructed using the large subunit terminase proteins from these and related 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.”

**Origin of the name of this taxon:** The name of this taxon is directed derived from the first virus of its type, Xanthomonas phage XAJ2.

**Historical aspects:** This lytic siphophage was isolated in Pecs, Hungary against Xanthomonas arboricola pv. juglandis by D. Domotor et al. (Enviroinvest Corp.)

**Electron micrograph:** N/A.

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Xanthomonas phage XAJ2 | [KU197014.1](https://www.ncbi.nlm.nih.gov/nuccore/KU197014.1) | 49.24 | 47.4 | [79](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/62856/465479|Xanthomonas phage XAJ2/viral segment/) | 100 | 100 |

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity; and phylogenetic analysis of the TerL proteins (Fig. 3) this is a cohesive genus.

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