

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

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| **Code assigned:** | ***2022.039B*** |  |
| **Short title:** Create a new subfamily (*Iiscvirinae*), with one existing genus (*Jilinvirus*) and one new genus (*Aryavirus*) (*Caudoviricetes*) | | |
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**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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| 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** |
|  |  |  |  |
|  |  |  |  |

**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**

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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: Add clarification for blue arrow in heatmap.  Proposer: clarification added to legend. |

**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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| 2022.039B.A.v1.Iiscvirinae\_nsf.xlsx |

**Abstract**

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| The genus *Jilinvirus* was created through Taxonomy Proposal 2019.004G. *Enterobacter virus Arya* is sufficiently dissimilar to members of the *Jilinvirus* to be considered part of a new genus, *Aryavirus*. A new subfamily, *Iiscvirinae*, was proposed to encompass these two genera. |

**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]  **Subfamily demarcation criteria:** Subfamilies are to be created when two or more genera are related below the family level. In practical terms, this usually means that they share a low degree of sequence similarity (usually about 40-50%) and that the genera form a clade in a marker tree phylogeny. [8] | |

**Supporting evidence**

1. **To create a new genus *Aryavirus* containing a single species**
2. **To create a new subfamily *Iiscvirinae***
3. **To move *Jilinvirus* and *Aryavirus* to this subfamily**
4. **To create a new genus *Aryavirus* containing a single species**

**Origin of the name of this taxon:** This taxon is named after Enterobacter phage Arya [11]

**Historical aspects:** This lytic phage Arya was isolated against Enterobacter sp. CT7 from the gut of the Formosan subterranean termite*, Coptotermes formosanus*. Its genome possesses an integrase pseudogene. The authors noted its close relationship to Escherichia phage vB\_EcoM\_ECO1230-10 and Escherichia phage vB\_EcoM-ep3.

**Electron micrograph:** N/A

**Genome summary:**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Enterobacter phage Arya | [NC\_031048.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_031048.1) | [KX231828.1](https://www.ncbi.nlm.nih.gov/nuccore/KX231828.1) | 41.92 | 54.1 | [61](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/46297/462694|Enterobacter phage Arya/viral segment/) | 1 | 100 | 100 |

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

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

**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 blue arrow points to the genome accession number for Enterobacter phage Arya.

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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 **red stars**. N/A

**Phylogeny:** The phylogenetic tree was constructed using the MCP proteins from Arya and related phages with phylogeny.fr in “one click” mode [6]. "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 [7] for details." The members of the *Aryavirus* are indicated with a **blue rectangle**.

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1. **To create a new subfamily *Iiscvirinae***

**Origin of the name of this taxon:** This taxon is named in honour of The Indian Institute of Science (IISc; https://iisc.ac.in/) which was established in 1909 by a visionary partnership between the industrialist Jamsetji Nusserwanji Tata, the Mysore royal family and the Government of India. It was at IISC that F.F. Dias and J.V. Bhat characterized phages for Aerobacter aerogenes (<https://pubmed.ncbi.nlm.nih.gov/14325890/>).

**Rationale:** Members of the two genera share approximately 60% overall DNA sequence similarity.

1. **To move *Jilinvirus* and *Aryavirus* to this subfamily**

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