

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

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| **Code assigned:** | ***2023.029B*** |  |
| **Short title:** To create a new subfamily *Guarnerosvirinae* with three genera [*Caudoviricetes*] | | |
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**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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**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)** | Y |

|  |  |  |
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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
| Guarnerosvirinae | Gabriel Guarneros Peña | Y |
|  |  |  |

**Submission dates**

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

|  |
| --- |
| 2023.029B.N.v1.Guarnerosvirinae\_nsf.xlsx |

**Abstract**

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| This new subfamily consists of three genera, *Torontovirus, Mechnikovvirus*, and *Beetrevirus*, which possess, on average, 39.0 kb (62.9 mol%G+C) genomes which encode 55 proteins. They share at least 28.1% DNA sequence similarity and 35 protein homologs (59.3%). These values are consistent with the establishment of a subfamily. The TBLASTX (ViPTree) analysis suggests that this subfamily and *Casadabanvirus* may form a new family. |

**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 [1,2] – 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].  **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 [10]. | |

**Supporting evidence**

**Preliminary statement:** A recent analysis of the *Beetrevirus* for new species revealed that this genus is not monophyletic.

**Proposals Data:**

1. **Create a new genus,** ***Torontovirus,* with seven species**
2. **Create a new genus *Mechnikovvirus,* with six species**
3. **Create a new subfamily, *Guarnerosvirinae*, for these two genera**
4. **Transfer *Beetrevirus* to this subfamily**

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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. Names highlighted in green represent current species; those in yellow are new species. Abbreviations: phg = phage; Pseu = Pseudomonas; -[P] = partial genome; -[CCG] = coding complete genome

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**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 line, green line and blue arrowhead and stars**.

**Taxonomic Proposals:**

1. **Create a new genus, *Torontovirus*, with seven species**

**Origin of the name of this taxon:** This taxon is named after the University of Toronto where many of the transposable Pseudomonas phages were isolated.

**Historical aspects:** In most cases these temperate phages were isolated from lysogenic strains in Canada and Mexico [Cady et al. 2012; Ramírez-Sánchez et al. 2023]

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage JBD25 | [JX495042.1](https://www.ncbi.nlm.nih.gov/nuccore/JX495042.1) | 39.55 | 62.5 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/52903/463945|Pseudomonas phage JBD25/viral segment/) | 100 | 100 |
| Pseudomonas phage Fc22 | [MH719191.1](https://www.ncbi.nlm.nih.gov/nuccore/MH719191.1) | 38.25 | 62.7 | [53](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83419/654428|Pseudomonas phage Fc22/viral segment/) | 80.4 | 90.9 |
| Pseudomonas phage Ps59 | [MH719195.1](https://www.ncbi.nlm.nih.gov/nuccore/MH719195.1) | 39.02 | 61.7 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83422/654431|Pseudomonas phage Ps59/viral segment/) | 71.9 | 81.8 |
| Pseudomonas phage Fc02 | [MH719189.1](https://www.ncbi.nlm.nih.gov/nuccore/MH719189.1) | 38.12 | 62.8 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83417/654426|Pseudomonas phage Fc02/viral segment/) | 81.3 | 89.1 |
| Pseudomonas phage H72 | [MH719193.1](https://www.ncbi.nlm.nih.gov/nuccore/MH719193.1) | 38.58 | 62.7 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83420/654429|Pseudomonas phage H72/viral segment/) | 82.8 | 90.9 |
| Pseudomonas phage H71 | [MH719190.1](https://www.ncbi.nlm.nih.gov/nuccore/MH719190.1) | 38.22 | 62.7 | [54](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83418/654427|Pseudomonas phage H71/viral segment/) | 80.8 | 85.4 |
| Pseudomonas phage UMP151 | [MK934841.1](https://www.ncbi.nlm.nih.gov/nuccore/MK934841.1) | 41.3 | 62.8 | [56](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/82303/596074|Pseudomonas phage UMP151/viral segment/) | 83.3 | 94.6 |

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

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

**Specific reference:** Cady KC, Bondy-Denomy J, Heussler GE, Davidson AR, O'Toole GA. The CRISPR/Cas adaptive immune system of Pseudomonas aeruginosa mediates resistance to naturally occurring and engineered phages. J Bacteriol. 2012 Nov;194(21):5728-38. doi: 10.1128/JB.01184-12. Epub 2012 Aug 10. PMID: 22885297; PMCID: PMC3486085.

Ramírez-Sánchez I, Magos-Castro M, Guarneros G. Transcriptional analysis in bacteriophage Fc02 of *Pseudomonas aeruginosa* revealed two overlapping genes with exclusion activity. Front Microbiol. 2023 Feb 3;14:1027380. doi: 10.3389/fmicb.2023.1027380. PMID: 36819063; PMCID: PMC9936078.

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive genus.

1. **Create a new genus** ***Mechnikovvirus*, with six species**

**Origin of the name of this taxon:** This taxon is named in honour of the Mechnikov Research Institute for Vaccines & Sera, Russian Academy of Medical Sciences where much of the pioneering studies on Pseudomonas transposable phages was conducted by Professor Victor Krylov.

**Historical aspects:** This group of phages includes several vB\_PaeS\_PM105, JBD67 and JBD18 which were recognized species in the genus *Beetrevirus*.

**Genome summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Pseudomonas phage JBD67 | [JX495043.1](https://www.ncbi.nlm.nih.gov/nuccore/JX495043.1) | 38.23 | 63.2 | [52](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/71807/399675|Pseudomonas phage JBD67/viral segment/) | 100 | 100 |
| Pseudomonas phage Ps60 | [MH719194.1](https://www.ncbi.nlm.nih.gov/nuccore/MH719194.1) | 39.68 | 63.2 | [56](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/83421/654430|Pseudomonas phage Ps60/viral segment/) | 81.5 | 96.1 |
| Pseudomonas phage vB\_Pae-SS2019XII | [MN536027.1](https://www.ncbi.nlm.nih.gov/nuccore/MN536027.1) | 39.7 | 63.6 | [55](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85374/740775|Pseudomonas phage vB_Pae-SS2019XII/viral segment/) | 82.8 | 92.3 |
| Pseudomonas phage vB\_Pae\_CF78a | [MK511059.1](https://www.ncbi.nlm.nih.gov/nuccore/MK511059.1) | 39.71 | 63.5 | [57](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/79123/494001|Pseudomonas phage vB_Pae_CF78a/viral segment/) | 89.4 | 94.2 |

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

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

**Conclusion:** On the basis of DNA (Fig. 1) and protein (Fig. 2) similarity this is a cohesive genus.

1. **Create a new subfamily, *Guarnerosvirinae*, for these genera**

**Origin of the name of this taxon:** This taxon is named in honour of Mexican virologist Gabriel Guarneros Peña (b. Mexico City, 1941). B.Sc. mayor in Chemistry, Bacteriology and Parasitology. M. Sc. in Biochemistry (CINVESTAV, Mexico City) and Ph. D in Molecular Biology (University of California, Berkeley). Phage work on site specific recombination in bacteriophage lambda and on expression of very short ORFs named minigenes in lambda genome. Recently switched to genomics of Pseudomonas aeruginosa phages. He was responsible for the isolation and characterization of many of the phages described in this Taxonomy Proposal. Currently: Profesor Emérito, Departamento de Genética y Biología Molecular, CINVESTAV, México.



**(reproduced from:** <https://genetica.cinvestav.mx/Personal-Acad%C3%A9mico/Dr-Gabriel-Guarneros-Pe%C3%B1a>**)**

**Rationale:** This new subfamily consists of three genera, *Davidsonvirus, Mechnikovvirus,* and *Beetrevirus*, which possess, on average, 39.0 kb (62.9 mol%G+C) genomes which encode 55 proteins. They share at least 28.1% DNA sequence similarity and 35 protein homologs (59.3%). These values are consistent with the establishment of a subfamily [10]. The TBLASTX (ViPTree) analysis suggests that this subfamily and *Casadabanvirus* may form a new family.

1. **Transfer *Beetrevirus* to this subfamily**

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

**Historical aspects:** This taxon was created through Taxonomy Proposal 2018.140B.A.v1.Beetrevirus. Based upon the VIRIDIC and ViPTree analyses presented above this taxon is not monophyletic

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