

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

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| **Code assigned:** | ***2023.011B*** |  |
| **Short title:** To add three new genera to the subfamily *Braunvirinae* [*Caudoviricetes*; *Drexlerviridae*] | | |
|  | | |

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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**

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

|  |
| --- |
| 2023.011B.N.v1.Braunvirinae\_3ng.xlsx |

**Abstract**

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| We have reassessed the subfamily *Braunvirinae* identifying three new genera: *Inhoffenstrassevirus, Augustepiccardvirus* and *Julespiccardvirus*. |

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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].  **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**

**Proposals:**

1. **Create a new single-species genus, *Inhoffenstrassevirus*.**
2. **Create a new single-species genus, *Augustepiccardvirus*.**
3. **Create a new single-species genus, *Julespiccardvirus*.**
4. **To add one new species to the genus *Rtpvirus*.**
5. **To transfer *Guelphvirus EC3a* to *Loudonvirus.***
6. **To add four new species to the genus *Veterinaerplatzvirus*.**
7. **To add one new species to the genus *Guelphvirus*.**

**Proposals Data:**

**A picture containing text, screenshot, line, colorfulness

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; Shig = Shigella; Ente = Enterobacteria; Esch = Escherichia. Because of the magnification we have attached a file Braunvirinae\_3ng\_Suppl.xlsx which permits easier visualization.

**![A close-up of a newspaper

Description automatically generated with low confidence]()**

**![A screenshot of a computer screen

Description automatically generated with low 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**.

**Taxonomic Proposals:**

1. **Create a new single-species genus, *Inhoffenstrassevirus*.**

**Origin of the name of this taxon:** The name of this taxon derives from the address (Inhoffenstr. 7B) of the Bioeconomy and Health Research, Leibniz-Institute DSMZ - German Collection of Microorganisms and Cell Cultures where this phage was isolated.

**Historical aspects:** Lytic siphophage Escherichia phage vB\_EcoS\_MM01 was isolated in Germany from horse dung against Escherichia coli.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage vB\_EcoS\_MM01 | [MK373793.1](https://www.ncbi.nlm.nih.gov/nuccore/MK373793.1) | 43.16 | 43.8 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/80028/559673|Escherichia phage vB_EcoS_MM01/viral segment/) | 1 | 100.0 | 100 |

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

1. **Create a new single-species genus, *Augustepiccardvirus*.**

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of one the first virus of its type, Escherichia phage AugustePiccard strain Bas01.

**Historical aspects:** This lytic siphophage was isolated against E. coli K-12 [Maffei et al. 2021].

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage AugustePiccard strain Bas01 | [MZ501051.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ501051.1) | 50.13 | 44.8 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/108323/1741295|Escherichia phage AugustePiccard/viral segment/) | 1 | 100.0 | 100 |

**Specific reference:** Maffei E, Shaidullina A, Burkolter M, Heyer Y, Estermann F, Druelle V, Sauer P, Willi L, Michaelis S, Hilbi H, Thaler DS, Harms A. Systematic exploration of Escherichia coli phage-host interactions with the BASEL phage collection. PLoS Biol. 2021 Nov 16;19(11):e3001424. doi: 10.1371/journal.pbio.3001424. PMID: 34784345; PMCID: PMC8594841.

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

1. **Create a new single-species genus, *Julespiccardvirus*.**

**Origin of the name of this taxon:** The name of this taxon derives directly from the name of one the first virus of its type, Escherichia phage JulesPiccard.

**Historical aspects:** This lytic siphophage was isolated from sewage plant inflow against E.coli K12 [Maffei et al. 2021].

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage JulesPiccard | [MZ501087.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ501087.1) | 47.73 | 44.7 | [89](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/108325/1741297|Escherichia phage JulesPiccard/viral segment/) | 1 | 100.0 | 100 |

**Specific reference:** Maffei E, Shaidullina A, Burkolter M, Heyer Y, Estermann F, Druelle V, Sauer P, Willi L, Michaelis S, Hilbi H, Thaler DS, Harms A. Systematic exploration of Escherichia coli phage-host interactions with the BASEL phage collection. PLoS Biol. 2021 Nov 16;19(11):e3001424. doi: 10.1371/journal.pbio.3001424. PMID: 34784345; PMCID: PMC8594841.

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

1. **To add one new species to the genus *Rtpvirus*.**

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

**Historical aspects:** This genus was established via taxonomy proposal 2019.100B. Lytic siphophage ZL19 was isolated by Gao et al. [2022]

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Bacteriophage RTP | [AM156909.1](https://www.ncbi.nlm.nih.gov/nuccore/AM156909.1) | 46.22 | 44.3 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/5671/891132|Escherichia phage Rtp/viral segment Unknown/) | 0 | 100.0 | 100 |
| Escherichia phage ZL19 | [OM258170.1](https://www.ncbi.nlm.nih.gov/nuccore/OM258170.1) | 47.88 | 44.5 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/116310/1896990|Escherichia phage ZL19/viral segment/) | 0 | 71.4 | 89.3 |

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

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

**Specific reference:** Gao LA, Wilkinson ME, Strecker J, Makarova KS, Macrae RK, Koonin EV, Zhang F. Prokaryotic innate immunity through pattern recognition of conserved viral proteins. Science. 2022 Aug 12;377(6607):eabm4096. doi: 10.1126/science.abm4096. Epub 2022 Aug 12. PMID: 35951700; PMCID: PMC10028730.

1. **To transfer** ***Guelphvirus EC3a* to *Loudonvirus.***

**Rationale:** *Guelphvirus* currently consists of two species, *Guelphvirus ACGM12* and *Guelphvirus EC3a* (TaxoProp 2019.100B). Recent VIRIDIC and ViPTree analyses (see above) reveal that *Guelphvirus EC3a* is more closely related to *Loudonvirus* than *Guelphvirus*, necessitating a move.

1. **To add four new species to the genus *Veterinaerplatzvirus*.**

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

**Historical aspects:** This genus was established via taxonomy proposal 2020.173B.R.Veterinaerplatzvirus. Lytic Escherichia siphophages phages vB\_EcoS\_FP, JeanPiccard, 2725-N35 and vB\_EcoD\_SU57 were isolated in Portugal (poultry farm). Switzerland (forest puddle), Russia and Sweden, respectively.

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage vB\_EcoS-12210I | [MK907226.1](https://www.ncbi.nlm.nih.gov/nuccore/MK907226.1) | 44.22 | 44.4 | [65](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/85512/743671|Escherichia phage vB_EcoS-12210I/viral segment/) | 1 | 100.0 | 100 |
| Escherichia phage vB\_EcoS\_FP | [MT682706.1](https://www.ncbi.nlm.nih.gov/nuccore/MT682706.1) | 43.76 | 44.1 | [68](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93321/927366|Escherichia phage vB_EcoS_FP/viral segment/) | 1(\*\*\*) | 75.0 | 84.6 |
| Escherichia phage JeanPiccard strain Bas02 | [MZ501080.1](https://www.ncbi.nlm.nih.gov/nuccore/MZ501080.1) | 47.15 | 44.5 | [83](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/108324/1741296|Escherichia phage JeanPiccard/viral segment/) | 1 | 70.6 | 87.7 |
| Escherichia phage 2725-N35 | [MN840485.1](https://www.ncbi.nlm.nih.gov/nuccore/MN840485.1) | 45.92 | 44.0 | [75](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/86971/760226|Escherichia phage 2725-N35/viral segment/) | 1 | 72.5 | 87.7 |
| Escherichia phage vB\_EcoD\_SU57 | [MT511058.1](https://www.ncbi.nlm.nih.gov/nuccore/MT511058.1) | 46.15 | 44.0 | [77](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/93291/927336|Escherichia phage vB_EcoD_SU57/viral segment/) | 1 | 70.1 | 86.1 |

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

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

**(\*\*\*) None indicated in GenBank record. Discovered using tRNAscan-SE at** [**http://lowelab.ucsc.edu/tRNAscan-SE/**](http://lowelab.ucsc.edu/tRNAscan-SE/) **[11]**

1. **To add one new species to the genus *Guelphvirus*.**

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

**Historical aspects:** This genus was established through Taxonomy Proposal 2019.100B. Lytic siphophage vB\_EcoS\_SCS31 was isolated in Kazakhstan.

**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Escherichia phage vB\_EcoS\_ACG-M12 | [JN986845.1](https://www.ncbi.nlm.nih.gov/nuccore/JN986845.1) | 46.05 | 43.5 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/15413/459750|Escherichia phage vB_EcoS_ACG-M12/viral segment Unknown/) | 1 | 100.0 | 100 |
| Escherichia phage vB\_EcoS\_SCS31 | [ON081052.1](https://www.ncbi.nlm.nih.gov/nuccore/ON081052.1) | 46.05 | 43.5 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/117099/1911700|Escherichia phage vB_EcoS_SCS31/viral segment/) | 1 | 93.4 | 100 |

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