

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

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| **Code assigned:** | ***2023.037B*** |  |
| **Short title:** To create fifty-two (52) species in the genus *Jerseyvirus* and abolish one species [*Caudoviricetes*] | | |
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**Author(s) and email address(es)**

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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** |
|  |  |  |  |
|  |  |  |  |

**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**

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| 2023.037B.N.v1.Jerseyvirus\_52ns\_ab1sp.xlsx |

**Abstract**

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| We have added 52 new species to the genus *Jerseyvirus*. |

**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]. | |

**Supporting evidence**

**Proposals Data:**

1. **Create fifty-two (52) new species in the genus, *Jerseyvirus***

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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. The names in white boxes are strains, while those in red boxes are existing species. Abbreviations: phg = phage; vir = virus; Salm = Salmonella. Because of the number of Jersey-like phages we have attached 2023.037B.N.v1.Jerseyvirus\_52ns\_ab1sp\_Suppl.xlsx to aid the reader.

**Taxonomic Proposals:**

1. **Create 52 new species in the genus, *Jerseyvirus***

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

**Historical aspects:** This taxon was established through Taxonomy Proposal 2013.030a-dB.A.v3.Jerseylikevirus with thirteen species: *Jerseyvirus AG11, Jerseyvirus Ent1, Jerseyvirus f18SE, Jerseyvirus jersey, Jerseyvirus L13, Jerseyvirus LSPA1, Jerseyvirus SE2, Jerseyvirus SETP3, Jerseyvirus SETP7, Jerseyvirus SETP13, Jerseyvirus SP101, Jerseyvirus SS3e,* and *Jerseyvirus wksl3.* Many more exemplars of these viruses have been deposited in GenBank. All of the viruses listed below conform to the criteria with which we define species [10].

**Genome summary:**

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| --- | --- | --- |
| Phage name | INSDC | Overall % DNA sequence identity (\*) |
| Salmonella phage SETP7 | NC\_022754.1 | 100.0 |
| Salmonella phage LSPA1 | KM272358.1 | 67.9 |
| Salmonella phage vB\_SalS\_TU03 | MZ560703.1 | 62.1 |
| Salmonella phage SS5 | MK972702.1 | 80.9 |
| Salmonella phage SE-W109 | KX649889.1 | 78.9 |
| Salmonella phage horsemountain | MT074482.1 | 77.2 |
| Salmonella phage skrot | MT074483.1 | 78.8 |
| Salmonella phage blauehaus | MT074473.1 | 79.7 |
| Salmonella phage wast | MT074451.1 | 80.9 |
| Salmonella virus VSt10 | MH424445.1 | 79.6 |
| Salmonella virus VSe101 | MN393078.1 | 79.3 |
| Salmonella phage vB\_StyS-sam | LC507823.1 | 79.5 |
| Salmonella phage vB\_SenS\_TUMS\_E19 | OL519843.1 | 81.9 |
| Salmonella phage vB\_SenS\_TUMS\_E4 | MZ955866.1 | 81.5 |
| Salmonella phage demigod | MT074431.1 | 80.1 |
| Salmonella phage templet | MT074462.1 | 79.4 |
| Salmonella phage 5sent1 | MT653144.1 | 79.6 |
| Salmonella phage sidste | MT074481.1 | 79.8 |
| Salmonella virus VSe103 | MH424443.1 | 77.2 |
| Salmonella phage NBSal007 | MT677934.1 | 81.8 |
| Salmonella phage F12013 | OP745619.1 | 81.8 |
| Salmonella phage PBSE191 | OM291373.1 | 79.4 |
| Salmonella phage vB\_SenS\_PVP-SE2 | MF431252.1 | 83.5 |
| Salmonella phage vB\_SenS-EnJE1 | MN336264.1 | 81.6 |
| Salmonella phage vB\_SenS\_S532 | OK108609.1 | 80.7 |
| Salmonella phage JD01 | MW715619.1 | 77.0 |
| Salmonella phage vB\_SenS\_S528 | OK108608.1 | 77.5 |
| Salmonella phage vB\_SenS-EnJE6 | MN336265.1 | 77.8 |
| Salmonella phage F118P13 | OM339548.1 | 81.0 |
| Salmonella phage vB\_SalS-S10 | OL770276.1 | 78.6 |
| Salmonella phage vB\_SalP\_LDW16 | OP484850.1 | 79.1 |
| Salmonella phage Shelanagig | MK931446.1 | 84.0 |
| Salmonella phage NBSal006 | MT677933.1 | 82.1 |
| Salmonella phage vB\_SenS\_ER23 | MW355465.1 | 80.8 |
| Salmonella phage vB\_SenS\_ER21 | MW355463.1 | 79.0 |
| Salmonella phage S102 | MH370360.1 | 75.4 |
| Salmonella phage S100 | MH370358.1 | 78.0 |
| Salmonella phage dunkel | MT074432.1 | 78.0 |
| Salmonella phage celemicas | MT074484.1 | 78.0 |
| Salmonella phage MET\_P1\_001\_43 | OP389270.1 | 75.4 |
| Salmonella phage LPSE1 | KY379853.1 | 76.9 |
| Salmonella phage BPS11Q3 | KX405002.1 | 80.3 |
| Salmonella phage LP31 | OL436139.1 | 76.0 |
| Salmonella phage CTH7 | ON409569.1 | 76.9 |
| Salmonella phage SHWT1 | MT740291.1 | 79.3 |
| Salmonella phage SLMP1 | MW201959.1 | 73.7 |
| Salmonella phage GRNsp50 | ON720977.1 | 74.7 |
| Salmonella phage fmb-p1 | MZ274225.1 | 76.6 |
| Salmonella phage T102 | ON996339.1 | 76.3 |
| Salmonella phage ZCSE9 | OP793478.2 | 74.0 |
| Salmonella phage vB\_SenS\_SB3 | MK578530.1 | 79.9 |
| Salmonella phage vB\_SenS\_ER1 | MW355461.1 | 79.5 |
| Salmonella phage SGPC | OK169616.1 | 79.8 |
| Salmonella phage STP03 | KY176369.1 | 74.9 |
| Salmonella phage pink | MT074430.1 | 75.3 |

**(\*) VIRIDIC analysis**

**The data highlighted in yellow confirms that neither of these two strains belongs to the *Jerseyvirus*.**

1. **Abolish species *Jerseyvirus L13***

The Salmonella phage L13 (KC832325), sole member of the species *Jerseyvirus L13*, is only represented in the database by an incomplete genome sequence. We therefore request the species to be abolished.

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