

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

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| **Code assigned:** | ***2022.020B*** |  |
| **Short title:** Create one new species in the genus *Teetrevirus* (*Autographiviridae*) and one new species in the genus *Felixounavirus* (*Caudoviricetes*) |
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**Author(s) and email address(es)**

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| Rujikan Nasanit  |

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

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**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**

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| --- | --- |
| **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 | Feb 16, 2022 |
| 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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| 2022.020B.N.v1.Caudoviricetes\_2nsp.xlsx |

**Abstract**

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| Genomes ofSalmonella phage vB\_SAg-RPN15 and Salmonella phage vB\_SAg-RPN213 were fully sequenced and identified as two novel species to be included in the genus *Teetrevirus* and *Felixounavirus*, respectively. |

**Text of proposal**

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| **Species demarcation criteria:**We have chosen 95% DNA sequence identity as the criterion for demarcation of species in a genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.  |

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**Supporting evidence**

**Proposal 1: To create new species *Salmonella* *virus RPN15* in the genus** ***Teetrevirus* (*Autographiviridae*)**

**History:** Salmonella phage vB\_SAg-RPN15 was isolated from a drain water sample collected from an open market in Nakhon Pathom province, Thailand. Phage isolation and propagation used SalmonellaAgonaCBn15 that was isolated from a chicken intestine.

vB\_SAg-RPN15 virions have icosahedral heads (head length = 58.0±3.8 nm; head width = 55.9±2.1 nm) and short non-contractile tails (tail length = 11.7±1.8 nm; tail diameter = 12.0±1.9 nm)

**GenBank Summary:** Salmonella phage vB\_SAg-RPN15 and its closely related sequences in *Teetrevirus* [1]

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. of CDSs | No. tRNA | % nt seq. ident. with RPN15\*\* |
| Citrobacter phage SH2 | NC\_031092.1 | KU687348.1 | 39.16 | 50.7 | 53 | 0 | 90.20 |
| Klebsiella phage 31 | - | MN149904.1 | 39.6 | 50.4 | 46 | 0 | 86.99 |
| Citrobacter phage phiCFP-1 | NC\_028880.1 | KP313531.1 | 38.63 | 50.3 | 43 | 0 | 86.51 |
| Klebsiella phage Kpn-11mx | - | MW296877.1 | 38.77 | 50.8 | 49 | 0 | 86.22 |
| Klebsiella phage KPP-5 | - | MW600722.1 | 38.25 | 50.8 | 40 | 0 | 85.98 |
| Klebsiella phage vB\_KpnP\_Emp27 | - | MN013074.1 | 38.6 | 50.7 | 45 | 0 | 85.81 |
| Enterobacter phage E-4 | - | KP791807.1 | 39.14 | 50.5 | 52 | 0 | 85.29 |
| Yersinia phage phiYe-F10 | NC\_047755.1 | KT008108.1 | 39.21 | 50.7 | 46 | 0 | 85.05 |
| Escherichia phage ECA2 | NC\_047766.1 | KX130726.1 | 38.89 | 50.5 | 47 | 0 | 84.25 |
| Enterobacter phage E-2 | NC\_029102.1 | KP791805.1 | 36.05 | 50.6 | 41 | 0 | 83.63 |
| Salmonella phage vB\_SAg-RPN15 | - | OL800605.1 | 38.5 | 50.4 | 47 | 0\* |  |

**\*** Aragorn (v1∙2∙41) was employed to find tRNAs on the genome (http://www.ansikte.se/ARAGORN/) [2]

\*\* The overall nucleotide identity was obtained by PAirwise Sequence Comparison (PASC) [3]

**BLASTN homologs:** A neighbour joining tree between complete genome sequence of Salmonella phage vB\_SAg-RPN15 and its closely related sequences in *Teetrevirus* was constructed on the basis of BLASTN analysis at NCBI.



**Phylogeny:** Phylogenetic analyses of the major capsid proteins (A) and terminase large subunit (B) of Salmonella phage vB\_SAg-RPN15, other closely related phages in *Teetrevirus* and other genera All sequences were aligned using MUSCLE [4]. The trees were constructed by MEGA7 [5] running on neighbor-joining method with 1,000 bootstrap replication [6]. Numbers on branches represent the bootstrap percentage greater than 50%.

**A) MCP**

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**B) TerL**

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**Proposal 2: To create new species *Salmonella* *virus RPN213* in the genus *Felixounavirus***

**History:** Salmonella phage vB\_SAg-RPN213 was isolated from a drain water sample collected from an open market in Nakhon Pathom province, Thailand. Phage isolation and propagation used SalmonellaAgonaPco213 that was isolated from a pig intestine.

vB\_SAg-RPN213 virions have icosahedral heads (head length = 67.0±2.3 nm; head width = 63.5±2.3 nm) and long contractile tails (tail length = 107.8±4.9 nm; tail diameter = 17.0±2.5 nm)

**GenBank Summary:** Salmonella phage vB\_SAg-RPN213 and its closely related sequences in *Felixounavirus* [1]

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq | INSDC | Size (kb) | GC% | No. of CDSs | No. tRNA | % nt seq. ident. with RPN213\*\* |
| Salmonella phage ph2-2 | - | OL474141.1 | 85.94 | 38.8 | 128 | 0 | 92.27 |
| Salmonella phage D1-2 | - | MN481367.1 | 86.88 | 38.7 | 128 | 23 | 91.60 |
| Salmonella phage BPSELC-1 | - | MN227145.1 | 87 | 38.8 | 125 | 19 | 91.45 |
| Salmonella phage BPS17W1 | NC\_042097.1 | MG646669.1 | 87.61 | 38.8 | 129 | 0 | 91.42 |
| Salmonella phage BPS17S6 | - | MG646671.1 | 87.63 | 38.8 | 129 | 0 | 91.41 |
| Salmonella phage vB Seyj1-1 | - | MW423797.1 | 88.8 | 38.7 | 129 | 0 | 90.38 |
| Escherichia phage JN01 | - | MN882542.1 | 88.36 | 38.8 | 97 | 0 | 90.05 |
| Salmonella phage BPS17L1 | NC\_042096.1 | MG646672.1 | 84.92 | 38.9 | 126 | 0 | 89.85 |
| Escherichia phage finno | - | MN850619.1 | 87.54 | 38.9 | 123 | 24 | 89.05 |
| Salmonella phage vB\_SPuM\_SP116 | NC\_027329.1 | KP010413.1 | 87.51 | 38.8 | 126 | 22 | 88.71 |
| Salmonella phage vB\_SAg-RPN213 | - | OL800606.1 | 86.12 | 38.7 | 131 | 22\* |  |

**\*** Aragorn (v1∙2∙41) was employed to find tRNAs on the genome (http://www.ansikte.se/ARAGORN/) [2]

\*\* The overall nucleotide identity was obtained by PAirwise Sequence Comparison (PASC) [3]

**BLASTN homologs:** A neighbour joining tree between complete genome sequence of Salmonella phage vB\_SAg-RPN213 and its closely related sequences in *Felixounavirus* was constructed on the basis of BLASTN analysis at NCBI.



**Phylogeny:** Phylogenetic analyses of the major capsid proteins (A) and terminase large subunit (B) of Salmonella phage vB\_SAg-RPN213, other closely related in *Felixounavirus* and other genera. All sequences were aligned using MUSCLE [4]. The trees were constructed by MEGA7 [5] running on neighbor-joining method with 1,000 bootstrap replication [6]. Numbers on branches represent the bootstrap percentage greater than 50%.

**A) MCP**

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**B) TerL**

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**References**

1. Sayers EW, Beck J, Brister JR, Bolton EE, Canese K, Comeau DC, et al. (2020) Database resources of the National Center for Biotechnology Information. Nucleic Acids Res 48:D9-D16. doi: 10.1093/nar/gkz899. PMID: 31602479.

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6. Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39:783–791. DOI: 10.2307/2408678.