

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.138B** |  |
| **Short title:** Create four new species in the genus *Rosemountvirus* (*Caudovirales*: *Myoviridae*) | | |
|  | | |

**Author(s) and email address(es)**

|  |  |
| --- | --- |
| Adriaenssens EM, Tolstoy I, Turner D, Kropinski AM | [evelien.adriaenssens@quadram.ac.uk](mailto:evelien.adriaenssens@quadram.ac.uk);  [tolstoy@ncbi.nlm.nih.gov](mailto:tolstoy@ncbi.nlm.nih.gov);  [dann2.turner@uwe.ac.uk](mailto:dann2.turner@uwe.ac.uk);  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com) |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Quadram Institute Bioscience, UK [EMA]  NCBI, USA [IT]  University of the West of England, UK [DT]  University of Guelph, Canada [AMK] |

**Corresponding author**

|  |
| --- |
| Andrew Kropinski |

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

|  |
| --- |
| *Caudovirales* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**ICTV study group comments and response of proposer**

|  |
| --- |
|  |

**Authority to use the name of a living person**

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
|  |  |  |
|  |  |  |
|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | May 2020 |
| Date of this revision (if different to above) |  |

**ICTV-EC comments and response of the proposer**

|  |
| --- |
|  |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

|  |
| --- |
| 2020.138B.R.Rosemountvirus.xlsx |

**Abstract**

|  |
| --- |
| Since its approval in 2019 many more species and strains of *Rosemountvirus* have been deposited with GenBank. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | **Species demarcation criteria:** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm. Members of the same species all share >95% nucleotide identity with all other members of the species. | |

**Supporting evidence**

**Source of the name of this taxon:** NA

**History:** NA

**Specific Reference:** NA

**VIRIDIC heatmap 1:** VIRIDIC (Virus Intergenomic Distance Calculator; 10) computes pairwise intergenomic distances/similarities amongst phage genomes. The green coloured genome corresponds to the only existing species in the genus *Rosemountvirus*. Black boxes indicate strains.



**GenBank summary**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Exemplar isolate | Accession | Genome size (bp) | GC% | # CDS | Nucleotide identity with type species exemplar (%)\* |
| Salmonella phage SE13 | MK770411.1 | 52,438 | 45.8 | 73 | 90.6 |
| Salmonella phage yarpen | MT074436.1 | 52,464 | 46.0 | 69 | 95.0 |
| Salmonella phage birk | MT074439.1 | 52,767 | 45.8 | 74 | 94.7 |
| Salmonella phage UPF\_BP2 | KX826077.1 | 54,894 | 46.0 | 70 | 95.9 |

\* type species exemplar: Salmonella phage BP63 (KM366099), nucleotide identity with VIRIDIC. Members of the same species all share >95% nucleotide identity with all other members of the species.

**Strain table**

|  |  |  |
| --- | --- | --- |
| **Phage** | **Accession** | **Belongs to species** |
| Salmonella phage emhyr | MT074444 | *Salmonella virus yarpen* |
| Salmonella phage renfri | MT074445 | *Salmonella virus yarpen* |
| Salmonella phage rivia | MT074438 | *Salmonella virus yarpen* |
| Salmonella phage nenneke | MT074437 | *Salmonella virus yarpen* |
| Salmonella phage zoltan | MT074443 | *Salmonella virus yarpen* |
| Salmonella phage emiel | MT074434 | *Salmonella virus yarpen* |
| Salmonella phage triss | MT074446 | *Salmonella virus yarpen* |
| Salmonella phage LSE7621 | MK568062 | *Salmonella virus BP63* |
| Salmonella phage vB\_SenM\_PA13076 | MF740800 | *Salmonella virus BP63* |
| Salmonella phage 8-19 | MN379740 | *Salmonella virus BP63* |
| Salmonella phage brunost | MT074441 | *Salmonella virus BP63* |
| Salmonella phage ciri | MT074442 | *Salmonella virus UPFBP2* |

**Electron micrograph:** NA

**Phylogeny:** NA

**References**

1. Sayers EW, Agarwala R, Bolton EE, Brister JR, Canese K, Clark K, et al. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2019;47(D1):D23-D28. doi: 10.1093/nar/gkz899. PMID: 31602479.
2. Tolstoy I, Kropinski AM, Brister JR. Bacteriophage Taxonomy: An Evolving Discipline. Methods Mol Biol. 2018;1693:57-71. doi: 10.1007/978-1-4939-7395-8\_6. PMID: 29119432.
3. O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, et al. Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic Acids Res. 2016;44(D1):D733-45. doi: 10.1093/nar/gkv1189. PMID: 26553804.
4. Agren J, Sundström A, Håfström T, Segerman B. Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. PLoS One. 2012;7(6): doi: 10.1371/journal.pone.0039107. PMID: 22723939.
5. Chan PP, Lowe TM. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 2019;1962:1-14. doi: 10.1007/978-1-4939-9173-0\_1. PMID: 31020551.
6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564.
7. Darling AE, Mau B, Perna NT. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One. 2010;5(6):e11147. doi: 10.1371/journal.pone.0011147. PMID: 20593022.
8. Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res. 2008;36(Web Server issue):W465-9. doi: 10.1093/nar/gkn180. Epub 2008 Apr 19. PMID: 18424797.
9. Anisimova M, Gascuel O. Approximate likelihood-ratio test for branches: A fast, accurate, and powerful alternative. Syst Biol. 2006;55(4):539-52. PMID: 16785212. DOI: 10.1080/10635150600755453.
10. Moraru C. VIRIDIC (Virus Intergenomic Distance Calculator) computes pairwise intergenomic distances/similarities amongst phage genomes. <http://kronos.icbm.uni-oldenburg.de/viridic/>