

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

|  |  |  |
| --- | --- | --- |
| **Code assigned:** | **2020.141B** |  |
| **Short title:** Create six new genera and 14 new species (*Ligamenvirales*: *Rudiviridae*) | | |
|  | | |

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

|  |  |
| --- | --- |
| Krupovic M, Baquero DP, Prangishvili D | [mart.krupovic@pasteur.fr](mailto:mart.krupovic@pasteur.fr); [diana-paola.baquero-uriza@pasteur.fr](mailto:diana-paola.baquero-uriza@pasteur.fr); [david.prangishvili@pasteur.fr](mailto:david.prangishvili@pasteur.fr) |

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

|  |
| --- |
| Institut Pasteur, France [MK, DPB, DP] |

**Corresponding author**

|  |
| --- |
| Mart Krupovic |

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

|  |
| --- |
| Bacterial and Archaeal Viruses Subcommittee |

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

|  |
| --- |
| Archaeal viruses SG, Bacterial and Archaeal Viruses Subcommittee |

**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 | July 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**

|  |
| --- |
| 2020.141B.R.Rudiviridae.xlsx |

**Abstract**

|  |
| --- |
| This proposal provides a justification for expansion of the family *Rudiviridae* through creation of 6 new genera and 14 new species. Furthermore, the existing genus, *Rudivirus*, is proposed to be renamed and one of the three species moved into a new genus. |

**Text of proposal**

|  |  |
| --- | --- |
| |  | | --- | | Family *Rudiviridae* includes rod-shaped, non-enveloped viruses with linear dsDNA genomes infecting hyperthermophilic archaea of the order Sulfolobales. Currently, the family includes a single genus, *Rudivirus*, with three species, *Acidianus rod-shaped virus 1*, *Sulfolobus islandicus rod-shaped virus 1* and *Sulfolobus islandicus rod-shaped virus 2* (type species). During the past decade, 16 additional rudivirus genomes have been sequenced but none has been officially classified (Table 1). Thirteen of these genomes have been sequenced from viruses isolates [1-4], whereas 3 (near) complete genomes were obtained by metagenomics [5-7] (Table 1).  Phylogenomic analysis of all available rudivirus genomes using the Genome-BLAST Distance Phylogeny method implemented in VICTOR [8] showed that the 19 sequenced rudiviruses fall into seven well-separated clades (Figure 1), roughly corresponding to the geographical origins of the virus isolation, suggesting local adaptation of the corresponding viruses [2]. Viruses within these clades (when more than one virus is present per clade) display over 50% sequence identity (Figure 2), as determined using Gegenees [9], which fragments the genomes and calculates symmetrical identity scores for each pairwise comparison based on BLASTn hits and a genome length. By contrast, between the clades the viruses share only fragments of the genome (typically below 50% of the genome/genes). For instance, ARV1 and SIRV2, two of the currently classified viruses, display 70.69% over only 19% of their genomes. Accordingly, viruses from the seven clades differ considerably in terms of the variable gene contents. For instance, viruses SIRV1 and SIRV2 isolated in Iceland share 11 genes that are absent from the viruses isolated from the United States [1]. Thus, we propose to establish six new genera for classification of the viruses forming the seven clades recognized by phylogenomic analysis. Furthermore, we propose renaming the existing genus, *Rudivirus*, to *Icerudivirus*, to avoid confusion due to the same stem in the family and genus names. Given that the clades generally correspond to the geographical locations of the isolation of the corresponding viruses, we propose the following names for the genera: *Usarudivirus, Mexirudivirus*, *Azorudivirus*, *Itarudivirus*, *Japarudivirus* and *Hoswirudivirus.* The latter name reflects the finding that members of this genus appear to experience frequent host switching events (i.e., hoswi-, for host switching) [2]. To assist future classification of rudiviruses, we propose that members of the same genus will form a monophyletic clade in phylogenomic analyses and share more than 50% of genome sequence similarity.  Species demarcation criteria have not been previously proposed, due to scarcity of available representatives. We propose to use a 95% global genome identity as a species demarcation criterion, to be consistent with the thresholds used for other prokaryotic viruses. Gegenees analysis has shown that viruses SIRV5, SIRV6 and SIRV7 (Table 1) share more than 95% sequence identity and should be considered as strains of the same virus. The assignment of unclassified rudiviruses to species and genera is provided in Table 2. Furthermore, we propose renaming the existing species to binomial format with freeform epithet, to match other proposed species. Namely, *Acidianus rod-shaped virus 1*, *Sulfolobus islandicus rod-shaped virus 1* and *Sulfolobus islandicus rod-shaped virus 2* would become *Itarudivirus ARV1*, *Icerudivirus SIRV1* and *Icerudivirus SIRV2*, respectively. | |

**Supporting evidence**

****

**Figure 1.** Inferred phylogenomic tree of all known members of the Rudiviridae family based on whole genome VICTOR [8] analysis at the amino acid level. The tree is rooted with lipothrixviruses, and the branch length is scaled in terms of the Genome BLAST Distance Phylogeny (GBDP) distance formula D6. Only branch support values >70% are shown. For each genome, the abbreviated virus name and GenBank/RefSeq accession number are indicated. The dashed line highlights the seven clades corresponding to the proposed genera. The tree is divided into colored blocks according to the proposed genus-level classification, with the names of the proposed genera indicated on the right.

****

**Figure 2.** Comparison of the rudivirus genome sequences using the Gegenees tool (BLASTN mode and cutoff threshold for non-conserved material of 40%).

**Table 1. Properties of rudiviruses.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Virus name** | **Abbreviation** | **Host** | **GenBank** | **GC%** | **Size, bp** | **Proteins** |
| Sulfolobus islandicus rod-shaped virus 1 | SIRV1 | *Sulfolobus islandicus* KVEM10H3 | AJ414696 | 25.3 | 32308 | 45 |
| Sulfolobus islandicus rod-shaped virus 2 | SIRV2 | *S. islandicus* LAL14/1 | AJ344259 | 25.2 | 35450 | 54 |
| Acidianus rod-shaped virus 1 | ARV1 | *Acidianus pozzuoliensis* | AJ875026 | 39.1 | 24655 | 41 |
| Sulfolobus islandicus rod-shaped virus 3 | SIRV3 | *S. islandicus* LAL14/1 | KX712143 | 25.5 | 32995 | 45 |
| Sulfolobus islandicus rod-shaped virus 4 | SIRV4 | *S. islandicus* M.16.27 | KY744231 | 25.6 | 35035 | 54 |
| Sulfolobus islandicus rod-shaped virus 5 | SIRV5 | *S. islandicus* NL10.C31.E08 | KY744233 | 25.4 | 36306 | 57 |
| Sulfolobus islandicus rod-shaped virus 6 | SIRV6 | *S. islandicus* Y08.82.36 | KY744235 | 25.5 | 35439 | 56 |
| Sulfolobus islandicus rod-shaped virus 7 | SIRV7 | *S. islandicus* M.16.30 | KY744232 | 25.6 | 34190 | 52 |
| Sulfolobus islandicus rod-shaped virus 8 | SIRV8 | *S. islandicus* M.16.4 | KY744229 | 25.1 | 36493 | 61 |
| Sulfolobus islandicus rod-shaped virus 9 | SIRV9 | *S. islandicus* M.16.4 | KY744228 | 24.9 | 36391 | 58 |
| Sulfolobus islandicus rod-shaped virus 10 | SIRV10 | *S. islandicus* M.16.4 | KY744230 | 25.4 | 32735 | 49 |
| Sulfolobus islandicus rod-shaped virus 11 | SIRV11 | *S. islandicus* Y08.82.36 | KY744234 | 25.8 | 33356 | 50 |
| Acidianus rod-shaped virus 3 | ARV3 | *A. brierleyi* POZ9 | MN876842 | 32 | 23666 | 33 |
| Metallosphaera rod-shaped virus 1 | MRV1 | *Metallosphaera sedula* POZ202 | MN876843 | 34.1 | 20269 | 27 |
| Saccharolobus solfataricus rod-shaped virus 1 | SSRV1 | *Saccharolobus solfataricus* POZ149 | MN876841 | 32.3 | 26097 | 37 |
| Stygiolobus rod-shaped virus | SRV | *Stygiolobus* sp. | FM164764 | 29.3 | 28096 | 37 |
| Acidianus rod-shaped virus 2 | ARV2 | metagenomics | KP282675 | 32.3 | 29763 | 43 |
| Sulfolobales Mexican rod-shaped virus 1 | SMRV1 | metagenomics | JX944686 | 46.6 | 27431 | 37 |
| Sulfolobales Beppu rod-shaped virus 1 | SBRV1 | metagenomics | MK064565 | 26.8 | 34025 | 60 |

Classified viruses are underlined.

**Table 2. Proposed classification of rudiviruses.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Virus name** | **Abbreviation** | **Species** | **Genus** |
| Sulfolobus islandicus rod-shaped virus 1 | SIRV1 | *Icerudivirus* *SIRV1\** | *Icerudivirus#* |
| Sulfolobus islandicus rod-shaped virus 2 | SIRV2 | *Icerudivirus SIRV2\** |
| Sulfolobus islandicus rod-shaped virus 3 | SIRV3 | *Icerudivirus SIRV3* |
| Sulfolobus islandicus rod-shaped virus 4 | SIRV4 | *Usarudivirus SIRV4* | *Usarudivirus* |
| Sulfolobus islandicus rod-shaped virus 5 | SIRV5 | *Usarudivirus SIRV5* |
| Sulfolobus islandicus rod-shaped virus 6 | SIRV6 | *Usarudivirus SIRV5* |
| Sulfolobus islandicus rod-shaped virus 7 | SIRV7 | *Usarudivirus SIRV5* |
| Sulfolobus islandicus rod-shaped virus 8 | SIRV8 | *Usarudivirus SIRV8* |
| Sulfolobus islandicus rod-shaped virus 9 | SIRV9 | *Usarudivirus SIRV9* |
| Sulfolobus islandicus rod-shaped virus 10 | SIRV10 | *Usarudivirus SIRV10* |
| Sulfolobus islandicus rod-shaped virus 11 | SIRV11 | *Usarudivirus SIRV11* |
| Acidianus rod-shaped virus 1 | ARV1 | *Itarudivirus ARV1@* | *Itarudivirus* |
| Acidianus rod-shaped virus 2 | ARV2 | *Hoswirudivirus ARV2* | *Hoswirudivirus* |
| Acidianus rod-shaped virus 3 | ARV3 | *Hoswirudivirus ARV3* |
| Metallosphaera rod-shaped virus 1 | MRV1 | *Hoswirudivirus MRV1* |
| Saccharolobus solfataricus rod-shaped virus 1 | SSRV1 | *Hoswirudivirus SSRV1* |
| Stygiolobus rod-shaped virus | SRV | *Azorudivirus SRV* | *Azorudivirus* |
| Sulfolobales Mexican rod-shaped virus 1 | SMRV1 | *Mexirudivirus SMRV1* | *Mexirudivirus* |
| Sulfolobales Beppu rod-shaped virus 1 | SBRV1 | *Japarudivirus SBRV1* | *Japarudivirus* |

\* - species renamed; *#* - genus renamed; @ - species renamed and moved to a new genus*.*

**References**

1. Bautista MA, Black JA, Youngblut ND, Whitaker RJ. Differentiation and Structure in Sulfolobus islandicus Rod-Shaped Virus Populations. Viruses. 2017; 9(5):120. doi: 10.3390/v9050120. PMID: 28534836
2. Baquero DP, Contursi P, Piochi M, Bartolucci S, Liu Y, Cvirkaite-Krupovic V, Prangishvili D, Krupovic M. New virus isolates from Italian hydrothermal environments underscore the biogeographic pattern in archaeal virus communities. ISME J. 2020; 14(7):1821-1833. doi: 10.1038/s41396-020-0653-z. PMID: 32322010
3. Erdmann S, Le Moine Bauer S, Garrett RA. Inter-viral conflicts that exploit host CRISPR immune systems of Sulfolobus. Mol Microbiol. 2014; 91(5):900-17. doi: 10.1111/mmi.12503. PMID: 24433295
4. Vestergaard G, Shah SA, Bize A, Reitberger W, Reuter M, Phan H, Briegel A, Rachel R, Garrett RA, Prangishvili D. Stygiolobus rod-shaped virus and the interplay of crenarchaeal rudiviruses with the CRISPR antiviral system. J Bacteriol. 2008; 190(20):6837-45. doi: 10.1128/JB.00795-08. PMID: 18723627
5. Gudbergsdóttir SR, Menzel P, Krogh A, Young M, Peng X. Novel viral genomes identified from six metagenomes reveal wide distribution of archaeal viruses and high viral diversity in terrestrial hot springs. Environ Microbiol. 2016; 18(3):863-74. doi: 10.1111/1462-2920.13079. PMID: 26439881
6. Liu Y, Brandt D, Ishino S, Ishino Y, Koonin EV, Kalinowski J, Krupovic M, Prangishvili D. New archaeal viruses discovered by metagenomic analysis of viral communities in enrichment cultures. Environ Microbiol. 2019; 21(6):2002-2014. doi: 10.1111/1462-2920.14479. PMID: 30451355
7. Servín-Garcidueñas LE, Peng X, Garrett RA, Martínez-Romero E. Genome sequence of a novel archaeal rudivirus recovered from a mexican hot spring. Genome Announc. 2013; 1(1):e00040-12. doi: 10.1128/genomeA.00040-12. PMID: 23405288
8. Meier-Kolthoff JP, Göker M. VICTOR: genome-based phylogeny and classification of prokaryotic viruses. Bioinformatics. 2017; 33(21):3396-3404. doi: 10.1093/bioinformatics/btx440. PMID: 29036289
9. 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):e39107. doi: 10.1371/journal.pone.0039107. PMID: 22723939