

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

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| **Code assigned:** | ***2023.012B*** |  |
| **Short title:** **To create seventeen (17) new species in the genus *Schiekvirus* andeleven (11) new species in the genus *Kochikohdavirus* (Subfamily: *Brockvirinae*, Family: *Herelleviridae*)** |
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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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| *Schitoviridae* Study Group, Bacterial and Archaeal Viruses Subcommittee*Herelleviridae* Study Group, Bacterial and Archaeal Viruses Subcommittee |

**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** |
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**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 |

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| **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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| 2023.012B.N.v1.Brockvirinae\_28ns.xlsx |

**Abstract**

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| Here, we propose the creation of seventeen (17) new species in the genus *Schiekvirus* and the creation of eleven (11) new species in the genus *Kochikohdavirus* based on genome-based comparisons. |

**Text of proposal**

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| Here, we propose the creation of seventeen (17) new species in the genus *Schiekvirus* and the creation of eleven (11) new species in the genus *Kochikohdavirus* based on genome-based comparisons.Several new candidates for the genus Schiekvirus were recently published [1-3]. Candidates for the genus *Kochikohdavirus* were recently published [4-6].**Origin of the name of proposed taxa:** The names of all proposed species were derived from (simplified) names of exemplar isolates.**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 VIRIDIC [7, 8]. The new species are:

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| *Schiekvirus Efsszw1* | MH791397.1 | Enterococcus phage EfsSzw-1 |
| *Schiekvirus Shef13* | OL799258.1 | Enterococcus phage phiSHEF13 |
| *Schiekvirus Tje1* | ON506927.1 | Enterococcus phage TJE1 |
| *Schiekvirus bill* | OM966901.1 | Enterococcus phage vB\_OCPT\_Bill |
| *Schiekvirus Gvesp1* | MZ333462.1 | Enterococcus phage GVEsP-1 |
| *Schiekvirus Pef771* | MN241318.1 | Enterococcus phage PEf771 |
| *Schiekvirus Efgrng* | MW004545.1 | Enterococcus phage EFGrNG |
| *Schiekvirus A2* | MT856905.1 | Enterococcus phage vB\_EfaM\_A2 |
| *Schiekvirus Tje2* | ON506928.1 | Enterococcus phage TJE2 |
| *Schiekvirus bop* | ON125307.1 | Enterococcus phage vB\_OCPT\_Bop |
| *Schiekvirus ben* | MN027503.1 | Enterococcus phage vB\_OCPT\_Ben |
| *Schiekvirus 163* | CAJDKA010000002.1 | Enterococcus phage 163 |
| *Schiekvirus Ccs1* | ON113170.1 | Enterococcus phage vB\_OCPT\_CCS1 |
| *Schiekvirus Porthos* | LR990835.1 | Enterococcus phage Porthos |
| *Schiekvirus Shef16* | OL799260.1 | Enterococcus phage phiSHEF16 |
| *Schiekvirus if6* | MT909815.1 | Enterococcus phage iF6 |
| *Schiekvirus sv113* | MZ147816.1 | Enterococcus phage 113 |
| *Kochikohdavirus kv149* | CAJDJZ010000002.1 | Enterococcus phage vB\_EfaH\_149 |
| *Kochikohdavirus Ef23* | MK721192.1 | Enterococcus phage vB\_EfaM\_Ef2.3 |
| *Kochikohdavirus Sw5* | ON286976.1 | Enterococcus phage Sw5 |
| *Kochikohdavirus Ef17h* | AP018714.1 | Enterococcus phage phiEF17H |
| *Kochikohdavirus Ef19g* | LC596379.1 | Enterococcus phage EF19G |
| *Kochikohdavirus PBEF19* | MN854830.2 | Enterococcus phage PBEF19 |
| *Kochikohdavirus car* | ON113168.1 |  Enterococcus phage vB\_OCPT\_Car |
| *Kochikohdavirus mda2* | MW633168.1 | Enterococcus phage MDA2 |
| *Kochikohdavirus kv53* | OQ420427.1 | Enterococcus phage 53 |
| *Kochikohdavirus bob* | ON113169.1 | Enterococcus phage vB\_OCPT\_Bob |
| *Kochikohdavirus EF24CP2* | AB609718.1 | Enterococcus phage phiEF24C-P2 |

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**Supporting evidence**

**Electron micrograph:** None available



VIRIDIC heat map: VIRIDIC (Virus Intergenomic Distance Calculator; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes [7, 8].

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The entire analysis was carried out by the VICTOR web service (<https://victor.dsmz.de>), a method for the genome-based phylogeny and classification of prokaryotic viruses [9]. All pairwise comparisons of the amino acid sequences were conducted using the Genome-BLAST Distance Phylogeny (GBDP) method [10] under settings recommended for prokaryotic viruses (Meier-Kolthoff and Göker, 2017).

The resulting intergenomic distances were used to infer a balanced minimum evolution tree with branch support via FASTME including SPR postprocessing [11] for D6. Branch support was inferred from 100 pseudo-bootstrap replicates each. Trees were rooted at the midpoint [12] and visualized with ggtree [13].

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