

**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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**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**

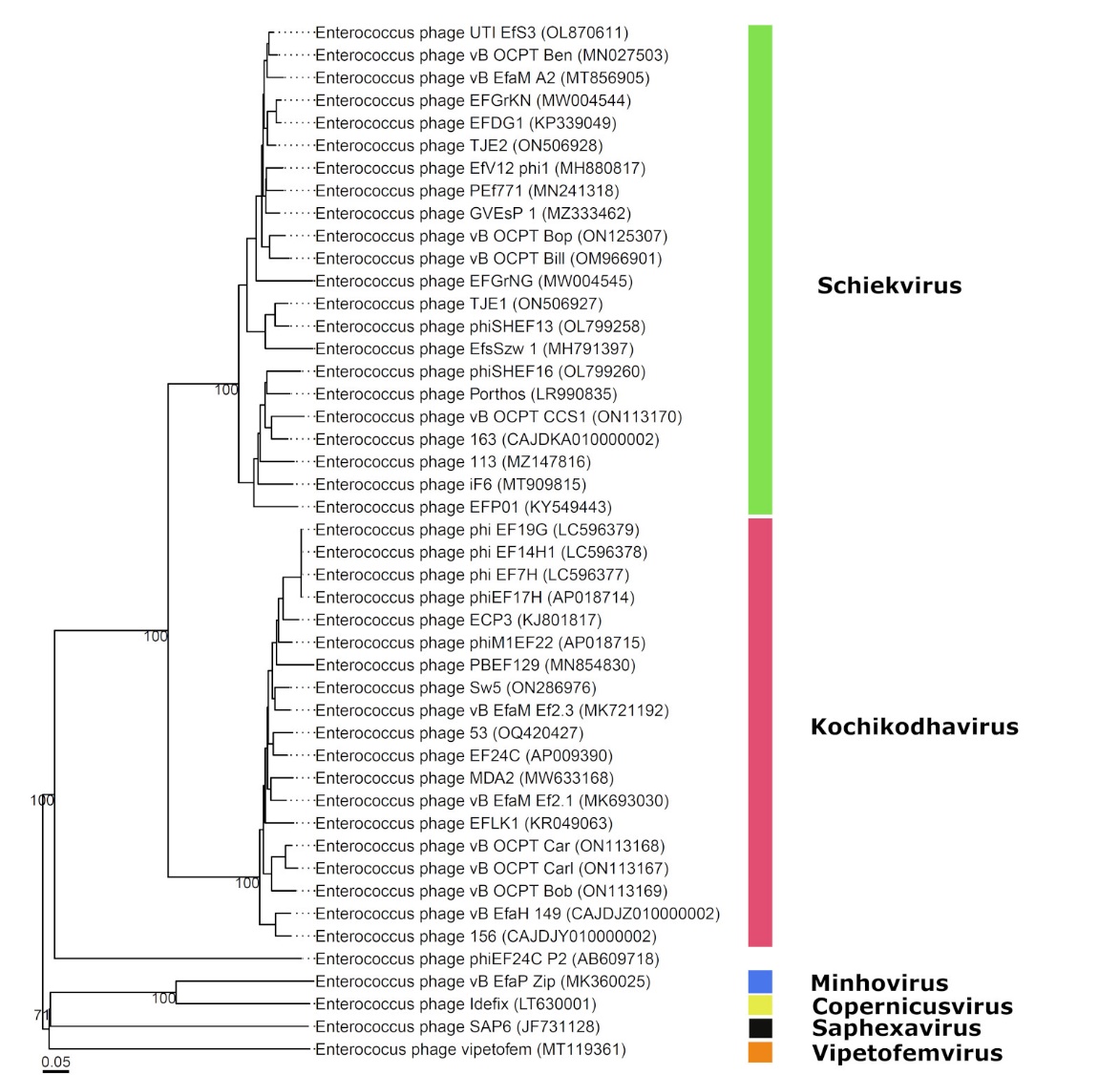
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**Supporting evidence**

**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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