

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

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| **Code assigned:** | **2020.070B** |  |
| **Short title:** Promote the genus *Hendrixvirus* to the rank of subfamily (*Hendrixvirinae*) and establish nine new genera (*Caudovirales*: *Siphoviridae*) | | |
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**List the ICTV Study Group(s) that have seen this proposal**

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| Lambda Study Group, Bacterial and Archaeal Viruses Subcommittee |

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

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

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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 | July 2020 |
| Date of this revision (if different to above) | November 2020 |

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

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

**Name of accompanying Excel module**

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| 2020.070B.R.Hendrixvirinae.xlsx |

**Abstract**

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| Proposal 2017.008B created the genus *HK97virus*, which was renamed *Hendrixvirus* in proposal 2018.007B. The current proposal promotes this taxonomic group to the level of a subfamily and defines 9 new genera and 3 new species within it. |

**Text of proposal**

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| |  | | --- | | **Background:** Proposal 2017.008B created the genus *HK97virus*, which was renamed *Hendrixvirus* in proposal 2018.007B. *HK97virus* was originally established based on a nucleotide similarity threshold of approximately 45% as assessed by a Gegenees blastn comparison. The ICTV now suggests approximately 70% nucleotide identity as a more appropriate genus demarcation threshold. To be more consistent with prevailing taxonomic principles and other genera of related phages, we propose to promote the *Hendrixvirus* cluster to the rank of subfamily, to be called *Hendrixvirinae*.  **Methods:** To support the proposed reorganization, 14 complete phage genomes were downloaded from GenBank, including 11 representing the ICTV-recognized species within *Hendrixvirus* and 3 that have been unofficially associated with *Hendrixvirus* by GenBank submitters or NCBI algorithms. An all-against-all nucleotide sequence comparison was conducted in VIRIDIC (1). Genus assignments were based on a 70% similarity threshold and species assignments were based on a 95% similarity threshold. Nine new genera and 3 new species within *Hendrixvirinae* are proposed based on Figure 1. Phylogenetic trees were constructed using the large terminase subunit (*terL*) and major capsid protein (MCP) genes. In these trees, 13 of the 14 phages proposed to comprise *Hendrixvirinae* appear monophyletic, with mEp235 (*Nochtlivirus*) sitting outside the main cluster (Figures 2A, B). However, across the genome as a whole, mEp235 shares 59-65% intergenomic similarity with the *Shamshuipovirus* phages. This is comparable to the degree of intergenomic similarity between *Shampshuipovirus* phages and all of the other phages in the proposed *Hendrixvirinae* subfamily. We hypothesize that this reflects a history of extensive recombination among these phages. While terminase and MCP are core phage genes, the prevalence of recombination among related phages means that individual core gene phylogenies may not accurately represent species and genus relationships. We therefore propose to leave mEp235 within the *Hendrixvirinae* for the time being, based on the level of whole genome similarity to other member phages, but acknowledge that this placement may need to be revised as subfamily demarcation criteria are refined.  **Genus Name Origins:** Six proposed genus names (*Yautsimvirus*, *Shamshuipovirus*, *Wongtaivirus*, *Kwaitsingvirus*, *Wanchaivirus, Saikungvirus*) are derived from the names of Districts within Hong Kong (Yau Tsim Mong, Sham Shui Po, Wong Tai, Kwai Tsing, Wan Chai, and Sai Kung, respectively), in recognition of the fact that these genera are typified by members of the Hong Kong (HK) series of phages. *Byrnievirus* is named for a chainmail shirt, since the HK97 capsid was the first phage in which the interlocking protein ring structures described as “biological chainmail” was found. Two genera typified by Mexican *E. coli* phages are named *Nochtlivirus* and *Cuauhtlivirus* after the Nahuatl words for prickly pear and eagle, respectively. | |

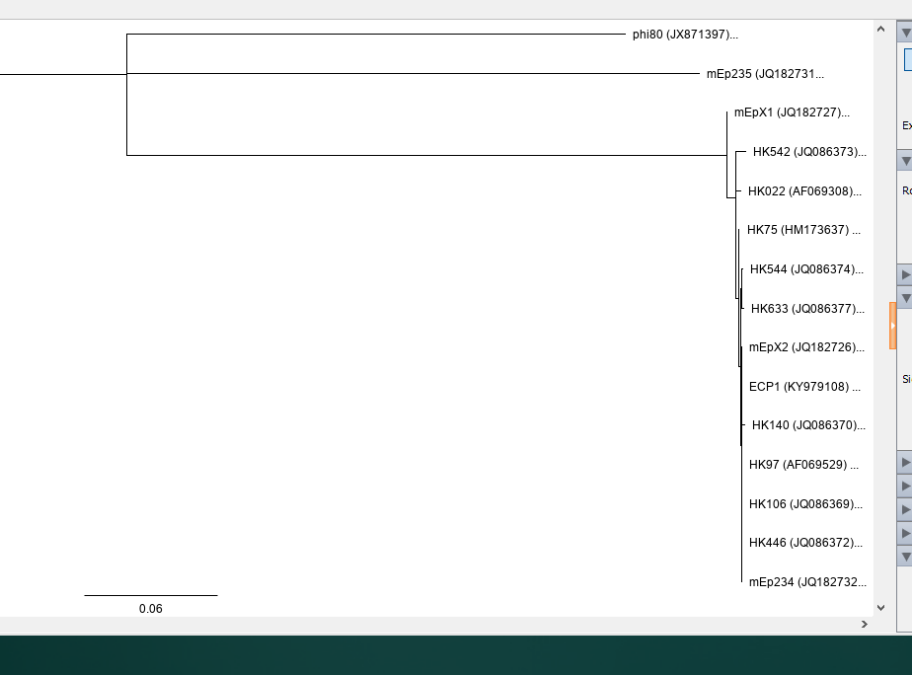
**Supporting evidence**

**Figure 1. VIRIDIC heatmap of proposed *Hendrixvirinae* phages.** Phage names are provided with GenBank accession numbers and indicate any previously recognized ICTV species assignments. New genera established in this proposal are marked in gold boxes and new species are indicated with red boxes.

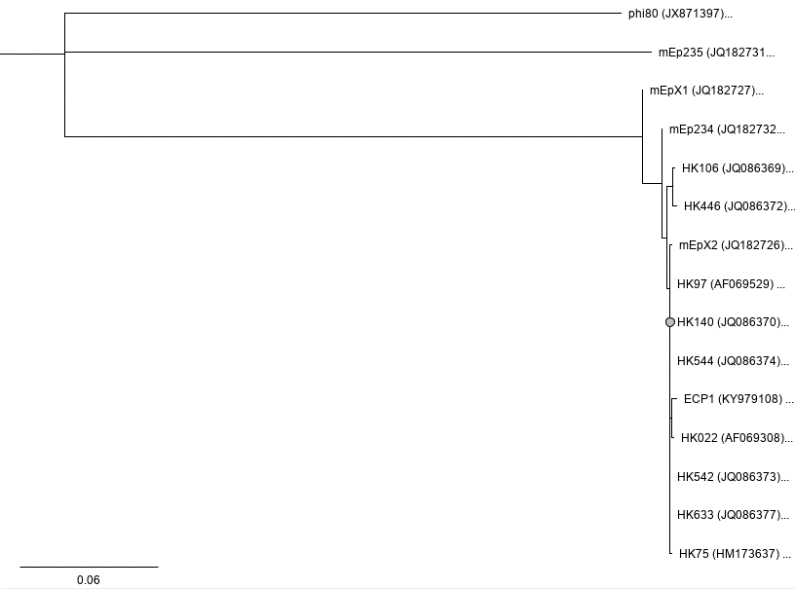
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**Figure 2. A) *terL* and B) MCP gene phylogenies for Hendrix*virinae*.** All 14 phages used for intergenomic similarity calculations were sufficiently annotated for inclusion in this analysis. In genomes where the gene was not explicitly annotated with its function, the encoding ORF was identified based on local gene synteny and primary nucleotide sequence. These are neighbor-joining trees (2) constructed in Geneious (v. 2020.2.4, Biomatters Ltd), each using a Tamura-Nei distance matrix (3), rooted using phi80 as the outgroup.



**A**



**B**

**References**

1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC – a novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. bioRxiv 2020.07.05.188268. <https://doi.org/10.1101/2020.07.05.188268>
2. Saitou, N.; Nei, M. (1 July 1987). "The neighbor-joining method: a new method for reconstructing phylogenetic trees". Molecular Biology and Evolution. 4 (4): 406–425. <https://doi.10.1093/oxfordjournals.molbev.a040454> PMID: 3447015
3. Tamura, Koichiro & Nei, Masatoshi. (1993). Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees. Mol Biol Evol 10: 512-26. <https://10.1093/oxfordjournals.molbev.a040023> PMID: 8336541