

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

**Part 1a: Details of taxonomy proposals**

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| **Title:** | Create a new species in the genus *Pahexavirus* |
| **Code assigned:** | 2025.055B.Pahexavirus\_1ns | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses |  |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:** |
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| **Optional – complete only if formally voted on by an ICTV Study Group:** | | | |
| **Study Group** | **Number of members** | | |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** |  |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required |  |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J - Reject |  |
| W - Withdrawn |  |

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| **Comments from the Executive Committee:** |
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**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:** |
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| **Revision date:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:** |
| *Brief description of current situation:*  *Proposed changes:*  *Justification:* |

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| **Text of General Proposal:** |
| *Background:*  *Proposed* *changes:*  *Justification:* |

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| **References:** |
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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |

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

<https://ictv.global/taxonomy/templates>

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| **Taxonomic changes proposed:** | | | |
| Establish new taxon | X | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Etymology (origin) of proposed taxonomic names:** | |
| **Taxon name** | **Etymology of the term** |
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| **Permission for use of names derived from a living person:** | | |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*, genus *Pahexavirus*, species *Pahexavirus LPPA1*  *Description of current taxonomy*:  The genus *Pahexavirus* was established in 2016 (proposal 2016.034a-dB.A.v1.Pa6virus) and the genus consists of 57 species.  *Proposed* *taxonomic change(s):*  Create a new species, “Pahexavirus LPPA1” in the genus Pahexavirus.  *Justification*:  We isolated a new Cutibacterium phage LPPA1. VIRIDIC and ViPTree analysis showed that LPPA1 has 89% identity with the species *Pahexavirus ouroboros*. *Cutibacterium* phage LPPA1 shares many properties with *P. ouroboros* but exhibits less than 95% identity with other *Pahexavirus* species to classify it as separate species of this genus. Thus, this proposal will place LPPA1 in the genus *Pahexavirus* as a new species. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*, genus *Pahexavirus*, species *Pahexavirus LPPA1*  *Description of current taxonomy*:  The genus *Pahexavirus* was established in 2016 (proposal 2016.034a-dB.A.v1.Pa6virus) and the genus consists of 57 species.  *Proposed* *taxonomic change(s):*  Create a new species, “Pahexavirus LPPA1” in the genus Pahexavirus.  *Demarcation criteria:*  Species demarcation: Two phages are assigned to the same species if their genomes are more than 95% identical over their genome length for isolates. These values can be calculated by a number of tools, such as BLASTn – usually calculated using intergenomic distance calculator VIRIDIC [1].  Genus demarcation: The Bacterial Viruses Subcommittee has established 70% nucleotide identity of the genome length as the cut-off for genera. Genus-level groupings should always be monophyletic in the signature genes, as tested with a phylogenetic tree. [2]  *Justification*:  A phylogenetic tree of *Cutibacterium phage* LPPA1 was constructed using VIPTree [3-4]. *LPPA1*, along with 80 other phages, formed a single clade, and these phages from this clade were subsequently selected for VIRIDIC analysis. VIRIDIC analysis computed the pairwise genomic distances and similarities between the phage genomes, revealing that *LPPA1* exhibited less than 95% similarity to other phages within the genus. In conclusion, we propose a new species, *Pahexavirus LPPA1*, within the genus *Pahexavirus.* |

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| **References:** |
| 1. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12(11):1268. PMID: 33172115 / PMCID: PMC7694805 doi: 10.3390/v12111268.  2. Turner D, Kropinski AM, Adriaenssens EM (2021) A Roadmap for Genome-Based Phage Taxonomy. Viruses 13(3):506. PMID: 33803862 / PMCID: PMC8003253 doi: 10.3390/v13030506.  3. Nishimura Y, Yoshida T, Kuronishi M et al (2017) ViPTree: the viral proteomic tree server. Bioinformatics 33(15):2379-2380. PMID: 28379287. doi: 10.1093/bioinformatics/btx157.  4. Rohwer F, Edwards R (2002) The Phage Proteomic Tree: a genome-based taxonomy for phage. J Bacteriol 184(16):4529-35. PMID: 12142423 / PMCID: PMC135240. doi: 10.1128/jb.184.16.4529-4535.2002.  5. Nishijima S, Nagata N, Kiguchi Y et al (2022) Extensive gut virome variation and its associations with host and environmental factors in a population-level cohort. Nat Commun 13(1):5252. PMID: 36068216 / PMCID: PMC9448778 doi: 10.1038/s41467-022-32832-w.  6. Kozlov AM, Darriba D, Flouri T et al (2019) RAxML-NG: a fast, scalable and user-friendly tool for maximum likelihood phylogenetic inference. Bioinformatics 35(21):4453-4455. PMID: 31070718 / PMCID: PMC6821337 doi: 10.1093/bioinformatics/btz305. |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
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| **Tables, Figures:** |

**ViPTree analysis:** ViPTree analysis ([https://www.genome.jp/viptree/](about:blank)) is based upon Rohwer and Edwards (2002) famous Phage Proteomic Tree. The phages of interest are indicated with **red box.** The phage LPPA1 is indicated with **red star**.

A screen shot of a computer

AI-generated content may be incorrect.

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes. The phage LPPA1 is indicated with **red star.**

A diagram of a bar code

AI-generated content may be incorrect.

**Origin of the name of this taxon:** None

**Historical aspects:** *Cutibacterium phage* LPPA1 was isolated in 2022 by Huazhong Agricultural University, using *Cutibacterium* as the host bacterium.

**Specific References:** None

**Genome summary:**

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| Phage name | INSDC | Size (Kb) | GC% | Protein | tRNA |
| *Cutibacterium phage LPPA1* | PP895300 | 29.365 | 54% | 52 | 0 |