

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | To create one (1) new species in the genus *Bifilivirus,* family *Paulinoviridae* | |
| **Code assigned:** | 2024.028B |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Deptula P | Department of Food Science, University of Copenhagen, Denmark | deptula@food.ku.dk | x |
| Sha Y | Department of Food Science, University of Copenhagen, Denmark | yuandong.sha@food.ku.dk |  |
| Potipimpanon S | Department of Food Science, University of Copenhagen, Denmark | siravudhood@gmail.com |  |
| Vogensen FK | Department of Food Science, University of Copenhagen, Denmark | fkv@food.ku.dk |  |
| Nielsen DS | Department of Food Science, University of Copenhagen, Denmark | dn@food.ku.dk |  |
| Knezevic P | Faculty of Sciences, University of Novi Sad, Serbia | petar.knezevic@dbe.uns.ac.rs |  |

**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:** | | | |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses | **x** |
| 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:** |
| Tubulavirales Study Group |

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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:** | 23/04/2024 |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept | **X** |
| 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:** | DD/MM/YYYY |

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

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| **Name of accompanying Excel module:** |
| 2024.028B.A.v1.Philemonvirus\_ns.xlsx |

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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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| **Is any taxon name used here derived from that of a living person:** | | **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*: This is a proposal for creating a new species within the genus *Bifilivirus*.  *Description of current taxonomy*:  *Proposed* *taxonomic change(s):* Addition of a new species *Bifilivirus philemonii*  *Justification*:  Filamentous phage Philemon was isolated from raw milk Emmental cheese on a dairy-associated strain of *Propionibacterium freudenreichii* PB4. The obtained TEM confirmed filamentous morphology (Fig. 1). Philemon forms plaques on three *P. freudenreichii* strains in our collection, including the strain TL18, which was used for characterization of phage B5 (though no plaquing was reported for phage B5) (1). The phage genome was sequenced with Illumina platform after formation of complementary strand with MDA technique. The genome is 5802 nt long, with 63 G+C %mol. Comparison with the only other representative of genus *Bifilivirus*, Propionibacterium virus B5 (NC\_003460.1) revealed that the genome of Philemon is 92.8% identical to the genome of the Propionibacterium virus B5, thus fulfilling the criteria for creation of a separate species (Table 1). The similarity of morphogenesis protein and CoaB (Table 1, Fig. 2) confirms that Philemon belongs to the genus Bifilivirus. We propose the name of the species – *Bifivilus philemonii*. |

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| **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*: species  *Description of current taxonomy*:  *Proposed* *taxonomic change(s)*:  *Demarcation criteria:* Phage Philemon is sufficiently different from the only known representative of the genus Bifilivirus  *Justification*: genome identity below 95% (genome is 93.86% identical to the genome of the *Propionibacterium* virus B5 over 99% of its genome span). |

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| **References:** |
| 1. Chopin,M.C., Rouault,A., Ehrlich,S.D., Gautier,M. 2002. Filamentous phage active on the gram-positive bacterium Page 24 of 35 additional material in support of this proposal References: Propionibacterium freudenreichii. J. Bacteriol. 184 (7), 2030-2033 2. Anisimova M., Gascuel O. Approximate likelihood ratio test for branchs: A fast, accurate and powerful alternative. Syst Biol. 2006, Aug;55(4):539-52. |

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| **Tables, Figures:** |

**Fig. 1.** Transmission electron microscopy image of the negatively stained P. freudenreichii strain during infection by phage Philemon at early stage (upper panel) and after 4,5 hours of incubation (lower panel)(credit: Horst Neve)

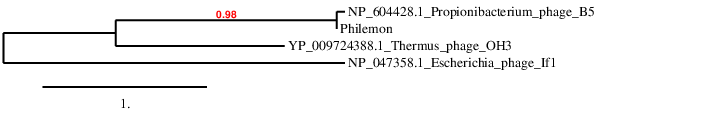
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**Table 1.** New species *Bifilivirius philemonii* (strain in bold, genus members highlihted in light blue) in family *Paulinoviridae* (Enterobacteria phage If1 is on outlier)

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|  | GenBank Access. No. | Genome lenght (nt) | Mol% G+C | No. CDS | DNA (% seq. Ident) | Proteome (No. of homologous proteins; E<10-3) | Zot | CoaB |
| **Philemon** |  | 6312 | 31.6 | 7 | 100 | 100 | 100 | 100 |
| Propionobacterium phage B5 | [NC\_003460](https://www.ncbi.nlm.nih.gov/nuccore/19718349) | 6136 | 33.8 | 7 | 92.8 | N.D. | 95.4 | 94.7 |
| Thermus phage OH3 | [NC\_045425](https://www.ncbi.nlm.nih.gov/nuccore/1784318017) | 6761 | 51.4 | 12 | 0 | N.D. | 20.4 | 24.8 |
| Enterobacteria phage If1 | [NC\_001954.1](https://www.ncbi.nlm.nih.gov/nucleotide/NC_001954.1?report=genbank&log$=nucltop&blast_rank=5&RID=59F5VC16013) | 8454 | 43.7 | 10 | 0 | N.D. | 0 | 14.7 |

**Fig. 2.** Phylogenetic analysis of the morphogenesis protein (A) and major coat protein (B) of phage Philemon and an outlier Escherichia virus If1, constructed using “one click” at phylogeny.fr (3). The new species *Bifilivirius philemonii* (strain in bold, genus members highlihted in light blue) in family *Paulinoviridae* (Enterobacteria phage If1 is on outlier)

A)



B)

