

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create two new species - *Camvirus vanseggelen* and *Camvirus verabelle* [subfamily Arquatrovirinae, class *Caudoviricites*]. | |
| **Code assigned:** | 2024.041B |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Name** | | **Affiliation** | **Email address** | **Corresponding author(s)** X |
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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:** |
| Actinophages 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:** | 02/04/2024 |

**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| W - Withdrawn |  |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:** |
| 2024.041B.A.v1.Camvirus\_2ns.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:** | | **Y/N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  The genus *Camvirus* is classified within the subfamily *Arquatrovirinae*, class *Caudoviricetes*  *Proposed* *taxonomic change(s):*  Create two new species in the genus *Camvirus*  *Justification*:  We have defined two new species, *Camvirus vanseggelen* and *Camvirus verabelle*, based upon phages isolated for host *Streptomyces coelicolor* from soil samples in the Netherlands at longitude N52°23’31” and latitude E4°34’49”*.* *Camvirus vanseggelen* contains a linear dsDNA genome of50426 bp (65,5% G+C) encoding 73 proteins. *Camvirus verabelle* contains a linear dsDNA genome of49832 bp (65,0% G+C) encoding 73 proteins. These new species can be included in the genus *Camvirus* together with *Streptomyces* phage Alsaber, *Streptomyces* phage Amela, *Streptomyces* phage phiCAM, *Streptomyces* phage Endor1, *Streptomyces* phage Endor2, *Streptomyces* phage Joe, *Streptomyces* phage Saftant and *Streptomyces* phage Sitrop. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Realm *Duplodnaviria*, kingdom *Heunggongvirae*, phylum *Uroviricota*, class *Caudoviricetes*  *Description of current taxonomy*:  The genus *Camvirus* is classified within the subfamily *Arquatrovirinae*, class *Caudoviricetes*  *Proposed* *taxonomic change(s):*  Create two new species in the genus *Camvirus*  *Demarcation criteria:*  Species demarcation criteria: 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 [1] – usually calculated using intergenomic distance calculator VIRIDIC [2].  Genus demarcation criteria: In search for criteria that create cohesive and distinct genera that are reproducible and monophyletic, 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. [3]  Family demarcation criteria: The family is represented by a cohesive and monophyletic group in the main predicted proteome-based clustering tools (ViPTree, GRAViTy dendrogram, vConTACT2 network). Members of the family share a significant number of orthologous genes (the number will depend on the genome sizes and number of coding sequences of members of the family; usually ca. 10%) [3].  *Justification*:  The phages detailed in this proposal conform to current demarcation criteria [3]. |

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| **References:** |
| 1. Sayers EW, Beck J, Bolton EE, Bourexis D, Brister JR, Canese K, Comeau DC, Funk K, Kim S, Klimke W, Marchler-Bauer A, Landrum M, Lathrop S, Lu Z, Madden TL, O'Leary N, Phan L, Rangwala SH, Schneider VA, Skripchenko Y, Wang J, Ye J, Trawick BW, Pruitt KD, Sherry ST. Database resources of the National Center for Biotechnology Information. Nucleic Acids Res. 2021 Jan 8;49(D1):D10-D17. doi: 10.1093/nar/gkaa892. PMID: 33095870  2. Moraru C, Varsani A, Kropinski AM. VIRIDIC-A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses. 2020 Nov 6;12(11):1268. doi: 10.3390/v12111268. PMID: 33172115; PMCID: PMC7694805. http://kronos.icbm.uni-oldenburg.de/viridic/  3. Turner D, Kropinski AM, Adriaenssens EM. A Roadmap for Genome-Based Phage Taxonomy. Viruses. 2021 Mar 18;13(3):506. doi: 10.3390/v13030506. PMID: 33803862; PMCID: PMC8003253.  4. Ongenae, V., Azeredo, J., Kropinski, A. M., Rozen, D., Briegel, A., & Claessen, D. (2022). Genome sequence and characterization of Streptomyces phage Pablito, representing a new species within the genus Janusvirus. Scientific Reports, 12(1), 17785.  5. Nishimura, Y., Yoshida, T., Kuronishi, M., Uehara, H., Ogata, H., & Goto, S. (2017). ViPTree: the viral proteomic tree server. Bioinformatics, 33(15), 2379–2380. https://doi.org/10.1093/bioinformatics/btx157  6. Turner D, Reynolds D, Seto D, Mahadevan P. CoreGenes3.5: a webserver for the determination of core genes from sets of viral and small bacterial genomes. BMC Res Notes. 2013;6:140. doi: 10.1186/1756-0500-6-140. PMID: 23566564. |

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| **Tables, Figures:** |

1. **To add two new species (*Camvirus vanseggelen* and *Camvirus verabelle*) tin thegenus *Camvirus*.**

**Origin of the name of this taxon:**

Vanseggelen is an old Dutch family name, while Verabelle is an uncommon girl’s name.

**Historical aspects:** These temperate phages were isolated in the Netherlands using host *Streptomyces coelicolor*. They are both siphoviruses.

**Electron micrograph:**

Phage Verabelle Phage Vanseggelen

**A black and white image of a black circle

Description automatically generatedA black and white speckled background

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**Genome summary:**

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| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| ***Streptomyces*  phage phiCAM** | **NC\_041856.1** | **JX889246** | **50.348** | **65.6** | **72** | **100** | **100** |
| *Streptomyces* phage Vanseggelen |  | OQ970438 | 50.426 | 65.5 | 73 | 74.3 | 84.8 |
| *Streptomyces* phage Verabelle |  | OQ970439 | 49.832 | 65.0 | 73 | 74.5 | 91.7 |

**(\*) determined using VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [6]**

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; VIRIDIC (Virus Intergenomic Distance Calculator; [2]; http://rhea.icbm.uni-oldenburg.de/VIRIDIC/) computes pairwise intergenomic distances/similarities amongst phage genomes.

A chart with numbers and a red line

Description automatically generated with medium confidence

**Phylogeny:** The phylogenetic tree was constructed using the whole genome sequences from the top 10 phages with the most similar genome sequences. *Streptomyces* phage Pablito [4] was chosen as an outlier. ViPTree was used to construct a viral proteomic tree [5].

A graph with lines and text

Description automatically generated with medium confidence