

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

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| **Code assigned:** | ***2022.041B*** |  |
| **Short title:** Create one new species in the genus *Janusvirus* (*Caudoviricetes*: *Arquatrovirinae*) | | |
|  | | |

**Author(s) and email address(es)**

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**Corresponding author**

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| Véronique Ongenae |

**List the ICTV Study Group(s) that have seen this proposal**

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| Bacterial Viruses Subcommittee, Actinophages Study Group |

**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** |
|  |  |  |  |
|  |  |  |  |

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

|  |  |
| --- | --- |
| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

|  |  |  |
| --- | --- | --- |
| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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|  |  |  |

**Submission dates**

|  |  |
| --- | --- |
| Date first submitted to SC Chair | February 2022 |
| 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**

|  |
| --- |
| 2022.041B.N.v1.Janusvirus\_1nsp.xlsx |

**Abstract**

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| We have proposed a new species, *Janusvirus pablito*, for a phage (Streptomyces phage Pablito) isolated from host *Streptomyces lividans* from soil samples in the Netherlands at longitude N52°23’31” and latitude E4°34’49”*.* This janusvirus contains linear ds DNA genomes of, on average, 48.49 kb (66.4 mol%G+C) and encode for 76 proteins. This new species can be included in the genus *Janusvirus* together with Streptomyces phage Hank144. |

**Text of proposal**

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| |  | | --- | | **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. [6]  **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%). [6] | |

**Supporting evidence**

**Proposals:**

1. **To add one new species (*Janusvirus pablito*) to *Janusvirus***

**Origin of the name of this taxon:** The name of the new species has originated from my dearest British short hair cat, called Pablo.

**Historical aspects:** This lytic phages was isolated in the Netherlands against *Streptomyces lividans*. It was originally called phage LA7 [3].

**Electron micrograph:** N/A

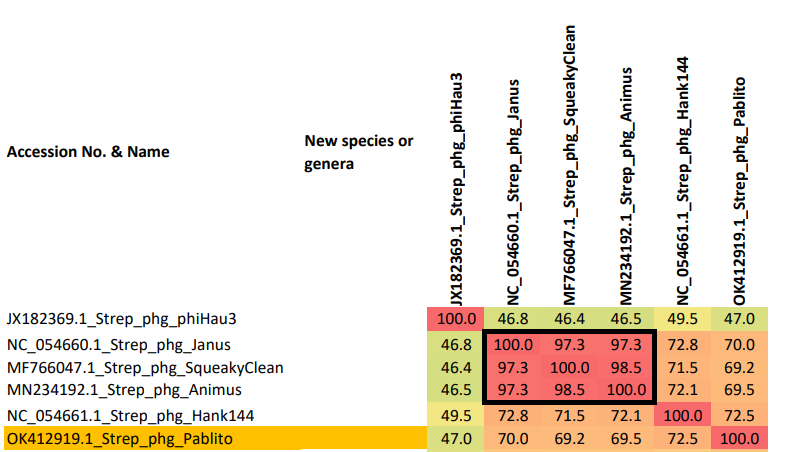
**Genome summary:**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | Overall % DNA sequence identity (\*) | Overall % homologous proteins (\*\*) |
| Streptomyces phage Janus | [NC\_054660.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_054660.1) | [MK392366.1](https://www.ncbi.nlm.nih.gov/nuccore/MK392366.1) | 50.63 | 67.0 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/76023/446681|Streptomyces phage Janus/viral segment/) | 100 | 100 |
| Streptomyces phage Pablito |  | OK412919.1 | 49.49 | 66.4 | 76 | 70.0 | 88.5 |
| Streptomyces phage Hank144 | [NC\_054661.1](https://www.ncbi.nlm.nih.gov/nuccore/NC_054661.1) | [MH669004.1](https://www.ncbi.nlm.nih.gov/nuccore/MH669004.1) | 50.55 | 66.3 | [78](https://www.ncbi.nlm.nih.gov/genome/browse/#!/proteins/72119/400255|Streptomyces phage Hank144/viral segment/) | 72.8 | 85.9 |

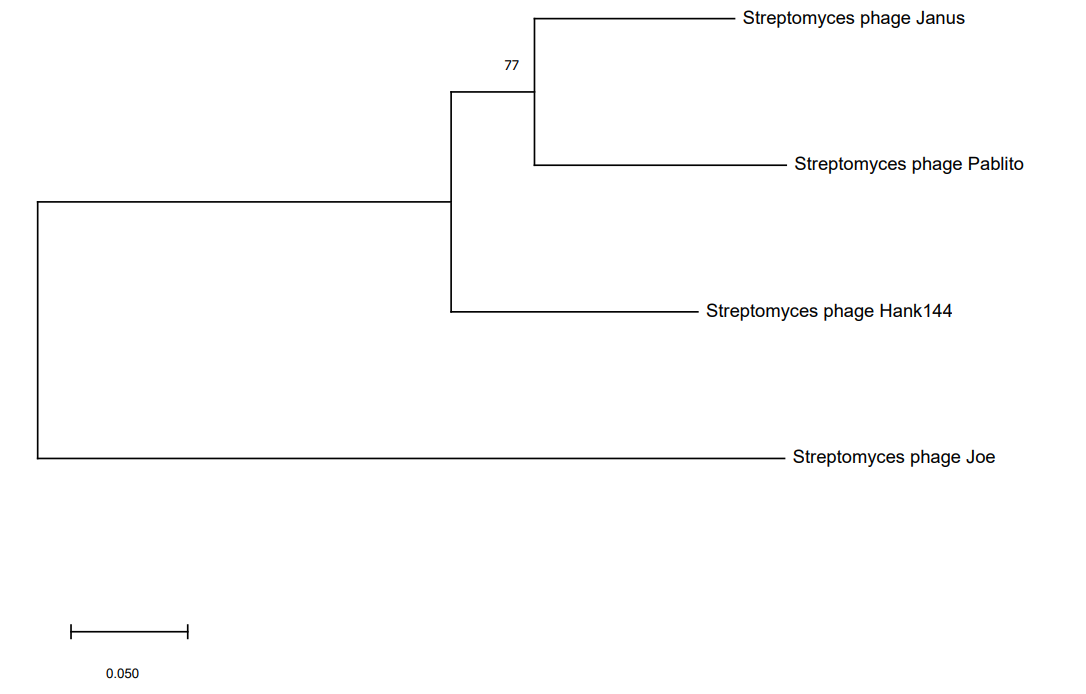
**(\*) determined using VIRIDIC [2]**

**(\*\*) determined using CoreGenes 3.5 [5]**

**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.



**Phylogenetic tree analysis:** MEGAX analysis [4] was used to create a phylogenetic tree of the closely related species. The phage of interest is indicated with a **red star**.



\*

**Phylogeny:** The phylogenetic tree was constructed using the major capsid head proteins from phages belonging to the genus *Janusvirus*. Streptomyces phage joe was chosen as an outlier. MUSCLE was used for multiple alignment and MEGAX to construct the maximum likelihood phylogenetic tree with 100 bootstraps

**References**

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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/>
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4. Sudhir Kumar, Glen Stecher, Michael Li, Christina Knyaz, and Koichiro Tamura (2018) MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549
5. 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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