

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

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| **Code assigned:** | ***2022.096B*** |  |
| **Short title:** Create a new genus (*Zhangqianvirus)* in the class *Caudoviricetes* |
|  |

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

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| --- | --- |
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**Author(s) institutional address(es) (optional)**

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**Corresponding author**

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| Yigang Tong |

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

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| Caudoviricetes Study Group, Bacterial Viruses Subcommittee |

**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** |
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|  |  |  |  |

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

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

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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 | May 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**

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| 2022.096B.N.v1.Zhangqianvirus\_ng.xlsx |

**Abstract**

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| A new genus *Zhangqianvirus* under the class *Caudoviricetes,* with a single species, *Staphylococcus* phage IME1354\_01, is proposed. |

**Text of proposal**

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| **Genus demarcation****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 – usually calculated using intergenomic distance calculator VIRIDIC [1].**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 [2]. |

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**Supporting evidence**

**Source of the name of this taxon:** This genus is named after the name of the first person to introduce grapes in ancient China, *Zhangqianvirus.*

**History:** A bacteriophage was induced from Staphylococcus cohnii strain 1354 with Mitomycin C.

**Specific Reference:** Tian F, Li J, Li L, et al. Molecular dissection of the first Staphylococcus cohnii temperate phage IME1354\_01. Virus Research 318:198812. doi: 10.1016/j.virusres.2022.198812. **[3]**.

**GenBank Summary:**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Phage name | RefSeq No. | INSDC | Size (Kb) | GC% | Protein | tRNAs |
| Staphylococcus phage IME1354\_01 | NC\_049931 | KY653126.1 | 42.706 | 34 | 64 | 0 |

**BLASTN homologs:** The genome has very low homology to all other bacteriophage sequences in the GenBank database. A complete genome sequence comparison using the BLASTn method revealed that the genome of Staphylococcus phage IME1354\_01 had a maximum nucleotide identity of 83.73% and 10% coverage with Staphylococcus phage vB\_SarS\_BM31. The low homology indicated that the newly sequenced bacteriophage likely represents a new genus with a single species.

**VIRIDIC heat map:** VIRIDIC (Virus Intergenomic Distance Calculator; 10) computes pairwise intergenomic distances/similarities amongst phage genomes [1].



**Electron micrograph:**



Transmission electron microscopy showed that this phage had an icosahedral capsid ~54 nm in diameter and a long, noncontractile tail.

**Phylogeny:**

The evolutionary history was inferred using the Neighbor-Joining method [1]. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [4]. The tree is drawn to scale, with branch lengths (next to the branches) in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the JTT matrix-based method [5] and are in the units of the number of amino acid substitutions per site. Evolutionary analyses were conducted in MEGA7 [6]. Phylogenetic trees of Staphylococcus phage IME1354\_01 were constructed with 1000 bootstrap replicates based on the (A) major capsid protein and (B) terminase large subunit.



**References**

**[1]** 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

**[2]** 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

**[3]** Tian F, Li J, Li L, et al. Molecular dissection of the first Staphylococcus cohnii temperate phage IME1354\_01. Virus Res.2022 May;318:198812. doi: 10.1016/j.virusres.2022.198812.

**[4]** Felsenstein J. CONFIDENCE LIMITS ON PHYLOGENIES: AN APPROACH USING THE BOOTSTRAP. Evolution. 1985 Jul;39(4):783-791. doi: 10.1111/j.1558-5646.1985.tb00420.x. PMID: 28561359.

**[5]** Jones DT, Taylor WR, Thornton JM. The rapid generation of mutation data matrices from protein sequences. Comput Appl Biosci. 1992 Jun;8(3):275-82. doi: 10.1093/bioinformatics/8.3.275. PMID: 1633570.

**[6]** Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. Mol Biol Evol. 2016 Jul;33(7):1870-4. doi: 10.1093/molbev/msw054. Epub 2016 Mar 22. PMID: 27004904