

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:** | Create a new genus, *Seraphanvirus*, containing two species (*Caudoviricetes*) | |
| **Code assigned:** | 2024.032B |

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| **Author(s), affiliation and email address(es):** | | | |
| **Name** | **Affiliation** | **Email address** | **Corresponding author(s)** X |
| Ganjoor MS | University of Isfahan, Iran | msg\_isrc@yahoo.com |  |
| Bouzari M | University of Isfahan, Iran | bouzari@sci.ui.ac.ir | X |
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**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:** |
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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:** | 09/12/2023 |

**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| W - Withdrawn |  |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:** |
| 2024.032B.A.v1.Sepahanvirus\_ng.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*:  Genus  *Description of current taxonomy*:  These phages are currently unclassified.  *Proposed* *taxonomic change(s):*  To create a new genus, *Sepahanvirus*, within the class *Caudoviricetes* comprising two species, vB\_Yru\_GN1 and YerA41.  *Justification*:  Phages vB\_Yru\_GN1 and phage YerA41 exhibit nucleotide sequence similarity that falls within the demarcation threshold for the creation of a new genus. |

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| * **Text of Taxonomy proposal:** |
| *Taxonomic rank(s) affected*:  Genus and species.  *Description of current taxonomy*:  Yersinia phages vB\_Yru\_GN1 and YerA41 are currently unclassified.  *Proposed* *taxonomic change(s)*:  A new genus, *Sepahanvirus* is proposed, named after the ancient name Sepahan of the city Isfahan, where vB\_Yru\_GN1 was isolated.  *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 [5].  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 [7].  *Justification*:  The vB\_Yru\_GN1 genome has very low homology to other bacteriophage sequences in the GenBank database. A complete genome sequence comparison using the BLASTn method revealed that the genome of Yersinia ruckery phage vB\_Yru\_GN1 (Table 1) had a maximum nucleotide identity of 97.95% and 94% coverage with Yersinia phage YerA41 [4]. Analysis with VIRIDIC demonstrates that these phages exhibit 92% nucleotide sequence similarity (Figure 1). Both vB\_Yru\_GN1 and YerA41 posses a myovirus morphology (Figure 2). Phylogenetic analysis using the Neighbor-joining method of the major capsid protein and DNA polymerase demonstrates that these phages form a monophyletic clade (Figure 3). |

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| **References:** |
| 1. Altschul SF, Madden TL, Schäffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic acids research 25:3389-3402  2. Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. evolution 39:783-791  3. Kumar S, Stecher G, Tamura K (2016) MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular biology and evolution 33:1870-1874  4. Leskinen K, Pajunen MI, Vilanova MVG-R, Kiljunen S, Nelson A, Smith D, Skurnik M (2020) YerA41, a yersinia ruckeri bacteriophage: determination of a non-sequencable DNA bacteriophage genome via RNA-Sequencing. Viruses 12:620  5. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC—A novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. Viruses 12:1268  6. Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular biology and evolution 4:406-425  7. Turner D, Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy. Viruses 13:506  8. Zuckerkandl E, Pauling L (1965) Evolutionary divergence and convergence in proteins. Evolving genes and proteins. Elsevier, pp 97-166 |

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| **Tables, Figures:** |

Table 1. Summary genome characteristics of bacterial viruses vB\_Yru\_GN1 and YerA41

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| **Phage name** | **Accession number** | **Size (bp)** | **GC%** | **Protein** | **tRNAs** |
| Yersinia ruckery phage vB\_Yru\_GN1 | LC779065 | 145093 | 32.1 | 205 | 2 |
| Yersinia phage YerA41 | MW570730 | 145577 | 32.3 | 213 | 2 |

A screenshot of a computer

Description automatically generated

Figure 1. VIRIDIC (Virus Intergenomic Distance Calculator) heatmap illustrating pairwise intergenomic similarities amongst phage genomes.

A close-up of a blurry black and white photo

Description automatically generated

Figure 2. Transmission electron micrograph of vB\_Yru\_GN1, showing a myovirus morphology. Virion dimensions are a head ~130 nm in diameter and a contractile tail and neck of ~ 215 nm in length (filled arrow) and phages with contracted tails of ~ 96 nm in length (empty arrows).

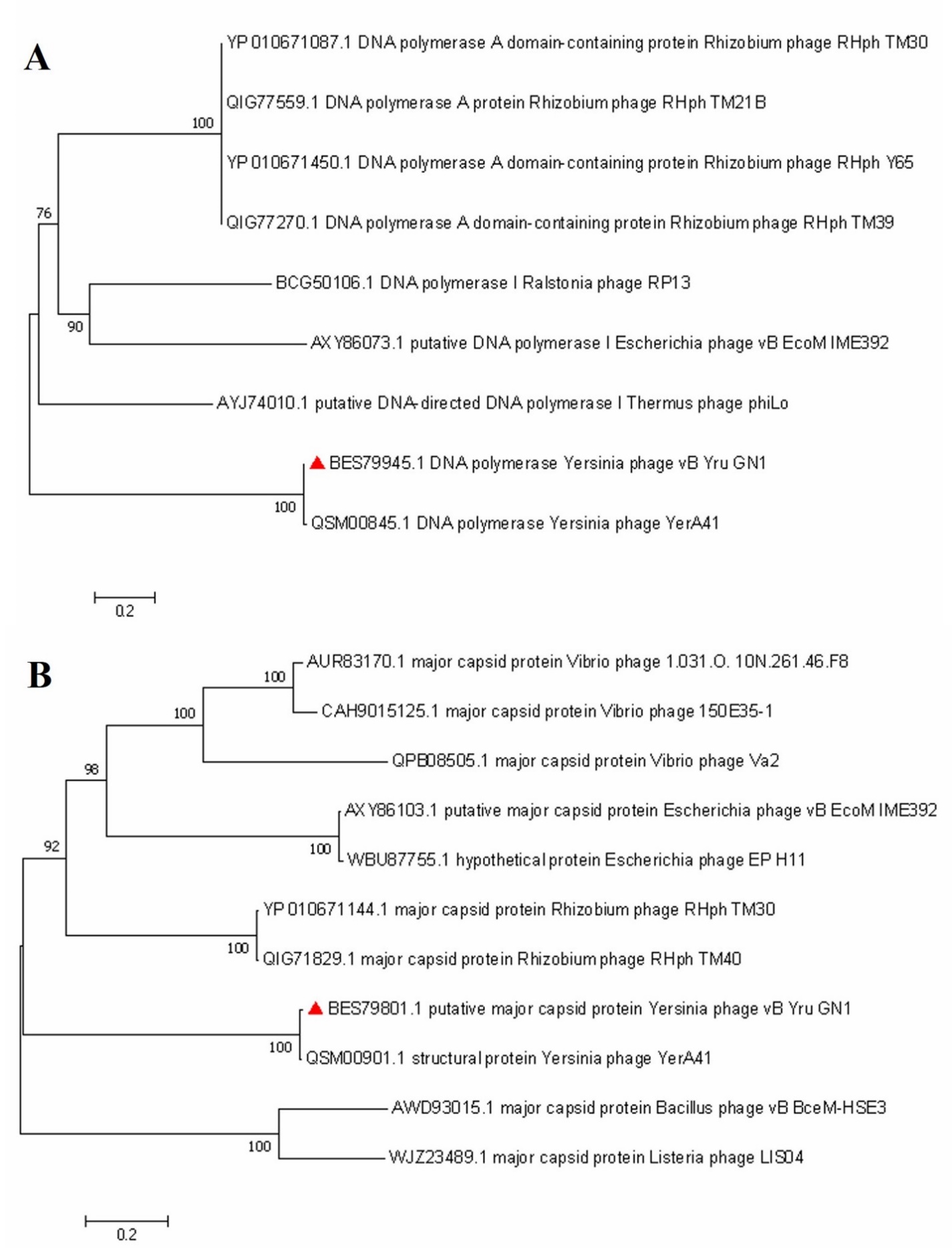


Figure 3. Neighbor-Joining phylogenetic trees [6] of (**A**) DNA polymerase and (**B**) major capsid proteins. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [2]. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method [8]. Evolutionary analyses were conducted in MEGA7 [3]. The red triangle indicates the phage species reported in this proposal.