

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:**  | Proposal of a new genus, *Acarajevirus*, harboring a new species belonging to the *Peduoviridae* family |
| **Code assigned:**  | 2025.089B.Acarajevirus\_1ng\_1ns |

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| **Author(s), affiliation and email address(es):**  |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation**  | **Email address**  | **Corr. author(s)**  |
| Poliane  | Alfenas-Zerbini | Universidade Federal de Viçosa, Microbiology Departament, Viçosa, Brazil | palfenas@ufv.br | x |
| Rafael R. | Rezende  | Universidade Federal de Viçosa, Microbiology Departament, Viçosa, Brazil | r.r.rezende@ufv.br |  |
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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:**  |
| Not applied |

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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:** |   |

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

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| 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| W - Withdrawn |  |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:** |  |

**Part 2:** **GENERAL PROPOSAL**

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| **Abstract for General Proposal:**  |
| *Brief description of current situation:* *Proposed changes:* *Justification:*  |
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| **Text of General Proposal:**  |
| *Background:* *Proposed* *changes:* *Justification:*  |

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| **References:** |
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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
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| **Tables, Figures:**  |

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

<https://ictv.global/taxonomy/templates>

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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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| **Etymology (origin) of proposed taxonomic names:**  |
| **Taxon name**  | **Etymology of the term** |
| “Acarajevirus” | The prefix “Acaraje” is the name of a typical Brazilian food from the region of isolation of Ralstonia phage AB1 |
| “bahia” | The specific epithet “alagoinhas” is the name of the Brazilian state where the Raltonia phage CA1 was isolated. |

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| **Permission for use of names derived from a living person:**  |
| **Taxon name** | **Full name of person from whom the name is derived** | **Attached**  |
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| **Abstract of Taxonomy Proposal:**  |
| *Taxonomic rank(s) affected*: *Peduoviridae* (*Caudoviricetes* class)*Description of current taxonomy*: *Peduoviridae* is orphan class family associated with *Caudoviricetes* order harboring a total of 58 genera and 126 species.*Proposed* *taxonomic change(s):* We proposed the Ralstonia phage AB1 be classified as new species “Acarajevirus bahia” belonging to a new genus named “Acajaevirus” associated with the family *Peduoviridae* (*Caudoviricetes* class)*Justification*: According to recommendation of ICTV to bacterial viruses taxonomy, the Ralstonia phage AB1 is related to other viruses from *Peduoviridae* family, but no sharing intergenomic similarity enough to be classified to establish species or genus. |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Recently, our team isolated and described a novel temperate phage that infects *Ralstonia solanacearum* and *Ralstonia pseudosolanacearum* named Ralstonia phage AB1 [1]. We had applied the ICTV recommendation to viruses classification [2, 3], and conclude this isolate comprises a new species belong to new genus inside *Peduoviridae* family. ]*Description of current taxonomy*: *Proposed* *taxonomic change(s)*: We used VIRIDIC v.1.0r3.6 [4] to compare the complete genome sequences of RS phage AB1 to those of related viruses in the RefSeq/GenBank database. First, we queried the NCBI nt/nr database to search for the sequences most similar to RS phages AB1. Next, we used VIRIDIC with default thresholds of intergenomic similarity to cluster sequences into species (95%) and genera (70%) (Fig. 1). Ralstonia phage AB1 is most similar to the Ralstonia phage RSY1 (species *Arsyunavirus RSY1*) (54.8% intergenomic similarity), which belongs to the genus *Arsyunavirus* (family *Peduoviridae*, class *Caudoviricetes*). Ralstonia phage RSY1 is a temperate phage that is wide- spread in *R. solanacearum* [5]. The six orthologous core genes of RS phage AB1 form monophyletic clades with other members from the *Peduoviridae* family (Fig. 2), according to the criteria for demarcation to that family. *Demarcation criteria:* To be classified as “Acarajevirus bahia” species, any caudovirus needs to share ≥ 95 % intergenomic similarity, and to be classified as a member of the “Acarajevirus” genus, it needs to share ≥ 70% and < 95% of intergenomic similarity [6]. *Justification*: We used VIRIDIC v.1.0r3.6 [37] to compare the complete genome sequences of our phage isolates to those of related viruses in the RefSeq/GenBank database. First, we queried the NCBI nt/nr database to search for the sequences most similar to RS phages AB1 and CA1. Next, we used VIRIDIC with default thresholds of intergenomic similarity to cluster sequences into species (95%) and genera (70%). |

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| **References:**  |
| 1. Januário BD, de Rezende RR, Morgan T, Alfenas-Zerbini P (2025) Description of two novel bacteriophages of the class Caudoviricetes that infect Ralstonia solanacearum and Ralstonia pseudosolanacearum. Arch Virol 170:86. https://doi.org/10.1007/s00705-025-06271-z2. Turner D, Shkoporov AN, Lood C, et al (2023) Abolishment of morphology-based taxa and change to binomial species names: 2022 taxonomy update of the ICTV bacterial viruses subcommittee. Arch Virol 2023 1682 168:1–9. https://doi.org/10.1007/S00705-022-05694-23. Simmonds P, Adriaenssens EM, Zerbini FM, et al (2023) Four principles to establish a universal virus taxonomy. PLOS Biol 21:e3001922. https://doi.org/10.1371/journal.pbio.30019224. Moraru C, Varsani A, Kropinski AM (2020) VIRIDIC—A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses. Viruses 12:1268. https://doi.org/10.3390/v121112685. Askora A, Kawasaki T, Fujie M, Yamada T (2017) Lysogenic Conversion of the Phytopathogen Ralstonia solanacearum by the P2virus ϕRSY1. Front Microbiol 8:1–11. https://doi.org/10.3389/fmicb.2017.022126. Turner D, Kropinski AM, Adriaenssens EM (2021) A roadmap for genome-based phage taxonomy. Viruses 13:506. https://doi.org/10.3390/v13030506 |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
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| **Tables, Figures:**  |

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Figure 1. Whole-sequence intergenomic similarity analysis performed using VIRIDIC for RS phage AB1. The dotted lines indicate the species' inclusion (⊂) in the genus. The heat map colors in panels A and B indicate the demarcation criteria for bacteriophages.



Figure 2. Figure S2. All members of Peduoviridae encode a set of 6 orthologous core genes: Terminase, large subunit; Portal protein; Capsid scaffolding protein; Major capsid protein; Terminase, small subunit; Capsid completion/stabilization protein (https://ictv.global/taxonomy/taxondetails?taxnode\_id=202200225&taxon\_ name=Peduoviridae). Multiple sequence alignments were done for each orthologous protein using Mafft v.7.471. The best evolutionary models were identified using ModelTest-NG v.0.1.7. Maximum likelihood trees were built using RaxML-NG v1.0.3 with 100 searches for the best-scoring tree and 1000 bootstrap replicates. The amino acid substitution model used was LG+G4, except for Capsid completion/stabilization protein, which was WAG+G4.