

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:**  | Create one new unassigned order in realm *Riboviria*, including four new families for four currently unassigned genera of plant satellite viruses |
| **Code assigned:**  | 2024.021P.A.v1.Riboviria\_1nord |

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| **Author(s), affiliation and email address(es):**  |
| **Name**  | **Affiliation**  | **Email address**  | **Corresponding author(s)** X |
| Krupovic M | Institut Pasteur, Université Paris Cité, Archaeal Virology Unit, Paris, France | mart.krupovic@pasteur.fr | 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 | **X** |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| There is currently no Study Group for these taxa. |

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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:** |  21/06/2024 |

**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| W - Withdrawn |  |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:**  |
| 2024.021P.A.v1.Riboviria\_1nord.xlsx |

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| **Taxonomic changes proposed:**  |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon | **X** | Promote taxon |  |
| Rename taxon | **X** | 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*: Species, genus, family*Description of current taxonomy*: *Riboviria*: unassigned family *Sarthroviridae* and genera *Albetovirus*, *Aumaivirus*, *Papanivirus*, and *Virtovirus**Proposed* *taxonomic change(s):* *Riboviria*: *Tombendovirales* to include family *Sarthroviridae* and two new families, *Pamosaviridae* (*Papanivirus*), and *Tomosaviridae* (*Virtovirus*); and *Riboviria*: *Tonesaviridae* (*Albetovirus, Aumaivirus*); renaming of all species in the four genera to fulfill the ICTV’s binomial naming mandate.*Justification*: Structural comparison of the satellite virus capsid proteins indicates that these viruses are not monophyletic and form two distinct assemblages.  |

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| * **Text of Taxonomy proposal:**
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| *Taxonomic rank(s) affected*: Species, genus, family*Description of current taxonomy*: Realm *Riboviria* currently includes one family, *Sarthroviridae*, and four genera that have not been assigned to other ribovirian ranks: *Albetovirus*, *Aumaivirus*, *Papanivirus*, and *Virtovirus*.*Proposed* *taxonomic change(s)*: Due to their overall, but distant, relationship, it is proposed to move genera *Papanivirus* and *Virtovirus*, each in a new family, and an unassigned family *Sarthroviridae* into one new order. We also propose to include genera *Albetovirus and Aumaivirus* into one new unassigned family. In addition, it is proposed to rename the species of the four genera to fulfill the binomial species naming mandate of the ICTV.*Demarcation criteria:*The species demarcation criteria remain the same. Membership in the family will be determined by phylogenetic analysis, whereas for inclusion into higher taxa, structure-based comparisons may be used.*Justification*: Plant satellite viruses have single-stranded (ss) RNA genomes of positive polarity that are packed into small capsids exhibiting T=1 icosahedral symmetry. The virions are constructed from 60 copies of the capsid protein (CP) that adopts the jelly-roll topology. In 2016, based on the CP sequence similarity, plant satellite viruses were classified into four “floating” genera, namely, *Albetovirus*, *Aumaivirus*, *Papanivirus* and *Virtovirus* (Krupovic et al., 2016). At the time, due to high sequence divergence, it was decided not to assign the genera to higher taxa. Recent developments in structural biology and bioinformatics prompted us to reassess the relationships among these satellite viruses and other viruses for which capsid protein structures became available.High resolution structures are available for members of three of the four genera, i.e., *Albetovirus*, *Papanivirus* and *Virtovirus*. Thus, we modeled the structure of a representative aumaivirus using AlphaFold2 (Jumper et al., 2021) and used DALI to perform all against-all-structural analysis of the jelly-roll capsid proteins of satellite viruses with icosahedral capsids, as well as other viruses with structurally similar CPs, as identified using FoldSeek (van Kempen et al., 2024). This analysis indicates that CPs of plant satellite viruses are not monophyletic and form two separate groups (Figure 1). The first group includes members of the genera *Albetovirus* and *Aumaivirus*, consistent with the earlier sequence-based comparisons that showed that CPs of viruses from the two genera share up to 29% sequence identity (Krupovic et al., 2016). Notably, CPs of these satellite viruses clustered with the CPs of plant geminivirids and nanovirids (Figure 1), in line with previous observations (Krupovic et al., 2009). The second cluster includes members of the genera *Papanivirus* and *Virtovirus*, and of family *Sarthroviridae*. The latter family includes a satellite virus, extra small virus (XSV), which together with its helper virus, Macrobrachium rosenbergii nodavirus (MrNV), infect giant freshwater prawns and cause white tail disease (Sahul Hameed et al., 2018).Based on these observations we suggest unifying genera *Albetovirus* and *Aumaivirus* within a new unassigned ribovirian family “*Tonesaviridae*”. Given that papaniviruses and virtoviruses are not more closely related to each other than they are to the sarthrovirid XSV, we propose assigning the two genera of plant satellite viruses to two new families, “*Pamosaviridae*” and “*Tomosaviridae*”, respectively. To recognize the relationship between families “*Pamosaviridae*”, “*Tomosaviridae*” and *Sarthroviridae*, we propose unifying them within a new order “*Tombendovirales*”.Finally, we propose renaming the species names of all plant satellite viruses to comply with the binomial species naming mandate of the ICTV:*Tobacco albetovirus 1 → Albetovirus alphatabaci**Tobacco albetovirus 2 → Albetovirus betatabaci**Tobacco albetovirus 3 → Albetovirus gammatabaci**Maize aumaivirus 1 → Aumaivirus maidis**Panicum papanivirus 1 → Papanivirus panici**Tobacco virtovirus 1 → Virtovirus tabaci*Etymologies of all proposed taxon names are provided in the excel module. |

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| **References:**  |
| Jumper J, Evans R, Pritzel A, Green T, Figurnov M, Ronneberger O, Tunyasuvunakool K, Bates R, Žídek A, Potapenko A, Bridgland A, Meyer C, Kohl SAA, Ballard AJ, Cowie A, Romera-Paredes B, Nikolov S, Jain R, Adler J, Back T, Petersen S, Reiman D, Clancy E, Zielinski M, Steinegger M, Pacholska M, Berghammer T, Bodenstein S, Silver D, Vinyals O, Senior AW, Kavukcuoglu K, Kohli P, Hassabis D. Highly accurate protein structure prediction with AlphaFold. Nature. 2021; 596(7873):583-589. doi: 10.1038/s41586-021-03819-2. PMID: 34265844Krupovic M, Kuhn JH, Fischer MG. A classification system for virophages and satellite viruses. Arch Virol. 2016; 161(1):233-47. doi: 10.1007/s00705-015-2622-9. PMID: 26446887Krupovic M, Ravantti JJ, Bamford DH. Geminiviruses: a tale of a plasmid becoming a virus. BMC Evol Biol. 2009 May 21;9:112. doi: 10.1186/1471-2148-9-112. PMID: 19460138Sahul Hameed AS, Ninawe AS, Nakai T, Chi SC, Johnson KL, ICTV Report Consortium. ICTV virus taxonomy profile: *Sarthroviridae*. J Gen Virol. 2018; 99(12):1563-1564. doi: 10.1099/jgv.0.001158.PMID: 30507372van Kempen M, Kim SS, Tumescheit C, Mirdita M, Lee J, Gilchrist CLM, Söding J, Steinegger M. Fast and accurate protein structure search with Foldseek. Nat Biotechnol. 2024; 42(2):243-246. doi: 10.1038/s41587-023-01773-0. PMID: 37156916   |

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| **Tables, Figures:**  |

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**Figure 1.** Relationships between jelly-roll capsid proteins of icosahedral viruses. The matrix and cluster dendrogram are based on the pairwise Z score comparisons calculated using DALI. The color scale indicates the corresponding Z scores. PDB identifiers are indicated next to the corresponding rows and columns. Current taxonomy of the corresponding viruses is provided in parenthesis next to the abbreviated virus names. The two groups of satellite viruses are highlighted with a colored background and the proposed taxa are indicated.