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The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2025

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

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| **Title:** | Create one (1) new species in the family *Alphaflexiviridae* |
| **Code assigned:** | 2025.002P.Alphaflexiviridae\_Allexivirus\_1nsp | |

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| **Author(s), affiliation and email address(es):** | | | | |
| **Given name (+middle initial(s))** | **Surname** | **Affiliation** | **Email address** | **Corr. author(s)** |
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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:** |
| *Alphaflexiviridae* SG |

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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** |
| *Alphaflexiviridae* SG |  |  |  |
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| **Submission date:** | 06/06/2025 |

**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| W - Withdrawn |  |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 3:** **TAXONOMIC PROPOSAL**

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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** |
| *Allexivirus sauroandrogyni* | Species epithet derived from the host genus ‘Sauropus’ and species ‘androgynus’. |
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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** X |
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| **Abstract of Taxonomy Proposal:** |
| *Taxonomic rank(s) affected*:  Genus, species    *Description of current taxonomy*:  The family *Alphaflexiviridae* currently includes 72 virus species in genera *Allexivirus* (14), *Botrexvirus* (3), *Lolavirus* (1), *Platypuvirus* (1), *Potexvirus* (52) and *Sclerodarnavirus* (1).  *Proposed* *taxonomic change(s):*  This taxonomic proposal considers the recognition of 1 new virus species belonging to genus *Allexivirus* within the family *Alphaflexiviridae.*    *Justification*:  Throughout the family, isolates of different species should have less than 72% nucleotide identity (or 80% amino acid identity) between their respective coat protein or polymerase genes (or proteins). Viruses from different genera usually have less than about 45% nucleotide identity in these genes. The nucleotide and amino acid sequences of the virus belonging to the newly proposed species fit well within these demarcation criteria. |

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| **Text of Taxonomy proposal** |
| *Taxonomic rank(s) affected*:  Genus, species  *Description of current taxonomy*:  The family *Alphaflexiviridae* currently includes 72 virus species in genera *Allexivirus* (14), *Botrexvirus* (3), *Lolavirus* (1), *Platypuvirus* (1), *Potexvirus* (52) and *Sclerodarnavirus* (1).  *Proposed* *taxonomic change(s)*:  This taxonomic proposal considers the creation of 1 new virus species belonging to the genus *Allexivirus* within the family *Alphaflexiviridae*  *Demarcation criteria:*  Throughout the family, isolates of different species should have less than 72% nucleotide identity (or 80% amino acid identity) between their respective coat protein or polymerase genes (or proteins). Viruses from different genera usually have less than about 45% nucleotide identity in these genes.  *Justification*:  **Creation of a novel species in the genus *Allexivirus* of the family *Alphaflexiviridae*.** The complete genome sequence of Sauropus androgynus virus (SaV) was determined using high throughput sequencing from total RNA extracted from *S. androgynus* plants [1]. The SaV genome is 8,007 nt long (accession number PQ177843) excluding the poly (A) tail and has UTRs of 94 nt and 197 nt at the 5' and 3' ends, respectively. The genome is organized into five ORFs; ORF 1 encodes the replicase, ORFs 2-4 encode the TGB 1, 2 and 3, and ORF5 encodes the CP. The SaV replicase shares highest 69.5% aa sequence identity with Arachis pintoi virus, whereas the SaV CP shares highest 56.4% aa sequence identity with blackberry virus E. Phylogenetic analyses with the SaV replicase (Figure 1) and CP (Figure 2) aa sequences placed the virus in the genus *Allexivirus* in the family *Alphaflexiviridae*.  Proposed new species name – “*Allexivirus sauroandrogyni”*; species epithet derived from the host genus ‘Sauropus’ and species ‘androgynus’. |

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| **References:** |
| [1] Zhu L.J., Su L.Y., Chen X., Pan S., Xia F., Han Y.H., Xu Z., Xu Q. (2025) Characterization of the complete genome of a novel allexivirus infecting Sauropus androgynus in China. Archives of Virology, 170, 4–7. https://doi.org/10.1007/s00705-024-06202-4 |

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| **Accompanying files:** | |
| **Filename** | **Description of contents** |
| 2025.002P.N.v2.Alphaflexiviridae\_Allexivirus\_1nsp | Spreadsheet |
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| **Tables, Figures:** |



**Figure 1.** Phylogenetic analysis of viruses in the family *Alphaflexiviridae* inferred using replicase amino acid sequences. Multiple sequence alignment of 74 replicase sequences was done using MUSCLE (Edgar, 2004). Best amino acid substitution method was inferred using MEGA 11 (Tamura et al., 2021). Maximum likelihood trees were inferred using RAxML-NG software (Kozlov et al., 2019) using the LG method considering the proportion of invariable sites (+I) and the variation of the substitution rate among sites according to a gamma distribution (+G). Best ML tree with bootstrap support values (1000 replicates) is shown. Only bootstrap values higher than 50% are displayed. Different colours mark different genera. Carnation latent virus (QJX15400.1) (genus *Carlavirus*, family *Betaflexiviridae*) was used as an outgroup. The sequence from Sauropus androgynus virus is marked with a red arrow.



**Figure 2.** Phylogenetic analysis of viruses in the family *Alphaflexiviridae* inferred using coat protein (CP) amino acid sequences. Multiple sequence alignment of 74 CP sequences was done using MUSCLE (Edgar, 2004). Best amino acid substitution method was inferred using MEGA 11 (Tamura et al., 2021). Maximum likelihood trees were inferred using RAxML-NG software (Kozlov et al., 2019) using the LG method considering the variation of the substitution rate among sites according to a gamma distribution (+G). Best ML tree with bootstrap support values (1000 replicates) is shown. Only bootstrap values higher than 50% are displayed. Different colours mark different genera. Carnation latent virus (QJX153999.1) (genus *Carlavirus*, family *Betaflexiviridae*) was used as an outgroup. The sequence from Sauropus androgynus virus is marked with a red arrow.