

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 genus *Arepavirus*, one (1) new species in genus *Macluravirus,* one 1 new species in genus *Poacevirus* and 2 new species in genus *Potyvirus* (*Patatavirales: Potyviridae*) |
| **Code assigned:**  | 2025.009P.Potyviridae\_5nsp |

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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:**  |
| *Potyviridae* Study Group  |

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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:** | 05/06/25  |

**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| W - Withdrawn |  |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** |
| *“Arepavirus karnatakense”* | Species name derived from the place the virus was found: Karnataka in India |
| *“Macluravirus amomi”* | Species name derived from the Latinized genus name of the host (*Amomum*) |
| *“Poacevirus avenae”* | Species name derived from the Latinized genus name of the host (*Avena*) |
| *“Potyvirus heraclei”* | Species name derived from the Latinized genus name of the host (*Heracleum*) |
| *“Potyvirus shilinense”* | Species name derived from the place the virus was found: Shilin county in China |

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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*: Genus, species *Description of current taxonomy*: The family *Potyviridae* includes 13 genera and 259 species. Genus *Arepavirus* is formed by 2 species, *Macluravirus* by 12 species, *Poacevirus* by 3 species and *Potyvirus* by 214 species. For the remaining 9 genera no recommendation for changes is proposed.*Proposed* *taxonomic change(s):* Creation of 5 new species: 1 species in the genus *Arepavirus*, 1 species in the genus *Macluravirus*, 1 species in the genus *Poacevirus* and 2 species in the genus *Potyvirus*, totaling 264 species in the family.Genus *Arepavirus: “Arepavirus karnatakense”*Genus *Macluravirus: “Macluravirus amomi”*Genus *Poacevirus: “Poacevirus avenae”*Genus *Potyvirus*: “*Potyvirus heraclei”; “Potyvirus shilinense”**Justification*:According to the ICTV Report chapter on *Potyviridae*, the 13 genera are distinguished based on biological criteria - primarily transmission by specific vectors - and molecular data, with members of different genera sharing less than 46% nucleotide sequence identity. Viruses from different species typically have complete ORF sequences that share less than 76% nucleotide identity and less than 82% amino acid identity. The genome sequences of the five proposed new viruses analyzed showed nucleotide and amino acid identities below the species demarcation thresholds. Additionally, biological data were available to support their classification as members of new species. |

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| **Text of Taxonomy Proposal:** *Taxonomic rank(s) affected*: Genus, species*Description of current taxonomy*: The family *Potyviridae* includes 13 genera and 259 species. Genus *Arepavirus* is formed by 2 species, *Macluravirus* by 12 species, *Poacevirus* by 3 species and *Potyvirus* by 214 species [1]. *Proposed* *taxonomic change(s)*: Creation of 5 new species: 1 species in the genus *Arepavirus*, 1 species in the genus *Macluravirus*, 1 species in the genus *Poacevirus* and 2 species in the genus *Potyvirus*, totaling 264 species in the family.Genus *Arepavirus: “Arepavirus karnatakense”*Genus *Macluravirus: “Macluravirus amomi”*Genus *Poacevirus: “Poacevirus avenae”*Genus *Potyvirus*: “*Potyvirus heraclei”; “Potyvirus shilinense”**Demarcation criteria:* Members of different species have complete ORF sequences that are generally <76% identical in nucleotide sequence and <82% identical in amino acid sequence [2]. Genome sequences based on assembly of NGS/HTS reads are considered if confirmed by Sanger sequencing. In considering the evidence for new species or genera in the family *Potyviridae*, the Study Group will evaluate each new case based on complete or near-complete genome sequence(s) together with host and biological characteristics.*Justification*:1. *“Arepavirus karnatakense”*[3]

**Virus name**: Areca palm necrotic ringspot virus 2 (ANRSV2) **Species name:**  *“Arepavirus karnatakense”***Genus:** *Arepavirus***Origin of name:** Species name derived from the location that the virus was found (Karnataka, India)**Isolates for which complete genomes are available:**Areca palm necrotic ringspot virus 2 KUN-1 (PQ197196) – exemplar isolateAreca palm necrotic ringspot virus 2 NER-1 (PQ197197)**Original hosts**:*Dypsis lutescens* (areca palm)**Justification for creating a new species:**The complete genomes of the two ANRSV2 isolates share 96% nt identity with one another and are thereby isolates of the same species. Their closest relatives (68-70% nt identity with 74-88% coverage) are areca palm necrotic ringspot virus (ANRSV) isolate XC-1 (MH395371) and areca palm necrotic spindle-spot virus (ANSSV) isolate HNBT (MH330686). Both ANRSV2 isolates are below the potyvirid species demarcation limit of <76% nt identity [2], confirming they represent members of a new species. The deduced polyproteins of the two ANRSV2 isolates share 99% aa identity with one another and 68-73% identity with the polyprotein sequences of ANRSV and ANSSV. These identities confirm the status of ANRSV2 isolates as belonging to a distinct species.HC-Pro1, HC-Pro2, P3, 7K, CI, 9K, NIa-VPg, NIa-Pro, NIb and CP of ANRSV2 isolates share a maximum of 54.6%, 64.4%, 58.0%, 81.4%, 78.3%, 51.8%, 83.3%, 75.7%, 72.8% and 85.7%, amino acid sequence identities, respectively, with the corresponding sequences of the other two arepaviruses.ANRSV2 clusters with ANRSV and ANSSV in phylogenetic analysis using maximum likelihood, placing it in genus *Arepavirus* (Figure 1). **Proteins and motifs**: The mature proteins cleaved from the polyprotein are identical in order and within the size range of typical potyviruses (Figure 2). The proteins are cleaved from the ORF into 10 mature proteins from conserved cleavage sites (Table 1). The small potyvirid ORF known as PIPO is present in ANRSV2. The conserved polymerase slippage motif is GA(7). It is present within the P3 coding region, allowing the translation of P3-PIPO in the +2 reading frame. In CI and NIb of ANRSV2, the conserved motif(s) associated with helicase activity (1094GSGKS(X)3P1102 and 1187DEXH1190) and replicase activity (2580GDD2582) were determined, while the conserved residues H1961, D1993, C2061, H2077 in the NIa-Pro active site and the conserved 2059GXCG2062 around the ‘C’ residue in the active site were located in NIa-Pro.The potyvirid-conserved HC-Pro motifs KITC and PTK linked to aphid transmission are not present. The CP of ANRSV2 and those of the other arepaviruses does not contain the conserved aphid transmission motif DAG or any of the five variations of DAG [4]. Predicted heptapeptide cleavage sites are reported in Table 1. **Natural transmission**: Unknown. The absence of the all three conserved aphid-transmission motifs suggests this virus is not transmitted by aphids. **Additional information**:The novel virus was found infecting symptomatic areca palms (Betel nut tree) in Karnataka, India. The other two arepaviruses, areca palm necrotic ringspot virus and areca palm necrotic spindle-spot virus, were isolated from the same host in Hainan Province, China.**Study Group recommendation**:The *Potyviridae* Study Group recommends that Areca palm necrotic ringspot virus 2 be assigned to a new species, for which we propose the name “*Arepavirus karnatakense”* in recognition of the location in India where it was first identified, and to distinguish it from areca palm necrotic ringspot virus isolates within *Arepavirus arecae*.1. *“Macluravirus amomi”* [5]

**Virus name:** tsaoko stripe mosaic virus (TkSMV)**Species name:** *“Macluravirus amomi”***Genus:** *Macluravirus***Origin of name:** species name derived from the host the virus was isolated, *Amomum tsaoko.***Isolates for which complete genomes are available:**Tsaoko stripe mosaic virus - FG2Z (PQ068101)**Original host**:*Amomum tsaoko* **Justification for creating a new species:**The complete genome of TkSMV-FG2Z shares 71.5% nucleotide and 75.9% amino acid sequence identity with its closest known relative, Alpinia oxyphylla mosaic virus (AloMV; MG978107) [5] ). This is below the potyvirid species demarcation limit of <76% nt identity and <82% aa identity [2], confirming it represents a member of a new species. Based on the full length nt sequences or aa sequences of the polyproteins of TkSMV, the 13 macluraviruses and other representative potyvirids, TkSMV clustered together with the macluraviruses in a phylogenetic tree and was most closely related to AloMV, another macluravirus that infects plants of the ginger family. In phylogenetic trees based on full-length genome and CP aa sequences, TkSMV was also most closely related to AloMV (Figure 1).**Proteins and motifs**: The polyprotein is predicted to be cleaved into nine mature proteins: HC-Pro (262 aa), P3 (304 aa), 7K (64 aa), CI (656 aa), 9K (80 aa), VPg (179 aa), NIa-Pro (217 aa), NIb (563 aa), and CP (301 aa) (Figure 3). A putative P3N-PIPO protein (57 aa) starting from a TA(6) motif was identified at nt 1356–1526 within the P3 region in the +2 reading frame. The conserved guanine (G) preceding hexa-adenine is replaced by thymine (T) in TsKMV, as it also is in large cardamom chirke virus. Highly conserved motifs of potyvirids are present in the TkSMV polyprotein, including 717GSGKSX3P725 and 810DESH814 in CI for RNA helicase activity; 1429LYD1431, which contains a tyrosine for linking VPg to the 5’end of the viral RNA; 2155GDD2157 in NIb for RNA-dependent RNA polymerase (RdRp) activity; and 2474WCANNGTSSE2483 and 2555AFDF2558 in CP. However, TkSMV lacks a P1 proteinase and has a shorter HC-Pro than most potyviruses. The aphid-transmission motifs ‘DAG’ in CP and ‘PTK’ and ‘KITC’ in HC-Pro are also absent in TkSMV. **Natural transmission**: Unknown. The absence of all three conserved aphid-transmission motifs suggests this virus is not transmitted by aphids. **Additional information**:The novel virus was found infecting symptomatic *Amomum tsaoko* plants in Fugong county, Yunnan Province, China. Transmission electron microscopy identified filamentous viral particles about 670 nm in length and 13 nm in width in the infected *A. tsaoko* plants. Illumina sequencing identified sequences with high similarity to macluraviruses and the complete genome was subsequently sequenced from overlapping PCR amplified fragments, 5’ and 3’ RACE.**Study Group recommendation**:The *Potyviridae* Study Group recommends that tsaoko stripe mosaic virus be assigned as a member of a new species, for which we propose the name “*Macluravirus amomi”* after the plant genus from which the virus was isolated1. *“Poacevirus avenae”* [6]

**Virus**: wild oat poacevirus 1 (WOPV1]**Proposed species name**: “*Poacevirus avenae”***Genus**: *Poacevirus* **Origin of name:** species name derived from the genus name of the host (*Avena*)**NCBI accession**: Wild oat poacevirus 1, isolate P2P5, complete genomeGenBank: PQ561517**Original host**: *Avena fatua***Symptoms of infection**: Yellowing and reddening of leaves and stunting of plants. **Note:** This virus was discovered in a mixed infection with wheat streak mosaic virus (genus *Tritimovirus*), barley stripe mosaic virus (genus *Hordeivirus*), and barley yellow dwarf virus(genus *Luteovirus*).**Morphology:** Not reported.**Country of isolation**: France**Sequencing approaches**: High-throughput sequencing (HTS) of ribosomal RNA-depleted total RNA from a pool of four symptomatic plants, Sanger sequencing of a 663 bp RT-PCR amplicon using virus-specific primers, and determination of 5' and 3’ terminal sequences by RACE. **Nucleotide sequence identity**: WOPV1 shares 44.6–58.1% nucleotide sequence identity with the three ICTV-ratified poaceviruses [Triticum mosaic virus (FJ263671), sugarcane streak mosaic virus (GQ388116); and Caladenia virus A (JX156425)], and 57.6% with a recently-described unratified poacevirus, Poaceae Liege poacevirus, isolate Latinne (ON137719).**Polyprotein sequence**: The WOPV1 genome encodes a large 3,189 amino acid polyprotein with all of the expected hallmarks of *Potyviridae* members.**Polyprotein identity**: Pairwise comparisons of complete polyprotein amino acid (aa) sequences showed that WOPV1 shares aa sequence identities of 39.6% with the orchid-infecting Caladenia virus A, 50.8% with sugarcane streak mosaic virus, 59.5% with Triticum mosaic virus, and 61.4% with Poaceae Liege poacevirus.Phylogenetic analysis based on pairwise alignments of polyprotein sequences of WOPV1 and other representative potyviruses showed that WOPV1 clusters with 100% bootstrap support with other poaceviruses (Figure 1).**Proteins and motifs**:The polyprotein encoded by the large ORF shows an overall arrangement (and sizes) of proteins and conserved motifs that are typical of potyvirids, i.e., P1, HC-Pro, P3, PIPO, 6K1, CI, 6K2, VPg, NIa-Pro, NIb, and CP.The putative protease cleavage sites could be identified along the polyprotein by comparison with those predicted for the other poaceviruses (Figure 4).The sequences of the CI and NIb proteins are the most conserved (71% and 71-74% aa sequence identity, respectively), and the P1 protein is the most divergent (45-47% aa sequence identity).**Natural transmission**: Not known. Some poaceviruses are transmitted by eriophyid mites. However, the zinc-finger-like motif H-(X2)-C-(X29)-C-(X2)-C, which is reportedly essential for mite transmission of the tritimovirus wheat streak mosaic virus, is incomplete in the N-terminal region of the HC-Pro protein of WOPV1.**Experimental transmission**: Unknown, not described.**Other host**s: Unknown, not described.**Study Group recommendation**: Based on the ICTV-recommended species demarcation criteria for the family (<76% nucleotide and <82% amino acid sequence identities in the complete ORF for members of the same genus [2]), WOPV1 represents a new species within genus *Poacevirus*, for which the name “*Poacevirus avenae*” is proposed*.*1. *“Potyvirus heraclei”* [7]

**Virus name**: Hogweed virus Y (HogVY) **Proposed species name:** “*Potyvirus heraclei”***Genus:** *Potyvirus***Origin of name:** species name derived from the generic name of the host (*Heracleum*)**Isolates for which complete genomes are available:**Hogweed virus Y isolate S1 (OR537212) isolated in North Yorkshire, UK – exemplar isolateHogweed virus Y isolate S37 (OR537213) isolated in Sleaford, UKHogweed virus Y isolate S4 (OR537214) isolated in North Yorkshire, UK**Original hosts**:Isolates S4 and S37 were from *Heracleum sphondylium* (hogweed), family Apiaceae.Isolate S1 was from *Anthriscus sylvestris* (cow parsley), family Apiaceae.**Justification for creating a new species:**The three HogVY isolates exhibit genome organisations typical of potyviruses. The complete genomes of isolates S1 and S4 share 99.8% nucleotide identity, while isolate S37 is more divergent, sharing 89.7% identity with the other two. All three isolates fall within the species demarcation limits (76% nucleotide identity for the genome, 82% amino acid identity for the large ORF) for potyviruses [2], supporting their classification as members of a single species.Comparative analysis shows that isolates S1 and S4 share 74.5–75.0% nucleotide identity with some turnip mosaic virus andlettuce mosaic virusisolates (KX579486, KX579485, KY111272, LC504570, KJ161176). Isolate S37 shares 68–69% nucleotide identity with isolates of lettuce mosaic virus andscallion mosaic virus(KJ161178, LC651507). The deduced polyproteins from the HogVY isolates share ~54% amino acid identity with the large ORFs of lettuce mosaic virus(AIA66377) and pecan mosaic-associated virus(OQ447475), which is below the species demarcation threshold for potyvirids. This supports recognition of these viruses as representing a distinct species.**Proteins and motifs**: The predicted mature proteins, cleaved from the polyprotein, are in the canonical order and size range typical of potyviruses. Ten mature proteins are generated from standard potyviral cleavage sites. The small PIPO ORF is present. The conserved polymerase slippage motif GA(₇) is found within the P3 coding region, allowing translation of P3-PIPO in the -1 reading frame. All conserved potyviral motifs appear in their expected positions [7].Transmission-associated motifs RITC and PTK were detected in the HC-Pro, and the NAG motif (a variant of the common DAG motif) was observed in the coat protein (CP).**Natural transmission**: Transmission by aphids was not experimentally confirmed. However, the presence of aphid transmission motifs (above) suggests that aphids may serve as vectors.**Additional information**:Mechanical inoculation of HogVY isolates onto indicator plants (Nicotiana benthamiana, N. occidentalis, N. rustica, N. tabacum, N. clevelandii, N. glutinosa, Chenopodium amaranticolor, C. quinoa, C. murale, Anthriscus cerefolium and Daucus carota) resulted in no observed transmission. Details of the detection methods used to assess transmission success were not reported.**Study Group recommendation**:The Potyviridae Study Group recommends that hogweed virus Y be recognized as a member of a new species, for which the species name Potyvirus heraclei was proposed [7], derived from the generic name of the primary host, Heracleum.1. *“Potyvirus shilinense”* [8]

**Virus**: Paris potyvirus 5 (ParPV-5)**Proposed species name**: “*Potyvirus shilinense”***Genus**: *Potyvirus***Origin of name:** Species name derived from the locality where the virus was found, Shilin, China**NCBI accession**: Paris potyvirus 5 isolate YShL-Paris, complete genomeGenBank: OR608917 (9631 nucleotides)**Original hosts**: *Paris polyphylla* var. yunnanensis (*Rhizoma paridis*)**Symptoms of infection**: ParPV-5, probably in coinfection with isolates of a capillovirus, induced leaf yellowing and necrosis, mottle, yellowing leaf edge, or yellowing and blistering on the leaves of *Paris polyphylla* var. *yunnanensis*.No obvious symptoms (asymptomatic) on the leaves of *P. polyphylla* var *yunnanensis*, *Nicotiana benthamiana*, *Cucumis sativus* and *Bidens pilosa* were observed upon inoculation with a full-length infectious cDNA clone of ParPV-5. Infection by the cDNA clone was confirmed by RT-PCR using ParPV-5-specifc primers.**Morphology:** filamentous virions of 750~800 nm in length.**Country of isolation**: Yunnan Province, China.**Sequencing approaches**: High-throughput sequencing (HTS), overlapping RT-PCR, 5' RACE, and Sanger sequencing**Nucleotide sequence identity**: ParPV-5 shares 52.4–68.9% nucleotide sequence identity with other known potyviruses **Polyprotein identity**: Pairwise comparisons of complete polyprotein amino acid (aa) sequences showed that ParPV-5 shares 37.6–70.1% identity with other potyviruses.**Proteins and motifs**: P1 of 312 aa, HC-Pro of 457 aa, P3 of 347 aa, PIPO ORF of 65 aa, 6K1 of 52 aa, CI of 634 aa, 6K2 of 53 aa, VPg of 190 aa, NIa-Pro of 243 aa, NIb of 517 aa, and CP of 284 aa (Figure 5).Protease cleavage sites: The P1 and HC-Pro correspond to Y/S and G/G cleavage sites, while predicted NIa-Pro cleavages are Q/G, Q/S, Q/S, Q/G, E/S, Q/S, Q/S (Figure 5).The following motifs were found:P1: 264GXSG267 (protease activity)HC-Pro: FRNKX12CDNQLD (symptomatology), HAKRFF (cell-to-cell movement), CCCVT (long distance movement), C-X72H (protease activity), KLSC and PTK (aphid transmission)A small PIPO ORF within the P3 ORF: GA6CI: GAVGSGKST (NTP binding); VLLLEPTRPL, DEXH, KVSATPP, LVYV, and GERIQRLGRVGR (potential helicase activity)NIa-Pro: HX34DX67GXCGX14H (proteolytic activity)NIb: SLKAEL (RNA polymerase activity), CHADGS, GNNSGQPSTVVDNTLMV, and GDD (RNA-dependent polymerase activity)CP: DAG (aphid transmission)**Natural transmission**: Unknown**Experimental transmission**: Infectious cDNA clone**Other host**s: *N. benthamiana,* *C. sativus* and *B. pilosa*, inoculated with the cDNA clone of ParPV-5, were infected, but were asymptomatic.**Study Group recommendation**: According to the species demarcation criteria for the genus *Potyvirus* established by the ICTV for the complete ORF (<76% identical in nucleotide sequence and <82% identical in amino acid sequence [2]), ParPV-5 represents a member of a new species in the genus *Potyvirus,* with a proposed name of “*Potyvirus shilinense*”. |

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| **References:**  |
| [1] Inoue-Nagata AK, Jordan R, Kreuze J, Li F, López-Moya JJ, Mäkinen K, Ohshima K, Wylie SJ, ICTV Report Consortium. ICTV Virus Taxonomy Profile: *Potyviridae* 2022. J Gen Virol. 2022 May;103(5). doi: 10.1099/jgv.0.001738. PMID: 35506996.[2] Adams MJ, Antoniw JF, Fauquet CM. Molecular criteria for genus and species discrimination within the family *Potyviridae*. Arch Virol. 2005 Mar;150(3):459-79. doi: 10.1007/s00705-004-0440-6. Epub 2004 Dec 10. PMID: 15592889.[3] Thava Prakasa Pandian R, Bhavishya, Kavi Sidharthan V, Rajesh MK, Babu M, Sharma SK, Nirmal Kumar BJ, Chaithra M, Hegde V. From the discovery of a novel arepavirus in diseased arecanut palms (*Areca catechu* L.) in India to the identification of known and novel arepaviruses in bee and plant transcriptomes through data-mining. Virology. 2024 Dec;600:110256. doi: 10.1016/j.virol.2024.110256. PMID: 39369672.[4] Nigam D, LaTourrette K, Souza PFN, Garcia-Ruiz H. Genome-wide variation in potyviruses. *Front Plant Sci*. 2019 Nov 12;10:1439. doi: 10.3389/fpls.2019.01439. PMID: 31798606; PMCID: PMC6863122.[5] Yu X, Zou X, Zhang L, Wu L, Yang Y, Li G, Dong J. Complete genome sequence of tsaoko stripe mosaic virus, a novel macluravirus found in *Amomum tsaoko*. Arch Virol. 2024 Nov 15;169(12):246. doi: 10.1007/s00705-024-06177-2.[6] Huang A, Marais A, Zhang Z, Candresse T. Complete genome sequence of a new poacevirus infecting wild oat (*Avena fatua* L.) in France. Arch Virol. 2024 Nov 28;169(12):256. doi: 10.1007/s00705-024-06187-0. PMID: 39607585.[7] Furrokh D, McGreig S, Adams IP, Barrett B, Fowkes A, Skelton A, Fox A., Vazquez-Iglesias I. Coding genome of a novel potyvirus, hogweed virus Y (HogVY). Journal of Plant Pathology2024;106(4):1839-42.[8] Lan P, He P, Mu A, Cao M, Wang Y, Zhou G, Chen X, Cai H, Li F. Molecular and biological characterization of infectious full-length cDNA clones of two viruses in *Paris yunnanensis*, including a novel potyvirus. Sci Rep. 2025 Jan 2;15(1):473. doi: 10.1038/s41598-024-84226-1. PMID: 39747256; PMCID: PMC11696918.[9] Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010). New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol. 59(3):307-21. doi: 10.1093/sysbio/syq010. PMID: 20525638.[10] Le SQ, Gascuel O (2008). An improved general amino acid replacement matrix. Mol Biol Evol. Jul;25(7):1307-20. doi: 10.1093/molbev/msn067. PMID: 18367465.[11] Darriba D, Posada D, Kozlov AM, Stamatakis A, Morel B, Flouri T (2020). ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. Mol Biol Evol. 37(1):291-294. doi: 10.1093/molbev/msz189. PMID: 31432070; PMCID: PMC6984357.  |

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| **Accompanying files:**  |
| **Filename** | **Description of contents** |
| 2025.009P.N.v2.Potyviridae\_5nsp | spreadsheet |
| 2025.009P.N.v1.Potyviridae\_5nsp\_Fig. 1 | Phylogenetic tree |

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| **Tables, Figures:**  |

**Table 1**. Predicted heptapeptide cleavage sites of the polyprotein of isolates KUN 1 and NER 1 of areca palm necrotic ringspot virus 2 (ANRSV2) compared with areca palm necrotic ringspot virus (ANRSV) isolate XC-1 and areca palm necrotic spindle-spot virus (ANSSV) isolate HNBT. Residues that differ from ANRSV2 are highlighted. Protein 1 (P1), Helper component protease (HC-Pro), Protein 3 (P3), Six Kilodalton protein 1 (6K1), Cytoplasmic Inclusion (CI), Six Kilodalton protein 2 (6K2), Viral Protein Genome-linked (VPg), Nuclear Inclusion a protease (NIa-Pro), Nuclear Inclusion b (NIb), and Capsid (Coat) Protein (CP).

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| **Virus** | **P1/HC-Pro** | **HC-Pro/P3** | **P3/6K1** | **6K1/CI** | **CI/6K2** | **6K2/VPg** | **VPg/NIa-Pro** | **NIa/NIb** | **NIb/CP** |
| ANRSV2 Kun1 | KDLFYV/T | FTYKVG/A | EKKEFQ/S | GSKEFQ/A | RCLEFQ/S | KEMNFE/G | KTKILE/C | DFVNFQ/M | NQKEFQ/M |
| ANRSV2 NER1 | KDLFYV/T | FTYKVG/A | EKKEFQ/S | GSKEFQ/A | RCLEFQ/S | KEMNFE/G | KTKILE/C | DFVNFQ/M | NQKEFQ/M |
| ANRSV XC1 | KDFFYG/V | FQYKVG/A | KRKEFQ/A | GGKEFQ/A | KCLEFQ/S | FVKEFE/A | PTKILE/C | DFENFQ/I | ASKEFQ/M |
| ANSSV HNBT | KDLFYG/V | FQYRVG/G | KNKEFQ/S | GGKEFQ/A | KCLEFQ/S | IAKEYE/V | PTKVLE/C | DFANFQ/M | ANKEFQ/M |

**Figure 1.** Phylogenetic tree was inferred using the complete polyprotein amino acid sequences of all ratified potyvirids with the complete genome sequence and the proposed new viruses highlighted with the phrase ‘recommended 2025’. The maximum likelihood (ML) tree was produced in PhyML v.3.1 [9] using the LG model [10] with gamma-distributed among-site rate variation; and a proportion of invariable sites was selected as the best substitution model by ModelTest-NG [11] from a degapped CLUSTAL X2 (Larkin et al., 2007) alignment of polyprotein amino acid sequences. Red dots in the major nodes indicate bootstrap values >90%, based on 100 pseudoreplicates. The scale bar represents 0.1 substitutions per site. The ML tree, midpoint rooted, was visualized using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/). The phylogenetic tree and corresponding sequence alignment are available to download from the Resources page.

Figure 1 is shown in the attachment.

**Figure 2**. Genome organisation of areca palm necrotic ringspot virus 2 with approximate positions of polyprotein cleavage sites. Not drawn to scale.



**Figure 3**. Genome organisation of tsaoko stripe mosaic virus with approximate positions of polyprotein cleavage sites. Not drawn to scale.



**Figure 4.** Genome organisation of wild oat poacevirus 1 with approximate positions of polyprotein cleavage sites. Not drawn to scale. (From [6])



**Figure 5.** Genome organisation of Paris potyvirus 5 with approximate positions of polyprotein cleavage sites. Not drawn to scale.