

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

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

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| **Title:**  | Create 1 new genus (*Phragmivirus*) with 2 species, and 8 new species in the genus *Potyvirus* (*Patatavirales: Potyviridae*) |
| **Code assigned:**  | 2024.012P.Uc.v1.Potyviridae\_1ng\_10nsp |

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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:** |  11/06/204 |

**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 | **X** |
| 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| W - Withdrawn |  |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:** |
| Following discussion, the EC suggested to remove SPVE as a new species, or to provide a better justification for the creation of a new species instead of considering it as an isolate of SPVC. In fact, the same host, the nt identity above the species demarcation threshold and the aa identity very close to the cut-off do not support the creation of a new species. Moreover, the references should be consolidated and moved to the appropriate section, and not embedded in the text. A new tree of better quality, if possible, should be removed from the proposal and provided separately as an appendix. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
| We discussed the comments of ICTV members regarding the proposal of sweet potato virus E as a member of a new species, and we agreed that its genome shares high identity with isolates of sweet potato virus C. We concluded that there is no enough evidence to classify it in a distinct species. Therefore, we decided to consider it as a variant of sweet potato virus C, and, thus, it was removed from our proposal. A new tree was constructed excluding sweet potato virus E from it.  |

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| **Revision date:** |  21/09/2024 |

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

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| **Name of accompanying Excel module:**  |
| 2024.012P.Uc.v1.Potyviridae\_1ng\_10nsp.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 within the family *Potyviridae* and species within the genus *Potyvirus* and the newly proposed *Phragmivirus**Description of current taxonomy*: According to the ICTV Report chapter on *Potyviridae*, twelve genera are differentiated by biological criteria, mainly transmission by specific vectors, and by molecular data, in which members of different genera are <46% identical in nucleotide sequence. Members of different species have complete ORF sequences that are generally <76% identical in nucleotide sequence and <82% identical in amino acid sequence. 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. *Proposed* *taxonomic changes:* Creation of one new genus (*Phragmivirus*), two new species in the genus *Phragmivirus* and eight new species in the genus *Potyvirus*:Genus *Phragmivirus**Phragmivirus phragmii**Phragmivirus spatinae*Genus *Potyvirus**Potyvirus aconiti**Potyvirus puerariae* *Potyvirus alilii**Potyvirus parisflavitessellati**Potyvirus catharanthiflavitessellati**Potyvirus polygonatimaculae**Potyvirus crocitessellati**Potyvirus galanthi**Justification*: the genomes of the proposed members in the new genus *Phragmitis* share sequence identity below the threshold for genera differentiation in the family *Potyviridae*; the proposed species have a genome strategy typical of members of genus *Phragmivirus* (2 species) and *Potyvirus* (8 species), and their nucleotide and amino acid sequences are below the threshold for species demarcation criteria for the genera. The characteristics of each new species and the new genus are described below.  |

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| **Text of Taxonomy proposal:**  |
| 1. **Creation ofone new genus:**

**Proposed genus name**: *Phragmivirus* **Family:** *Potyviridae***Origin of the name:** genus name derived from the latinized name of the host genus in which the first virus was described.**Members of proposed new genus for which complete genomes are available:**Common reed chlorotic stripe virus (CRCSV) isolate Tianshui (KY612317) Spartina mottle virus (SpMV) isolates DSMZ PV-0970 (MN788417), Q1371 (MW314142) and Q1372 (MW314143) **Original hosts**:*Phragmites australis*: common reed chlorotic stripe virus isolate Tianshui *Spartina* sp.:Spartina mottle virus isolate DSMZ PV-0970*Cynodon dactylon* × *C. transvaalensis*: Spartina mottle virus isolates Q1371 and Q1372 **Justification for creating a new genus:**Adams et al., 2005: ‘…*Most species had 50–55% nt identity to other members of their genus in their ORFs.’**‘…For the entire ORF, genus demarcation criteria were <46% nt identity…’*The complete genome sequences of CRCSV isolate Tianshui and SpMV isolate Q1372 share 53% nt identity. The analyses below are based on the sequence of isolate Q1372 of SpMV and isolate Tianshui of CRCSV.The complete genomes of these two viruses shared 33-47% nucleotide identities with members of other genera of the family *Potyviridae*: rymoviruses (46-47%), potyviruses (45-46%), arepaviruses (43%), tritimoviruses (42%), the brambyvirus and the bevemovirus (39%), roymoviruses and ipomoviruses (38%), macluraviruses (36%), the celavirus (35%) and bymoviruses (33%).The deduced polyproteins of the above isolates of CRCSV and SpMV share 46% aa identity. They share 14-33% identities with members of other genera of the family *Potyviridae*: rymoviruses (33%), potyviruses (31-32%), arepaviruses (18%), tritimoviruses (22%), the brambyvirus (23%), the bevemovirus (20%), roymoviruses (21%), ipomoviruses (19%), macluraviruses (18%), the celavirus (14%) and bymoviruses (17%) (Figure 1).Thus, CRCSV and SpMV are phylogenetically closer to one another than to viruses classified in other genera within family *Potyviridae*. Sequence identities closely follow the guidelines of Adams et al. (2005) and Inoue-Nagata et al. (2022), supporting their assignment into a new genus. **Genome sequence sizes**: CRCSV: 9426 ntSpMV: 9346-9376 nt**Polyprotein sequence**: CRCSV: 3014 aaSpMV: 3024-3029 aa**Shared molecular features:****Proteins and motifs**: The mature proteins cleaved from the polyproteins of both viruses are identical in order and within the size range to those of viruses in genus *Potyvirus.* They differ from potyviruses mainly in phylogeny (Fig 1). The proteins are cleaved from the ORF into 10 mature proteins from conserved cleavage sites, and PIPO is encoded by a small frame-shifted gene embedded within the P3 cistron (Fig. 2, Table 1). The small potyvirid ORF known as PIPO is present. The conserved polymerase slippage motif is G2A6 in CRCSV and G1A6 in SpMV. They are present within the P3 coding region of both viruses, allowing the translation of P3-PIPO in the −1 reading frame (Chung et al., 2008). Gene order, functional motifs and architecture of CRCSV, as shown in Yuan et al. (2017), closely resemble those predicted for SpMV (Fig 2).The potyvirid-conserved HC-Pro motifs KITC (IMQC in SpMV, LFQC in CRCSV) and PTK (ATE in SpMV, PIE in CRCSV) linked to aphid transmission are not present in either virus. The CP of SpMV does not contain the conserved aphid transmission motif DAG (DSD in SpMV), but the CRCSV CP has the DAE variation of DAG (Nigam et al., 2019), which is also found in the aphid-transmitted potyvirus chilli veinal mottle virus. *Ipomovirus**Poacevirus**Tritimovirus**Macluravirus**Bymovirus**Brambyvirus****Phragmivirus****Potyvirus**Rymovirus***Figure 1**. Phylogenetic analysis (Neighbor-Joining) of complete polyprotein sequences of representative viruses of different genera in the family *Potyviridae*. Common reed chlorotic strip virus and Spartina mottle virus (indicated by black dots) are members of proposed new genus *Phragmivirus*. **Table 1**. Predicted heptapeptide cleavage sites of the polyproteins of common reed chlorotic stripe virus (CRCSV) and Spartina mottle virus (SpMV).

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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** |
| CRCSV | 234LQLEHF/S | 692KNYRVG/G | 1038GRITLQ/A | 1091ETITLQ/S | 1730GVINLQ/S | 1783DRVYLE/A | 2000NGIQLE/C | 2240KALELQ/S | 2753DVITLQ/A |
| SpMV | 224MRLIHY/S | 664KHYLVG/G | 1010KDITLQ/A | 1063ETIMLQ/S | 1703GVITLQ/S | 1756DGFLLE/S | 1965DSLNLE/G | 2203ATLNLQ/S | 2715DTFQLQ/A |

Residues common to cleavage sites of both viruses are shaded in yellow. Numbers indicate the position of the first amino acid residue of each protein. Protein 1 (P1), Helper component protease (HC-Pro), Protein 3 (P3), Pretty Interesting *Potyviridae* Open reading frame (PIPO), 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).**Figure 2**. Genome organisation of known phragmiviruses showing approximate positions of the 5’ and 3’ untranslated regions (UTR), Protein 1 (P1), Helper component protease (HC-Pro), Protein 3 (P3), Pretty Interesting *Potyviridae* Open reading frame (PIPO), 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). Not drawn to scale.**Natural transmission**: Unknown. The absence of all three conserved aphid-transmission motifs in both viruses suggests these viruses are not transmitted by aphids. **Additional information**:Thomas et al. (2021) proposed the novel genus name ‘Sparmovirus’ following Spartina mottle virus. However, common reed chlorotic stripe virus has priority, being published by Yuan et al. in 2017, and the *Potyviridae* SG recommends the genus name *Phragmivirus* to acknowledge the host of the first virus described from this group. **Study Group recommendation**:The *Potyviridae* Study Group recommends the creation of a new genus, tentatively named *Phragmivirus*, named after the botanical name of the host, *Phragmites australis* (common reed), of common reed chlorotic stripe virus. Two viruses currently meet the criteria for inclusion in this proposed genus: they are common reed chlorotic stripe virus and Spartina mottle virus.1. **Creation of 2 new species in the genus *Phragmivirus*:**

**2.1) Virus name:** Common reed chlorotic stripe virus (CRCSV)**Proposed species name**: *Phragmivirus phragmii***Genus:** *Phragmivirus***Origin of names:** species name derived from the latinized genus name of the host**Genome available:**The complete genome of isolate Tianshui of common reed chlorotic stripe virus (CRCSV) is available (KY612317) Note: The GenBank accession KY612317 describes the sequence of reed chlorotic stripe virus, but this virus is identified as common reed chlorotic stripe virus in the publication of Yuan et al. (2017).**Authors:** Yuan,W., Du,K., Fan,Z. and Zhou,T.**Author location:** Plant Pathology, China Agricultural University, No. 2 Yuanmingyuan West Road, Beijing, Beijing 100193, China**Publication:** Yuan W, Du K, Fan Z, Zhou T. Complete genomic sequence of common reed chlorotic stripe virus, a novel member of the family Potyviridae. Arch Virol. 2017 Nov;162(11):3541-3544. doi: 10.1007/s00705-017-3454-6. Epub 2017 Jul 13. PMID: 28707269.**Original host**:*Phragmites australis***Symptoms of infection**:streaked chlorosis and necrosis on leaves**Country of isolation**: China**Sequencing approach(es)**: Illumina, RT-PCR, RACE and sequencing**Genome sequence**: CRCSV: 9426 nt**Nucleotide sequence identity**: The complete genome sequence of CRCSV isolate Tianshui shares closest (51%) nt identity with Spartina mottle virus (SpMV) isolates DSMZ PV-0970 (MN788417), Q1371 (MW314142) and Q1372 (MW314143). The complete genome of the Tianshui isolate of CRCSV shares 33-47% nucleotide identities with members of other genera of the family *Potyviridae*: rymoviruses (46-47%), potyviruses (45-46%), arepaviruses (43%), tritimoviruses (42%), the brambyvirus and the bevemovirus (39%), roymoviruses and ipomoviruses (38%), macluraviruses (36%), the celavirus (35%) and bymoviruses (33%).**Polyprotein sequence**: CRCSV: 3014 aa**Polyprotein identity**: The deduced polyproteins of the above isolate of CRCSV shares 45-46% aa identity with SpMV isolates. It shares 14-33% identities with members of other genera of the family *Potyviridae*: rymoviruses (33%), potyviruses (31-32%), arepaviruses (18%), tritimoviruses (22%), the brambyvirus (23%), the bevemovirus (20%), roymoviruses (21%), ipomoviruses (19%), macluraviruses (18%), the celavirus (14%) and bymoviruses (17%).Species demarcation identities are below those recommended by Adams et al. (2005) and Inoue-Nagata et al. (2022) (<76%), supporting its assignment into a novel species. **Proteins and motifs**: The mature proteins cleaved from the polyprotein of CRCSV are identical in order and within the size range to those of viruses of genus *Potyvirus.* They differ from potyviruses mainly in phylogeny (Fig. 1). The proteins are cleaved from the ORF into 10 mature proteins from conserved cleavage sites. The small potyvirid ORF known as PIPO is present. The conserved polymerase slippage motif is G2A6 in CRCSV, present within the P3 coding region, allowing the translation of P3-PIPO in the −1 reading frame (Chung et al., 2008).Gene order, functional motifs and architecture of CRCSV are shown in Yuan et al. (2017).The potyvirid-conserved HC-Pro motifs KITC (LFQC in CRCSV) and PTK (PIE in CRCSV) linked to aphid transmission are not present. The CP of CRCSV held the DAE variation of DAG (Nigam et al., 2019), which is also found in the aphid-transmitted potyvirus chilli veinal mottle virus. **Natural transmission**: Unknown. The absence of the all three conserved aphid-transmission motifs suggests CRCSV is not transmitted by aphids. **Experimental transmission**: CRCSV was mechanically transmissible to *Cucumis sativus* plants*.***Additional information**: This is a wild plant virus from China. To date it has been identified only from *Phragmites australis* and only from Gansu Province.**Study Group recommendation**:The *Potyviridae* Study Group recommends the creation of a new species, tentatively named *Phragmivirus phragmii,* for which common reed chlorotic stripe virus isolate Tianshui is the exemplar. Note, the genus *Phragmivirus* will be created if common reed chlorotic stripe virus and Spartina mottle virus are accepted as representatives of new species, and if a new genus composed of these two species is also accepted.**2.2) Virus name**: Spartina mottle virus (SpMV)**Species name:** *Phragmivirus spartinae***Genus:** *Phragmivirus***Origin of names:** species name derived from the latinized genus name of the host**Isolates for which complete genomes are available:**Spartina mottle virus isolate DSMZ PV-0970 (MN788417)Spartina mottle virus isolate Q1371 (MW314143)Spartina mottle virus isolate Q1372 (MW314142)**Original hosts**:*Spartina* sp: SpMV isolate DSMZ PV-0970 *Cynodon dactylon* × *C. transvaalensis*: SpMV isolates Q1371 and Q1372**Justification for creating a new species:**The complete genome sequences of SpMV share greatest nt identity (51%) with common reed chlorotic stripe virus (CRCSV) isolate Tianshui (KY612317).The complete genomes of these three SpMV isolates share 79-87 % nucleotide identities with one another, which is marginally above the species demarcation limit of <76% recommended by Adams et al. (2005) placing these isolates together within one species. They share 33-47% nucleotide identities with other members of the family *Potyviridae* as follows: rymoviruses (46-47%), potyviruses (45-46%), arepaviruses (43%), tritimoviruses (42%), the brambyvirus and the bevemovirus (39%), roymoviruses and ipomoviruses (38%), macluraviruses (36%), the celavirus (35%) and bymoviruses (33%).The deduced polyproteins of the SpMV isolates share 91-97% aa identities with one another. They share 45-46% aa identify with the CRCSV isolate. The SpMV genome sequences shared 14-33% identities with other members of the family *Potyviridae*: rymoviruses (33%), potyviruses (31-32%), arepaviruses (18%), tritimoviruses (22%), the brambyvirus (23%), the bevemovirus (20%), roymoviruses (21%), ipomoviruses (19%), macluraviruses (18%), the celavirus (14%) and bymoviruses (17%).SpMV and CRCSV and are phylogenetically closer to one another than to viruses classified in other genera within family *Potyviridae*. Sequence identities closely follow the guidelines of Adams et al. (2005), and Inoue-Nagata et al. (2022), supporting their assignment into one genus. **Genome size**: SpMV: 9346 nt**Polyprotein size**: SpMV: 3029 aa**Proteins and motifs**: The mature proteins cleaved from the polyprotein are identical in order and within the size range of typical potyviruses. SpMV differs from potyviruses mainly in phylogeny (Fig. 1). The proteins are cleaved from the ORF into 10 mature proteins from conserved cleavage sites, and PIPO is encoded by a small frame-shifted gene embedded within the P3 cistron. The small potyvirid ORF known as PIPO is present. The conserved polymerase slippage motif is G1A6 in SpMV. It is present within the P3 coding region, allowing the translation of P3-PIPO in the −1 reading frame (Chung et al., 2008). Gene order, functional motifs and architecture of common reed chlorotic stripe virus, as shown in Yuan et al. (2017), closely resembles that predicted for spartina mottle virus.The Potyvirid-conserved HC-Pro motifs KITC (IMQC in SpMV) and PTK (ATE in SpMV) linked to aphid transmission are not present. The CP of SpMV does not contain the conserved aphid transmission motif DAG (DSD in SpMV) or any of the five variations of DAG (Nigam et al., 2019). **Natural transmission**: Unknown. The absence of the all three conserved aphid-transmission motifs suggests this virus is not transmitted by aphids. **Additional information**:Thomas et al. (2021) note the virus does not fit into established genera within family *Potyviridae*, and proposed the novel genus name ‘*Sparmovirus*’ following Spartina mottle virus. **Study Group recommendation**:The *Potyviridae* Study Group recommends the creation of a new species identified as *Phragmivirus spartinae*, depending on the creation of the genus *Phragmivirus*. This genus will be created if Spartina mottle virus and common reed chlorotic stripe virus are accepted as representatives of new species, and if a new genus composed of these two species is also accepted. The isolate DSMZ PV-0970 (MN788417) is proposed as the exemplar virus for *Phragmivirus spartinae*. 1. **Creation of 8 new species in the genus *Potyvirus*:**
	1. **Virus**: Aconitum virus 2 (AcV2)

**Proposed species name**: *Potyvirus aconiti***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized host genus name **NCBI accession**: MZ389235 – Aconitum mosaic virus isolate YZYi-WTThis accession will be renamed to Aconitum virus 2.**Authors**: [Jie Yang](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Yang+J&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Ping-Xiu Lan](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Lan+PX&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Yun Wang](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Wang+Y&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Jin-Ming Li](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Li+JM&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Ruhui Li](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Li+R&cauthor_id=37958540)[2](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-2), [Steve Wylie](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Wylie+S&cauthor_id=37958540)[3](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-3), [Xiao-Jiao Chen](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Chen+XJ&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Gen-Hua Yang](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Yang+GH&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Hong Cai](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Cai+H&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1), [Fan Li](https://pubmed.ncbi.nlm.nih.gov/?sort=pubdate&term=Li+F&cauthor_id=37958540)[1](https://pubmed.ncbi.nlm.nih.gov/37958540/#full-view-affiliation-1)**Author location:*** 1State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, Kunming 650201, China.
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**Publication**: Yang J, Lan PX, Wang Y, Li JM, Li R, Wylie S, Chen XJ, Yang GH, Cai H, Li F. Virome analysis of *Aconitum carmichaelii* reveals infection by eleven viruses, including two potentially new species. Int J Mol Sci. 2023 Oct 25;24(21):15558. doi: 10.3390/ijms242115558. PMID: 37958540; PMCID: PMC10650655.Note: Yang and co-workers published the description of this new potyvirus named Aconitum potyvirus 1. Firstly, isolate YZYi-WT was deposited as Aconitum mosaic virus (MZ389235) in 2021. It was detected from a *Aconitum carmichaelii* plant, but the authors later found that this potyvirus could be detected from symptomless *A. carmichaelii* plants. So, the authors changed the virus name to Aconitum potyvirus 1. However, another potyvirus identified as Aconitum potyvirus 1 (isolate AcoPV1-MY, OP271473) was already registered at GenBank. The isolate YZYi-WT was then deposited as Aconitum mosaic virus (MZ389235). Isolates MY and YZYi-WT are distinct enough to be considered as different species. To avoid further confusion, the authors preferred to name the isolate YZYi-WT as Aconitum virus 2 (AcV2).**Original hosts**: *Aconitum carmichaelii***Symptoms of infection**: Not clear, as the plants presented infection with multiple viruses**Country of isolation**: China, Zhangyi, Yunnan province**Sequencing approach(es)**: Illumina and resequencing through Sanger of overlapping RT-PCR products and 5’ RACE**Genome sequence**: The complete genomic sequence of Aconitum virus 2 (MZ389235) is 9453 nt, excluding the poly(A) tail. It has a 5’ UTR of 91 nt and a 3’ UTR of 176 nt. Note: The same virus is referred to as Aconitum mosaic virus in the GenBank description and as Aconitum potyvirus 1 in the Yang et al. (2023) publication. **Nucleotide sequence identity**: A pairwise comparison was performed between the complete genomic and polyprotein sequences of AcV2 and those of other potyviruses. AcV2 shares genomic sequence identity below 57% and polyprotein sequence identity below 55% with other potyviruses. All these values fall below the current species delineation criteria for potyvirids, with <76% nt identity with the complete genome and <80% aa identity with the polyprotein (Inoue-Nagata et al., 2022). **Polyprotein sequence**: AcV2 encodes a large ORF, and the polyprotein is predicted to comprise 3061 aa residues. Nine highly conserved proteolytic cleavage sites in the polyprotein were identified by comparison with the consensus protease recognition motifs of selected potyviruses, which resulted in ten putative mature proteins of P1 (287 aa), HC-Pro (456 aa), P3 (358 aa), 6K1 (53 aa), CI (633 aa), 6K2 (53 aa), VPg (187 aa), NIa-Pro (249 aa), NIb (515 aa), and CP (270 aa). The small ORF PIPO within the P3 of potyviruses was also identified by the presence of GA6 in AcV2 (nt 2794–2800).**Polyprotein identity**: AcV2 polyprotein sequence shares <80% aa identity with the polyprotein of other potyviruses.**Proteins and motifs**:Most conserved motifs were found in the AcV2 sequence by comparing the deduced polyprotein sequences with those of other known potyviruses. These motifs include 195HX8DX33SGX22RG263 (proteolytic activity) in P1; 312CX8CX18CX2C343 (putative zinc finger binding motif), 602IGN604 (cell-to-cell and long-distance movement), 466FRNKX12CDNQLD487 (symptomatology), 577CCCVT581 (long-distance movement), and 627GYCY630 (cysteine proteinases) in HC-Pro; four motifs, including 1355KVSATPP1361, 1406LVYV1409, 1457VATNIIENGVTL1468, and 1501GERIQRLGRVGR1512, related to potential helicase activity in CI; 2080HX34D67GXCGX14H2201 (proteolytic activity) in NIa-Pro; four motifs, including 2447SLKAEL2452, 2480CVDDFN2485, 2584GNNSGQPSTVVDNTIMV2600, and 2626GDD2629, related to RNA-dependent polymerase activity in NIb; and 2975YMPRYG2980, 2994AFDF2997, and 3014QMKAAA3019 motifs in CP. Additionally, three motifs associated with aphid transmission—337RITC340 and 595PTK597 in HC-Pro and 2797DAG2799 in CP. Most conserved motifs were found in the AcV2 sequence by comparing the deduced polyprotein sequences with those of other known potyviruses. **Natural transmission**: Evidence of transmission through seeds**Experimental transmission**: No information**Other host**s: No information**Study Group recommendation**: The *Potyviridae* Study Group recommends acceptance of Aconitum virus 2 as a member of a new species named *Potyvirus aconiti* with isolate YZYi-WT (MZ389235) as the exemplar sequence. * 1. **Virus**: Kudzu chlorotic ring blotch virus (KudCRBV)

**Proposed species name**: *Potyvirus puerariae***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized genus name of the host**NCBI accession**: OQ148665, Kudzu chlorotic ring blotch virus isolate Ack01, complete genome.**Authors**: Aboughanem-Sabanadzovic N, Stephenson RC, Allen TW, Henn A, Moore WF, Lawrence A and Sabanadzovic S.**Author location**:Nina Aboughanem-Sabanadzovic1,2, Ronald Christian Stephenson2, Thomas W. Allen3, Alan Henn2, William F. Moore2, Amanda Lawrence4, and Sead Sabanadzovic21Institute for Genomics, Biocomputing and Biotechnology, Mississippi State University,Mississippi State, MS 39762, USA; 2 Department of Biochemistry, Molecular Biology, Entomology and Plant Pathology, Mississippi State University, Mississippi State, MS 39762, USA;3 Delta Research and Extension Center, Mississippi State University, Stoneville, MS 38776, USA;4Institute for Imaging and Analytical Technologies, Mississippi State University,Mississippi State, MS 39762, USA**Publication**: Aboughanem-Sabanadzovic, N.; Stephenson, R.C.; Allen, T.W.; Henn, A.; Moore, W.F.; Lawrence, A.; Sabanadzovic, S. Characterization of a putative new member of the genus Potyvirus from kudzu (*Pueraria montana* var. *lobata*) in Mississippi. Viruses, 2023, 15, 2145. https://doi.org/10.3390/v15112145**Original hosts**:*Pueraria montana* var. lobata**Symptoms of infection**:Chlorotic ring blotches and distinct line patterns**Country of isolation**: The United States**Sequencing approach(es)**: Sanger and high-throughput genome sequencing**Genome sequence**: Isolate Ack01(OQ148665): complete genome, 9686 bp.**Nucleotide sequence identity**: In the initial BLAST alignments performed on complete nucleotide sequences, kudzu chlorotic ring blotch virus (KudCRBV) shared the greatest level of identities (87% and 94%, respectively) with the two near-complete sequences deposited in GenBank as wisteria vein mosaic virus isolates Ce-JH (WVMV-Ce-JH; LC729727) and JEBUp (WVMV-JEBUp; MT603851). However, identity with a complete sequence of an original isolate of WVMV from Beijing (WVMV-Beijing; AY656816) was found to be only 76.2% - a value too close to the currently applied species demarcation criteria (<76% nt identity). Similar values were obtained in comparisons with an Iranian WVMV isolate with complete sequences available in GenBank (WVMV-Ir; MN514947).In phylogenetic analyses performed on complete amino acid sequences of the polyproteins of reference potyviral isolates, the virus from kudzu was placed in a well-supported subclade composed of soybean mosaic virus (SMV), watermelon mosaic virus (WMV), and wisteria vein mosaic virus (WVMV) within the “bean common mosaic virus clade” (“BCMV clade”, synonym: “BCMV group”) of potyviruses. Indeed, KudCRBV-Ack01 represents a sister branch to WVMV (Beijing isolate), with mutual evolutionary distances comparable to those between SMV and WMV. KudCRBV shared similar levels of identity, around 73-74%, with SMV and WMV isolates.Note: BLAST analysis of the KudCRBV sequence showed that the closest match is the soybean virus A isolate JB from Korea, deposited in GenBank (MH428831) on August 18, 2020. It should be noted that the soybean virus A sequence was registered before KudCRBV (June 14, 2023), so naming the virus as soybean virus A would be preferred. However, the sequence of the soybean virus A was determined by Illumina, and there is no additional information about the virus. All biological information is provided for the KudCRBV isolate. Therefore, the name "kudzu chlorotic ring blotch virus" is proposed for this virus.Two wisteria vein mosaic virus sequences: (1) MT603851 (JEBU-P) and (2) LC729727 (Ce-JH) should be corrected as KudCRBV sequences based on the high whole-genome nucleotide sequence identities among them.**Polyprotein sequence**: 3095aa**Polyprotein identity**:Not described**Proteins and motifs**:A large, 3095-codon-long ORF covering approximately 96% of the whole genome, codes for a polyprotein with an estimated Mr of 353.8 kDa (~354 K). Similar to other potyviruses, this 354K polyprotein is presumably cleaved by three virus-encoded proteases to give ten mature products (from N- to C-terminus): P1, HC-Pro, P3, 6K1, CI, 6K2, Nla-VPg, Nla-Pro, Nlb, and CP. Analyses of the amino acid sequences showed the presence of conserved motifs reported in orthologs of other potyviruses. The three amino acid motifs reported to have a function in the potyvirus aphid-mediated virus transmission have been identified in the HC-Pro (PTK and KITC) and CP proteins (DAG). PIPO was found overlapping the P3 coding region of the large ORF (nt positions 2931-3158).**Natural transmission**:Not described**Experimental transmission**: Kudzu chlorotic ring blotch virus can be transmitted by cotton and potato aphids, and mechanically to soybean and beans.**Other host**s:Not described**Study Group recommendation**:The Study Group recommends that kudzu chlorotic ring blotch virus is a member of a new species in the genus *Potyvirus*. The proposed species name is *Potyvirus puerariae*, with the exemplar sequence OQ148665.* 1. **Virus**: Lily virus A (LVA)

**Proposed species name**: *Potyvirus alilii***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized genus name of the host with the addition of ‘A’ to discriminate from other lily viruses**NCBI accession**: OR879085 (isolate DSMZ PZ-0455)JN127335 (isolate Bate1)OM201232 (isolate BJ)**Authors**: Knierim, D., Margaria, P., Menzel, W. and Winter, S. (isolate DSMZ PZ-0455)1Wylie, S.J., Luo, H., Li, H. and Jones, M.G. (isolate Bate1)2Chen, L. and Li, Y. (isolate BJ)3**Author location**: 1Plant Virus Department, Leibniz Institute, DSMZ-German Collection of Microorganisms and Cell Cultures, Inhoffenstrasse 7B, Braunschweig 38124, Germany (isolate DSMZ PZ-0455)2Plant Virus Group, WA State Agricultural Biotechnology Centre, Murdoch University, South Street, Perth, WA6150, Australia (isolate Bate1)3School of Grassland Science, Beijing Forestry University, Qinghua East Road 35, Haidian District, Beijing 100083, China (isolate BJ)**Publication**: Unpublished (isolate DSMZ PZ-0455)Wylie et al. (2012) Multiple polyadenylated RNA viruses detected in pooled cultivated and wild plant samples. Arch. Virol. 157 (2), 271-284 (2012) (isolate Bate1)Unpublished (isolate BJ)**Original hosts**:*Lilium martagon* x *Lilium tsingtauense* (isolate DSMZ PZ-0455)*Lilium longiflorum* (isolate Bate1)‘Lily’ (isolate BJ)**Symptoms of infection**:Not described**Country of isolation**: Germany (isolate DSMZ PZ-0455)Australia (isolate Bate1)China (isolate BJ)**Sequencing approach(es)**: HTS isolate Bate 1 (partial genome). Unknown for other isolates.**Genome sequence**: 9472 nt (isolate DSMZ PZ-0455) complete genome7900 nt (isolate Bate1) partial genome7900 nt (isolate BJ) partial genome**Nucleotide sequence identity**: The complete and partial genome sequences of three lily virus A isolates share high nt identities with one another (95%) over 82% of the complete genome of the virus. When compared to other viruses, the complete genome sequence of lily virus A shares the closest identities (69% nt identity over 85-89% of complete genomes) with isolates of lily mottle virus (e.g., isolate Bate5 JN127341 and isolate Baishan-Jingyu MT795719) and 89% identities with partial genome sequences of Rembrandt tulip-breaking virus (e.g. MK368780), both members of genus *Potyvirus*. Note: The nt identities of lily virus A and lily mottle virus isolates are below the species demarcation identities accepted for potyviruses (Adams et al., 2005; Inoue-Nagata et al., 2022), indicating they can be assigned to different species.**Polyprotein sequence**: 3112 aa **Polyprotein identity**: The deduced aa sequence of the polyprotein of the complete genome of lily virus A shared greatest aa identities with the two partial lily virus A sequences (98%) and with complete polyproteins of lily mottle virus (71%).**Proteins and motifs**: The polyprotein encoded by the typical large potyvirid ORF is predicted to be cleaved into 10 mature proteins (positions for polyprotein cleavage sites given for isolate DSMZ PZ-0455 under protein accession WPR15555), as is typical of members of genus *Potyvirus*. Polyprotein sites are identical for the three lily virus A isolates but differ from those of lily mottle virus. The small potyvirid ORF PIPO is present, and its position is recorded under accession WPR15555). The conserved PIPO initiation site is G1A7 at nt positions 2983-2990. Conserved functional motifs closely resemble those of other potyviruses.**Natural transmission**: not described, but the presence of conserved potyvirid aphid transmission motifs indicates aphid transmission is possible.**Experimental transmission**: Yes, in *Chenopodium quinoa* (isolate DSMZ PZ-0455) **Other host**s: Described naturally only in species of *Lilium* to date.**Additional information**:This virus appears widely distributed (Germany, China and Australia) in lilies yet not widely reported – to date having only three sequences provided over a 12-year period.**Study Group recommendation**:The *Potyviridae* Study Group recommends that lily virus A isolate DSMZ PZ-0455 be considered as the exemplar isolate representing a new species in genus *Potyvirus*, for which the name *Potyvirus alilii* is proposed* 1. **Virus**: Paris yunnanensis mosaic chlorotic virus (PyMCV)

**Proposed species name**: *Potyvirus parisflavitessellati***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized genus name of the host and the symptoms induced by this virus**NCBI accession**: Paris yunnanensis mosaic chlorotic virus isolate 2021PPY33, complete genomeGenBank: ON871824.1**Authors**: Zhang,B., Li,Q., Hu,J., Zhang,L., Dong,X., Ji,P. and Dong,J.**Author location**: Institute of Medicinal Plant Cultivation, Academy of Southern Medicine, Yunnan University of Chinese Medicine, No. 1076 Yuhua Road, Chenggong District, Yunnan, Kunming 650500, China**Publication**: Zhang, B., Li, Q., Hu, J., Zhang, L., Dong, X., Ji, P., & Dong, J. (2023). Complete genome sequence analysis of a new potyvirus isolated from Paris polyphylla var. yunnanensis. Archives of Virology, 168(2), 43. https://doi.org/10.1007/s00705-022-05655-9**Original hosts**: *Paris polyphylla* var. yunnanensis**Symptoms of infection**: Mosaic and chlorotic symptoms**Country of isolation**: China, Lijiang, Yunnan**Sequencing approach(es)**: Illumina, RT-PCR and RACE**Genome sequence**: 9571 nucleotides long (excluding poly(A) tail)5' UTR length: 171nt long3' UTR length: 216 nt long**Nucleotide sequence identity**: Range from 54.2 to 59.6% with other potyviruses. Closest identity of 59.6% with Thunberg fritillary mosaic virus (AJ851866.1). All these values fall below the current species delineation criteria for potyvirids, with <76% nt identity with the complete genome and <80% aa identity with the polyprotein (Inoue-Nagata et al., 2022). **Polyprotein sequence**: Two open reading frames present:Polyprotein with 3061 amino acids Out-of-frame PIPO after G1A7 motif at position 2901 (within the P3) with 54 amino acids.**Polyprotein identity**: Range from 51.8 to 57.9% with 14 other potyviruses. Closest identity is 57.9% with Iris potyvirus A (QXU69567.1)**Proteins and motifs**:Predicted gene products for P1, HC-Pro, P3, 6K1, CI, 6K2, NIa consisting of NIa-Pro and VPg, NIb, and CPPIPO region within P3 to generate P3N-PIPO. Potential protease cleavage sites are recognizable but not reported. The P1 and HC-Pro correspond to F/S and G/G cleavage sites, while predicted NIa-Pro cleavages are Q/A, Q/S, Q/S, Q/A, E/S, Q/D, and Q/S.Other recognizable motives: HC-Pro PTK; NIb GDD motif; CP NAG motif**Natural transmission**: Not known – aphid transmission suspected based on NAG motif in CP.**Experimental transmission**: not known**Other host**s: not known**Study Group recommendation**: The *Potyviridae* Study Group recommends accepting Paris yunnanensis mosaic chlorotic virus as a member of a new species, with the binomial name *Potyvirus flavitessellati* and the isolate 2021PPY33 (ON871824) as the exemplar sequence.Note that Paris yunnanensis is not a recognised species, rather it is *Paris polyphylla* var. *yunnanensis*. The virus name misrepresents the host name.* 1. **Virus**: Periwinkle mild yellow mosaic virus (PwMYMV)

**Proposed species name**: *Potyvirus* *catharanthiflavitessellati***Genus**: *Potyvirus* **Origin of names:** species name derived from the latinized name of the host genus and the symptom induced by this virus.**NCBI accession**: Periwinkle mild yellow mosaic virus isolate HRLP1.poty1, complete genomeGenBank: PP382205 (9936 nt)Periwinkle mild yellow mosaic virus isolate HRLP1.poty1.HTS, complete genomeGenBank: PP382206 (9936 nt)Periwinkle mild yellow mosaic virus isolate HRLP1.poty2, complete genomeGenBank: PP382207 (9944 nt)Periwinkle mild yellow mosaic virus isolate HRLP1.poty2.HTS, partial genomeGenBank: PP382208 (9829 nt)**Authors**: Alabi, O.J., Stevens, K., Oladokun, J.O., Villegas, C., Hwang, M., Al Rwahnih, M., Tian, T., Hernendez, I., Ouro-Djobo, A., Setamou, M. and Jifon, J.**Author location** Plant Pathology & Microbiology, Texas A&M AgriLife Research & Extension Center, 2401 E. Hwy. 83, Weslaco, TX 78596, USA**Publication**: Alabi, O. J., Stevens, K., Oladokun, J. O., Villegas, C., Hwang, M. S., Al Rwahnih, M., Tian, T., Hernandez, I., Ouro-Djobo, A., Sétamou, M., & Jifon, J. L. (2024). Discovery and characterization of two highly divergent variants of a novel potyvirus species infecting Madagascar periwinkle (*Catharanthus roseus* L.). Plant Disease, 10.1094/PDIS-02-24-0459-RE. Advance online publication. https://doi.org/10.1094/PDIS-02-24-0459-RE**Original hosts**: *Catharanthus roseus* (Gentianales: Apocynaceae), known as periwinkle**Symptoms of infection**: Foliar mild yellow mosaic**Country of isolation**: USA, Harlingen, Cameron County, Texas (GPS: 26.207953, 97.699583)**Sequencing approach(es)**: Illumina and resequencing through Sanger overlapping RT-PCR and RACE**Genome sequence**: 9905 and 9915 nucleotides long (excluding poly(A) tails) for two variants found in the same plant and named PwMYMV-1 and PwMYMV-25' UTR length: 154 and 155 nt long for PwMYMV-1 and PwMYMV-2, respectively3' UTR length: 235 and 238 nt long for PwMYMV-1 and PwMYMV-2, respectively**Nucleotide sequence identity**: The two variants, PwMYMV-1 and PwMYMV-2 shared maximum identities with isolates of pokeweed mosaic virus (53-54%), potato yellow blotch virus (53%), potato virus A (53%), tobacco vein mottling virus (51-52%), and sunflower ring blotch virus (50%). The shared complete polyprotein aa identities between PwMYMV-1 and PwMYMV-2 and other potyviruses were below 50%. All these values fall below the current species delineation criteria for potyvirids, which include <76% nt identity with the complete genome and <80% aa identity with the polyprotein (Inoue-Nagata et al., 2022). **Polyprotein sequence**: Two open reading frames present:Polyproteins with 3171 and 3173 amino acids for PwMYMV-1 and PwMYMV-2, respectively. Out-of-frame PIPO after G2A7motif at position 3277 and 3275 (within the P3) with 83 and 79 amino acids for PwMYMV-1 and PwMYMV-2, respectively.The two variants shared identities of 77.4% nt and 84.1% aa, close to the stipulated ICTV thresholds, hence they should be considered as highly divergent genetic variants of PwMYMV.**Polyprotein identity**: Pairwise comparisons of complete polyprotein aa sequences showed that PwMYMV-1 and PwMYMV-2 shared maximum identities with isolates of pokeweed mosaic virus (53-54%), potato yellow blotch virus (53%), potato virus A (53%), tobacco vein mottling virus (51-52%), and sunflower ring blotch virus (50%).**Proteins and motifs**:Predicted gene products for P1, HC-Pro, P3, 6K1, CI, 6K2, NIa consisting of NIa-Pro and VPg, NIb, and CPPIPO region within P3 to generate P3N-PIPO.Protease cleavage sites: The P1 and HC-Pro correspond to Y/S and G/G cleavage sites, while predicted NIa-Pro cleavages are Q/A, Q/S, Q/S, Q/G, E/G, Q/G, and Q/A.Other recognizable motives in HC-Pro: RITC and PTKNIb: GDD motifCP: DAG motif**Natural transmission**: Aphid transmission suspected (*Aphis gossypii* individuals found in the original plant, but transmission not tested)**Experimental transmission**: not known**Other host**s: not known**Additional information**:**Study Group recommendation**: The *Potyviridae* Study Group recommends acceptance of periwinkle mild yellow mosaic virus as a member of a new species, named *Potyvirus catharanthiflavitessellati* with isolate HRLP1.poty1 (PP382205) as the exemplar sequence. * 1. **Virus**: Polygonatum kingianum mottle virus (PKgMV)

**Proposed species name**: *Potyvirus polygonatimaculae***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized host genus name and the symptoms induced by this virus.**NCBI accessions**: 1ON428226 (isolate HJ-21YV029)2MN873572 (isolate QJ)  **Authors of complete genome sequence**: 1Wang,M., Su,X., Zhang,F., Zheng,K. and Zhang,Z.2Zhao,M., Wen,G., Chen,Z. and Yang,L.**Author location**: 1Biotechnology and Genetic Germplasm, Resources Research Institute, Yunnan Academy of Agricultural Sciences, 2238# Beijing, Panlong Prefecture, Kunming, Yunnan, 650205, P.R. China2Key Laboratory of Ministry of Education - Agriculture Biodiversity for Plant Disease Management, Yunnan, Agricultural University, No. 95 Jinhei Highway, Panlong District, Kunming City, Kunming, Yunnan 650201, China**Publication**: Wang M, Su X, Zhang F, Wang T, Zheng K, Zhang Z. Complete genome sequence of Polygonatum kingianum mottle virus infecting *Polygonatum kingianum* Coll. et Hemsl in Yunnan, China. Arch Virol. 2024 Feb 1;169(2):39. doi: 10.1007/s00705-024-05965-0. PMID: 38300368**.** **Original hosts**: *Polygonatum* *kingianum***Symptoms of infection**: dwarf, leaf yellowing, and curling (isolate HJ-21YV029)**Country of isolation**: Shizong, Yunnan Province, China (isolate HJ-21YV029)**Sequencing approach(es)**: HTS, RT-PCR, RACE (isolate HJ-21YV029) **Genome sequence**: isolate HJ-21YV029: 10,002 nucleotides (nt) and a large open reading frame (nt 108 to 9,746). The ORF starts with an AUG codon (nt 108–110) and ends with a UGA codon (nt 9,744–9,746).**Nucleotide sequence identity**: Pairwise comparisons revealed that the PKgMV polyprotein shares 50.5–68.6% nt sequence identity with reported members of the genus *Potyvirus*, which matches the current demarcation criteria for new species in the genus *Potyvirus* (< 76% nt sequence identity and < 82% aa sequence identity in the complete polyprotein ORF). The polyprotein sequence of PKgMV has the highest sequence identity (84.7% nt and 94% aa sequence identity) to that of the unpublished PKgMV isolate QJ (MN873572), suggesting PKgMV and PKgMV-QJ should be assigned to the same species in the genus *Potyvirus*. Note: The TEM analysis revealed the presence of filamentous viral particles measuring 780 nm × 11 nm in the infected *P. kingianum* plant. In addition, several pinwheel inclusions and bundle inclusions were observed in the cytoplasm of *P. kingianum* cells.**Polyprotein sequence**: the genome encodes a polyprotein of 3,212 amino acids (aa) (363.68 kDa)**Polyprotein identity**: Pairwise comparisons revealed that the PKgMV polyprotein shares 43.1–72.2% aa sequence identity with reported members of the genus *Potyvirus*. **Proteins and motifs**: The polyprotein has nine predicted cleavage sites, resulting in 10 mature proteins: P1 (432 aa), HC-Pro (459 aa), P3 (352 aa), 6K1 (52 aa), CI (643 aa), 6K2 (53 aa), NIa-Pro (243 aa), NIb (517 aa), and CP (267 aa). In addition, a putative PIPO protein (74 aa) is embedded within the P3 protein of the polyprotein. The PKgMV polyprotein contains the typical highly conserved potyviral motifs, including (1) 381GXSG384 in P1; (2) 485KITC488, 614FRNKX11CDNQLD635, 648HAKRFF653, 725CCCVT729, 743PTK745, 750IGN752, 775GYCY778, 780NIFLAML786, and 835AELPRILVDH844 in HC-Pro; (3) 1400VLLLEPTRPL1409, 1496KVSATPP1502, 1547LVYV1550, 1598VATNIIENGVTL1609, and 1642GERIQRLGRVGR1653 in CI; (4) 2598SLKAEL2603, 2617FTAAPLD2663, and 2631CVDDFN2636 in NIb; and (5) 2953DAG2954, 3061MVWCIDNGTSP3071, 3077WVMMDGN3083, 3124PYMPRYG3130, 3144AFDF3147, and 3189EDTERH3194 in CP.**Natural transmission**: Not tested**Experimental transmission**: Not tested**Other host**s: Not tested **Study Group recommendation**:The *Potyviridae* Study Group recommends acceptance of Polygonatum kingianum mottle virus as a member of a new species named *Potyvirus polygonatimaculae*. The isolate HJ-21YV029 (ON428226) is indicated as the exemplar sequence.* 1. **Virus**: Saffron yellow mosaic virus (SYMV)

**Proposed species name**: *Potyvirus crocitessellati***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized name of the host genus and the symptoms induced by this virus.**NCBI accession**: GenBank: OK632024 (isolate IR)**Authors**: Tavoosi,M., Moradi,Z. and Mehrvar,M.**Author location**:Mohsen Mehrvar Department of Plant Pathology, Faculty of Agriculture, Ferdowsi University of Mashhad, P.O. Box, Mashhad, 91779-1163, Iran**Publication**: Tavoosi, M., Moradi, Z. & Mehrvar, M. Virome analysis of potyvirus populations infecting saffron in Iran: the discovery of a novel potyvirus. Eur J Plant Pathol 168, 453–466 (2024). https://doi.org/10.1007/s10658-023-02767-z**Original hosts**: Saffron (*Crocus sativus*)**Symptoms of infection**:pale chlorotic local lesions in *Chenopodium quinoa.* Note: symptomatic infected saffron samples were co-infected with two or three of the following potyviruses: saffron yellow mosaic virus, saffron latent virus, and turnip mosaic virus.**Country of isolation**: Iran**Sequencing approach(es)**: RNA-Seq libraries were created using the TruSeq stranded total RNA sample preparation kit (Illumina, San Diego, CA). The sequencing was done in paired-end mode (2 × 151 bp) on an Illumina NovaSeq 6000. The CLC Genomics Workbench version 20 was used to *de novo* assemble the raw reads (CLC Bio-Qiagen, Aarhus, Denmark). Sanger sequencing using virus-specific primers and two-step reverse transcriptase-polymerase chain reaction (RT-PCR) was used to confirm the RNA deep sequencing. **Genome sequence**: 9541 nucleotides long (excluding poly(A) tail). The 5' UTR and 3' UTR of the obtained sequence were 78 and 169 nt long, respectively.**Nucleotide sequence identity**: For the genomic nucleotide sequence, SYMV-IR revealed the highest sequence identity (63%) with bean yellow mosaic virus (BYMV; NC\_003492) and clover yellow vein virus (CYVV; NC\_003536). The thresholds for species demarcation using nucleotide identity values for the individual coding regions are not exceeded for any cistron (54–63% nucleotide identity across the genome). SYMV-IR formed a well-differentiated clade with high bootstrap support within the BYMV group. No evidence of recombination for SYMV-IR and other potyviruses could be detected.Note: The 5’ and 3’ termini are not reported to be verified by Rapid Amplification of cDNA Ends (RACE). **Polyprotein sequence**: Two open reading frames - one of which encoded a polyprotein comprised of 3132 amino acids and the other in the + 2 reading frame within the P3 cistron encoded a PIPO protein of 64 amino acids.**Polyprotein identity**: The aa sequence identity of the whole polyprotein of SYMV is 63% with BYMV and CYVV. NIb (72/71%), CI (69/66%), HC-Pro (73%), VPg (60/63%), NIa-Pro (63%), and CP (73%) proteins of SYMV shared aa sequence identities with those of BYMV and CYVV. The identity of P1 and P3 was as low as 7.33–24.39% and 11.87–44.86%, respectively.**Proteins and motifs**: The ten putative mature proteins of SYMV-IR follow the known order in other potyviruses: P1, HC-Pro, P3, 6K1, CI, 6K2, NIa consisting of NIa-Pro and VPg, NIb, and CP.Nine potential protease cleavage sites were identified in the polyprotein at amino acid positions 320, 777, 1125, 1179, 1814, 1867, 2057, 2300, and 2819 resulting in ten mature functional proteins. The P1 and HC-Pro had F/S and G/G cleavage sites, whereas NIa-Pro had Q/A, Q/S, Q/S, Q/A, E/S, Q/S, and Q/S cleavage sites. For example the motifs G266-X-SG269 in P1; R371ITC374 (the underlined aa has been substituted for K in KITC), F500RNK503, C611CCTT615, P629TK631, I636GS638, C663-72X-H736 in HC-Pro, E810PF-X7-SP-X2-L-X-S-X2-N-X-G-X2-E-X5-W840, G1264AVGSGKSTG1273, D1353ECH1356, V1482ATNIIENGVTL1493 in CI, H2103-34X-D-67X-G-X-CG-14X-H2224 in NIa-Pro; S2471LKAEL2476, C2546DADGSQFDSS2556, G2608NNSGQPSTVVDNTLMV2624, G2651DD2653 in NIb, M2947VWCIENGTSP2957, R2988-43X-D3032, A3030FDF3033, and Q3050MKAAA3055 in CP.**Natural transmission**: Aphid transmission is suspected based on the existing NAG motif in CP. NAG is one of the most frequent deviations of DAG in potyviruses which has been proven to be as efficient in aphid transmission as the canonical DAG motif (Atreya et al., 1991).**Experimental transmission**: Mechanically transmissible.**Other host**s: Experimental host for mechanical transmission *Chenopodium quinoa.* Note: symptomatic saffron plant samples were coinfected with two or more of the following potyviruses: saffron yellow mosaic virus, saffron latent virus, and turnip yellow mosaic virus.**Study Group recommendation**: The recommendation of the Study Group is to accept saffron yellow mosaic virus as a member of a new species of genus *Potyvirus* with the name *Potyvirus crocitessellati* and with the exemplar sequence isolate IR (OK632024).* 1. **Virus**: Snowdrop virus Y (SVY)

**Proposed species name**: *Potyvirus galanthi***Genus**: *Potyvirus***Origin of names:** species name derived from the latinized genus name of the host **NCBI accessions**: Snowdrop virus Y isolate 4241-SVY-HTS polyprotein gene, complete cds GenBank: OP871788SVY isolate SA66 complete cds GenBank LC757029SVY isolate SA59 partial cds. GenBank LC790724SVY isolate SA48 partial cds. GenBank LC790723SVY isolate SA40 partial cds. GenBank LC790722SVY isolate 14590-SVY-HTS partial cds GenBank OP871783Snowdrop virus Y isolate BC28 polyprotein gene, partial cds GenBank MH886519.1.Snowdrop virus Y polyprotein gene, partial cds GenBank: EU927399.1**Authors of complete genome sequence**: Forde,S.M.D., Harju,V., Skelton,A., Adams,I.P., Fowkes,A.R., Pufal,H., McGreig,S., Conyers,C., Ward,R., Frew,L., Buxton-Kirk,A., Kelly,M. and Fox,A.**Author location**: Fera Science Ltd, Sand Hutton, York YO41 1LZ, United Kingdom**Publication**: Forde, S.M.D., Harju, V., Skelton, A., Adams, I., Fowkes, A., Pufal, H. et al. (2023) First report of Snowdrop virus Y and Turnip yellows virus in *Narcissus* sp. in the United Kingdom. New Disease Reports, 48, e12200. https://doi.org/10.1002/ndr2.12200**Original hosts**: *Galanthus* ‘Gerald Parker’ (snowdrop, EU927399), *Muscari neglectum* (grape hyacinth, MH886519), *Narcissus* sp. (Daffodil, OP871788, LC757029, LC790724, LC790723, LC790722, OP871783)**Symptoms of infection**: Not described.**Country of isolation**: UK, Australia, Korea**Sequencing approach(es)**: HTS and Sanger**Genome sequence**: Full genome 10,554 nt (OP871788)**Nucleotide sequence identity**: The SVY isolates share very high nt sequence identity (>98%) with one another, and 73-77% nt identity with fragments of closest known relatives – maize dwarf mosaic virus, yam mosaic virus, leek yellow stripe virus, and others. All these values are very close to the current species delineation criteria for potyvirids of <76% nt identity with the complete genome and <80% aa identity with the polyprotein (Inoue-Nagata et al., 2022). **Polyprotein sequence**: 3381 aa**Polyprotein identity**: Closest matches were 83-100% with other partial SVY sequences, and ~50% with Jasmine virus T, Polygonatum kingianum viruses 1, 2, and 5, Ranunculus mild mosaic virus, celery mosaic virus, and others. **Proteins and motifs**: Typical potyvirus motifs were identified, including those for aphid transmission (Inoue-Nagata et al., 2022).**Natural transmission**: Unknown, but the motifs generally associated with aphid vector transmission are present.**Experimental transmission**: Not reported.**Other host**s: As above.**Additional information**: SVY has been identified from the UK, Korea, and Australia in ornamental flower cultivars of three species, all typically propagated asexually from bulbs. Thus, it is reasonable to assume that SVY is transported to new locations via the international trade in flower bulbs. Its known host range of *Galanthus* and *Narcissus* (family Amaryllidaceae) and *Muscari* (family Asparagaceae) suggests SVY may be capable of infecting other monocotyledonous plants, especially those in the described genera and families. The presence of aphid transmission motifs suggests secondary transmission by insect vectors is possible. **Study Group recommendation**:Snowdrop virus Y was named by Monger after it was first isolated in a plant of *Galanthus* ‘Gerald Parker’ (snowdrop) from which a partial genome sequence was obtained. The complete genome sequence of snowdrop virus Y was later obtained from a *Narcissus* sp. plant. It shared >98% identity with the partial sequences previously provided by Monger and by Wylie et al. (2019). The complete genome sequence usually shares <76% nt identity with other described potyviruses, thereby satisfying its classification as a distinct species (Adams et al., 2005; Inoue-Nagata et al., 2022). We recommend naming the virus Snowdrop virus Y and the species *Potyvirus galanthi* after the first host (snowdrop) in which it was described. We propose that the exemplar virus from *Narcissus* be the isolate 4241-SVY-HTS. |

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| **Tables, Figures:**  |

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Fig. 1. Phylogenetic tree constructed using the complete polyprotein amino acid sequences of viruses in the family *Potyviridae*, aligned with MUSCLE. Confidence values were calculated by bootstrapping with 1000 repetitions using the Neighbor-Joining method implemented in MEGA 11. The proposed new species in the genus *Potyvirus* are highlighted in yellow, and those in the proposed new genus *Phragmivirus* are highlighted in blue.



