

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2023.012P** |  |
| **Short title:** Create five new species in the genus *Potyvirus* (*Patatavirales: Potyviridae*) |
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**Author(s) and email address(es)**

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| --- | --- |
| Inoue-Nagata AK, Wylie SJ, Jordan R, Kreuze JF, Li F, Lopez-Moya JJ, Makinen K, Ohshima K | alice.nagata@embrapa.br;s.wylie@murdoch.edu.au;ramon.jordan@ars.usda.gov;j.kreuze@cgiar.org;fanli@ynau.edu.cnjuanjose.lopez@cragenomica.es;kristiina.makinen@helsinki.fi;ohshimak@cc.saga-u.ac.jp |

**Author(s) institutional address(es) (optional)**

|  |
| --- |
| Embrapa Hortaliças, Brasília, DF, Brazil [AKI-N]Murdoch University, Perth, Australia [SJW]Floral & Nursery Plants Research Unit, U.S. National Arboretum, ARS, USDA, Washington, DC, USA [RJ]International Potato Center, Lima, Peru [JK]Yunnan Agricultural University, Kunming, China [LF]Centre for Research in Agricultural Genomics, CRAG (CSIC-IRTA-UAB-UB), Barcelona, Spain [JJL-M]University of Helsinki, Helsinki, Finland [KM]Saga University, Saga, Japan [KO] |

**Corresponding author**

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| Alice Kazuko Inoue Nagata (alice.nagata@embrapa.br) |

**List the ICTV Study Group(s) that have seen this proposal**

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| *Potyviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| *Potyviridae* | 8 | 0 | 0 |
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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | June 16, 2023 |
| Date of this revision (if different to above) | July 4, 2023 |

**ICTV-EC comments and response of the proposer**

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**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.012P.A.v1.Potyviridae\_5ns |

**Abstract**

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| The *Potyviridae* Study Group proposes the creation of five new species, all in the genus *Potyvirus*. The sequence of the genome polyprotein coding region of the proposed viruses differs from those of accepted species being below the threshold for species demarcation within the genus *Potyvirus* of 76% nucleotide identity, as described in the text of proposal.The proposed new species are: *Potyvirus miscanthi**Potyvirus tetraparis**Potyvirus passiflory**Potyvirus polygonati**Potyvirus thevetiae* |

**Text of proposal**

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| **Description of each proposed new species****1) Virus**: Miscanthus sinensis mosaic virus isolate WA (MsiMV)**Proposed species name**: *Potyvirus miscanthi* (etymology: host name)**Genus**: *Potyvirus***NCBI accession**: OL312763**Authors**: Zacharie Leblanc, Marie‐Emilie Gauthier, Ruvini Lelwala, Candace Elliott, Cassie McMaster, Robin Eichner, Kevin Davis, Lia Liefting, Jeremy Thompson, Adrian Dinsdale, Mark Whattam, Julie Pattemore, Roberto A. Barrero**Author location**:eResearch Office, Queensland University of Technology, Brisbane, QLD 4000, Australia **Publication**: Leblanc et al. 2022.**Original hosts**: *Miscanthus sinensis***Symptoms of infection**: A silver grass plant (*Miscanthus sinensis* cultivar "Morning Light") imported from the USA in 1985 into Western Australia, Australia, was analyzed at the Plant Quarantine Station, Rydalmere, New South Wales, and maintained there for biological indexing. Mechanical inoculation resulted in mosaic symptoms in *Zea mays* cv. Supagold. Filamentous virus particles were detected by transmission electron microscopy.**Country of isolation**: Australia (imported from the USA)**Sequencing approach(es)**: Next-generation sequencing and assembly of 21-22 nt small RNA sequences, confirmed by Illumina and long-read Oxford Nanopore Technology, resulting in identical assembled genome sequences.**Genome sequence**: 9604 nucleotides excluding the poly(A) tail.**Nucleotide sequence identity**: The complete sequence of MsiMV-WA shares 74% or less nucleotide sequence identity with those of other potyviruses. Phylogenetic analysis confirmed the distinct relationship of the genome sequence to previously reported potyvirus sequences and placed them within the genus *Potyvirus* with sorghum mosaic virus being the closest relative, and grouped with other potyviruses infecting monocolyledoneous plants. These results show that this virus represents a separate species within the genus *Potyvirus*.**Polyprotein sequence**: 3071 amino acids.**Polyprotein identity**: The complete polyprotein sequence of MsiMV-WA shares 78.5 % amino acid sequence identity with isolates of sorghum mosaic virus, and less with other potyviruses.**Proteins and motifs**: The usual potyvirus gene products are present in the MsiMV polyprotein yielding the expected cleaved mature products. Cleavage sites correspond to those of other polyproteins in viruses of the genus *Potyvirus*. The PIPO region (237 nts) preceded by the RNA slippage motif (G2A6) is present embedded in the P3 region. Several conserved motifs found in members of the genus *Potyvirus* are also found in MsiMV-WA, including some of those associated with aphid transmission (PTK in HC-Pro and DAG in the CP), although the variant EITC is replacing the KITC motif in HC-Pro.**Natural transmission**: Unknown, but probably aphids for wild isolates.**Experimental transmission**: Unknown, MsiMV-WA was found in a single imported plant and only information about its infectivity on *Zea mays* was mentioned.**Other hosts**: Not known**Additional information**: The biological information available is very limited, with only one isolate conserved in a single plant maintained in a quarantine facility since its isolation. **Study Group recommendation**: The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus miscanthi* with the common name of Miscanthus sinensis mosaic virus and acronym MisMV. 2) **Virus**: Paris potyvirus 4 isolate YLJ (ParPV-4)**Proposed species name**: *Potyvirus tetraparis* (etymology: host name and original name)**Genus**: *Potyvirus***NCBI accession**: OP374157 **Authors**: Wu and Tang**Author location**: College of Landscape and Horticulture, Yunnan Agricultural University, Kunming, Yunnan, China**Publication**: Lan et al. 2022; doi: 10.3389/fmicb.2022.1045750. **Original hosts**: *Paris polyphylla* var. *yunnanensi***Symptoms of infection**:Several types of symptoms were observed in*Paris polyphylla* var. *yunnanensi*, but authors did not associate any specifically with ParPV-4.**Country of isolation**: China**Sequencing approach(es)**: High-throughput RNA-Seq from a pool of 9 and 11 symptomatic leaf samples. Sequence was confirmed by RT-PCR with overlapping virus-specific primers and 5’RACE.**Genome sequence**: 9509 nucleotides excluding the poly (A) tail**Nucleotide sequence identity**: ParPV-4 shows 53.0–57.8% with other potyviruses.**Polyprotein sequence**: 3063 amino acids **Polyprotein identity**: ParPV-4 shows 39.3–51.9% amino acid identity to other potyviruses**Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites are present in the ParPV-4 polyprotein. These are predicted to cleave the polyprotein in 10 mature proteins containing typical conserved motives in the proteins for which they are known. The small ORF PIPO within the P3 of potyviruses is also identified by the presence of GA6.**Natural transmission**: unknown, but probably aphids due to presence of typical conserved motives associated with aphid transmission.**Experimental transmission**: Not performed**Other host**s: Only tested and found in *Paris polyphylla* var. *yunnanensi***Additional information**:RT-PCR screening of *Paris polyphylla* plants found average infection rates of 3.3%. Filamentous particles of 700 ~ 800 nm in length were detected by transmission electron microscopy in the bulks of symptomatic plants.**Study Group recommendation**:The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus tetraparis* with the common name of Paris potyvirus 4 and acronym ParPV-4.

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3) **Virus**: Passiflora virus Y Shaoguan isolate (PaVY)**Proposed species name**: *Potyvirus passiflory* (etymology: host name and original name)**Genus**: *Potyvirus***NCBI accession**: MW165064 **Authors**: Chen,B., L,L., Wu,D., Song,X., Cao,Y. and Yan,F.**Author location**: Institute of Plant Virology, Ningbo University, Fenghua Road, Jiangbei District, No. 818, Ningbo, Zhejiang 315000, China**Publication**: Chen et al. 2021. **Original hosts**: Passion fruit plant**Symptoms of infection**:Yellow and green mosaic, ringspots, chlorotic spots and curling were observed In the infected passion fruit leaves. **Country of isolation**: Shaoguan, in Guangdong province, China**Sequencing approach(es)**: NGS RNA-Seq sequencing (Illumina NovaSeq 6000 platform). Coding sequence confirmed by RT-PCR with overlapping virus-specific primers, 5’ and 3’ UTR by 5’ and 3’ RACE.**Genome sequence**: 9728 bp (9681 bp without poly(A))**Nucleotide sequence identity**: PaVY-SG shares >83% identity with incomplete sequence of Passiflora foetida virus Y (GenBank accession No. LC466655), another PaVY isolate from Japan. BLAST searches performed with the complete genome sequence of PaVY-SG suggest that the virus may correspond to a new potyvirus, with the best match being paris mosaic necrosis virus from potyviruses, with which it shares 67.1% nucleotide identity. **Polyprotein sequence**: 3084 amino acids **Polyprotein identity**: Shares about 69.3% amino acid identity with the best match in NCBI, paris mosaic necrosis virus from potyviruses. More than 63% identity with several viruses in BCMV subgroup of potyviruses.**Proteins and motifs**: The polyprotein of PaVY is predicted to be proteolytically cleaved into 10 mature peptides and it has similar but not identical cleavage sites with other viruses in the genus *Potyvirus*. The possibility for production of PIPO protein. The conserved aphid transmission motif DAG found in members of the genus *Potyvirus* is also found in PaVY-SG.**Natural transmission**: unknown, but probably aphids.**Experimental transmission**: not reported**Other host**s: Wild passiflora, various legumes including *Pisum sativum, Vigna unguiculata, and Macroptilium atropurpureum* **Additional information**: PaVY was first discovered in Australia and the Indonesian Province of Papua in 2004. Since then, partial or complete CP sequences with >90% amino acid sequence identity to the original PaVY isolate have been identified in various plant species, including wild and cultivated passiflora and various legumes, including *Pisum sativum, Vigna unguiculata*, and *Macroptilium atropurpureum*.**Study Group recommendation**:The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus passiflory* with the common name of Passiflora virus Y and acronym PaVY.4) **Virus**: Polygonatum mosaic-associated virus 1 isolate S21MP21 SR (PMaV1)**Proposed species name**: *Potyvirus polygonati* (etymology: host name)**Genus**: *Potyvirus***NCBI accession**: OP380926 **Authors**: Qiannan Li, Boxin Zhang, Jingyu Hu, Lei Zhang, Pengzhang Ji, Jiahong Dong**Author location**: School of Chinese Materia Medica and Yunnan Key Laboratory of Southern Medicinal Resource, Yunnan University of Chinese Medicine, Yunnan, China**Publication**: Li et al. (2023). **Original hosts**: *Polygonatum cyrtonema* Hua**Symptoms of infection**:mosaic**Country of isolation**: China**Sequencing approach(es)**: Two pairs of degenerate primers specific for potyviruses were used to amplify the CI gene sequence and 3’-terminal sequence of the genome, and the expected 700-bp and 1100-bp fragments were obtained. Then High-throughput RNA-Seq was carried out. Sequence was confirmed by RT-PCR and RACE with virus-specific primers.**Genome sequence**: 9619 nucleotides excluding the 3’-terminal poly(A) tail.**Nucleotide sequence identity**: PMaV1 shares 71.50% genome sequence identity with Polygonatum kingianum virus 4 of the genus *Potyvirus*.**Polyprotein sequence**: 3109 amino acids **Polyprotein identity**: PMaV1 shares 80.00% amino acid sequence identity with Polygonatum kingianum virus 3 of the genus *Potyvirus*. **Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites are present in the PMaV1 polyprotein. Predicted that the PMaV1 polyprotein is proteolytically cleaved into 10 mature peptides and that PMaV1 has similar cleavage sites to other viruses in the genus *Potyvirus*. Most of the conserved motifs found in members of the genus *Potyvirus*, including those associated with aphid transmission, are also found in PMaV1.**Natural transmission:** unknown, but probably aphids.**Experimental transmission**: PMaV1 could infect *Polygonatum* spp. and *Nicotiana tabacum* by mechanical inoculation. **Other host**s:Not recorded.**Additional information**:Phylogenetic trees based on the polyprotein sequences, genome sequences, and coat protein sequences of PMaV and other potyviruses showed that PMaV1 formed an independent sub-branch of the clade containing PKV3 and PKV4.Taken together, the results indicate that PMaV1 infecting *Polygonatum cyrtonema* should be considered a member of a novel species in the genus *Potyvirus*.**Study Group recommendation**:The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus passiflory* with the common name of Polygonatum mosaic-associated virus 1 and acronym PMaV1.5) **Virus**: Thevetia white spot virus isolate Amazonas (ThWSV)**Proposed species name**: *Potyvirus thevetiae* (etymology: host name)**Genus**: *Potyvirus***NCBI accession**: OM263475 **Authors**: Canada-Bautista *et al.* (2022)**Author location**: Facultad de Ciencias de la Vida, Escuela Superior Politécnica del Litoral, ESPOL, Km 30.5 Vía Perimetral Campus Gustavo Galindo, Guayaquil, Ecuador **Publication**: Canada-Bautista *et al.* (2022) **Original hosts**: *Thevetia ahouai* **Symptoms of infection**:White spots on leaves, black ringspots on the stems and fruit discoloration. Koch’s Postulates were satisfied, as below.**Country of isolation**: Equador. city of Guayaquil **Sequencing approach(es)**: Two isolates (Amazonas, Espol) were sequenced using high-throughput RNA-Seq. Given the low coverage of isolate Amazonas, a series of overlapping primers were designed to amplify and re-sequence it by cloning each RT-PCR fragment followed by Sanger sequencing. 5’ and 3’ terminal RACE used to confirm termini.**Genome sequence**: ‘Isolate Amazonas’ 9912 nt (OM263475) and ‘Isolate Espol’ 9904 nt (OM263476) **Nucleotide sequence identity**: BLASTn searches revealed that isolates ThWSV-Amazonas and ThWSV-Espol share 81% nt identity with one another and approximately 73% nt sequence identity (83% coverage) with their closest relative, a metagenomic potyvirus sequence (isolate UPHV-3.CD-W) from an unidentified perennial herb in the same family (Apocynaceae) as *T. ahouai* in a papaya orchard of Chiapas, Mexico (Alcala-Briseno *et al.,* 2020) (accession no. MN203192). When the complete genome sequence of this potyvirus was compared to both isolates of the Thevetia potyvirus, the identity was 69%. **Polyprotein sequence**: 3182 aa isolate Amazonas, 3181 aa isolate Espol **Polyprotein identity**: The two ThWSV isolates share 87% aa identity with one another, and about 72% amino acid identity with an unnamed potyvirus (QHB15168) from Mexico, and 61% with Asclepias potyvirus A (QED42798). **Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites are present in the ThWSV polyprotein. Predicted that the ThWSV polyprotein is proteolytically cleaved into 10 mature peptides and that ThWSV has similar cleavage sites to other viruses in the genus *Potyvirus*. Most of the conserved motifs found in members of the genus *Potyvirus*, including those associated with aphid transmission, are also found in ThWSV.**Natural transmission**: unknown, but probably aphids based on the presence of aphid-transmission-related motifs, such as KITC in isolate Amazonas (KIAC in isolate Espol) and PTK in the HC-Pro and DAG in the CP **Experimental transmission**: Symptomatic leaves infected with each virus isolate were used for mechanical inoculation of *T. ahouai* virus-free seedlings (n = 15 for each isolate). White spots were observed on non-inoculated young leaves (n = 7 for isolate Amazonas and n = 8 for isolate Espol) at an average of 15 days post-inoculation, with no differences between the symptoms induced by the two isolates. The presence of the virus in the inoculated plants was confirmed by RT-PCR and Sanger sequencing using virus-specific primers. Inoculated plants were maintained under controlled conditions, and symptoms were monitored for one year. The original symptoms, including white spots on leaves and fruit discoloration, were reproduced in the inoculated plants, and no other virus-like sequences were found in the HTS data sets. Taken together, these findings suggest that the new potyvirus is the causal agent of symptoms. **Other host**s: Unknown**Additional information**:Note, the virus was named by the authors Thevetia white spot virus (ThWSV) in their paper (Cañada-Bautista et al., 2022) but they re-named it Thevetia ringspot virus when they submitted the sequences to GenBank. Much of the nucleotide divergence between the two isolates occurs in the 5’ end of the genome encoding the 5’UTR and the P1 cistron. **Study Group recommendation**:The *Potyviridae* Study Group recommends that Thevetia white spot virus isolate Amazonas be considered as representative of a new species, *Potyvirus thevetiae.*

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**Supporting evidence**

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Figure 1. Phylogenetic tree constructed by alignment of the polyprotein amino acid sequence of all members of *Potyviridae* with the complete genome sequence available and those proposed new viruses. Alignment was performed by Muscle, and the phylogenetic tree was constructed using bootstrap test of Phylogeny and the Poisson Model with 4000 replications, implemented in MEGA11.

**References**

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