

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

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| **Code assigned:** | **2022.010P** |  |
| **Short title:** **Create six new species in the genus *Potyvirus* and one in the genus *Macluravirus* (*Patatavirales: Potyviridae*)** |
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**Author(s) and email address(es)**

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**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 | May 20, 2022 |
| Date of this revision (if different to above) | May 23, 2022 |

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

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

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**Name of accompanying Excel module**

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| 2022.010P.N.v1.Potyviridae\_7ns.xlxs |

**Abstract**

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| The *Potyviridae* Study Group proposes the creation of seven new species. The new viruses are six in genus *Potyvirus*: *P. anemones, P. cliviaflavilineae, P. gladioli, P. tagetis, P. scorzaureum*, and *P. thladiatessellati*; and one in genus *Macluravirus*: *M. amomulineae*.  |

**Text of proposal**

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| **Description of each proposed new species****1) Virus**: Anemone mosaic virus isolate NL (AnMV)**Proposed species name**: *Potyvirus anemones***Genus**: *Potyvirus***NCBI accession**: LC604019 (E)**Authors**: Yuya Imamura, Moritsugu Oishi, Yuji Fujiwara and Hironobu Yanagisawa**Author location**: Tsukuba Farm, Yokohama Plant Protection Station, Nagamine, Tsukuba, Ibaraki 305-0052, JapanNarita Branch, Yokohama Plant Protection Station, Aza-Tennamino, Komaino, Narita, Chiba, 282-0021, Japan**Publication**: Imamura et al., 2021.**Original hosts**: *Anemone* spp.**Symptoms of infection**: An anemone plant (*Anemone blanda* cv. Charmer) that originated from bulbs imported from the Netherlands showing leaf mosaic was observed during a field inspection at a post-entry quarantine farm in Japan (Imamura et al., 2021). This plant was double-infected with anemone mosaic virus (AnMV) and ranunculus mild mosaic virus (RanMMV).**Country of isolation**: Japan (imported from the Netherlands)**Sequencing approach(es)**: Next-generation sequencing. Sequence confirmed by RT-PCR with overlapping virus-specific primers.**Genome sequence**: 9698 nucleotides excluding the poly(A) tail.**Nucleotide sequence identity**: The complete polyprotein sequence of AnMV-NL shares 58.0−63.0% nucleotide sequence identity with those of other potyviruses. Phylogenetic analysis confirmed the distinct relationship of the AnMV genome sequence to the previously reported potyvirus sequences and placed them within the genus *Potyvirus*. These results show that this virus represents a separate species within the genus *Potyvirus*.**Polyprotein sequence**: 3088 amino acids.**Polyprotein identity**: The complete polyprotein sequence of AnMV-NL shares 46.0−57.0 % amino acid sequence identity with those of other potyviruses.**Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites were present in the AnMV polyprotein. It was predicted that the AnMV polyprotein is proteolytically cleaved into 10 mature peptides and that AnMV 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, were also found in AnMV-NL.**Natural transmission**: Unknown, but probably aphids.**Experimental transmission**: Unknown, AnMV-NL was found co-infected with a ranunculus mild mosaic virus (RanMMV) isolate in an anemone plant, hence it was difficult to examine host reactions of this virus.**Other host**s: Not known**Additional information**: AnMV is known to cause flower breaking and distortion with leaf mottling, is transmitted by aphids, and is very similar to Brassica nigra virus and cabbage black ringspot virus based on its biological properties (Hollings, 1957). Both AnMV and these viruses are synonyms for turnip mosaic virus (TuMV) in the datasheet (CABI invasive species compendium, 2019). However, the coat protein (CP) sequence of AnMV was amplified from diseased *Anemone blanda* in the Netherlands in 2011 and was reported to be a distinct potyvirus (Pham et al., 2011). Consequently, AnMV is classified as “Related, unclassified potyvirus” in the ICTV 10th report (Wylie et al., 2017).**Study Group recommendation**: The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus anemones* with the common name of Anemone mosaic virus and acronym AnMV. **References**:CABI invasive species compendium (2019). Datasheet Turnip Mosaic Virus (cabbage A virus mosaic). [https://www.cabi.org/ISC/datasheet/54306. Accessed 1 Dec 2019](https://www.cabi.org/ISC/datasheet/54306.%20Accessed%201%20Dec%202019). Hollings M (1957). Anemone MOSAIC–A virus disease. Ann Appl Biol 45:44–61. https://doi.org/10.1111/j.1744-7348.1957.tb00442.xImamura Y, Oishi M, Fujiwara Y, Yanagisawa H (2021). Complete genome sequences of anemone mosaic virus and ranunculus mild mosaic virus isolated from anemone imported from the Netherlands into Japan. *Archives of virology*, *166*(8), 2337–2341. https://doi.org/10.1007/s00705-021-05133-8Pham KTK, de Kock MJD, Lemmers MEC, Derks AFLM (2011). Molecular identification of potyviruses infecting bulbous ornamentals by the analysis of coat protein (CP) sequences. Acta Hortic 901:167–172. https://doi.org/10.17660/ActaHortic.2011.901.21Wylie SJ, Adams M, Chalam C, Kreuze J, López-Moya JJ, Ohshima K, Praveen S, Rabenstein F, Stenger D, Wang A, Zerbini FM, ICTV Report Consortium (2017). ICTV virus taxonomy profile: potyviridae. J Gen Virol 98:352–354. https://doi.org/10.1099/jgv.0.0007402) **Virus**: Clivia yellow stripe virus isolate 19-3026 (ClYSV)**Proposed species name**: *Potyvirus cliviaflavilineae***Genus**: *Potyvirus***NCBI accession**: MT533610 (E), MT533611 (A)**Authors**: David A. Read, Dirk Swanevelder, Gerhard Pietersen and Genevieve D. Thompson**Authors location**: Agricultural Research Council (ARC), Biotechnology Platform, 100 Old Soutpan Road, Onderstepoort, Pretoria 0110, South AfricaARC - Plant Health and Protection, Private Bag X134, Queenswood, Pretoria 0121, South AfricaDepartment of Genetics, Stellenbosch University, Stellenbosch 7600, South AfricaGene Vantage, 34 Monte Carlo Crescent, Kyalami Business Park, Johannesburg 1684, South Africa**Publication**: Read et al., 2021.**Original hosts**: *Clivia* sp*.***Symptoms of infection**: Two clivia plants were used for RNA isolation for metagenomic studies, and one virus was detected in both samples. The isolate 19-3026 (MT533610) was detected in a plant displaying severe chlorotic streaks, while isolate 19-3027 (MT533611) in a plant with mild chlorotic streaks. There is no information if other viruses were present in a mixed infection.**Country of isolation**: South Africa**Sequencing approach(es)**: Next-generation sequencing. Authors informed that the presence of the virus was confirmed by RT-PCR.**Genome sequence**: ClYSV, 9799 nucleotides excluding the poly(A) tail.**Nucleotide sequence identity**: The complete nucleotide sequence of isolate 19-3026 (MT533610) shares 100% identity with the sequence of a second isolate, 19-3027 (MT533611), and 61.0% maximum identity with plum pox virus (KC347608), the closest potyvirus nucleotide sequence.**Polyprotein sequence**: 3133 amino acids**Polyprotein identity**: The complete polyprotein amino acid sequence shares 48.1% maximum identity with turnip mosaic virus, the closest potyvirus protein sequence.**Proteins and motifs**: Not reported.**Natural transmission**: Unknown, but probably aphids.**Experimental transmission**: Unknown. The virus was identified by metagenomics.**Other host**s: Unknown**Additional information**: The virus was identified in two clivia plants collected in the same field. Their sequences share 100% nucleotide identity, indicating that this virus likely infect clivia plants.**Study Group recommendation**: The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus cliviaflavilineae* with the common name of Clivia yellow stripe virus, and acronym ClYSV. **References**:[Read DA, Roberts R, Swanevelder D, Pietersen G, Thompson GD. Novel viruses associated with plants of the family Amaryllidaceae in South Africa. Arch Virol. 2021 Oct;166(10):2817-2823. doi: 10.1007/s00705-021-05170-3. Epub 2021 Jul 19. PMID: 34279720.://www.cabi.org/ISC/datasheet/54306. Accessed 1 Dec 2019](https://www.cabi.org/ISC/datasheet/54306.%20Accessed%201%20Dec%202019)3) **Virus**: Gladiolus mosaic virus (GdMV)**Proposed species name**: *Potyvirus gladioli***Genus**: *Potyvirus***NCBI accession**: KU981083 (isolate Taean)(E), MH886516 (isolate BC31)(A)**Authors**: 1. Cho, S.Y., Lim, S., Kim, H., Yi, S.I. and Moon, J.S. (2016)
2. Wylie, S.J., Tran, T.T., Nguyen, D.Q., Koh, S.H., Chakraborty, A., Xu, W., Jones, M.G.K. and Li, H (2019)

**Author location**: **1.** Seed Testing & Research Center, Korea Seed & Variety Service, Gimcheon, Republic of Korea.Molecular Biofarming Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea.Biosystems and Bioengineering Program, University of Science and Technology, Daejeon, Republic of Korea.**2.** Plant Biotechnology Research Group-Virology, Western Australian State Agricultural Biotechnology Centre, School of Veterinary and Life Sciences, Murdoch University, Murdoch, WA 6150, Australia Jiangsu Academy of Agricultural Sciences, Nanjing, China **Publication**: Cho et al., 2016; Wylie et al., 2012; 2019.**Original hosts**: *Gladiolus* sp*.* (isolate Taean), *Iris x hollandica* (isolate BC31)**Symptoms of infection**:Yellow leaf stripes and mottling **Country of isolation**: Republic of Korea (South Korea), Australia**Sequencing approach(es)**: High throughput sequencing (Illumina platforms) followed by RT-PCR and Sanger sequencing with virus-specific primers to confirm. RACE used to determine 5’ end in the Korean sample. **Genome sequence**: 9475 nt (isolate Taean), 8779 nt (isolate Bate9, partial genome), 9463 nt (isolate BC31) excluding 3’-terminal poly(A) tail. **Nucleotide sequence identity**: The two complete GdMV sequences share >97% pairwise nt identity with one another and 80-97% nt identities with five near complete sequences (below). The complete sequences share 71-73% nt and 75-79% aa sequence identities with the complete genome sequences of Ornithogalum mosaic virus (OrMV) isolates SW3.1 (JQ807995), OrMV-SW3.3 (JQ807996) and OrMV-KP (JQ807997), marginally below the species demarcation criteria for potyviruses of <76% nt and <82% aa identities.**Polyprotein sequence**: 3157 aa (isolate Taean), 3154 aa (isolate BC31)**Polyprotein identity**: Greatest amino acid identities of 77-81% were with the complete genome sequences of OrMV isolates SW3.1 (JQ807995), OrMV-SW3.3 (JQ807996) and OrMV-KP (JQ807997)**Proteins and motifs**: The GdMV polyprotein was predicted to be cleaved to produce 10 functional proteins: P1 (266 aa), HC-Pro (455 aa), P3 (348 aa), 6K1 (52 aa), CI (634 aa), 6K2 (53 aa), VPg (192 aa), NIa-Pro (243 aa), NIb (518 aa), and CP (253 aa). **Natural transmission**: unknown, but probably aphids.**Experimental transmission**: Not recorded **Other host**s: *Ornithogalum* sp., *Lachenalia* sp., *Iris xiphium***Additional information**: Isolate Taean was initially classified within *Ornithogalum mosaic virus*, but it is sufficiently divergent from the Ornithogalum mosaic virus type isolate KP (JQ807997) that we propose it represents the exemplar isolate of a new species with a common name of Gladiolus mosaic virus*.* This division was first proposed by Wylie et al. (2019), based on sequence identities with OrMV isolates below 76% nt and 82% aa, the species demarcation criteria accepted by the ICTV. These authors also showed consistent differences in the polyprotein cleavage sites between OrMV and GdMV isolates. We propose that the Ornithogalum mosaic virus isolate Taean (JQ807997) is considered an isolate of Gladiolus mosaic virus. The proposed new virus is supported by two complete and five near-complete genomic sequences. Isolate Taean is proposed as theexemplarisolate of the species because of priority; it was the first complete genome sequence (KU981083) available. Four near-complete genomes of this virus exist from South Africa that share 80-84% nt identity with isolate Taean (1-4 below) and one from Australia that shares 98% nt identity with isolate Taean (5 below): 1. Isolate D\_Meta-contig26605-RC from *Ornithogalum* sp. (KY769735, 6941 nt,84% nt identity)
2. Isolate D\_Meta-contig25080-RC from *Ornithogalum* sp. (KY769734, 9086 nt, 80% nt identity)
3. Isolate E\_Meta-contig4807-RC from *Lachenalia* sp. (KY769751, 9471 nt, 83% nt identity)
4. Isolate E\_Meta-contig19-RC from *Lachenalia* sp. (KY769722, 9116 nt, 83% nt identity)
5. Isolate Bate9 from *Iris xiphium* (JN127345, 8779 nt, 98% nt identity)

All hosts recorded to date are members of families Iridaceae and Asparagaceae. **Study Group recommendation**:The *Potyviridae* Study Group recommends that isolate Taean be considered as the exemplar isolate of a new species proposed as *Potyvirus gladioli* with the common name of Gladiolus mosaic virus, and acronym of GdMV. **References**: Cho, S.Y., Lim, S., Kim, H., Yi, S.I. and Moon, J.S., 2016. Complete genome sequence of Ornithogalum mosaic virus infecting *Gladiolus* spp. in South Korea. *Genome Announcements*, *4*: e00816-16. (isolate Taean)Wylie, S.J., Luo, H., Li, H. and Jones, M.G., 2012. Multiple polyadenylated RNA viruses detected in pooled cultivated and wild plant samples. *Archives of Virology*, *157*: 271-284. (isolate Bate9)Wylie, S.J., Tran, T.T., Nguyen, D.Q., Koh, S.H., Chakraborty, A., Xu, W., Jones, M.G.K. and Li, H., 2019. A virome from ornamental flowers in an Australian rural town. *Archives of Virology*, *164*:2255-2263. (isolate BC31)4) **Virus**: Marigold mosaic virus isolate BJ (MMV)**Proposed species name**: *Potyvirus tagetis***Genus**: *Potyvirus***NCBI accession**: MW546936 (E)**Authors**: Yin, H.**Author location**: College of Bioscience and Resource Environment, Beijing University of Agriculture, Beijing, China**Publication**: Yin et al., 2021. **Original hosts**: Marigold (*Tagetes erecta*)**Symptoms of infection**: The symptoms that associate specifically with MMV are still to be investigated. The virus was identified by deep sequencing, and then detected in plants showing viral symptoms or asymptomatic, and co-infected with other viruses.**Country of isolation**: China**Sequencing approach(es)**: Deep sequencing of PCR-amplified small RNA library and ribo-depleted total RNA sequencing by Illumina HIseq2500. RACE for both 5’ and 3’end was performed and at least five independent clones were sequenced. **Genome sequence**: 9841 nucleotides excluding the poly(A)**Nucleotide sequence identity**: Complete genome nt sequence analysis showed sequence identity 57% with some turnip mosaic virus (TuMV) and plum pox virus (PPV) isolates. BLAST searches performed with the complete genome sequence of MMV isolate BJ suggest that the virus may correspond to a new potyvirus. **Polyprotein sequence**: 3196 amino acids **Polyprotein identity**: Shares about 57% amino acid identity with Polygonantum kingianum virus with 90% sequence coverage. CP shares highest aa identity (63.5%) with the CP of TuMV. These identity percentages confirm that MMV corresponds to a new potyvirus.**Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites were present in the MMV polyprotein. Predicted that the MMV polyprotein is proteolytically cleaved into 10 mature peptides and that MMV has similar cleavage sites to other viruses in the genus *Potyvirus*. NIb/CP site cleavage between Q/N, which is rare but not unique in potyviruses. Most of the conserved motifs found in members of the genus *Potyvirus*, including those associated with aphid transmission, were also found in MMV.**Natural transmission**: unknown, but probably aphids.**Experimental transmission**: Experimental transmission is still to be studied.**Other host**s: not known**Additional information**:Sang and Varma, Phytopath Z. 84, 10-17, 1975, used the name Marigold mosaic virus for an icosahedral virus. However, the sequence in NCBI which is found with the key word Marigold mosaic virus is only the potyvirus. Ref. Sang and Varma. 1974 Marigold Mosaic Virus. Phytopath. Z., 84, 10-17. **Study Group recommendation**:The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species of genus *Potyvirus,* proposed as *Potyvirus tagetis* with the common name of marigold mosaic virus, and acronym MMV. **References**:Yin H, Dong Z, Wang X, Lu S, Xia F, Abuduwaili A, Bi Y, Li Y. Metagenomic Analysis of Marigold: Mixed Infection Including Two New Viruses. Viruses. 2021 Jun 28;13(7):1254. doi: 10.3390/v13071254. PMID: 34203118; PMCID: PMC8310094.5) **Virus**: Scorzonera virus A (SCoVA) isolate SK**Proposed species name**: *Potyvirus scorzaureum***Genus**: *Potyvirus***NCBI accession**: MW972223 (E)**Authors**: Igori, D., Cho, H.S., Kim, H.S., Park, J.M., Lee, H.J., Kwon, S.Y., Moon, J.S**Author location**: Plant System Engineering Research Center,Korea Research Institute of Bioscience and Biotechnology, 125 Gwahak-ro, Yuseong-gu, Daejeon, Daejeon 34141, South Korea**Publication**: Igori et al., 2021**Original hosts**: *Scorzonera austriaca* **Symptoms of infection**:Mild leaf mosaic and mild yellowing **Country of isolation**: South Korea**Sequencing approach(es)**: A cDNA library was built from an rRNA-depleted library using a Ribo-Zero rRNA Removal Kit. Subsequently, the sample library was sequenced using the BGISEQ platform to generate 100-bp paired-end reads. Sanger sequencing was subsequently used to confirm most of the genomic sequence, and 5’ and 3’ RACE used to confirm ends. **Genome sequence**: 9867 nucleotides excluding 3’-terminal poly(A) tail. **Nucleotide sequence identity**: Highest nucleotide sequences identity (54%) was with lettuce mosaic virus (KJ161185) **Polyprotein sequence**: 3168 amino acids **Polyprotein identity**: Highest amino acid sequence identity (50%) was with lettuce mosaic virus (KJ161185) **Proteins and motifs**: The SCoVA polyprotein was predicted to be cleaved to produce 10 functional proteins: P1 (355 aa), HC-Pro (458 aa), P3 (358 aa), 6K1 (52 aa), CI (647 aa), 6K2 (53 aa), VPg (194 aa), NIa-Pro (243 aa), NIb (520 aa), and CP (288 aa). The predicted cleavage sites are similar to those of lettuce mosaic virus isolates. PIPO was identified by the presence of the typical G1A6 motif. Analysis of the SCoVA polyprotein aa sequence revealed the conserved functional motifs typical of potyviruses, including FRNK, PTK, GDD and DAG and others. **Natural transmission**: unknown, but probably aphids.**Experimental transmission**: Not recorded **Other host**s: Not recorded**Additional information**:**Study Group recommendation**:The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species proposed as *Potyvirus scorzaureum* with the common name as Scorzonera virus A, acronym SCoVA. **Reference:**Igori, D., Cho, H.S., Kim, H.S., Park, J.M., Lee, H.J., Kwon, S.Y. and Moon, J.S., 2021. Complete genome sequence and genome organization of scorzonera virus A (SCoVA), a novel member of the genus *Potyvirus*. *Archives of Virology*, *166*: 2901-2904.6) **Virus**: Thladiantha dubia mosaic virus Harbin-NEFU isolate (acronym ThDMV)**Proposed species name**: *Potyvirus thladiatessellati***Genus**: *Potyvirus***NCBI accession**: MF420353 (E); MK396781 (A)**Authors**: Zhao, N., Zhao, M., Zheng, B.-J. and Lin, B.-X.**Author location**: College of Life Science, Northeast Forestry University, Harbin, China**Publication**: Zhao et al., 2019. **Original hosts**: Manchurian tuberground (*Thladiantha dubia*)**Symptoms of infection**:severe mosaic symptoms**Country of isolation**: China**Sequencing approach(es)**: isolate Harbin-NEFU isolate. cDNA synthesis with random hexamers and PCR amplification followed by amplicon sequencing (at least three independent clones). 5’ and 3’end sequences were generated by RACE, at least three independent clones were sequenced.**Genome sequence**: 10112 nucleotides excluding poly(A)**Nucleotide sequence identity**: The highest nt sequence identity (73.8%) with papaya leaf distortion mosaic virus Hainan-DF isolate (PLDMV). Nt identity at the CP cistron is 81.6%.BLAST searches performed with the complete genome sequence of ThDMV suggest that the virus may correspond to a new potyvirus. **Polyprotein sequence**: 3260 amino acids **Polyprotein identity**: Shares about 79% amino acid identity of polyprotein sequence with isolates of papaya leaf distortion mosaic virus. The species demarcation criteria, based upon the polyprotein, is generally accepted as <82 % amino acid identity, proposing ThDMV is a member of a new species in genus *Potyvirus*.**Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites were present in the ThDMV polyprotein. Predicted that the ThDMV polyprotein is proteolytically cleaved into 10 mature peptides and that ThDMV has similar cleavage sites to other viruses in the genus *Potyvirus*. Most of the conserved motifs found in members of the genus *Potyvirus*, including DAG associated with aphid transmission, were also found in ThDMV.**Natural transmission**: unknown, but probably aphids.**Experimental transmission**: ThDMV was mechanically inoculated to 23 plant species*.* Only *T. dubia* developed visible symptoms but *Solanum nigrum* and *Solanum tuberosum* tested positive by RT-PCR four weeks after inoculation with ThDMV. **Other host**s: Potato, which is susceptible in controlled conditions, was found to be a host also under natural conditions.**Additional information**:The particles associated with the 10112 nt long ThDMV RNA were found to be only 650 nm in length. The length of the particle is questionable.**Study Group recommendation**:The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species of genus *Potyvirus* proposed as *Potyvirus thladiatessellati* with the common name Thlandiantha dubia mosaic virus, and acronym ThDMV. **References**:Zhao N., Zheng B., Lin B., Zhao M and Jiang L. 2019. Thladiantha dubia mosaic virus: a novel potyvirus infecting Manchurian tubergourd (Thladiantha dubia) in northeast China. Plant Disease 103, 2933-2939. https://doi.org/10.1094/PDIS-09-18-1665-RE7) **Virus**: Large cardamon chirke virus (LCCV) **Proposed species name**: *Macluravirus amomulineae***Genus**: *Macluravirus***NCBI accession**: MT110148 (E); BK013139 (A)**Authors**: Jo and Cho**Author location:** Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, 1, Gwanak-ro, Gwanak-gu, Seoul 08826, Korea**Publication:** Mandal et al. (2013); Sharma et al. (2019); Sidharthan et al. (2021)**Original hosts:** *Amomum subulatum* (large cardamon)**.** **Symptoms of infection**:Not reported for MT110148, named Amomum potyvirus A, isolate Won\_8200, from India. The sequence MT110148 shares 99% identity with partial sequences of large cardamon chirke virus (LCCV), and 100% identity with the complete sequence of LCCV assembled using transcriptome sequences (Sidharthan et al., 2021). The symptom of large cardamon plants infected with LCCV is commonly known as ‘chirke’, which is characterized by light and dark green streaks on the leaf lamina of *Amomum subulatum,* while leaf deformation and severe mosaic symptoms along with green streaks were observed in *Capsicum annuum*. It indicates that the virus named Amomum potyvirus A is an isolate of LCCV, reported previously in large cardamon plants from India. **Country of isolation**: India**Sequencing approach(es)**: Illumina**Genome sequence**: 8200 nucleotides, excluding the polyadenylated tail.Nucleotide sequence identity: BLAST and EMBOSS Needle searches showed that the 8200bp near-complete genome sequence of Amomum potyvirus A isolate Won\_8200 shares >98% identity with the near-complete genome sequence (8292bp) of large cardamom chirke virus (LCCV) of *Amomum subulatum* (large cardamom) isolate Gangtok from India reported in 2021 (Accession number BK013139; Sidharthan et al., 2021), and the partial polyprotein gene (1776nt) of LCCV ChK-1 isolate from *A. subulatum*, India (Accession number JN257715), in this case, the first LCCV description published in 2013 (Mandal et al., 2013), and the partial coat protein gene (810bp) of three LCCV isolates (DK1-DK3) from *Capsicum annuum* (chilli), India (Accession number MH899147-MH899149; Sharma et al., 2019). **Polyprotein sequence**: 2632 amino acids **Polyprotein identity**: Shares about 100% amino acid identity with cardamom chirke virus (LCCV) isolate Gangtok (ABG74927). **Proteins and motifs**: Not reported, but showed to be similar to that of LCCV isolate Gangtok.**Natural transmission:** unknown, but probably aphids such as *Rhopalosiphum maidis* and *Myzus persicae,* thesameas LCCV (Mandal et al., 2013).**Experimental transmission**: Not reported, but showed to be similar to those of LCCV such as sap transmissibility.**Other host**s: *Capsicum annuum* (chilli).**Additional information**: Not reported.**Study Group recommendation**:The *Potyviridae* Study Group recommends that Amomum potyvirus A and large cardamon chirke virus are classified in the same species for which the species name of *Macluravirus amomulineae* and the common name of large cardamon chirke virus (LCCV) are proposed in the genus *Macluravirus*. **References**:Mandal B, Vijayanandraj S, Shilpi S, Pun KB, Singh V, Pant RP, Jain RK, S. Varadarasan S, Varma A (2013). Disease distribution and characterization of a new macluravirus associated with chirke disease of large cardamom. Annals of Applied Biology, 160: 225–236.Sharma SK, Chanu NT, Anand YR, Singh YH, Singh S, Raj C, Baranwal VK, Rai R, Sanabam R, Roy SS, Ansari MA, Prakash N (2019). First report of large cardamom chirke virus, a Macluravirus naturally infecting chili crop in India. Plant Disease, 103(4):777.Sidharthan VK, Sharma SK, Baranwal VK (2021). The first near-complete genome sequence of large cardamom chirke virus mined from the transcriptome dataset of large cardamom. Plant Gene, 28:100324. |

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**Supporting evidence**

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Fig. 1. Polyprotein amino acid sequences of all members of *Potyviridae* with complete genome sequences were aligned with the sequences of the proposed new viruses. Alignment was done with Muscle implemented in Mega11 by the Neighbor-Joining method in a Bootstrap test of phylogeny with 189 taxa. The common name was used for the identification of each taxon. The new viruses are highlighted in gray.

**References**

References in the text.