

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

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| **Code assigned:** | **2021.006P** |  |
| **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](mailto:alice.nagata@embrapa.br);  [s.wylie@murdoch.edu.au](mailto:s.wylie@murdoch.edu.au);  [Ramon.Jordan@ars.usda.gov](mailto:Ramon.Jordan@ars.usda.gov);  [j.kreuze@cgiar.org](mailto:j.kreuze@cgiar.org);  [fanlikm@126.com](mailto:fanlikm@126.com);  [juanjose.lopez@cragenomica.es](mailto:juanjose.lopez@cragenomica.es);  [kristiina.makinen@helsinki.fi](mailto:kristiina.makinen@helsinki.fi);  [ohshimak@cc.saga-u.ac.jp](mailto: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]  Consejo Superior de Investigaciones Científicas, Madrid, Spain [JJL-M]  Viikki Plant Science Centre [KM]  Saga University [KO] |

**Corresponding author**

|  |
| --- |
| 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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**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 27, 2021 |
| Date of this revision (if different to above) | August 5, 2021 |

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

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| The Excel file was corrected |

**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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| 2021.006P.A.v1.Potyvirus\_5ns\_3as.xlxs |

**Abstract**

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| The *Potyviridae* Study Group proposes the creation of five new species, and the abolishment of three species. The new species are named according to the binomial rule: *Potyvirus achyrantis, Potyvirus ashitabae, Potyvirus mirabilis, Potyvirus fountaingrassi*, and *Potyvirus pleioblasti*. The following species were abolished from the *Potyviridae* species list because they were not assigned to an existing genus: *Common reed chlorotic stripe virus, Longan witches broom-associated virus*, and *Spartina mottle virus*. The Study Group will analyze all *Potyviridae*-related sequences, and, if appropriate, will create new genera for classification of all accepted species. |

**Text of proposal**

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| |  | | --- | | 1. **Virus**: Achyranthes virus A (AcVA)   **Proposed species name**: *Potyvirus achyrantis*  **Genus**: *Potyvirus*  **NCBI accession**: MT513101  **Authors**: Igori D., Lim, S., Kwon, S-Y., Cho, H., Park, JM., Kim, H-S., Lee, H-J., Lee S-H., Moon, JS.  **Author location**: Plant Systems Engineering Research Center, Korea Research Institute of Bioscience and Biotechnology, Dajeon 34141, Korea – jsmoon@kribb.re.kr  **Publication**: Igori et al., 2020.  **Original hosts**: *Achyranthes bidentata*  **Symptoms of infection**:Mild leaf mosaic and milt mottling in *Achyranthes bidentata*  **Country of isolation**: Korea and China  **Sequencing approach(es)**: RNA from a pool of 67 plants, including a plant of *A. bidentata*. High-throughput RNA-Seq, Illumina HiSeq 2500. Sequence confirmed by Sanger sequencing of RT-PCR amplicons with overlapping virus-specific primers and of 5’ and 3’ rapid amplification of cDNA ends (RACE) fragments using the *A. bidentata* sample.  **Genome sequence**: 9491 nucleotides  **Isolate:** SK  **Nucleotide sequence identity**:  Pairwise comparisons showed that the AcVA genome shares 47.81–57.78% nucleotide (nt) sequence identity at the complete genome level, 41.89–56.41% amino acid (aa) sequence identity at the polyprotein level, and 50–63.8% aa sequence identity at the coat protein level with the closest members of genus *Potyvirus,* includingBasella rugose mosaic virus and Freesia mosaic virus.  **Polyprotein sequence**: 3103 amino acids and PIPO  **Polyprotein identity**: Most of the conserved functional motifs typical of potyviruses were identified, including 509FRNK512 (RNA silencing suppressor) and 638PTK640 (aphid transmission) motifs in HCPro; 1276GSGKS-X3-P1284 (potential helicase activity), 1491VATNIIENGVTL1502 (potential helicase activity), 1535GERIQRLGRVGR1546 (potential helicase activity), and 1362DECH1365 (potential helicase activity) motifs in CI; 2619GNNSGQPSTVVDNT2632 (RNA-dependent polymerase activity) and 2663GDD2665 (RNA-dependent polymerase activity) motifs in NIb; and a 2832DAG2834 (aphid transmission) motif in CP.  **Natural transmission**: not tested.  **Experimental transmission**: not tested.  **Other host**s: no report  **Additional information**:  Another potyvirus was identified in China (Wu et al. 2020) in the same host. The complete genome sequence (9482 nt) was determined after RT-PCR of partial fragments. The sequence (MT648692) shared 75.8% nucleotide identity and 84.8% amino acid identity to that of AcVA reported by the Koreans (Igori et al. 2020). They concluded that it may be an isolate of AcAV. Its sequence in GenBank is entitled achyranthes bidentata mosaic virus isolate Zhejiang.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that Achyrantes virus A be considered as the exemplar isolate of a new species in the genus *Potyvirus* for which the species name *Potyvirus achyranthis* is proposed.   1. **Virus**: Ashitaba mosaic virus (AshMV)   **Proposed species name**: *Potyvirus ashitabae*  **Genus**: *Potyvirus*  **NCBI accession**: MN853672  **Authors**: Aya Sakamoto, Azusa Kanagawa, Maya Kubota, Hideo Hoshi, Keiko T. Natsuaki. Aya\_1\_Sakamoto@member.metro.tokyo.jp  **Author location**: Tokyo Metropolitan Islands Area Research and Development Center for Agriculture, Forestry and Fisheries, 4341‑11 Okago, Hachijo‑machi, Tokyo 100‑1401, Japan  **Publication**: Sakamoto et al., 2021  **Original hosts**: *Angelica keiskei*  **Symptoms of infection**:mosaic, chlorotic spots, and vein clearing. AshMV-AA infected six plant species from three families: chlorotic spots on the leaves of *Chenopodium quinoa* and *C. amaranticolor;* fewer leaves produced by *Apium graveolens* and *Petroselinum crispum;* and mosaic on leaves of *Nicotiana benthamiana* and *A. keiskei*.  **Country of isolation**: Japan  **Sequencing approach(es)**: RT-PCR products cloned in pGEM-T and Sanger-sequenced, including 5’ and 3’ RACE fragments.  **Genome sequence**: 9,651nucleotides  **Isolate:** AshMV-AA  **Nucleotide sequence identity**: AshMV-AA nucleotide sequence shares 60.5% with carrot thin leaf virus (CTLV).  **Polyprotein sequence**: 3,133 amino acids and PIPO  **Polyprotein identity**: AshMV-AA amino acid sequence shares 58.7% with the polyprotein of CTLV. Most motifs typical of potyviruses are present in the following functional proteins: H-X8-D-X31-GXSG in P1; FRNK and GYCY-X71-H in HC-Pro; GAVGSGKST, VLLLEPTRPL, and DEXH in CI; H-X34-D-X67-GXCG-X14-H in NIa; and CDADGS and GDD in NIb . Additionally, the DAG motif in CP and the KITC and PTK motifs in HC-Pro, which are involved in aphid transmission, were also detected, suggesting the virus is most likely transmitted by aphids.  **Natural transmission**: not tested.  **Experimental transmission**: mechanically transmissible  **Other hosts**: *Chenopodium quinoa,* *C. amaranticolor, Apium graveolens,* and *Petroselinum crispum*  **Additional information**:  A phylogenetic analysis of the CP genes indicated the occurrence of two genotypes, Genotype A and Genotype B. The nucleotide identity within Genotype A and within B was 98.0–99.7%. In contrast, the nucleotide and amino acid identities between the two genotypes were 77.2–78.1% and 79.4–80.9%, respectively.  **Study Group recommendation**:  The *Potyviridae* Study Group recommend ashitaba mosaic virus as the exemplar isolate of a new member of the genus *Potyvirus* for which the species name *Potyirus ashitabae* is proposed.   1. **Virus**: Mirabilis crinkle mosaic virus, isolate MJ [MiCMV-MJ]   **Proposed species name**: *Potyvirus mirabilis*  **Genus**: *Potyvirus*  **NCBI accession**: MT247721  **Authors**: Wang et al. (2012); Zhang et al. (2020); Li et al. (2020)  **Author location**: School of Life Sciences, Biocontrol Engineering Research, Center of Plant Disease and Pest, Biocontrol Engineering Research Center of Crop Disease and Pest of Yunnan Province, Yunnan University, Kunming 650091, China  **Publication**: Zhang et al. (2020)  **Original hosts**: *Mirabilis jalapa* (China; MT247721, MT247722) [Several publications]  *Phytolacca americana* (Japan; LC603132) [No publication]  **Symptoms of infection**:Mosaic and crinkle symptoms were observed on the leaves of *Mirabilis jalapa.*  **Country of isolation**: China (also found in Japan)  **Sequencing approach(es)**: Sanger sequencing of overlapping PCR amplicons generated with virus-specific and degenerate primers coupled with 5’ and 3’ RACE protocols.  **Genome sequence**: 9666 nucleotides  **Isolate:** MiCMV-MJ  **Nucleotide sequence identity**: MiCMV isolate MJ (MT247721) shares 98.96-99.94% identity with the original 2012 Chinese isolate [then named Basella rugose mosaic virus, isolate MJ (MG656405)] and another Chinese MiCMV, isolate MJ-19 of (MT247722), respectively. All three of these isolates share 90.5% identity with the Japanese isolate MiCMV-PA (LC603132). All four of these isolates only share ~73% identity (100% query coverage) with correctly named Basella rugose mosaic virus isolates and less than 63% identity with other potyviruses.  **Polyprotein sequence**: 3080 amino acids  **Polyprotein identity**: All four MiCMV isolates (BaRMV-MJ, MiCMV-MJ, MiCMV -M19 and MiCMV-PA) share 94.33 to 99.84% amino acid identity with each other and only 72-73% identity with correctly named Basella rugose mosaic virus isolates.  **Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites were present in the MiCMV polyprotein. Predicted that the MiCMV polyprotein is proteolytically cleaved into 10 mature peptides and that MiCMV 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 MiCMV-MJ.  **Natural transmission**: Unknown, but probably aphids (see experimental transmission).  **Experimental transmission**: The original virus found in *Mirabilis jalapa* [named Basella rugose mosaic virus (BaRMV-MJ)] was shown to be mechanically transmissible to *Mirabilis jalapa, Chenopodium amaranticolor*, *C. quinoa*, and *Nicotiana benthamiana*. What was called BaRMV-MJ could also be transmitted by *Myzus persicae* in a non-persistent manner. Mechanical inoculation of infectious clones (Li et al., 2020) made from RNA from the original BaRMV-MJ (now named MiCMV-MJ) were shown to have the same symptoms and host range as those shown by sap-inoculation.  **Other hosts:** Not reported.  **Additional information**: The virus isolated from *Mirabilis jalapa* in China was first described in 2012 (Wang et al, 2012) and was subsequently identified to be a probable isolate of Basella rugose mosaic virus (BaRMV) based on CP sequence similarity to sequences in three BaRMV isolates (75.2%–77.3% sequence identity). Once the complete genome was sequenced (Zhang et al., 2020) the nucleotide sequence similarities of the other gene regions were all below the corresponding species demarcation threshold and the virus was renamed Mirabilis crinkle mosaic virus, isolate MJ.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that this virus be considered as representative of a new species for which the species name *Potyvirus mirabilis* is proposed.   1. **Virus**: Pennisetum alopecuroides mosaic virus (PalMV)   **Proposed species name**: *Potyvirus fountaingrassi*  **Genus**: *Potyvirus*  **NCBI accession**: MT790493  **Authors**: Liu, X., Chen, X., Liu, S., Du, K., Wang, P., Jiang, T., Cao, M., Li, X., Fan, Z., Zhou, T  **Author location**: The corresponding author (Tao Zhou) is located in: State Key Laboratory for Agro-Biotechnology, and Ministry of Agriculture and Rural Affairs, Key Laboratory for Pest Monitoring and Green Management, Department of Plant Pathology, China Agricultural University, Beijing 100193, China.  Other locations of authors:  Guangdong Provincial Key Laboratory for Plant Epigenetics, Longhua Institute of Innovative Biotechnology, College of Life Sciences and Oceanography, Shenzhen University, Shenzhen 518060, China.  National Citrus Engineering Research Center, Citrus Research Institute, Southwest University, Chongqing 400712, China.  Department of Plant Pathology, Shandong Agricultural University, Taian 271018, China.  **Publication**: Liu et al. (2021).  **Original hosts**: Pennisetum grass(*Pennisetum alopecuroides* L.)  **Symptoms of infection**: The infected pennisetum grass plants, found (June 2016) in Haidian District in Beijing, exhibited dwarf phenotype, leaf chlorosis and delayed flowering. Flexuous filamentous virions were detected in TEM in them.  **Country of isolation**: China  **Sequencing approach(es)**: Total RNA extracted from symptomatic leaves was used to construct a small RNA library and for high-throughput sequencing. Reads from 18 to 25 nts in length (18 million) were assembled and mapped to the viral genome in both sense and antisense orientations, being the most abundant of 21 and 22 nts. Contigs cover the majority of the genome, with a few gaps. Primers designed in known sequences were used to complete the genomic sequence by RT-PCR, and the extremities were confirmed by 5' and 3' RACE PCR.  **Genome sequence**: The complete sequence (9717 nts followed by a poly(A) tail) was deposited in GenBank with accession number MT790493. The reference is still not available for public consultation on May 2021, but the authors provided upon request a draft of the provisional version (attached as annex).  **Isolate:** PalMV-Haidian  **Nucleotide sequence identity**: Authors performed a comparison with 42 representative genomes of potyviruses, including another potyvirus previously found in the same plant species and named Pennisetum mosaic virus (PenMV, accession NC\_007147). The closest relative to PalMV was johnson grass mosaic virus (JGMV, accession NC\_003606), with identities of 72% (nt) and 65% (aa).  **Polyprotein sequence**: The genome encodes a polyprotein of 3131 aa flanked by 5' UTR (142 nts) and 3'UTR (176 nts). Mature gene products after proteolytic cleavage include the usual organization of P1, HC-Pro, P3, 6K1, CI, 6K2, NIa-Vpg, Nia-Pro, NIb and CP. The conserved out-of-frame PIPO (267 nts) was present within the P3 gene product and translatable as P3N-PIPO after polymerase slippage at the unique GA6 motif (position 2773-9 in the genome).  **Polyprotein identity**: The cleavage of the 10 mature proteins in the polyprotein were predicted at aa positions 262, 723, 1070, 1122, 1775, 1828, 2017, 2259 and 2776.  **Proteins and motifs**: Several conserved motifs typical for potyviruses were found in the polyprotein sequence, including those for protease activities, helicase and RNA-dependent polymerase activities, and vector transmission.  **Natural transmission**: Unknown vector, probably aphids based on conservation of motifs.  **Experimental transmission**: The virus can be mechanically inoculated to monocotyledonous plants such as maize, millet, wheat, sorghum and rice. Common indicator plants, *Chenopodium* and *Nicotiana* species, did not show symptoms and the virus was not detected by RT-PCR.  **Other host**s: Unknown  **Additional information**:  No other sequences (partial or complete genome) with sufficient similarity to be considered different isolates of the same virus could be identified through BLAST searches in GenBank. The virus is clearly different from Pennisetum mosaic virus (PenMV), for which the binomial name *Potyvirus penniseti* would be preferred.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that PalMV should be considered as the exemplar isolate of a new species in the genus *Potyvirus* for which the species name *Potyvirus fountaingrassi* is proposed.  ANNEX  LOCUS Seq1 9734 bp RNA linear 03-NOV-2019  DEFINITION UNVERIFIED: Pennisetum alopecuroides mosaic potyvirus.  ACCESSION Seq1  VERSION  KEYWORDS UNVERIFIED.  SOURCE Pennisetum alopecuroides mosaic potyvirus  ORGANISM Pennisetum alopecuroides mosaic potyvirus  Unclassified.  REFERENCE 1 (bases 1 to 9734)  AUTHORS Liu,X., Chen,X. and Zhou,T.  TITLE Direct Submission  JOURNAL Submitted (21-JUL-2020) China agricultural university, College of  Plant Protection, No.2 Yuanmingyuan west road, Beijing, Beijing  100193, China  COMMENT GenBank staff is unable to verify sequence and/or annotation  provided by the submitter.  Bankit Comment: ALT EMAIL:chenximelon@126.com  Bankit Comment: TOTAL # OF SEQS:1.  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*Potyvirus*  **NCBI accession**: isolate J1 **LC573287**, isolate J2 LC573288  **Authors**: Kosuke Katsu, Takamichi Nijo, Tetsuya Yoshida, Yukari Okano, Masanobu Nishikawa, Akio Miyazaki, Kensaku Maejima, Shigetou Namba and Yasuyuki Yamaji  **Author location**: Department of Agricultural and Environmental Biology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo, 113-8657, Japan  **Publication**: Katsu et al., 2021  **Original hosts**: Bamboo  **Symptoms of infection**: Mosaic symptoms in bamboo  **Country of isolation**: Japan  **Sequencing approach(es)**: 1) RT-PCR products obtained with universal potyvirus primers were sequenced. 2) cDNA libraries were constructed from the isolated RNA samples for paired-end sequencing using an NEBNext Ultra II RNA Library Prep Kit for Illumina (New England Biolabs, USA). Sequencing was performed with a MiSeq instrument (Illumina, USA) and a MiSeq Reagent Kit v. 2. This resulted in two large virus-like contigs of 9,615 (sample 1) and 9,601 (sample 2) nt in length. 3) 5’ and 3’ ends were verified from six fragments amplified with the 5′ RACE system kit v.2 (Invitrogen, USA) and RT-PCR with a specific and an oligo(dT) primer.  **Genome sequence**: Sequencing of two isolates, J1 and J2, of PleMV resulted in revelation of the genomic RNA sequences consisting of 9,634 and 9643 nucleotides, respectively.  **Nucleotide sequence identity**: PleMV isolate J1 share 80.55% identity on the nucleotide level with PleMV isolate J2 (query cover 93%) proposing that they are two isolates of the same species.  PleMV isolates J1 and J2 have the highest nt sequence identity of 71.4% and 71.5% with the potyvirus johnsongrass mosaic virus (JGMV, Z26920.1). Here the sequence coverages of the comparisons were 49% and 45%.  **Polyprotein sequence**: 3081 (LC573287) and 3084 (LC573288) amino acids.  **Polyprotein identity**: The large ORFs of the isolates showed the highest sequence identity to those of JGMV (KT833782): 69.4% (isolate J1) and 69.9% (isolate J2) at the aa level. The level of sequence identity of PleMV large ORF was between 41,7-45,4% with five randomly selected potyviruses (PVY, PVA, TuMV, TEV and PPV) with query cover varying between 88-96%,  **Proteins and motifs**: Nine conserved potyvirus proteolytic cleavage sites were present in the PleMV polyprotein proposing that these cleavages result into 10 protein products. Both isolates contain the required sequence elements for production of PIPO from a short ORF. Sequence motifs that are typical for potyviruses are present.  **Natural transmission**: Unknown, probably aphids as predicted from the PTK and DAG motives in HCPro and CP, respectively.  **Experimental transmission**: not reported  **Other host**s: not reported  **Additional information**:  Samples were found to be infected by potyviruses with immunoStrip for Potyvirus Group (Agdia, USA) prior to sequencing.  **Study Group recommendation**:  The *Potyviridae* Study Group recommends that PleMV should be considered as the exemplar isolate of a new species for which the name *Potyvirus pleioblasti* is proposed.  **6) Abolishment of current species within the family *Potyviridae* not assigned to a genus**  The Study Group proposes to abolish the following species from the *Potyviridae* species list because they were not assigned to an existing genus: *Common reed chlorotic stripe virus, Longan witches broom-associated virus*, and *Spartina mottle virus*.  The Study Group will analyze all *Potyviridae*-related sequences, and, if appropriate, will create new genera for classification of all accepted species. | |

**Supporting evidence**

Comparison of genome wide nucleotide sequence of the proposed new *Potyvirus* species with selected potyviruses (reference sequences)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Viruses and  Ref sequences | Viruses evaluated for acceptance | | | | | |
| AcVA | AshMV | MiCMV | PalMV | PleMV |
| AcVA | 100.0 | 60.1 | 62.2 | 60.5 | 59.9 |
| AshMV | 60.1 | 100.0 | 61.0 | 60.0 | 60.4 |
| MiCMV | 62.2 | 61.0 | 100.0 | 60.2 | 59.5 |
| PalMV | 60.5 | 60.0 | 60.2 | 100.0 | 68.0 |
| PleMV | 59.9 | 60.4 | 59.5 | 68.0 | 100.0 |
| BaRMV | 62.8 | 61.8 | 70.7 | 60.8 | 60.1 |
| CABMV | 61.9 | 61.6 | 62.1 | 60.6 | 60.3 |
| CTLV | 60.5 | 64.5 | 60.7 | 61.0 | 60.5 |
| JGMV | 60.8 | 60.3 | 60.0 | 67.3 | 67.7 |

Sequence accessions and names:

AcVA – Achyranthes virus A – MT513101

AshMV – ashitaba mosaic virus – MN853672

MiCMV – Mirabilis crinkle mosaic virus – MT247721

PalMV – Pennisetum alopecuroides mosaic virus – MT790493

PleMV – Pleiobastus mosaic virus – LC573287

BaRMV – Basella rugose mosaic virus – DQ821938

CABMV – Cowpea aphid-borne mosaic virus – AF348210

CTLV – Carrot thin leaf virus – JX156434

JGMV – Johnsongrass mosaic virus – Z26920

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