This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
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| **Code assigned:** | ***2017.007P*** | | | | (to be completed by ICTV officers) |
| **Short title:** Nine new species in family *Potyviridae* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1** **X 2 X 3  4 X** | | | |
| **Author(s):** | | | | | |
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| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | *Potyviridae* | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
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| Date first submitted to ICTV: | | | | 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

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| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.007P.N.v1.Potyviridae\_9sp** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| Blawid, R., Rodrigues, K.B., de Moraes Rêgo, C., Inoue-Nagata, A.K. and Nagata, T., 2016. Complete genome sequence of tobacco mosqueado virus. *Archives of Virology* 161: 2619-2622.  Cho, S.Y., Kim, H., Yi, S.I., Lim, S., Park, J.M., Cho, H.S., Kwon, S.Y. and Moon, J.S., 2017. First Report of Impatiens flower break virus Infecting *Impatiens walleriana* in South Korea. *Plant Disease* 101: 394  Desbiez, C., Verdin, E., Tepfer, M., Wipf-Scheibel, C., Millot, P., Dafalla, G. and Lecoq, H., 2016. Characterization of a new cucurbit-infecting ipomovirus from Sudan. *Archives of Virology* 161: 2913-2915.  References  Gibbs A.J., Trueman J.W.H. and Gibbs M.J. 2008. The bean common mosaic virus lineage of potyviruses: where did it arise and when? *Archives of Virology* 153: 2177–2187  Igori, D., Hwang, U.S., Lim, S., Zhao, F., Kwon, S.Y. and Moon, J.S., 2016. The first complete sequence and genome structure of Daphne virus Y. *Archives of Virology* 161: 2905-2908  Jordan R. and Guaragna M. (2007): Characterization of a new potyvirus, Impatiens flower break virus, infecting New Guinea *Impatiens*. *Phytopathology* 97: Supplement S54  Mederos, D.C., Bejerman, N., Trucco, V., de Breuil, S., Lenardon, S. and Giolitti, F., 2017. Complete genome sequence of sunflower ring blotch virus, a new potyvirus infecting sunflower in Argentina. *Archives of Virology* 1-4. doi:10.1007/s00705-017-3275-7  Ohshima, K., Korkmaz, S., Mitoma, S., Nomiyama, R. and Honda, Y., 2016. First genome sequence of wild onion symptomless virus, a novel member of *Potyvirus* in the turnip mosaic virus phylogenetic group. *Genome Announcements*: 4 e00851-16.  Seo, E.Y., Lim, S., Hammond, J., Moon, J.S. and Lim, H.S., 2016. Complete genome sequence of a novel potyvirus, Callistephus mottle virus, identified in *Callistephus chinensis*. *Archives of Virology* 161: 3281-3283.  Su, X., Fu, S., Qian, Y., Zhang, L., Xu, Y. and Zhou, X., 2016. Discovery and small RNA profile of pecan mosaic-associated virus, a novel potyvirus of pecan trees. *Scientific Reports* 6: 26741  Zheng Y, Gao S, Padmanabhan C, Li R, Galvez M, Gutierrez D, Fuentes S, Ling K-S, Kreuze J, Fei Z., 2017. VirusDetect: An automated pipeline for efficient virus discovery using deep sequencing of small RNAs. Virology 500: 130-138. |

|  |
| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Proposal to create eight new species in genus *Potyvirus***

In *Potyviridae*, species of all genera are distinguished by the following criteria:

1. Sequence relatedness: different species have nucleotide identities of less than about 76% across the entire ORF or the coat protein, and amino acid identities are less than about 80%. Differences in polyprotein cleavage sites may help distinguish species.
2. Host range and host responses to infection.
3. Inclusion body morphology
4. Antigenic properties

In many cases, information addressing only criteria (i) and (ii) is available.

Barbacena virus Y

A leaf sample of an unidentified weed with yellowing and mosaic-like symptoms was collected from a tomato field in Barbacena, Brazil, in February 2013. As part of a larger study to evaluate a procedure for novel virus detection, sRNAs were extracted and assembled. A contig of 9837 nt was identified containing a single ORF that had significant nucleotide identity to known potyviruses. Sanger sequencing of overlapping PCR products was used to validate the authenticity of the assembly. A complete genome sequence of 9837 nt (KU685505) was assembled from the Sanger sequences that had 99% sequence identity to the initial assembly. The virus was tentatively named Brazilian weed virus Y (Zheng et al., 2017). It has all genomic characteristics of a member of the genus *Potyvirus* and is most closely related to viruses in the potato virus Y (PVY) subgroup as shown by phylogenetic analysis (Fig 1). The polyprotein sequence has 60-63% (nt) and 60-64% (aa) identity with viruses in the PVY group, including tomato necrotic stunt virus, Bidens mottle virus, potato virus Y, sunflower chlorotic mottle virus, pepper severe mosaic virus, Verbena virus Y, pepper yellow mosaic virus, pepper mottle virus, Brugmansia mosaic virus, Brugmansia suaveolens mottle virus, Peru tomato mosaic virus, potato virus V and wild potato mosaic virus. The genetic distance and phylogenetic analysis justify the creation of a new species, for which we propose the name *Barbacena virus Y*. The authors have approved the species name.

Callistephus mottle virus

Leaves showing severe mottling symptoms were collected from China aster (*Callistephus chinensis* (L.) Nees) in South Korea and submitted to high-throughput total cDNA sequencing. A single contig covering the near complete genome of a potyvirus was assembled from the paired end reads and the 5´and 3´ends were completed using corresponding RACE reactions. The genomic RNA of Callistephus mottle virus (CalMV) isolate DJ consisted of 9,859 nucleotides (excluding the poly(A) tail) (KX013584) and contains the typical open reading frame of potyviruses, encoding a putative large polyprotein of 3,154 amino acids. The identified virus was most closely related to plum pox virus and members of the Apium virus Y (ApVY) subgroup (Fig 1) by sharing 50-52 % polyprotein amino acid sequence identity, which is well below the threshold used to discriminate species within the genus, justifying its placement into a new species. The name *Callistephus mottle virus* was proposed for this new species (Seo et al., 2016).

Daphne virus Y

Daphne virus Y (DVY) was first reported from *Daphne* spp. in New Zealand in 1975, and then in Germany in 1991 and in Republic of Korea in 2006. There was the nucleotide sequence of the 3’ terminal region of a DVY genome from New Zealand made available in 2007 (EU179854). A total of 97 *Daphne odora* Thunb. plant samples with virus-like symptoms were collected from different places in the Republic of Korea during 2014 (Igori et al., 2016). DVY isolate SK isolate was sequenced to reveal it had a genome 9,448 nucleotides long, excluding the poly-A tail, with typical potyvirus organization (KU556609). Percent identities of the complete genome of DVY to those of potyviruses varied from 46.3% to 61.4% at the nucleotide level and from 37.8% to 62.5% at the amino acid level. The complete genome had the highest nucleotide sequence identity of 61.4% with an isolate of Daphne mosaic virus (DapMV, DQ299908) (Fig 1). The nucleotide and amino acid identities and phylogenetic analysis justify the creation of a new species, *Daphne virus Y*, in genus *Potyvirus*.

Impatiens flower break virus

Impatiens flower break virus (IFBV) was initially isolated in the USA from “several New Guinea *Impatiens* cultivars” showing colour breaking symptoms on flower petals (Jordan & Guaragna 2007). Leaves and flowers from symptomatic plants tested positive in ELISA with a potyvirus broad-spectrum reacting monoclonal antibody and contained inclusion bodies typical of a potyvirus. A partial genome sequence consisting of the 3′-terminal region of the virus was sequenced and phylogenetic analysis of the 6546 nt fragment (GenBank AY864851) revealed that the new potyvirus, tentatively named Impatiens flower break virus, was most closely related to members of the bean common mosaic virus cluster of potyviruses (Gibbs et. al. 2008) (Fig 1). It shared greatest nt identity across the coding region of its genome with isolates of east Asian passiflora virus and bean common mosaic virus (67%); its polyprotein sequence was closest to an isolate of yambean mosaic virus (67%). The virus has been mechanically transferred to, and symptoms reproduced in, healthy *Impatiens* cultivars (Jordan & Guaragna 2007). The same virus was recently identified as causal pathogen for virus-like symptoms on leaves of *Impatiens walleriana* in South Korea based on various molecular analyses. The complete genome sequence was obtained by *de novo* assembly of contigs. The newly sequenced genome shared 99% nt identity with the previously available partial genome. The complete genome sequence of the Korean isolate, which was 9622 nt long, was deposited in GenBank as IFBV isolate Asan (KU981084) (Cho et. al. 2017).

Pecan mosaic-associated virus

A survey conducted to identify viruses of woody plants in southeast China lead to the detection of a virus infecting pecan trees (*Carya illinoensis*). Electron microscopy analysis revealed the presence of filamentous particles in symptomatic tissues. To characterize the virus, the complete sequence was obtained by deep sequencing of small RNAs, and completed by RT-PCR amplification and RACE-PCR to determine the 5' and 3' terminal regions. The assembled genome sequence revealed a structure compatible with a member of the genus *Potyvirus* with 9310 nt (KT633868). Sequence comparisons of the CP region and of the full-length genome of the virus pecan mosaic-associated virus (PMaV) isolate LA was closest to lettuce mosaic virus with 61% nt and 67% aa identities (Fig 1), and provided similarities below the threshold used to discriminate species within the genus, justifying its placement into a new species. The name *Pecan mosaic-associated virus* was proposed by the authors for a new species typified by PMaV-LA (Su et al., 2016).

Sunflower ring blotch virus

This virus was found from sunflower in Argentina where sunflower is the second most widely cultivated oilseed crop. The virus causes ring blotch symptoms and is mechanically transmitted. ELISA was positive using potyvirus group antiserum but negative with antisera against sunflower chlorotic mottle virus (SuCMoV) and sunflower mild mosaic virus (SuMMoV), two known potyviruses that infect sunflower there. The complete genome sequence of sunflower ring blotch virus (SuRBV) isolate Chaco was determined to be 9555 nt (KX856009) (Mederos et al., 2017). Phylogenetic analyses revealed that the virus belongs to the PVY subgroup (Fig 1) and is most close to SuCMoV and Bidens mosaic virus (BiMV), sharing 69.1% and 70.6% identities at the nt level, respectively. At the amino acid level, five (6K1, CI, VPg, NIb and CP) of the ten viral proteins (excluding P3N-PIPO) of SuRBV) are 79 to 86% identical to those of SuCMoV and BiMV. The authors propose creation of a new species in the genus *Potyvirus* named *Sunflower ring blotch virus* to accommodate SuRBV-Chaco.

Tobacco mosqueado virus

This virus was initially detected in PVY-resistant tobacco plants (*Nicotiana tabacum*) in southern Brazil (Blawid et al., 2016). The mild mottling ("mosqueado" in Portuguese) symptoms resembled those induced by PVY, but the plants tested negative for this virus in serological assays. The tobacco mosqueado virus (TMosqV) isolate RS-01 genome is 9896 nucleotides (nt) long, excluding the poly-A tail (KT834407), and has a typical potyvirus organization. The complete genome has the highest nucleotide sequence identity of 68.5 % with pepper yellow mosaic virus (PepYMV, AB541985) and 68.2 % with Brugmansia mosaic virus (JX874139) (Fig 1). The coat protein coding region has the highest nucleotide sequence identity of 74.0 % with PepYMV (AB541985) and the highest amino acid sequence identity of 77.9 % with Peru tomato mosaic virus (CAE82257). The virus is sap-transmissible and, besides *N. tabacum*, was also shown to infect *N. benthamiana*, *N. rustica* and *Physalis pubescens*. *Tobacco mosqueado virus* is proposed as a new species in *Potyvirus*.

Wild onion symptomless virus

Samples of wild onion were collected in 2012 from a fruit orchard in Iznik, western Turkey. The host species was not identified—there are several species of wild onion indigenous to Turkey. Analysis of an RT-PCR product using generic primers revealed a potyvirus-like sequence resembling members of the turnip mosaic virus subgroup within *Potyvirus*. Generic primers were used to amplify the complete genomes of two isolates of the virus. The two sequences of wild onion symptomless virus (WOSV) isolates Tur256-1 and Tur256-2 (LC159494, LC159495) were both 9369 nt long and shared 99.97% nucleotide identity. They shared 60-67% nt identity with isolates of turnip mosaic virus, Narcissus late season yellows virus, Narcissus yellow stripe virus, scallion mosaic virus, and Japanese yam mosaic virus (Ohshima et al., 2016) (Fig 1). The genetic distance and phylogenetic analysis of WOSV justify the creation of a new species in *Potyvirus*, for which the authors proposed the name *Wild onion symptomless virus*.

**Proposal to create one new species in genus *Ipomovirus***

Coccinia mottle virus

A virus tentatively named Coccinia mottle virus (CocMoV) was detected in a sample of the cucurbit Coccinia grandis collected in central Sudan in 2012 (Desbiez et al., 2016). Small RNAs of 21-24 nt were sequenced by Illumina HiSeq. The fragments were assembled into two contigs of 573 nt and 8747 nt, and a gap between them was filled using Sanger sequencing after RT-PCR amplification. The complete or near-complete genome sequence of Coccinia mottle virus isolate Su12-25 was 9767 nt (KU935732). Its genomic organization was similar to that of ipomoviruses cucumber vein yellowing virus (CVYV) and squash vein yellowing virus (SqVYV), with a deduced polyprotein of 3145 aa containing P1a, P1b and P3N-PIPO. Nucleotide sequence identity was 68 % with CVYV, 59-60 % with SqVYV and other ipomoviruses cassava brown streak virus and Ugandan cassava brown streak virus (Fig 1), and less than 50 % with viruses of other genera within the Potyviridae. Preliminary biological and epidemiological studies indicate that CocMoV has a narrow natural host range within the cucurbits, and a low prevalence. CocMoV isolate Su12-25 was transmitted by the Mediterranean biotype of Bemisia tabaci but not by the aphid Myzus persicae. *Coccinia mottle virus* is proposed as a new member of *Ipomovirus*.

**Figure 1** Estimated phylogeny of deduced polyprotein sequences of completely sequenced representative viruses of ratified species within family *Potyviridae*, genera *Brambyvirus, Bymovirus, Ipomovirus, Macluravirus, Poacevirus, Potyvirus, Rymovirus, Tritimovirus*, and two proposed new genera, Roymovirus and Bevemovirus (shown in red font, see separate proposal), were used. Ten proposed new virus species, including eight species in genus *Potyvirus*, one species in genus *Ipomovirus* and one species in proposed new genus Bevemovirus, are indicated by a red dot. The tree was deduced in Mega v7.0.21 after alignment in Muscle using the Neighbor-joining method with 1000 bootstrap replications. Bootstrap support for branches is shown at the junctions of branches where it was >60%. Evolutionary distances were calculated using the Poisson correction method and branch lengths are proportional to genetic distance in units of amino acid substitutions per site.

Accession codes corresponding to the nucleotide sequence of each virus genome sequence used in the tree are: Agropyron mosaic virus, AY623626; Algerian watermelon mosaic virus, EU410442; Apium virus Y, HM363516; Arracacha mottle virus, DQ925486; artichoke latent virus, KP405232; Asparagus virus 1, KJ830760; banana bract mosaic virus, HM131454; Barbacena virus Y, KU685505; barley mild mosaic virus (RNA1), D83408; Basella rugose mosaic virus, DQ821939; bean common mosaic necrosis virus, U19287; bean common mosaic virus, U19287; bean yellow mosaic virus, D83749; beet mosaic virus, AY206394; bellflower veinal mottle virus, KY491536; Bidens mosaic virus, KF649336; Bidens mottle virus, AF538686; blackberry virus Y, AY994084; blue squill virus A, JQ807999; broad-leafed dock virus A, KU053507; brome streak mosaic virus, Z48506; Brugmansia mosaic virus, JX867236; Brugmansia suaveolens mottle virus, AB551370; Caladenia virus A, JX156425; Calla lily latent virus, EF105297; Callistephus mottle virus, KX013584; Canna yellow streak virus, GQ421689; carrot thin leaf virus, JX156434; Catharanthus mosaic virus, KP742991; cassava brown streak virus, FN434437; celery mosaic virus, HQ676607; chilli ringspot virus, JQ234922; chilli veinal mottle virus, GQ981316; Chinese yam necrotic mosaic virus, AB710145; clover yellow vein virus, AB011819; Coccinia mottle virus, KU935732; cocksfoot streak virus, AF499738; Colombian datura virus; JQ801448; cowpea aphid-borne mosaic virus, KM655833; cucumber vein yellowing virus, AY578085; Cyrtanthus elatus virus A, JQ723475.; Daphne mosaic virus, DQ299908; Daphne virus Y, KU556609; dasheen mosaic virus, AB219545; donkey orchid virus A, JX156422; East Asian Passiflora virus, AB246773; Freesia mosaic virus, FM206346; Fritillary virus Y, AM039800; Gloriosa stripe mosaic virus, EF427894; Habenaria mosaic virus, EF427894; Hardenbergia mosaic virus, HQ161081; Hippeastrum mosaic virus, JQ395040; Hordeum mosaic virus, AY623627; Impatiens flower break virus, KU981084; Japanese yam mosaic virus, AB027007; Jasmine virus T, KT222674; Johnsongrass mosaic virus, Z26920; Keunjorong mosaic virus, JF838187; Konjac mosaic virus, AB219545; leek yellow stripe virus, KP258216; lettuce Italian necrotic virus; KP769852; lettuce mosaic virus, KF268954; lily mottle virus, AB570195; Lupinus mosaic virus, EU847625; maize dwarf mosaic virus, AM110758; Moroccan watermelon mosaic virus, EF579955.; Narcissus degeneration virus, AM182028; Narcissus late season yellows virus, KC691259; Narcissus yellow stripe virus, KC691259; oat mosaic virus (RNA1), AJ306718; oat necrotic mottle virus, AY377938; onion yellow dwarf virus, KJ451436; Ornithogalum mosaic virus, JQ807995; Panax virus Y, GQ916624; papaya leaf distortion mosaic virus, AB088221; papaya ringspot virus, KC345607; passion fruit woodiness virus, HQ122652; pea seed-borne mosaic virus, AJ252242; peanut mottle virus, AF023848; pecan mosaic-associated virus, KT633868; Pennisetum mosaic virus, AY642590; pepper severe mosaic virus, AM181350; pepper veinal mottle virus, DQ645484; pepper yellow mosaic virus, AB541985; Peru tomato mosaic virus, AJ437280; plum pox virus, AY953267; pokeweed mosaic virus, JQ609095; potato virus A, Z21670; potato virus V, KP849483; potato virus Y, U09509; rose yellow mosaic virus, JF280796; ryegrass mosaic virus, Y09854; scallion mosaic virus, AJ316084; shallot yellow stripe virus, AJ865076; sorghum mosaic virus, U57358; soybean mosaic virus, S42280; squash vein yellowing virus, EU259611; sugarcane mosaic virus, GU474635; sugarcane streak mosaic virus, GQ388116; sunflower chlorotic mottle virus, GU181199; sunflower mild mosaic virus, JQ350738; sunflower ring blotch virus, KX856009; sweet potato feathery mottle virus, AB439206; sweet potato latent virus, KC443039; sweet potato mild mottle virus, Z73124; sweet potato virus 2, JN613807; sweet potato virus C; GU207957; sweet potato virus G, JQ824374; tamarillo leaf malformation virus, KM523548.; Telosma mosaic virus, DQ851493; Thunberg fritillary mosaic virus, AJ851866; tobacco etch virus, DQ986288; tobacco mosqueado virus, KT834407; tobacco vein banding mosaic virus, EF219408; tobacco vein mottling virus, U38621; tomato necrotic stunt virus, JQ314463; Triticum mosaic virus, FJ669487; turnip mosaic virus, AF169561; Vanilla distortion mosaic virus, KF906523; Verbena virus Y, EU564817; wheat yellow mosaic virus (RNA1), FJ361765; wild onion symptomless virus, LC159494; wild potato mosaic virus, AJ437279; wild tomato mosaic virus, DQ851495; Wisteria vein mosaic virus, AY656816; yambean mosaic virus, JN190431; yam chlorotic mosaic virus, KT724961; yam mild mosaic virus, JX470965; yam mosaic virus, U42596; Zantedeschia mild mosaic virus, AY626825; Zea mosaic virus, JQ692088; zucchini shoestring virus, KU355553; zucchini tigre mosaic virus, KC345607; zucchini yellow mosaic virus, L31350.

