This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

| | | |
|---|---|---|
| **Code assigned:** | ***2014.009aP*** | (to be completed by ICTV officers) |

**Short title:** Create 12 species in the genus *Potyvirus*, family *Potyviridae*
(e.g. 6 new species in the genus *Zetavirus*)

| **Modules attached** (modules 1 and 9 are required) | | | | | |
|---|---|---|---|---|---|
| | **1** ☒ | **2** ☒ | **3** ☐ | **4** ☐ | **5** ☐ |
| | **6** ☐ | **7** ☐ | **8** ☐ | **9** ☒ | |

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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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses) | Potyviridae |

**ICTV-EC or Study Group comments and response of the proposer:**

*EC comments:* Suggest remove accent from tigré. Clarify the basis of the phylogenetic tree.

*Response:* Done.

*Study Group comment re: recent change in the proposed name of one species (Dec 16/2014)*
After receiving advice that the botanical name *Vallota speciosa* had been superseded by the name *Cyrtanthus elatus*, and that the naming conventions of the ICTV prohibited Vallota speciosa virus as an official name, the Potyvirus Study Group voted unanimously to rename the virus Cyrtanthus elatus virus A, thus recognizing the current scientific name of the host, and addressing the virus naming conventions of the ICTV.

| | |
|---|---|
| Date first submitted to ICTV: | June 2014 |
| Date of this revision (if different to above): | August 2014 |

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

| Code | ***2014.009aP*** | (assigned by ICTV officers) |
|---|---|---|

**To create 12 new species within:**

| | |
|---|---|
| Genus: | ***Potyvirus*** |
| Subfamily: | |
| Family: | ***Potyviridae*** |
| Order: | |

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

| **Name of new species:** | **Representative isolate:** | **GenBank sequence accession number(s)** |
|---|---|---|
| *Bidens mosaic virus* | SP01 | KF649336 |
| *Blue squill virus A* | Wanneroo | JN416599 |
| *Brugmansia mosaic virus* | D-437 | JX874139 |
| *Calla lily latent virus* | M19 | EF105297 |
| *Habenaria mosaic virus* | Ha-1 | AB818538 |
| *Keunjorong mosaic virus* | Cheongwon | JF838187 |
| *Lupinus mosaic virus* | LU2 | EU847625 |
| *Panax virus Y* | WS2 | GQ916624 |
| *Tomato necrotic stunt virus* | MX9354 | JQ314463 |
| *Cyrtanthus elatus virus A* | Marijiniup7 | JQ723475 |
| *Verbena virus Y* | Michigan | EU564817 |
| *Zucchini tigre mosaic virus* | Q10 | KC345605 |

**Reasons to justify the creation and assignment of the new species:**

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The family *Potyviridae* consists of plant viruses with a single stranded, positive sense RNA genome and flexuous, filamentous particles. Genomes have a VPg covalently linked to the 5'-end and the 3'-terminus is polyadenylated. Genomes encode a large polyprotein that is self-cleaved into a set of functional proteins that is strongly conserved throughout the family. The genus *Potyvirus* is easily the largest in the family and has economically important members in all parts of the world. They are transmitted by aphids in a non-persistent manner. The genome is monopartite and the polyprotein is cleaved into 10 products. Each of these proteins has at least some strongly conserved motifs and the cleavage sites also have distinctive patterns. An additional small ORF named PIPO has also been identified which is expressed with the N-terminal part of the P3 protein by ribosomal frameshift.

According to criteria published in the ICTV 9th Report (Adams et al., 2011), species are distinguished by the following criteria:

- Genome sequence relatedness: different species have CP aa sequence identity less than ca. 80%; and nt sequence identity less than 76% either in the CP or over the whole genome. There are also differences in polyprotein cleavage sites.
- Host range and key host reactions; lack of cross protection.
- Different inclusion body morphology.
- Antigenic properties: serological relatedness may help in distinguishing species.

Polyproteins of viruses in the same genus have >40% aa identity (Adams et al., 2005).

The 12 viruses all appear to represent new species in the genus. For each, there is at least one complete genome sequence in the public domain and this shows the expected ORFs, conserved motifs and cleavage sites. The molecular criteria to create new species have been satisfied and there are peer-reviewed publications giving the provenance of the virus(es) and in many cases additional biological data. Phylogenetic analysis of the complete polyprotein coding sequence (Annex Figure 1) also supports the placement of these viruses within the genus and as distinct species.

**Bidens mosaic virus**

Bidens mosaic virus (BiMV), a virus first reported from Brazil in 1961, and sunflower chlorotic mottle virus (SCMoV) were both considered strains of the species *Potato virus Y* for a while based on the analysis of coat protein sequences (see Inoue-Nagata et al., 2006). Sunflower chlorotic mottle virus was recognised as a distinct species in 2012 (proposal 2010.020aP) following publication of its complete genome sequence (Bejerman et al., 2010) and BiMV was then considered a strain of SCMoV as its coat protein (the only part of the genome then sequenced) had about 85% aa identity to SCMoV. The complete sequence of an isolate (SP01) of bidens mosaic virus has recently been determined (KF649336; Sanches et al., 2014) and this, too, seems to be a distinct species when the entire genome is considered. Isolate SP01 was obtained from symptomatic plants of *Bidens pilosa* L., and sap transmitted to various plants. Plants that subsequently became infected included *Chenopodium quinoa, C. amaranticolor, Helianthus annus, Pisum sativum* and various species of *Nicotiana*. Total RNA was extracted from infected *Chenopodium quinoa* leaves and the genome amplified by RT-PCR for sequencing, using universal primers for members of the family *Potyviridae* to amplify conserved regions and specific primers derived from the sequences obtained to amplify the gaps between. The 5'-end of the genome was determined by RACE. Primers designed from the sequence were used to verify the presence of BiMV in the other infected plant species. The complete genome consisted of 9557 nt encoding a predicted polyprotein of 348 kDa in which the typical potyvirus motifs and cleavage sites could be recognised. BiMV-SP01 was most closely related to SCMoV (73% nt and 76% aa identity over the entire polyprotein) and, as expected was also related to other members of the PVY group. The genetic differences and some differences in host range support the designation of *Bidens mosaic virus* as a species distinct from *Sunflower chlorotic mottle virus*.

**Blue squill virus A**

Wylie et al (2012) used deep sequencing to examine a number of Australian wild plants for viruses. A sequence of 9433 nt assembled from a plant of *Chamaescilla corymbosa* (R. Br.) Benth., (blue squill) appeared to represent about 96% of the genome of a potyvirus (blue squill virus A; BSVA) with about 72% nt (77% aa) identity over the entire sequence to Hardenbergia mosaic virus (HarMV) and slightly less to passion fruit woodiness virus. The

coat proteins of BSVA and HarMV have about 80% aa identity. This isolate (KP1) was deposited in GenBank with accession number JN052072. The sequence lacks the 5'-terminus but otherwise has all the features of a potyvirus. Primers designed from this sequence were used to amplify substantial parts of a similar sequence (c. 90% nt identity after Sanger sequencing) from a second site (Wanneroo; accession JN416599). Subsequently, a further isolate of BSVA was discovered by deep sequencing of RNA from a wild plant of the orchid *Diurus corymbosa*. This isolate (SW3.1) is complete and has 87% nt (95% aa) identity over the entire genome to isolate KP1. BSVA was also detected in another plant in the same population using an RT-PCR-based assay with specific primer. These data provide convincing proof of the existence of a virus in both *C. corymbosa* and *D. corymbosa* that should be classified in a new species.

**Brugmansia mosaic virus**

A suspected virus disease was identified from an arborescent *Brugmansia x candida* Pers. (syn. *Datura candida* Pers.) tree growing in Colombia. The causal agent was aphid transmissible at low rates. In mechanical transmission tests, the virus had an extensive host range causing systemic infections in plants belonging to four different families and nine genera, with the preponderance belonging to the Solanaceae. Viral particles were purified from infected tobacco tissue, and purified virions were inoculated into healthy tobacco plants to recreate the symptoms. The virions had a mean length of 720-729 nm, and infected cells contained inclusion bodies typical of potyvirus infections. Analysis of infected tissues and purified virions with a panel of potyvirus-specific antibodies confirmed identification as a potyvirus which was named Brugmanisa mosaic virus (BruMV). The sequence of isolate D-437 RNA was determined using a combination of RT-PCR and next-generation sequencing. De novo assembly of 454 sequences generated two scaffolds that covered approximately 8 kb of virus sequence as assessed by TblastN searches against a plant virus database. PCR primers were designed from these contigs to verify the sequence and fill in the remaining gaps. The results revealed that the viral RNA is 9761 nucleotides in length (GenBank accession number JX874139) with a genome organization typical of potyviruses. D-437 has the greatest nucleotide sequence identity to pepper mottle virus (PepMoV), at 72 % over the whole genome. Their coat proteins have 76% aa identity.

A South Korean (SK) isolate of BruMV has also been reported from *B. suaveolens.* Its complete sequence, mostly determined from sequencing of RT-PCR products, is 9781 nucleotides in length (accession number JX867236) and it shares complete nucleotide and polyprotein amino acid sequence identities of 85.6 % and 93.1 %, respectively, with isolate D-437.

**Calla lily latent virus**

Chen et al., (2004; 2006) reported the isolation of a virus from calla lilies (*Zantedeschia* spp.) in Taiwan. Isolate M19 is capable of inducing local lesions on *Chenopodium quinoa*. Typical potyvirus-like flexuous particles were consistently detected in infected plants, and a 1.3-kb DNA fragment was amplified from these plants by reverse-transcription polymerase chain reaction (RT-PCR) using potyvirus degenerate primers. The PCR product was cloned and its sequence analyzed (AF469171). This partial sequence suggested that the virus represented a new species in the Bean common mosaic virus (BCMV) group. After expressing the CP by the vector pET28b and purification from *E. coli* culture, polyclonal antibodies were prepared in rabbits and used to detect the virus in calla lilies. It did not react with at least five calla lily infecting potyviruses, including *Dasheen mosaic virus, Bean yellow mosaic virus, Konjak mosaic virus, Turnip mosaic virus,* and *Zantedeschia mild mosaic virus*. Indirect ELISA and

SDS-immunodiffusion tests showed that M19 was serologically related, but distinct from members of the BCMV group of potyviruses. The virus was frequently detected in calla lily plants collected from several major calla lily production townships in Taiwan. Among 86 field samples positively reacting to the antibody, 77 of them exhibited evident systemic mosaic symptoms, but these symptomatic plants were confirmed to be infected simultaneously by other viruses. Nine plants were found to be infected by the new virus alone. These plants were confirmed to have remained symptomless throughout a 6-month observation period. The name calla lily latent virus (CLLV) was therefore proposed. Subsequently, three complete sequences from Taiwan have been made available, including one of the original isolate M19 (EF105297). This confirms that CLLV is a member of the BCMV subgroup most closely related to Watermelon mosaic virus (WMV) and Soybean mosaic virus (respectively 74% and 71% nt identity over the entire genome). The coat proteins of CLLV and WMV have 82% aa identity, slightly above the normal threshold for species demarcation but the differences in the rest of the genome are more than sufficient to justify the creation of a new species.

**Habenaria mosaic virus**

Habenaria mosaic virus (HaMV) has been reported from *Habenara radiata* plants (Orchidaceae) in Japan (Inouye et al., 1998). The virus causes mosaic symptoms and is sap-transmissible to some experimental plant species, but *H. radiata* is currently the only known systemic host. The virus has long been believed to be a potyvirus because of its filamentous particle length of ca. 750 nm, non-persistent mode of transmission by aphids, and formation of typical cylindrical inclusions in infected cells. Furthermore, HaMV shows distant serological relationships to several potyviruses, including WMV, and was thus suspected to be a new potyvirus. The complete sequence of isolate Ha-1 has now been determined (Kondo et al., 2014; accession number AB818538). This isolate had been isolated by single lesion transfer using the experimental host, *Chenopodium quinoa*. The virus was purified from mechanically inoculated leaves of *C. quinoa*, and RNA extracted from purified particles was used for sequencing using an RT-PCR approach. The virus has all the expected characteristics of a member of the genus *Potyvirus* and its genome is 55-59 % identical at the nt sequence level to Chilli veinal mottle virus and its related viruses. Corresponding coat protein aa identities are less than 70%.

**Keunjorong mosaic virus**

In 2008, a novel potyvirus was found infecting keunjorong [*Cynanchum wilfordii* (Maxim.) Hemsley], which is traditionally used for medicinal purposes in Asia, and was tentatively designated keunjorong mosaic virus (KjMV) (Lee et al., 2010). Several herbaceous hosts were mechanically inoculated with extracts from diseased Keunjorong plants collected in Cheongwon, Korea, but only *Chenopodium quinoa* developed symptoms (chlorotic local lesions on the inoculated leaves and systemic chlorotic spots on upper leaves). The virus was then maintained and propagated in *C. quinoa*, which was used as a virus source for purification. Viral RNA was extracted from the purified viral particles and RT-PCR was used to amplify sections of the genome for sequencing with ten primer pairs designed for potyvirus sequence amplification. The 5'-terminus was determined by RACE. The complete KjMV genomic RNA (accession JF838187) was found to be 9,611 nt in size with an organization typical of potyviruses. The highest complete genome sequence identity with other potyviruses (57.5 %) was with peanut mottle virus (PeMoV) and freesia mosaic virus. The coat proteins of KjMV and PeMoV have 68% aa identity.

**Lupinus mosaic virus**

This virus was first discovered in 2009 in samples of garden lupin (*Lupinus polyphyllus*) in the south of the Czech Republic showing mild mosaic symptoms and interveinal yellowing (Sarkisova & Petrzik, 2009). Filamentous virus particles of 690 nm in length were visible under the electron microscope and first results, including a coat protein sequence, suggested the presence of a new potyvirus, which was named lupine mosaic virus (LuMV). The virus was maintained in a glasshouse by mechanical inoculation to *Nicotiana benthamiana*, *Chenopodium quinoa* and *L. polyphyllus* plants. RNA was isolated from infected leaves of *L. polyphyllus* with mild mosaic symptoms and RT-PCR was used to amplify sections of the genome for sequencing using specific and degenerate potyvirid primers. The 5'-terminus was determined by RACE. The complete genomic RNA of this isolate (LU2) was found to be 9,611 nt in size with an organization typical of potyviruses. The complete sequence (EU847625; Sarkisova & Petrzik, 2011) has 10,113 nt and comparisons of its polyprotein sequence show that it is quite distant from other viruses in the genus. The most closely related viruses are plum pox virus (PPV) and scallion mosaic virus with respective amino acid identities of 54 and 52% over the entire polyprotein. The coat proteins of LuMV and PPV have 64% aa identity. Although the virus name 'lupine mosaic virus' is used in the publication and in the GenBank accession, a 'lupine' virus could be derived from a wolf and we therefore propose to use the unambiguous 'Lupinus' (the genus name of the host plant) in the official species name.

**Panax virus Y**

A probable potyvirus consistently associated with leaf distortion and mosaic symptoms in the perennial Chinese medicinal plant sanqi (*Panax notoginseng* (Burk.) F. H. Chen) was first identified by electron microscopy and by its weak reaction to potyvirus-specific antibodies in ELISA. dsRNA was extracted from symptomatic plants and fragments were amplified by RT-PCR using random and oligo-DT primers. Primers designed from these sequence and degenerate potyvirus-specific primers were then used to amplify larger sections of the genome for sequencing. The genome extremities were determined by RACE. The complete nucleotide sequence of isolate WS2 (GQ916624) was composed of 9,750 nt and was predicted to encode a polyprotein of 351.5 kDa (Yan et al., 2010). The name Panax virus Y (PanVY) was proposed. Comparisons with other fully-sequenced potyviruses indicated that it was most closely related to plum pox virus (PPV) with 56.3% nt and 53.3% aa identity over the entire genome/polyprotein. The coat proteins of PanVY and PPV have 50% aa identity. Analysis by the Study Group indicates that the virus is a little more closely related to Celery mosaic virus and Apium virus Y (about 63% nt identity to both over the entire genome), a relationship supported by the phylogenetic analysis. Nevertheless, the genetic distances from all currently accepted species still comfortably exceed the expected threshold for species discrimination.

**Tomato necrotic stunt virus**

Deep sequencing of siRNAs from a Mexican sample of tomato led to the discovery of a putative new potyvirus, named tomato necrotic stunt virus (ToNSV). Two contigs covering most of the typical potyvirus genome were obtained. The virus was transmissible by mechanical inoculation, inducing plant stunting, necrosis, and leaf and fruit deformation symptoms on the inoculated tomato plants. It causes serious damage in some Mexican tomato crop production systems. To obtain a complete virus genome and to validate the authenticity of this novel virus, overlapping RT-PCR products were produced using primers derived from the two contigs. In general, the sequences obtained from Sanger sequencing were in agreement with those generated from the siRNA assembly, with only three nucleotide differences. After completion of the terminal sequencing, the final complete and validated virus genome for the newly identified virus (isolate MX9354) was determined to comprise 10,057 nt (GenBank

Accession No. JQ314463; Li et al., 2012). ToNSV has less than 60% nucleotide sequence identity over the whole genome to other known potyviruses and appears to be a distant member of the potato virus Y group. The coat proteins of ToNSV and PVY have 67% aa sequence identity.

A second Mexican isolate (MX5) has since also been sequenced (accession JX846918; Li et al., 2014). It was almost identical to isolate MX9354 and was shown to induce stunting and chlorotic to necrotic leaf symptoms on tomato plants. In host-range assays, the virus systemically infected many species in the family *Solanaceae* and locally infected some species in the families *Amaranthaceae*, *Brassicaceae* and *Cucurbitaceae*. A sensitive and reliable real-time RT-PCR assay was developed using crude tissue extract.

**Cyrtanthus elatus virus A**

A potyvirus infecting some Narcissus plants in Australia was first identified by Wylie et al., 2010 on the basis of 3'-terminal sequences of 3 isolates (GU812282-4) obtained using conserved potyvirus primers. The coat protein sequences were similar to one another and to some coat protein sequences of a virus named Vallota speciosa virus (ValSV) obtained from the UK (FJ032248) and New Zealand (DQ417604), which had previously been deposited in GenBank (but without any peer-reviewed publications). The complete sequence of a further isolate (Marijiniup7, accession number JQ723475) was subsequently obtained from a different sample by Illumina sequencing (Wylie & Jones, 2012). Its coat protein sequence was 99% identical to those of the partially-sequenced isolates obtained earlier. The most closely related current species was *Narcissus degeneration virus* with 65% nt and 63% aa identity over the entire genome/polyprotein (73% aa identity in the coat protein).

After receiving advice that the botanical name *Vallota speciosa* had been superseded by the name *Cyrtanthus elatus*, and that the naming conventions of the ICTV prohibited Vallota speciosa virus as an official name, the Poytvirus Study Group voted unanimously to rename the virus Cyrtanthus elatus virus A, thus recognizing the current scientific name of the host, and addressing the virus naming conventions of the ICTV.

**Verbena virus Y**

Specimens of the ornamental plant Verbena with mottling symptoms were examined by Kraus et al., and shown to contain a mixture of three viruses. Virus purification failed to separate the different viruses but by shotgun cloning two of the viruses were identified as Broad bean wilt virus 1 (genus *Fabavirus*) and coleus vein necrosis virus (genus *Carlavirus*) (Kraus et al., 2008). The third virus appeared to be a previously undescribed potyvirus, named Verbena virus Y (VVY). A combination of shotgun cloning, RT-PCR, and RACE was then used to obtain the complete genome of VVY from the purified virus mixture (Kraus et al., 2010). The virus genome (accession number EU564817) is 9,742 nt long and is most similar to isolates of *Potato virus Y* and *Pepper mottle virus*, sharing 63% nucleotide identity over the length of the genomes and 80% aa identity in the coat protein. The virus was transmitted experimentally by mechanical inoculation and sometimes by aphids to several other solanaceous plants (infection confirmed by RT-PCR with specific primers and by sequencing of the products).

**Zucchini tigre mosaic virus**

Papaya ringspot virus (PRSV) is a very important pathogen of papaya and curcubits wherever they are cultivated. Two major groups of isolates are distinguished. Type P isolates infect papaya and cucurbits while PRSV-W isolates only infect cucurbits (W is for watermelon). In

1982, virus-like symptoms different from those of PRSV-W were observed in zucchini squash (*Cucurbita pepo* L) fields in Guadeloupe (French West Indies) and a potyvirus serologically distinct from known cucurbit-infecting ones was found to be the aetiological agent . From its biological properties and serological studies, this virus was designated as PRSV-T, T referring to the main symptom, a leaf discoloration resembling a tiger stripe pattern (tigré in French) in zucchini squash (Quiot-Douine et al., 1986). PRSV-T isolates were reported from several parts of the world and serological studies showed that the types W and P were more related to each other than to PRSV-T. Molecular and biological characterization of several PRSV isolates was then used to resolve the status of PRSV-T. The full-length nucleotide sequence of PRSV-W isolate E2 and PRSV-T isolates Q10 from Guadeloupe (Caribbean), VET-026 from Venezuela (South America), Re01-25 from Réunion Island (Indian Ocean) and E11-045 (France) were obtained using potyvirus-wide or specific primers (accessions numbers: KC345609, KC345605, KC345606, KC345607 and KC345608, respectively; Romay et al., 2014). PRSV-W isolate E2 shared 83- 98% nt identity with sequenced PRSV-W and PRSV-P isolates but the PRSV-T isolates had only 69-71% nt identity over the entire genome with isolates of PRSV (78% aa identity in the coat protein), which was the most closely related virus. Other members of the PRSV cluster, Algerian watermelon mosaic virus and Moroccan watermelon mosaic virus, had 61- 62% nt identity with PRSV-T isolates, which had 83-89% nt identity amongst themselves. These data support the establishment of a new species in the PRSV cluster to accommodate the PRSV-T isolates and the name *Zucchini tigre mosaic virus* is proposed. The different viruses can also be distinguished by their symptoms on various cucurbit hosts.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

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additional material in support of this proposal

**References:**


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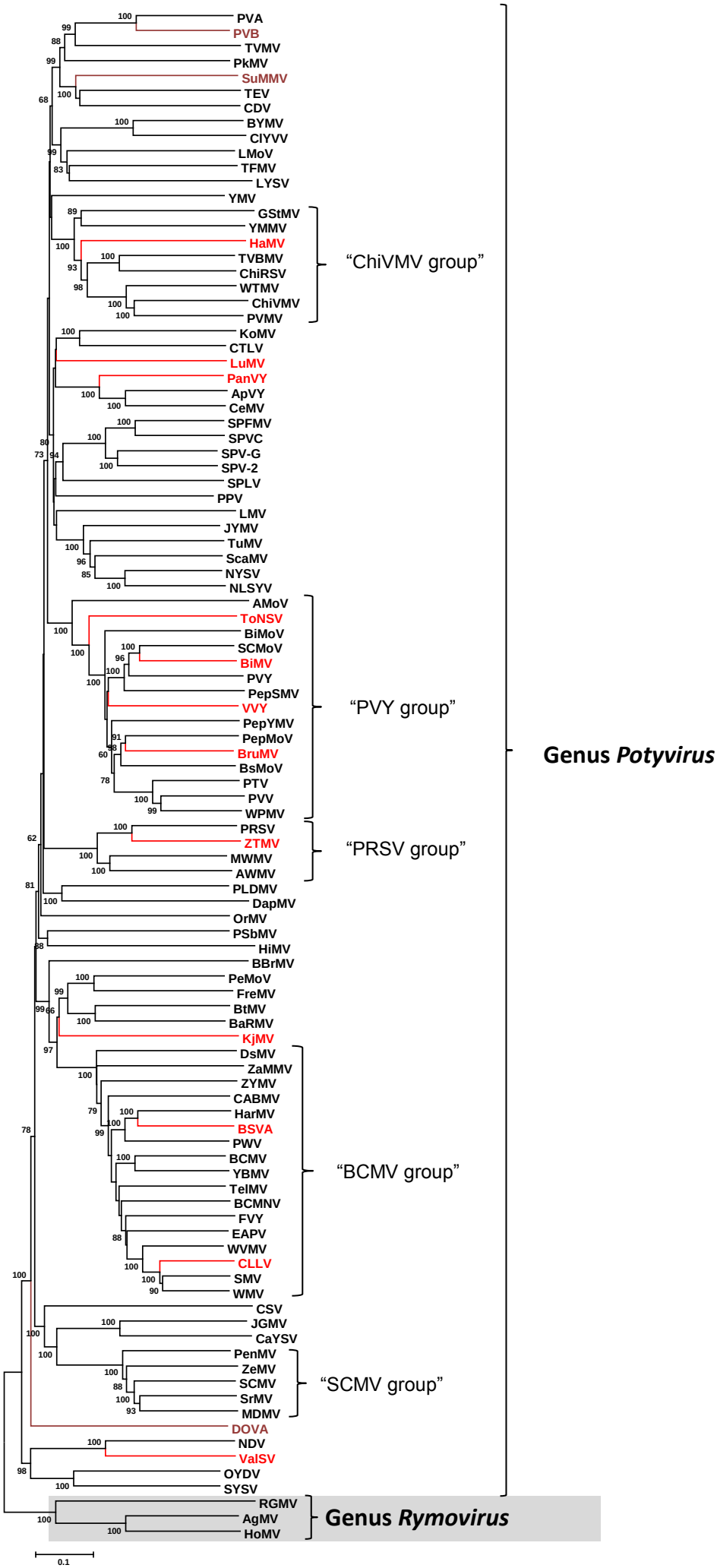
Zhao F, Lim S, Yoo RH, Lim HS, Kwon SY, Lee SH, Moon JS (2013). Complete genome sequence of a South Korean isolate of Brugmansia mosaic virus. Arch. Virol. 158(9):2019-2022


**Annex:**

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Figure 1: Distance (Maximum composite likelihood) phylogenetic tree using the codon-aligned complete polyprotein nucleotide sequences of fully sequenced members of the genera *Rymovirus* and *Potyvirus*. Each branch in black represents a single isolate of an approved species, the branches in red represent the species proposed here and the currently unclassified viruses DOVA, PVB and SuMMV are in brown. Tree produced in MEGA5.10 with 10,000 bootstrap replicates. Values at the branches give % bootstrap support (where >60%). Abbreviations are: AgMV, Agropyron mosaic virus; AMoV, Arracacha mottle virus; ApVY, Apium virus Y; AWMV, Algerian watermelon mosaic virus; BaRMV, Basella rugose mosaic virus; BBrMV, Banana bract mosaic virus; BCMNV, Bean common mosaic necrosis virus; BCMV, Bean common mosaic virus; BiMoV, Bidens mottle virus; BiMV, Bidens mosaic virus; BruMV, Brugmansia mosaic virus; BsMoV, Brugmansia suaveolens mottle virus; BSVA, Blue squill virus A; BtMV, Beet mosaic virus; BYMV, Bean yellow mosaic virus; CABMV, Cowpea aphid-borne mosaic virus; CaYSV, Canna yellow streak virus; CDV, Colombian datura virus; CeMV, Celery mosaic virus; ChiRSV, Chilli ringspot virus; ChiVMV, Chilli veinal mottle virus; CLLV, Calla lily latent virus; ClYVV, Clover yellow vein virus; CSV, Cocksfoot streak virus; CTLV, Carrot thin leaf virus; DapMV, Daphne mosaic virus; DOVA, Donkey orchid virus A; DsMV, Dasheen mosaic virus; EAPV, East Asian passiflora virus; FreMV, Freesia mosaic virus; FVY, Fritillary virus Y; GStMV, Gloriosa stripe mosaic virus; HaMV, Habenaria mosaic virus; HarMV, Hardenbergia mosaic virus; HiMV, Hippeastrum mosaic virus; HoMV, Hordeum mosaic virus; JGMV, Johnsongrass mosaic virus; JYMV, Japanese yam mosaic virus; KjMV, Keunjorong mosaic virus; KoMV, Konjac mosaic virus; LMoV, Lily mottle virus; LMV, Lettuce mosaic virus; LuMV, Lupinus mosaic virus; LYSV, Leek yellow stripe virus; MDMV, Maize dwarf mosaic virus; MWMV, Moroccan watermelon mosaic virus; NDV, Narcissus degeneration virus; NLSYV, Narcissus late season yellows virus; NYSV, Narcissus yellow stripe virus; OrMV, Ornithogalum mosaic virus; OYDV, Onion yellow dwarf virus; PanVY, Panax virus Y; PeMoV, Peanut mottle virus; PenMV, Pennisetum mosaic virus; PepMoV, Pepper mottle virus; PepSMV, Pepper severe mosaic virus; PepYMV, Pepper yellow mosaic virus; PkMV, Pokeweed mosaic virus; PLDMV, Papaya leaf distortion mosaic virus; PPV, Plum pox virus; PRSV, Papaya ringspot virus; PSbMV, Pea seed-borne mosaic virus; PTV, Peru tomato mosaic virus; PVA, Potato virus A; PVB, Potato virus B; PVMV, Pepper veinal mottle virus; PVV, Potato virus V; PVY, Potato virus Y; PWV, Passion fruit woodiness virus; RGMV, Ryegrass mosaic virus; ScaMV, Scallion mosaic virus; SCMoV, Sunflower chlorotic mottle virus; SCMV, Sugarcane mosaic virus; SMV, Soybean mosaic virus; SPFMV, Sweet potato feathery mottle virus; SPLV, Sweet potato latent virus; SPV-2, Sweet potato virus 2; SPVC, Sweet potato virus C; SPVG, Sweet potato virus G; SrMV, Sorghum mosaic virus; SuMMV, Sunflower mild mosaic virus; SYSV, Shallot yellow stripe virus; TelMV, Telosma mosaic virus; TEV, Tobacco etch virus; TFMV, Thunberg fritillary mosaic virus; TNSV, Tomato necrotic stunt virus; TuMV, Turnip mosaic virus; TVBMV, Tobacco vein banding mosaic virus; TVMV, Tobacco vein mottling virus; ValSV, Vallota speciosa virus; VVY, Verbena virus Y; WMV, Watermelon mosaic virus; WPMV, Wild potato mosaic virus; WTMV, Wild tomato mosaic virus; WVMV, Wisteria vein mosaic virus; YBMV, Yambean mosaic virus; YMMV, Yam mild mosaic virus; YMV, Yam mosaic virus; ZaMMV, Zantedeschia mild mosaic virus; ZeMV, Zea mosaic virus; ZTMV, Zucchini tigré mosaic virus; ZYMV, Zucchini yellow mosaic virus.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