This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

For guidance, see the notes written in blue, below, and the help notes in file Taxonomic\_Proposals\_Help\_2018.

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

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| **Code assigned:** | ***2018.026P*** | (to be completed by ICTV officers) |
| **Short title:** Seven new species in genus *Potyvirus* |
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| **Author(s):** |
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|  |  |
| --- | --- |
| Wylie, Stephen (SG Chair) | s.wylie@murdoch.edu.au |
| Kreuze, Jan F. | j.kreuze@cgiar.org |
| Lopez-Moya, Juan Jose | juanjose.lopez@cragenomica.es |
| Makinen, Kristiina | kristiina.makinen@helsinki.fi |
| Inoue-Nagata, Alice Kazuko | alice.nagata@embrapa.br |
| Ohshima, Kazusato | ohshimak@cc.saga-u.ac.jp |
| Wang, Aiming | aiming.wang@agr.gc.ca |

 |
| **Corresponding author with e-mail address:** |
|

|  |  |
| --- | --- |
| Wylie, Stephen | s.wylie@murdoch.edu.au |

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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:** |
|       |
|  |
| Date first submitted to ICTV: | May 1st, 2018 |
| Date of this revision (if different to above): |       |

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

**Part 2:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

| **Text of proposal:** |
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|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2018.026P.N.v1.Potyvirus\_7sp.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2017\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| 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.
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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 precursor polyprotein (except in the case of genus *Bymovirus*, which is bipartite and encodes two polyproteins) that is self-cleaved into a set of functional proteins that is strongly conserved throughout the family.

Species demarcation criteria for the Potyviridae:

• Genome sequence relatedness: different species have coat protein amino acid pairwise identity less than about 80%, or the complete ORF of less than about 82%. The nucleotide pairwise identity is less than 76% between 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.

The seven viruses described below are proposed to represent new species in the genus *Potyvirus*. 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 of pairwise identity to create new species have been satisfied. Phylogenetic analysis of the complete polyprotein coding sequences (Figure 1) supports the placement of these viruses as distinct species within genus *Potyvirus*.

**Seven proposed new taxa in genus *Potyvirus***

1. **African eggplant mosaic virus**

The complete genomic sequence (MF997470) of a virus isolate tentatively named African eggplant mosaic virus (AEMV isolate 2013-281) (9646 nt) was determined from RNA extracted from African eggplant (*Solanum aethiopicum*), also known as Ethiopian eggplant and bitter tomato, collected from Tanzania in 2012 and 2013. Three naturally infected plants were identified. The authors of the sequence were contacted and they reported testing the AEMV isolate on plants of *Solanum aethiopicum, S. melongena* (eggplant)*, S. lycopersicum* (tomato*), Capsicum annuum* (bell pepper) and *C. chinense* (chili pepper)using *Myzus nicotianae*and manual inoculation*.* Mosaic symptoms and systemic virus infection occurred only on *S. aethiopicum*and *S. lycopersicum*; there was no virus transmission to or reproduction in *S. melongena, C. annuum* and *C. chinense* as confirmed by RT-PCR using virus-specific primers.

The sequence of AEMV 2013-281 was generated using Illumina technology. The deduced amino acid sequence shares closest pairwise identities of 70-75% (71-74% nt identity) with isolates of other Solanaceae-infecting potyviruses pepper veinal mottle virus, chilli veinal mottle virus and wild tomato mosaic virus. A formal description of the virus has not been published.

The *Potyviridae* study group proposes classifying African eggplant mosaic virus as a member of a new, homonymous species within genus *Potyvirus*.

1. **Cucurbit vein banding virus**

A new potyvirus, tentatively named cucurbit vein banding virus (CVBV), was detected in squash (*Cucurbita maxima*) with strong symptoms in San Pedro (Buenos Aires, Argentina) (Perotto *et al*., 2018). By sequencing of RNA preparations from these samples by NGS (Illumina HiSeq 1500 - no mention if samples were pooled), two near-complete potyvirus sequences for isolates 3.1 and 4.1 were assembled (KY657266, KY657267, respectively). They shared ~88% nucleotide (~93% amino acid) identity to each other, while maximum identity of 48% was found with plum pox virus at the amino acid level of the polyprotein. The genomic RNA consisted of 9968 and 9813 nucleotides, respectively, and displayed typical potyvirus organization. Isolation and inoculation of the virus to a cucurbit plant were not done. The name of the virus was defined after finding a field grown plant with a putative single infection with CVBV, while all other plants, including those used for NGS analysis, had mixed infection with other viruses. No vector is described. Two internal primer pairs were designed and field samples were tested. This test demonstrated that the virus was present in other areas of Argentina. Phylogenetic analysis showed the CVBV sequences cluster with other potyvirus sequences.

The *Potyviridae* study group proposes classifying CVBV isolate 3.1 as the type isolate of a new species *Cucurbit vein banding virus* within genus *Potyvirus*.

1. **Mediterranean ruda virus**

A novel potyvirus was isolated from plants of *Ruta montana* (mountain rue) growing in an evergreen oak forest of the Iberian Peninsula, and it was named Mediterranean ruda virus (MeRV) isolate ParP17 (Rodríguez-Nevado et al., 2017). MeRV occurred in 123 of 171 wild mountain rue plants tested. The virus can systemically infect plants of *Capsicum annuum*, *Nicotiana benthamiana*, and *Solanum lycopersicum*. The complete genome of the virus was determined using high-throughput sequencing on an Illumina platform. The genome was 9160 nt in length and has a typical potyvirus organisation. The sequence was assigned GenBank accession MF953305. The percentage of nucleotide identity of the MeRV-ParP17 genome with that of the other potyviruses ranged from 50% to 66%, showing highest identity (65% nt identity) with isolates of bean yellow mosaic virus and clover yellow vein virus.

The *Potyviridae* study group proposes classifying Mediterranean ruda virus as a prototype of a new species within genus *Potyvirus* named *Mediterranean ruda virus*.

1. **Paris mosaic necrosis virus**

This virus, named Paris mosaic necrosis virus (PMNV), was reported from a wild plant of *Paris polyphylla* var. *yunnanensis* in southern China (Lan et al., 2017), which is an herbaceous perennial plant related to lilies. The virus causes mottle, necrotic and mosaic symptoms on leaves. A short cDNA fragment of the virus was initially cloned by RT-PCR using potyvirus group primers followed by DNA sequencing. The complete genome sequence was subsequently obtained by an overlapping amplicon cloning strategy (a total of 8 amplicons with 150-250 nt overlapping regions). The complete genome sequence of PMNV isolate PMNV-cn is 9660 nt excluding the polyA tail (GenBank accession MF509898). It contains one large ORF encoding a polyprotein of 353 kDa, and includes the nine semi-conserved proteolytic cleavage sites typical of potyviruses. A short ORF resulting from transcriptional slippage in the P3 cistron to generate P1-HCpro-P3N-PIPO was also identified, as is typical of the genomic organization of potyviruses. Phylogenetic analyses of the large ORF showed that the virus belongs to the BCMV group within genus *Potyvirus*; its genome shares sequence identity of about 72-73% at the nt level with isolates of soybean mosaic virus and Wisteria vein mosaic virus, and 72-74% at the aa level with isolates of watermelon mosaic virus and soybean mosaic virus and proposed virus saffron latent virus.

Analyses using the CP sequence of PMNV revealed sequence identity of 87% and 91% identity at nt and aa levels, respectively, with the 3’UTR, complete CP and partial NIb sequence of Paris vietnamensis mottle virus (KM609326.1, PVMV). Only 1.7 kb of the genome sequence of PVMV is available. These high identities suggest that PMNV and PVMV are isolates of the same virus. If we accept that PMNV and PVMV are isolates of the same virus, the name Paris vietnamensis mottle virus has priority over Paris mosaic necrosis virus because its partial sequence was published in 2015, three years before that of PVMV. However, a full genome sequence does not support the name Paris vietnamensis mottle virus; it is possible, for instance, that PVMV is a recombinant virus and the unknown upstream part of its genome differs from that of PMNV. Therefore, the *Potyviridae* study group proposes creation of a new species within genus *Potyvirus* named *Paris mosaic necrosis virus* and represented by PMNV-cn.

1. **Saffron latent virus**

A virus infecting saffron (*Croccus sativus*) was found in numerous samples of randomly selected plants surveyed in the 2011-2015 period in Iran (Parizad et al., 2017). Serologically based analysis suggested the presence of a member of the genus *Potyvirus*, and the complete genome sequence of the virus was obtained, consisting in 9693 nts, excluding the poly-A tail (accession number KY562565). Sequence comparisons of the complete genome showed highest nt identities with isolates of East Asian passiflora virus and proposed species Paris mosaic necrosis virus (69%), soybean mosaic virus, bean common necrosis mosaic virus, and Wisteria vein mosaic virus (68%). These values were below the threshold used to discriminate species within the genus, and consequently the virus isolate was considered to represent a new species, tentatively named saffron latent virus isolate Ir-Kh1, with the acronym SaLV. Virus specific primers designed in the CP genomic region were used to verify the high prevalence of the virus in saffron fields in Iran.

The *Potyviridae* study group proposes that SaLV, isolate Ir-Kh1 represents a new species *Saffron latent virus* in the genus *Potyvirus.*

1. **Sudan watermelon mosaic virus**

Sudan watermelon mosaic virus (SuWMV) isolate Su94-54 was collected in 1994 in Eastern Sudan near Gadamballia from a snake cucumber (*Cucumis melo* var. *flexuosus*) showing symptoms of mosaic and leaf deformations (Desbiez et al., 2017). To preserve the infectivity over time, extracts from the dry material were ground in phosphate solution and mechanically inoculated on zucchini at various time periods until the present day. To obtain the complete genome sequence of isolate Su94-54, total RNA was extracted from dried leaf material and NGS was done of 18–30 nt small RNAs. The genome sequence was assembled from short, overlapping reads. It was 10,232 nt in length and assigned GenBank accession KY623505. PASC analyses indicated that nucleotide identity across the complete genome was around 70% with its closest known relative, Moroccan watermelon mosaic virus (MWMV). SuWMV appears to be an interspecific recombinant between wild melon vein banding virus-like viruses and MWMV-like viruses. The virus was transmissible by the aphid *Myzus persicae*. An antiserum was developed against SuWMV and it was used to screen 750 samples collected in Sudan 1992 -1999, and 207 samples collected 2002 - 2012. Of the first period, 17% of samples tested positive for SuWMV, and for the second period only one sample (0.5%) was positive. Partial NIb-CP RT-PCR products were obtained from 40 samples (accessions KY623506-545), and phylogenetic analysis revealed two well-supported molecular clades without obvious relation to the host or the place of sampling.

The *Potyviridae* study group proposes that Sudan watermelon mosaic virus represents a new homonymous species within the genus *Potyvirus*.

1. **Wild melon vein banding virus**

Wild melon vein banding virus (WMVBV) isolate Su03-07 was collected in Tayba Block, Sudan, during a survey of cucurbit species in December 2003 (Desbiez et al., 2017). The wild melon *Cucumis melo* var. agrestis exhibited mild vein banding and mosaic symptoms. The virus induced a rapid top necrosis on cultivated melon (*Cucumis melo*) cv ‘Védrantais’, a mosaic and vein banding in cv. ‘Ouzbèque’, and local lesions and no systemic symptoms in WMR29, a PRSV resistant accession. A survey was done and WMVBV was found only in Sudan and in a rather limited geographic area. It was found mainly in wild hosts, suggesting that this virus is endemic in wild hosts –cucurbits or others, either annual or perennial- and it infects cultivated cucurbits only occasionally. The sequence of the genome was obtained by RT-PCR amplification using generic PRSV-group primers, and internal primers were designed to fill in the gaps. Sequence was obtained using the Sanger method. The genome sequence was 10,152 nt, assigned GenBank accession KY623506. The virus was transmissible by the aphid *Myzus persica*e. The full-length nucleotide sequence shared about 60% identity to the full-length sequences of the other members of the papaya ringspot virus group (PRSV) within genus *Potyvirus*, including PRSV, Moroccan watermelon mosaic virus, and zucchini tigre mosaic virus. There was no evidence for recombination with other members of the PRSV group.

The *Potyviridae* study group proposes that Wild melon vein banding virus represents a new species within the genus *Potyvirus* for which name *Wild melon vein banding virus* is proposed.

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**Figure 1.** Estimated phylogeny of deduced polyprotein sequences of completely sequenced representative viruses of recognized species in genera *Bevemovirus*, *Brambyvirus, Bymovirus, Ipomovirus, Macluravirus, Poacevirus, Potyvirus, Roymovirus*, *Rymovirus,* and *Tritimovirus* in the family *Potyviridae* were used. Seven proposed new species in genus *Potyvirus* are indicated by red dots. Two proposed species unassigned a genus are indicated by blue dots. The tree was deduced in Mega v7.0.21 after alignment in Muscle using Neighbor-joining 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: African eggplant mosaic virus, MF997470; 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; common reed chlorotic stripe virus, KY612317; cowpea aphid-borne mosaic virus, KM655833; cucumber vein yellowing virus, AY578085; cucurbit vein banding virus, KY657266; 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; longan witches’ broom-associated virus, KY649478; Lupinus mosaic virus, EU847625; maize dwarf mosaic virus, AM110758; Mediterranean ruda virus, MF953305; 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; Paris mosaic necrosis virus, MF509898; 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; saffron latent virus, KY562565; scallion mosaic virus, AJ316084; shallot yellow stripe virus, AJ865076; sorghum mosaic virus, U57358; soybean mosaic virus, S42280; squash vein yellowing virus, EU259611; Sudan watermelon mosaic virus, KY623505; 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 melon vein banding virus, KY623506; 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.

| **References:** |
| --- |
| Adams, M.J., Antoniw, J.F. and Fauquet, C.M., 2005. Molecular criteria for genus and species discrimination within the family Potyviridae. *Archives of Virology*, *150*: 459-479.Desbiez, C., Wipf-Scheibel, C., Millot, P., Verdin, E., Dafalla, G. and Lecoq, H., 2017. New species in the papaya ringspot virus cluster: Insights into the evolution of the PRSV lineage. *Virus Research*, *241*, pp.88-94.Lan, P., Zhao, J., Zhou, Y., Li, Y., Shen, D., Liao, Q., Li, R. and Li, F., 2017. Complete genome sequence of Paris mosaic necrosis virus, a distinct member of the genus *Potyvirus*. *Archives of Virology*, pp.1-4.Parizad, S.; Dizadji, A.; Koobi Habibi, M.; Winter, S.; Kalantari, S.; Garcia-Arenal, F. and Ayllon, M.A. 2017. Prevalence of saffron latent virus (SaLV), a new potyvirus species, in saffron fields of Iran. *Journal of Plant Pathology*, *99*: 802.Perotto, M.C., Pozzi, E.A., Celli, M.G., Luciani, C.E., Mitidieri, M.S. and Conci, V.C., 2018. Identification and characterization of a new potyvirus infecting cucurbits. *Archives of Virology*, *163*:719-724.Rodríguez-Nevado, C., Montes, N. and Pagán, I., 2017. Ecological factors affecting infection risk and population genetic diversity of a novel potyvirus in its native wild ecosystem. *Frontiers in Plant Science*, *8*. |