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:** | ***2018.027P*** | | (to be completed by ICTV officers) |
| **Short title:** Two proposed unassigned species in *Potyviridae* | | | |
|  | | | |
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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: | | | May 1st, 2018 |
| Date of this revision (if different to above): | | |  |

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

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| **Name of accompanying Excel module:** 2018.027P.N.v1.Potyviridae\_2sp.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. |

**Two proposed new species not assigned to a genus in *Potyviridae***

The two proposed species below, common reed chlorotic stripe virus and Longan witches’ broom-associated virus, could not readily be placed in existing genera under accepted demarcation criteria (Adams et al 2005). These species are not currently assigned a genus.

1. **Common reed chlorotic stripe virus**

An isolate of a virus named common reed chlorotic stripe virus (CRCSV isolate Tianshui) was collected in 2015 in Gansu Province, China, from common reed (Phragmites australis) plants showing chlorotic stripe symptoms on leaves (Yuan *et al*., 2017). The virus was detected using the deep sequencing of small RNAs on the Illumina platform. The cDNA of the full genomic sequence of CRCSV was determined using the amplified products by RT-PCR. The genome consists of 9426 nt and contains a large open reading frame typical of members of the *Potyviridae* encoding a polyprotein of 3067 amino acids. Putative proteolytic cleavage sites were identified. The polyprotein was predicted to cleave into 10 mature proteins, typical of potyviruses. The sequence shared low nt sequence identity (35%-37% amino acid identity) with known members of the family Potyviridae. Neighbor-joining analyses of amino acid sequences of the CP and complete ORF revealed that both sequences clustered with high bootstrap support between rymoviruses and the brambyvirus. Analysis of motifs conserved within many members of the family revealed that all were present, although those strongly associated with aphid transmission, KITC, PTK and DAG, were changed to LFQC, PIE and DAE, respectively, suggesting that this virus is not transmitted by aphids. The authors propose that CRCSV may represent a member of a new genus within *Potyviridae*. Its genome sequence is assigned GenBank code KY612317 under the name reed chlorotic stripe virus.

The *Potyviridae* study group proposes classifying common reed chlorotic stripe virus as a representative of a new species in family *Potyviridae*, not assigned to any of the existing genera. We propose the name *Common reed chlorotic stripe virus* for this new unassigned species in the family.

1. **Longan witches’ broom-associated virus**

Witches’ broom disease is caused by stress that is brought on by pests or disease. Typical symptoms include leaf malformation, premature leaf falling and generation of bushy twigs and short internodes. The causative agent for longan witches’ broom disease (LWBD) has remained unknown in spite of the recognition of the disease as early as in 1948 (Chen *et al*., 2001). Samples showing symptoms of LWBD were collected from an experimental green house in Hanoi, Vietnam. Filamentous particles were detected in negatively-stained electron micrographs. The sequence of isolate Han1 was determined using an Illumina platform. Trinity pipeline was used for the *de novo* assembly of the quality-infiltered NGS reads. The assembly resulted in identification of one large contig 9322 bp in length encoding a polyprotein calculated to be of 3086 amino acids. After verifying that this sequence originated from the longan samples, 5’ and 3’RACE was used to obtain a full-length sequence of 9428 nucleotides, poly(A)-tail excluded, of longan witches broom-associated virus isolate Han 1 (LWBaV; KY649478) (Seo et al., 2017).

Sequence analysis showed the genome has characteristics typical of the members of the *Potyviridae*. The deduced 344 kDa polyprotein may be potentially cleaved into 10 typical potyviral proteins. The coding regions is surrounded by 5’ and 3’ untranslated regions of 117 and 50 nt, respectively, and the 3’end is poly(A)-tailed.

LWBaV shared very low sequence identity with the other members of family *Potyviridae*. A comparison between LWBaV and representative viruses of various genera in the family *Potyviridae* indicated that the identity in the genomic nucleotide sequences varied between 3.7-7.8% and polyprotein amino acid sequences between 17.5%-24.3%. In the phylogenetic tree constructed on the full-length genomic RNA sequences LWBaV is positioned closest to genus *Tritimovirus*, but there is no support to include LWBaV to that genus. At the amino acid level, the polyprotein’s closest is rose yellow mosaic virus (RoYMV; genus *Roymovirus*) sharing 35% amino acid identity with 85% coverage. On the genomic RNA sequence level, LWBaV and RoYMV don’t cluster together, but when the phylogenetic tree is constructed on the basis of the full length amino acid sequence there is strong bootstrap support for positioning LWBaV and RoYMV together in the same clade. Like RoYMV, LWBaV lacks the conserved aphid transmission motifs KITC, PTK and DAG, indicating it may not be transmitted by aphids. According to ML phylogenetic tree presented in Seo *et al*., 2017, the support for the internal nodes leading to divisions between *Ipomovirus, Tritimovirus* and *Poacevirus* genera is low. Symptomatic longan plants contained the virus, and the non-symptomatic ones didn’t contain the virus, but to fulfil the rest of Koch’s postulates requires further experiments.

The *Potyviridae* study group proposes that longan witches’ broom-associated virus represents a new species, named *Longan witches broom associated virus*. We also propose that the new species remains unassigned to any of the existing genera until more data is acquired to clarify its relationship to rose yellow mosaic virus.

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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. The two proposed species unassigned a genus are indicated by blue dots. Seven proposed new species in genus *Potyvirus* are indicated by red 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:** |
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| 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.  Chen, JY., Chen J.Y., and Xu, X.D., 2001. Advances in research of longan witches’ broom disease. *Acta Horticulturae*, 558:413-416.  Seo, J.K., Kim, M.K., Kwak, H.R., Kim, J.S. and Choi, H.S., 2017. Complete genome sequence of longan witches’ broom-associated virus, a novel member of the family *Potyviridae*. *Archives of Virology*, 162:2885-2889.  Yuan, W., Du, K., Fan, Z. and Zhou, T., 2017. Complete genomic sequence of common reed chlorotic stripe virus, a novel member of the family *Potyviridae*. *Archives of Virology*, 162:3541-3544. |