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.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

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

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| **Code assigned:** | ***2019.017P*** | |  |
| **Short title:** Create two new species in genus *Macluravirus* | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| |  |  | | --- | --- | | Wylie S, Kreuze JF, Lopez-Moya JJ, Makinen K, Inoue-Nagata AK, Ohshima K, Wang A | s.wylie@murdoch.edu.au;  j.kreuze@cgiar.org;  juanjose.lopez@cragenomica.es;  kristiina.makinen@helsinki.fi;  alice.nagata@embrapa.br;  ohshimak@cc.saga-u.ac.jp;  aiming.wang@agr.gc.ca | | | | |
| **Corresponding author** | | | |
| Steve Wylie | | | |
| **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: | | |  |
| 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:** |
| --- |
|  |

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

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| **Name of accompanying Excel module:** 2019.017P.A.v1.Macluravirus\_2sp.xlxs |

**Alpinia oxyphylla mosaic virus**

A newly-described virus, tentatively named Alpinia oxyphylla mosaic virus (AloMV) isolate Alpo, was detected from symptomatic plants of *Alpinia oxyphylla* in Haikou, Hainan Province, China (Hu *et al*., 2018). Transmission to experimental host plants was not described. TEM revealed flexuous filamentous potyvirid-like particles of about 15x770 nm.

An RNA preparation was used to construct a cDNA library that was sequenced using an Illumina HiSeq 4000 high-throughput sequencing platform, and the sequence was confirmed by RT-PCR using specific and random primers. Rapid amplification of cDNA ends (RACE) was used to confirm the 5’ and 3’ termini of the genome sequence.

The complete genome sequence of AloMV-Alpo was determined. The genome is 8213 nucleotides in length. The genome sequence of AloMV was assigned GenBank accession MG978107. It is predicted to encode a polyprotein of 2626 amino acid residues. The genome and its protein products display the genome organization and motifs of a typical macluravirus. Like other macluraviruses, the genome lacks a cistron that encodes the P1 protein of potyviruses. As usual, the PIPO ORF located within the AloMV P3 cistron is predicted to be translated by frameshift at A6, but it is unusual in that the preceding nucleotide of A6 is ‘C’ rather than the conserved ‘G’ seen in most potyvirids. The same ‘C’ occurs in the PIPO of some bymoviruses and also in the macluravirus, cardamon mosaic virus (CdMV).

The polyprotein sequence shares 48-68% amino acid identity with those of other macluraviruses, the closest relative being CdMV. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities, which suggests Alpinia oxyphylla mosaic virus isolate Alpo represents a novel taxon.

The *Potyviridae* study group proposes that Alpinia oxyphylla mosaic virus represents a new species, named *Alpinia oxyphylla mosaic virus*, within the genus *Macluravirus*, with ‘Alpo” (AloMV-Alpo) being the exemplar isolate.

**Yam chlorotic necrosis virus**

A newly-described virus, tentatively named yam chlorotic necrosis virus (YCNV), was detected in yam (*Dioscorea* *alata*) showing foliar yellowing, necrosis, mottle, and crisping. The YCNV isolate YJish was found in infected plants growing in a field in Jianshui, Anning and Lufeng counties, Yunnan Province, China, in 2016 (Lan *et al.*, 2019).

RNA preparations from five symptomatic plants were used to construct a cDNA library, and the partial genome of the virus was obtained using deep sequencing.

The complete genome sequence of YCNV-YJish was determined by RT-PCR amplification of the entire viral genome and subsequent sequencing. The genome is 8261 nucleotides in length. The genome sequence of YCNV-YJish was assigned GenBank accession MG755240. It is predicted to encode a polyprotein of 2627 amino acid residues. It displays the organization of a typical malcluravirus in the family *Potyviridae*.

Specific primers were used for detection of the virus in 273 yam leaf samples by RT-PCR. The virus occurred in 26.4% of the plants.

The genome and polyprotein sequences of YCNV-YJish share 64% nucleotide and amino acid identities, respectively, with yam chlorotic necrotic mosaic virus isolate YS (YCNV, KT724961) in the genus *Macluravirus*. The deduced amino acid sequence of the polyprotein shares 64% identity with the same virus isolate. These identities are below the ICTV-accepted demarcation limits of <76% nucleotide and <82% amino acid identities, which suggests YCNV-YJish represents a novel taxon.

The *Potyviridae* study group proposes that yam chlorotic necrosis virus represents a new species, named *Yam chlorotic necrosis virus*, within the genus *Macluravirus*, with ‘YJish” (YCNV-YJish) being the exemplar isolate.

Note: YCNV isolate W10-223 (accession MH341583) from India shares 82% nt identity with YCNV-YJish (Filloux *et al.*, 2018). Its genome was submitted to GenBank after that of YCNV-YJish and represents the second isolate of this proposed new species.

| **References:** |
| --- |
| Filloux, D., Fernandez, E., Loire, E., Claude, L., Galzi, S., Candresse, T., Winter, S., Jeeva, M.L., Makeshkumar, T., Martin, D.P. and Roumagnac, P., 2018. Nanopore-based detection and characterization of yam viruses. Scientific Reports 8:17879  Hu, W., Li, Z., Wang, X., Liu, W., Huang, C., Miao, W. and Cui, H., 2018. Complete genomic sequence of a novel macluravirus, alpinia oxyphylla mosaic virus (AloMV), identified in *Alpinia oxyphylla*. Archives of Virology 163:2579-2582.  Lan, P., Meng, Y., Shen, P., Li, R., Ma, Y., Tan, S., Chen, H., Cao, M. and Li, F., 2018. Complete genome sequence of yam chlorotic necrosis virus, a novel macluravirus infecting yam. Archives of Virology 163:2275-2278. |

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**Figure 1 -** Estimated phylogeny of deduced polyprotein sequences of completely sequenced representative viruses of species in genera *Arepavirus*, *Bevemovirus*, *Brambyvirus, Bymovirus, Celavirus, Ipomovirus, Macluravirus, Poacevirus, Potyvirus, Roymovirus*, *Rymovirus* and *Tritimovirus* in the family *Potyviridae*. Proposed new species in genera *Arepavirus* (proposed new genus), *Celavirus* (proposed new genus), *Macluravirus*, *Potyvirus,* and *Roymovirus* are indicated by a red dot. The tree was deduced in Mega v7.0.26 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; Alpinia oxyphylla mosaic virus, MG978107; Apium virus Y, HM363516; Areca palm necrotic ringspot virus, MH395371; Areca palm necrotic spindle-spot virus, MH330686; 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 latent virus, MH932227; 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; Dendrobium chlorotic mosaic virus, MK241979; Dioscerea mosaic virus, MH206616; donkey orchid virus A, JX156422; East Asian Passiflora virus, AB246773; East Asian Passiflora distortion virus, LC379162; Freesia mosaic virus, FM206346; fritillary virus Y, AM039800; Gloriosa stripe mosaic virus, EF427894; Gomphocarpus mosaic virus, LC228573; 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; lily virus Y, MF543013; longan witches’ broom-associated virus, KY649478; Lupinus mosaic virus, EU847625; maize dwarf mosaic virus, AM110758; Mashua virus Y, MH680824; 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; Passiflora edulis symptomless virus, MH379332; 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; Platycodon mild mottle virus, MH779625; plum pox virus, AY953267; pokeweed mosaic virus, JQ609095; potato virus A, Z21670; potato virus V, KP849483; potato virus Y, U09509; potato yellow blotch virus, JX294310; 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 chlorotic necrosis virus, MG755240; 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.