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**

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.019P*** | |  |
| **Short title:** Create two new species and one new genus (*Arepavirus*)in the family *Potyviridae* | | | |
| **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:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | | June 19, 2019 |
| Date of this revision (if different to above): | | |  |

|  |
| --- |
| **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:** |
| --- |
|  |

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

|  |
| --- |
| **Name of accompanying Excel module:** 2019.019P.A.v1.Arepavirus\_ngen.xlxs |

**Areca palm necrotic spindle-spot virus**

A previously undescribed virus tentatively named areca palm necrotic spindle-spot virus (ANSSV), isolate HNBT, was detected in symptomatic plants of *Areca catechu* (areca palm) in Hainan Island, China in 2017 (Yang *et al*., 2018). Infected plants exhibited chlorosis, necrosis and spindle-spot symptoms. Transmission to experimental host plants was not described. TEM revealed flexuous filamentous, potyvirid-like particles of about 15x780 nm.

An RNA preparation was used to construct a cDNA library from small RNAs using Illumina technology. Forty-four contigs of 56-300 bp were assigned to the new virus. Primers were designed from the contig sequences, and the entire sequence of the genome determined using the Sanger method of sequencing overlapping amplicons.

The complete genome sequence of ANSSV is 9437 nucleotides in length, and the sequence was assigned GenBank accession MH330686. A polyprotein of 3019 amino acid residues was deduced. The genome and its protein products display the genome organization typical of a macluravirus. Like macluraviruses, the polyprotein encodes eight predicted cleavage sites and lacks a cistron that encodes a P1 protein. The typical potyviridal PIPO ORF is located within the ANSSV P3 cistron and is predicted to be translated by a frameshift at G(A)7. Other conserved potyvirid motifs were detected, confirming its membership in the *Potyviridae*.

The ANSSV polyprotein shares closest identities (31-32% amino acid sequence identity over 86%-95% coverage) with known macluraviruses. Although nucleotide sequence comparisons of the large ORF of ANSSV are closest (41-45% pairwise identities) to those of macluraviruses, these identities are marginally below the inter-genus identity values of <46% for the family *Potyviridae*.

In summary, pairwise identities of ANSSV-HNBT are below the ICTV-accepted demarcation limits for existing species and genera within *Potyviridae*, which suggests Areca palm necrotic spindle-spot virus represents a novel species within a novel genus, related to, but distinct from, *Macluravirus*.

The *Potyviridae* Study Group proposes that areca palm necrotic spindle-spot virus isolate HNBT represents a novel, homonymous species (the type species, *Areca palm necrotic spindle-spot virus* ) in the proposed novel genus *Arepavirus* in the family *Potyviridae*.

Etymology: AREca PAlm necrotic spindle-spot VIRUS

**Areca palm necrotic ringspot virus**

A previously undescribed virus tentatively named areca palm necrotic ringspot virus (ANRSV), isolate XC1, was detected from one symptomatic plant of *Areca catechu* (areca palm) in Qionghai, Hainan Island, China, in 2017 (Yang *et al*., 2019). Infected plants exhibited symptoms of necrotic ringspots on the lower and middle leaves of trees, but not on the top leaves. An RT-PCR assay was developed, and the average incidence of the virus was 19% across eight production regions. Transmission to experimental host plants was not described. TEM revealed flexuous filamentous, potyvirid-like particles of about 15x780 nm.

An RNA preparation was used to construct a cDNA library from small RNAs using Illumina HiSeq2500 technology. Of the 29 million raw sequences obtained, 1.6 million matched the virus genome sequence. The viral reads were *de novo* assembled into 24 contigs (65-599 nucleotides) that matched the virus. Primers were designed from contig sequences, and the entire sequence of the genome was determined using the Sanger method by sequencing nine RT-PCR-generated amplicons. The 5’ and 3’ terminal sequences were confirmed by RACE. Coat protein sequences of 27 isolates were obtained from four regions, and these were deposited in GenBank (e.g. MH395372).

The complete genome sequence of ANRSV is 9434 nucleotides in length, and the sequence was assigned the GenBank accession number MH395371. A polyprotein of 3019 amino acid residues was deduced. The genome differs from other potyvirids in that it has two HC-Pro like cistrons, HC-Pro1 and HC-Pro2, at the 5’ end of the genome, and no P1 cistron. Both HC-Pro cistrons are believed to encode cysteine proteases. The typical potyvirid PIPO ORF is located within the ANSSV P3 cistron and is predicted to be translated by a frameshift at G(A)7. Other conserved potyvirid motifs were detected, confirming its membership in the *Potyviridae*.

The ANRSV polyprotein shares 31-33% amino acid sequence identity over 81%-89% coverage with seven macluraviruses. Although nucleotide sequence comparisons of the large ORF of ANRSV are closest (38-42% pairwise identities) to those of macluraviruses, these identities are below the genus demarcation value of <46% for the family *Potyviridae*. The ANRSV polyprotein is closest (75% amino acid identity, 73% nucleotide identity) to that of an isolate of the proposed new species areca palm necrotic spindle-spot virus (see above).

In summary, pairwise identities of ANRSV-XC1 are below the ICTV-accepted demarcation limits for species and genera within *Potyviridae*. The *Potyviridae* Study Group proposes that areca palm necrotic ringspot virus isolate XC1 represents a novel species within proposed novel genus *Arepavirus* in family *Potyviridae* for which we propose the name *Areca palm necrotic ringspot virus*.

| **References:** |
| --- |
| Yang, K., Ran, M., Li, Z., Hu, M., Zheng, L., Liu, W., Jin, P., Miao, W., Zhou, P., Shen, W. and Cui, H. (2018) Analysis of the complete genomic sequence of a novel virus, areca palm necrotic spindle-spot virus, reveals the existence of a new genus in the family *Potyviridae*. Archives of Virology, 163:3471-3475.  Yang, K., Shen, W., Li, Y., Li, Z., Miao, W., Wang, A. and Cui, H. (2019) Areca palm necrotic ringspot virus, classified within a recently proposed genus Arepavirus of the family *Potyviridae*, is associated with necrotic ringspot disease in areca palm. Phytopathology, doi 10.1094/PHYTO-06-18-0200-R. |



**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.