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:** | ***2019.020P*** |  |
| **Short title:** Create one new genus *Celavirus* including one new species in the family *Potyviridae* |
| **Author(s) and email address(es):** |
|

|  |  |
| --- | --- |
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 |
| **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:** 2019.020P.A.v1.Celavirus\_1ngen.xlxs |

**Celery latent virus**

Celery latent virus (CeLV) was first described in the 1960s and 1970s (Brandes and Luisoni, 1966; Bos et al., 1978) from the Netherlands in asymptomatic celeriac (*Apium graveolens* var. *rapaceum*). Bos et al (1978) described 16 experimental hosts, including species of *Amaranthus*, *Apium*, *Chenopodium*, *Nicotiana*, *Pisum*, *Spinacia* and *Trifolium*. They were unable to transmit CeLV using five aphid species, but seed transmission was high in celeriac (34%) and *C. quinoa* (67%), and confirmed in *Amaranthus*. TEM revealed virus particles with an average length of 885 nm, with no pinwheel inclusion bodies visible in infected cells.

A new paper (Rose et al., 2019) describes experiments that repeated and confirmed much of the earlier work on CeLV, and contributed the complete genome sequence and analysis thereof. Isolate CeLV-Ag097 is described from an asymptomatic plant of leaf celery (*A. graveolens* var. *secalinum*) in Italy. When inoculated to other apiaceous plants, it asymptomatically infected plants of celeriac and celery (*A. graveolens* var. *dulce*). Systemic infection occurred in *C.* *quinoa*, where symptoms consisted of yellow (ring-) spots, and symptomless systemic infection on *N. benthamiana* was recorded. The virus was sap- and seed-transmissible, and it was not transmissible by five aphid species. No cytoplasmic cylindrical (“pinwheel”) inclusions were visible in the infected tissue. Virions were flexuous filamentous particles about 900 nm in length and possess a single-stranded and monopartite RNA genome.

cDNA synthesised from the ssRNA viral genome was sequenced using both Sanger and NGS methods. The genome sequence of 11,519 nucleotides was assigned GenBank accession MH932227. CeLV-Ag097 has the largest genome of known potyvirids. It also has several genome features not found in other potyvirids. The genome contains a single large open reading frame (ORF) that is flanked by an unusually-short 5′ untranslated region (UTR) of 13 nt and an unusually-long 3′ UTR consisting of 586 nt. Unique among potyvirids, the 3’UTR is not polyadenylated. The large ORF is deduced to encode a polyprotein of 3,640 amino acid residues. Like other potyvirids, the CeLV polyprotein has a putative P3N-PIPO (Pretty Interesting Potyvirus (Potyviridae) Open-reading-frame) ORF, but the PIPO shares very low amino acid sequence identities (about 18 %) with other potyvirids. Typical potyviridae-like protease cleavage sites were not identified for the N-terminal two-thirds of the polyprotein, although this region possesses a number of sequence motifs typical of potyvirids. However, many characteristic potyvirid motifs were not present. For example, motifs characteristic of the HC-Pro such as K-I-T-C, I-G-N, C-C/S-C, F-R-N-K, P-T-K and G-Y-C-Y, were absent.

Pairwise comparison of the nucleotide sequence of the large ORF with those of other potyvirids revealed closest values of 44.2% with blackberry virus Y (BlVY, genus *Brambyvirus*), 40.9% with bellflower veinal mottle virus(BVMoV, genus *Bevemovirus*), 18.7% with rose yellow mosaic virus and ryegrass mosaic virus (genera *Roymovirus* and *Rymovirus*, respectively), and 15.4% with Chinese yam necrotic mosaic virus (CYNMV, *Macluravirus*). The amino acid sequence of the large ORF shares only 10-14% identity with other potyvirids. The nuclear inclusion b (NIb) gene of CeLV shared nucleotide identities of 45.1% with BIVY, 36.4% with Triticum mosaic virus (TriMV, genus *Poacevirus*), 23.3% with BVMoV, and 19.4% with potato virus Y (*Potyvirus*). The coat protein (CP) gene shared nucleotide sequence identities of 43.7% with BIVY, 39.5% with sweet potato mild mottle virus (SPMMV, genus *Ipomovirus*), 18.2% with CYNMV, and 13.8% with TriMV. Phylogenetic analysis places CeLV-Ag097 basal to all other potyvirids.

These sequence identities are well below the ICTV-accepted species demarcation limits of <76% nucleotide and <82% amino acid identities for polyproteins (Adams et al., 2005), which confirms that celery latent virus represents a novel species. Further, the unusual genomic features and sequence identities below the genus demarcation criterion of <46% warrant creation of a new genus for celery latent virus. Rose et al (2019) proposed the generic name Celavirus (etymology: CElery LAtent VIRUS).

Should celery latent virus be assigned to family *Potyviridae*? Differences between the sequence of CeLV-Ag097 and other potyviruses are significant. However, the Study Group considers that three main pieces of evidence favour assigning CeLV to the Potyviridae:

1. Its genome contains a large ORF encoding a polyprotein which can potentially be cleaved into the potyvirid-like proteins CI, NIa, NIb and CP.
2. The potyvirid-like PIPO occurs at a genome position very similar to that of other potyvirids.
3. Its flexuous filamentous particles measuring about 900 nm in length, which is in line with virions of other potyvirids.

Thus, the Study Group proposes that celery latent virus represents a very unusual new species in family *Potyviridae*, named *Celery latent virus*, and that its significant differences from all other known potyvirids warrants creation of a new genus, *Celavirus.*

| **References:** |
| --- |
|  Adams M.J., Antoniw J.F., Fauquet C.M. (2005) Molecular criteria for genus and species discrimination within the family *Potyviridae*. Archives of Virology 150:459-479.Bos, L., Diaz-Ruiz, J.R., Maat, D.Z. (1978) Further characterization of celery latent virus. Netherlands Journal of Plant Pathology 84:61-79.Brandes J., Luisoni E. (1966) Untersuchungen über einige Eigenschaften von zwei gestreckten Sellerieviren. Journal of Phytopathology 57:277-288.Rose H., Doering I., Vetten H.-J., Menzel W., Richert-Poeggeler K.R., Maiss E. (2019) Complete genome sequence and construction of an infectious full-length cDNA clone of celery latent virus - an unusual member of a putative new genus within the *Potyviridae*. Journal of General Virology 100:308-320. |



**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.