This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2016.005aP***	(to be completed by ICTV officers)

Short title: Create one new species in the genus *Pomovirus*, family *Virgaviridae*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 11 are required)	**2** ☒ **3** ☐ **4** ☐ **5** ☐ **6** ☐ **7** ☐ **8** ☐ **9** ☐ **10** ☐

Author(s):

Adams MJ, Gil JF, Adams I, Boonham N, Nielsen SL, Nicolaisen M, Adkins S, Bragard C, Gilmer D, Li D, MacFarlane SA, Man WS, Melcher U, Ratti C, Ryu KH

Corresponding author with e-mail address:

Mike Adams (mike.adams.ictv@gmail.com

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Virgaviridae and Benyviridae

ICTV Study Group comments (if any) and response of the proposer:

Approved unanimously

Date first submitted to ICTV: June 2016
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for **one** isolate of each new species proposed.

Code	***2016.005aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Pomovirus***
Subfamily:	
Family:	***Virgaviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
Colombian potato soil-borne virus	IS9	KT225271 (RNA1), KT225272 (RNA2), KT225273 (RNA3)

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 11

The genus *Pomovirus* contains viruses with a tripartite ssRNA+ genome encapsidated in rigid rod-shaped particles. Where known, the vectors are root-infecting fungoid protists. Viruses in other genera of the family *Virgaviridae* have different numbers of genome components and/or different modes of transmission (seed, nematodes, mechanical) but there are clear phylogenetic relationships between some of the major gene products. Genome organization is conserved within each of the genera. In members of the genus *Pomovirus* the largest RNA encodes a replication protein of 145-150 kDa with a 'leaky' stop codon that, when suppressed, extends the protein into an RdRp domain and results in a product of about 210 kDa. The second RNA encodes the major coat protein of about 20 kDa, again with a 'leaky' stop codon that, when suppressed, extends the protein to about 90kDa; this larger product plays a role in transmission by the vector. The smallest RNA encodes a 'triple gene block' (involved in virus cell-to-cell movement) and (in some virus isolates) a small cysteine-rich protein that may be a silencing suppressor (Annex Fig. 1). All RNA segments have a tRNA-like structure at the 3' terminus that contains an anticodon for valine in isolates of the current species.

Species discrimination criteria within the genus as listed in the 9th report are:

- Differences in host range,
- Effects in infected tissue: different inclusion body morphology,
- Transmission: different vector species,
- Serology: virions are distantly related serologically,
- Genome: different numbers of genome products (presence or absence of a gene for a cysteine-rich protein).
- Sequence: less than about 80% identical over whole sequence,

- Sequence: less than about 90% identical in CP amino acid sequence.

Gil et al (2016) reported the detection and characterization of two genetically distinct pomoviruses from the soil of potato fields in Colombia. The viruses were baited from soil on *Nicotiana benthamiana* and potato and could be multiplied and maintained on *N. benthamiana* in which they caused stunting, leaf curling and mild mosaic symptoms. Sequences obtained by NGS from bait plants grown in soil from three separate sites were clearly those of pomoviruses. The coding-complete sequences of the expected 3 genome components of two closely-related isolates (IS9 and IS13) were obtained and named Colombian potato soil-borne virus (CPSbV). Some sequences of a second genetically-distinct pomovirus (IS16) were also obtained from a third soil sample but only from two of the genome components. These probably represent a further species but are not being proposed at this stage.

The three genomic RNA components of CPSbV isolate IS9 are 6170, 3164 and 3028nt long and have an organization typical of the genus *Pomovirus* although without the cysteine-rich protein on the smallest RNA that is present in isolates of the type member, potato mop-top virus (PMTV). The predicted tRNA-like structure at the 3' terminus of each RNA contains an anticodon for leucine. Amino acid sequence comparisons show that CPSbV has 72% identity to PMTV in the RdRp, 79% in the coat protein and 78% in the first (and largest) of the TGB proteins. Phylogenetic analysis (Annex Fig. 2) shows that the proteins of PMTV isolates from different geographical regions are very similar to one another, probably reflecting dispersal via planting material from the Andes region where potatoes originate. The products of CPSbV form a distinct clade well separated from PMTV isolates. Genetic distance, the distinctive 3'-termini, phylogenetic analysis and the absence of the cysteine-rich protein support the creation of a new species for isolates of CPSbV.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Gil J.F., Adams I., Boonham N., Nielsen S.L., Nicolaisen M. (2016). Molecular and biological characterisation of two novel pomo-like viruses associated with potato (*Solanum tuberosum*) fields in Colombia. Arch. Virol. 161(6):1601-1610.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Figure 1. Genome organization of potato mop-top virus (PMTV), the type member of the genus *Pomovirus*. RNA-1 encodes the replication proteins, RNA-2 encodes the coat protein and a readthrough domain necessary for vector transmission. RNA-3 encodes the triple block proteins that are required for cell-to-cell movement and a small cysteine-rich protein (light green). The solid squares indicate a 3'-terminal tRNA-like structure that accepts valine. Other members of the genus have similar organization but beet soil-borne virus and beet virus Q do not have the cysteine-rich protein. Colombian potato soil-borne virus, the subject of this proposal, also lacks the cysteine-rich protein and its tRNA-like structure accepts leucine.

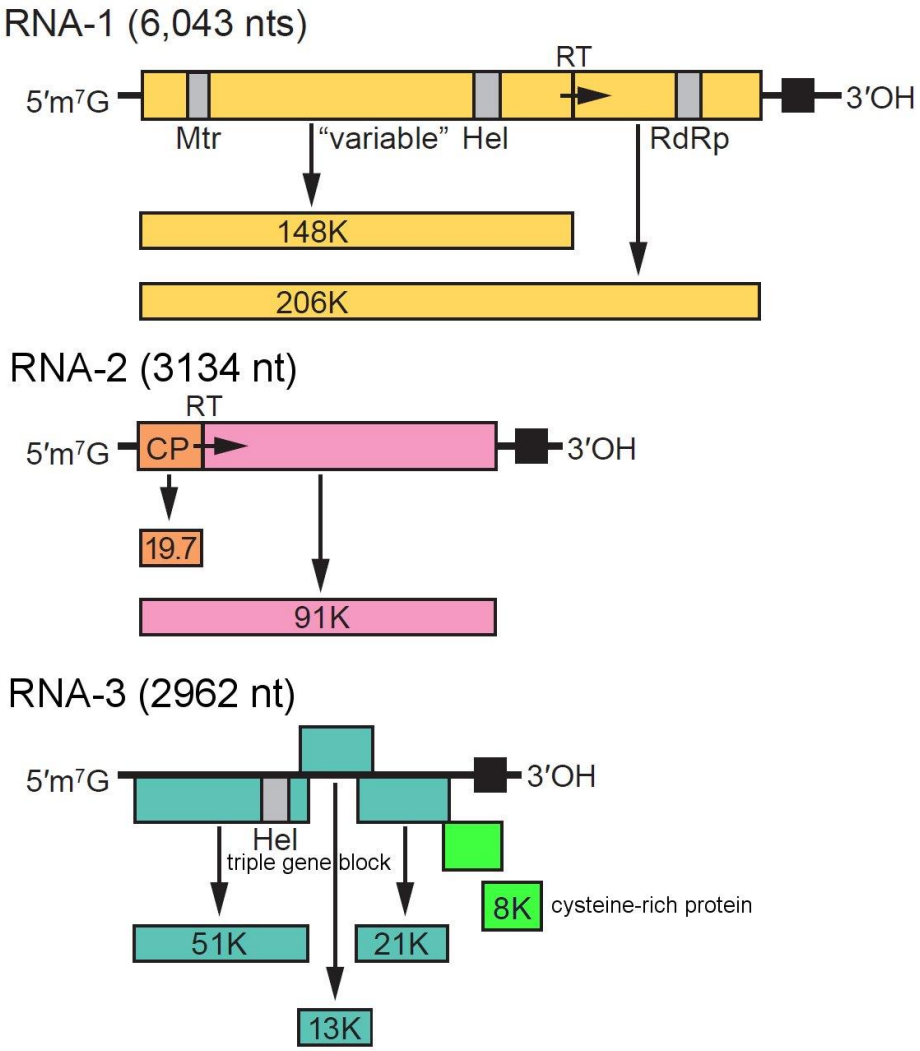

Figure 2. Phylogenetic trees showing the relationships between the major protein products for each fully-sequenced isolate of members of the genus *Pomovirus*. Trees are based on amino acid alignments obtained by MUSCLE with some manual curation and were calculated in MEGA6 using the Maximum Likelihood method based on the JTT matrix-based model. The percentage of trees from 1000 replicates in which the associated taxa clustered together is shown next to the branches where >60%. The Replicase tree is for the entire readthrough protein of RNA1. CP, major coat protein from RNA2. TGB, concatenated alignment of the three triple gene block proteins from RNA3. Potato mop-top (PMTV) isolates are shown in blue and the geographical origin of the isolates is shown in the Replicase tree. Colombian potato soil-borne virus (CPSbV) isolates representing the proposed new species are shown in red. Other viruses are: beet soil-borne virus (BSBV), broad bean necrosis virus (BBNV) and beet virus Q (BVQ). Sequence accession numbers are also shown.