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:	***2014.010a-dP***	(to be completed by ICTV officers)

Short title: create a new genus, *Rosadnavirus*, in the family *Caulimoviridae*
(e.g. 6 new species in the genus *Zetavirus*)

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

Author(s) with e-mail address(es) of the proposer:

ADW Geering, a.geering@uq.edu.au

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)	Caulimoviridae Study Group

ICTV-EC or Study Group comments and response of the proposer:

SG comment: There is agreement about the need to create a new virus genus to include rose yellow vein virus and also support for the new name.

EC comment: The EC did not have difficulty with the creation of the proposed new genus but suggested some modifications to improve the proposal. The wording in the figure legend of the phylogenetic tree should state that the tree was built using the maximum likelihood method (the current phrasing is confusing). The SG should also confirm which virus was used as an outgroup and ensure that the tree is properly rooted. In the title page, replace "yes" by "Caulimoviridae SG"

AG comment: The wording in the figure legend has been revised. The outgroup has been clarified. "Yes" has been replaced by "Caulimoviridae Study Group" in the title page.

Date first submitted to ICTV:	June 2014
Date of this revision (if different to above):	September 2014

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	***2014.010aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Rosadnavirus (new)***
Subfamily:	
Family:	***Caulimoviridae***
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:**	**GenBank sequence accession number(s)**
Rose yellow vein virus		JX028536.1

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 9

Rose yellow vein virus (RYVV) is clearly a new virus species in the *Caulimoviridae* as it has isometric virions, a circular double-stranded DNA genome, a unique genome organization, is distantly related to any other described virus species in the family and is graft transmissible. A new genus is proposed to accommodate this virus (see below) and a detailed justification for the creation of the species and genus is given below.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2014.010bP***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Caulimoviridae***
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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2014.010cP***	(assigned by ICTV officers)

To name the new genus: *Rosadnavirus*

Assigning the type species and other species to a new genus

Code	***2014.010dP***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Rose yellow vein virus

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

Rose yellow vein virus (RYVV) is clearly a new species and a representative of a new genus of the *Caulimoviridae* for the following reasons:

1. RYVV encodes a polyprotein containing aspartic protease, reverse transcriptase (RT) and RNase H (RH) domains. Family *Caulimoviridae* is the only group of viruses in the plant kingdom (other than the long terminal repeat retrotransposons in the *Pseudoviridae* and *Metaviridae*) that incorporates a reverse transcription step in its replication cycle. RYVV lacks an integrase enzyme and contains a viral movement protein (MP), features that distinguish the *Caulimoviridae* from the *Pseudoviridae* and *Metaviridae*. The genome of RYVV is composed of double-stranded DNA and is circular, based on the ability to PCR-amplify the whole genome using outward pointing primers. Virions are isometric and similar in size to *Cauliflower mosaic virus*, although slightly smaller in diameter. Finally, RYVV groups within the *Caulimoviridae* in a phylogenetic analysis of conserved RT-RH gene sequences (Fig. 1, Annex).

2. RYVV has a unique genome organization (Fig. 2, Annex), which is the primary criterion for distinguishing genera within the *Caulimoviridae*. Based on virion shape, RYVV is

distinguishable from the genera *Tungrovirus* and *Badnavirus*, which have bacilliform-shaped virions. RYVV has eight putative ORFs that potentially encode proteins ≥ 10 kDa. The only other genera in the *Caulimoviridae* that have this many ORFs are *Caulimovirus* and *Soymovirus*. An obvious difference in the genome organization of RYVV and the genera *Caulimovirus*/*Soymovirus* is that in the former, the ORFs that encode the MP and capsid protein (CP) partially overlap one another but in different reading frames, whereas in the latter, there are 2-3 ORFs between the MP and CP, including those that encode the aphid transmission factor (ATF) and the virion-associated protein (VAP). Furthermore, RYVV does not have homologue of the *Caulimovirus*/*Soymovirus* ATF.

The three other genera in the *Caulimoviridae* with isometric virions are *Cavemovirus*, *Solendovirus* and *Petuvirus*. For the genus *Cavemovirus*, the MP and CP derive from a polyprotein that is post-translationally processed and the genes are in opposite order to RYVV. For the genus *Solendovirus*, the MP and CP are coded by separate and neighbouring ORFs but like the genus *Cavemovirus*, the order of these genes is opposite to RYVV. For the genus *Petuvirus*, there is only a single ORF encoding a large polyprotein that contains the precursors of all necessary replication, movement, transmission and structural proteins.

3. At 9.3 kbp, the genome of RYVV is the largest known of any species in the *Caulimoviridae*, and of those with isometric virions, the next largest is the soymovirus *Blueberry red ringspot virus*, at 8.3 kbp.

4. RYVV has a maximum of 29-33% amino acid sequence identity with homologous proteins of other members of the *Caulimoviridae*, which is a magnitude typical of different genera.

Origin of the new genus name:

Rosadnavirus: derived from *Rosa* DNA virus, where rose is the generic epithet of rose and DNA refers to the composition of the virus genome. Rosadnavirus follows the previous convention set for *Badnavirus*, which derives from 'bacilliform DNA virus'.

Reasons to justify the choice of type species:

Rose yellow vein virus is the first and so far the only representative of this new genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Monotypic genus.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Mollov D, Lockhart B, Zlesak DC, Olszewski N (2013) Complete nucleotide sequence of rose yellow vein virus, a member of the family *Caulimoviridae* having a novel genome organization. *Archives of Virology* **158**: 877-880.

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.

Annex 1. Information supporting proposal of nomination of new genus, Rosadnavirus, in the *Caulimoviridae*.

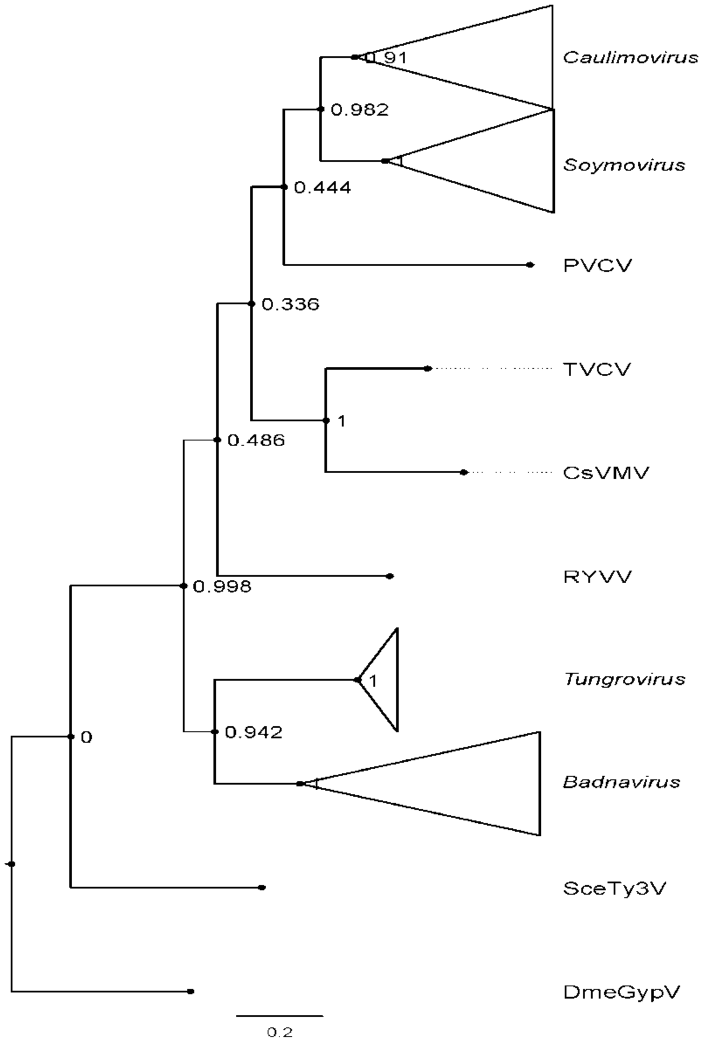

Figure 1. Phylogram of the *Caulimoviridae* built using the maximum likelihood method provided in the MEGA 6.06 suite of software. Reverse transcriptase-RNase H1 gene sequences, equivalent to nucleotides 4449-5648 of the cauliflower mosaic virus genome (NCBI accession NC_001497.1), were used for phylogenetic inference. Abbreviations are: PVCV, *Petunia vein clearing virus* (type species, genus *Petuvirus*); TVCV, *Tobacco vein clearing virus* (type species, genus *Solendovirus*); CsVMV, *Cassava vein mosaic virus* (type species, genus *Cavemovirus*); RYVV (rose yellow vein virus; unassigned). The phylogram has been rooted using *Saccharomyces cerevisiae Ty3 virus* (SceTy3V, type species of genus *Metavirus*) and *Drosophila melanogaster Gypsy virus* (DMeGypV, type species of genus *Errantivirus*). Clades containing caulimovirus, soymovirus, tungrovirus and badnavirus species have been collapsed. Bootstrap values for 500 replicates are shown in the nodes of the branches.

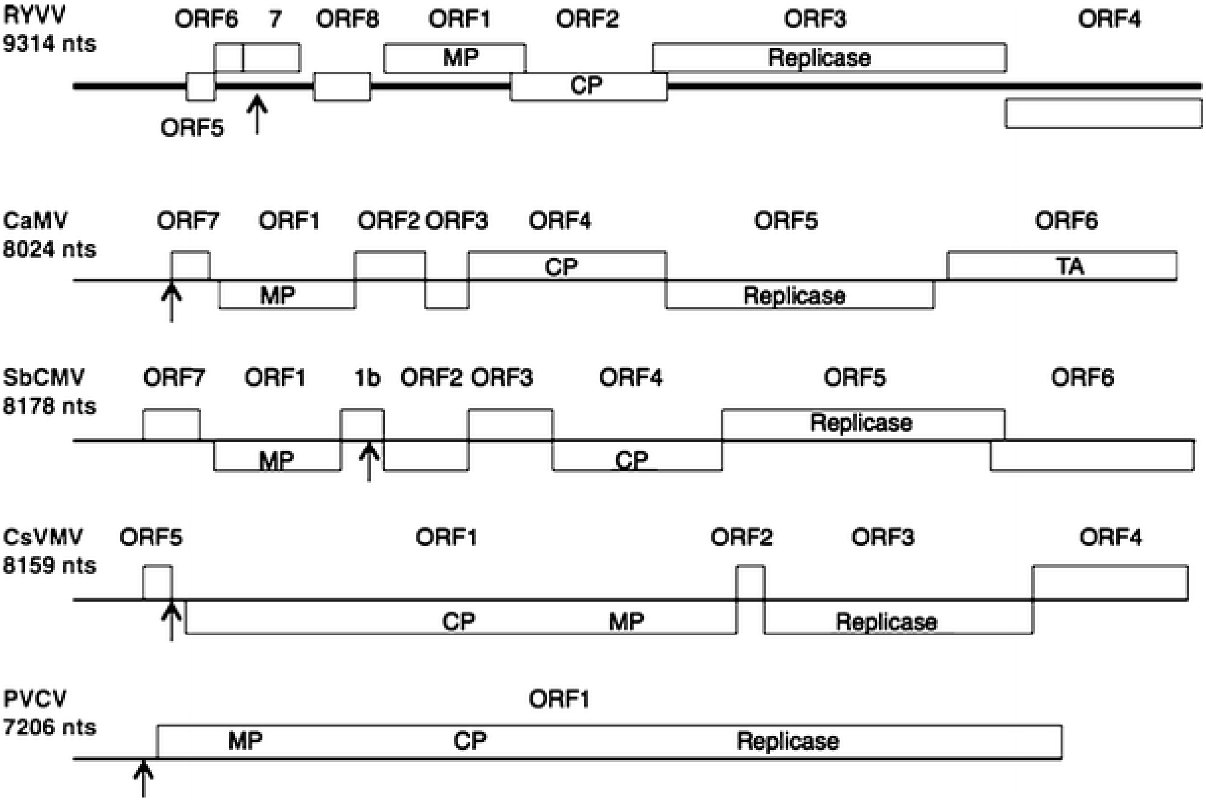

Figure 2. Comparison of the genome organisation of rose yellow vein virus (RYVV) with the type species of other genera with isometric virions in the *Caulimoviridae*. Abbreviations are: ORF, open reading frame; MP, movement protein; CP, capsid protein; CaMV, *Cauliflower mosaic virus* (genus *Caulimovirus*); SbCMV, *Soybean chlorotic mottle virus* (genus *Soymovirus*); CsVMV, *Cassava vein mosaic virus* (genus *Cavemovirus*); PVCV, *Petunia vein clearing virus* (genus *Petuvirus*). An open box represents an ORF and the upward-pointing arrow, the position of the tRNA^{MET} consensus sequence. The replicase polyprotein contains the aspartic protease, reverse transcriptase and RNaseH enzyme precursors. Figure extracted from paper by Mollov *et al*., 2013).