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:	***2016.013aP***	(to be completed by ICTV officers)

Short title: One new species in the genus *Caulimovirus*
(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** ☐ **11** ☒

Author(s):

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Corresponding author with e-mail address:

Pierre-Yves Teycheney; teycheney@cirad.fr

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

Date first submitted to ICTV: July 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	***2016.013aP***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Caulimovirus***
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: (only 1 per species please)**	**GenBank sequence accession number(s)**
Atractylodes mild mottle virus	AMMV-ES	KR080327.1

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 11

Atractylodes mild mottle virus is considered a new caulimovirus species for the following reasons:

1. A complete genome sequence of *Atractylodes mild mottle virus* (AMMV) was assembled from deep sequencing reads of cDNA obtained from *Atractylodes macrocephala* plants showing mild mottling symptoms. Overlapping PCR amplicons covering the entire genome were obtained from symptomatic plants and sequenced by the Sanger method. The 8,105-nt genome contains six ORFs and has a genome organization typical of members of the family *Caulimoviridae*.
2. In phylogenetic analyses using ORF3 nucleotide sequences corresponding to the conserved RT/RNAseH domains, AMMV groups within the genus *Caulimovirus* (Fig. 1). AMMV is most closely related to the caulimovirus *Soybean Putnam virus* (SPuV), to which it shares 78.7% nucleotide identity within the RT-RNase H domains (Table 1), which is below the 80% demarcation threshold for species within the genus *Caulimovirus*.
3. The ends of the pregenomic RNA have been mapped and terminal redundancy demonstrated, as typical of all members of the *Caulimoviridae*.

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Lim S, Igori D, Zhao F, Yoo RH, An TJ, Lim HS, Lee SH, Moon JS (2015) Complete genome sequence of a tentative new caulimovirus from the medicinal plant *Atractylodes macrocephala*. Arch Virol. 160: 3127-31.

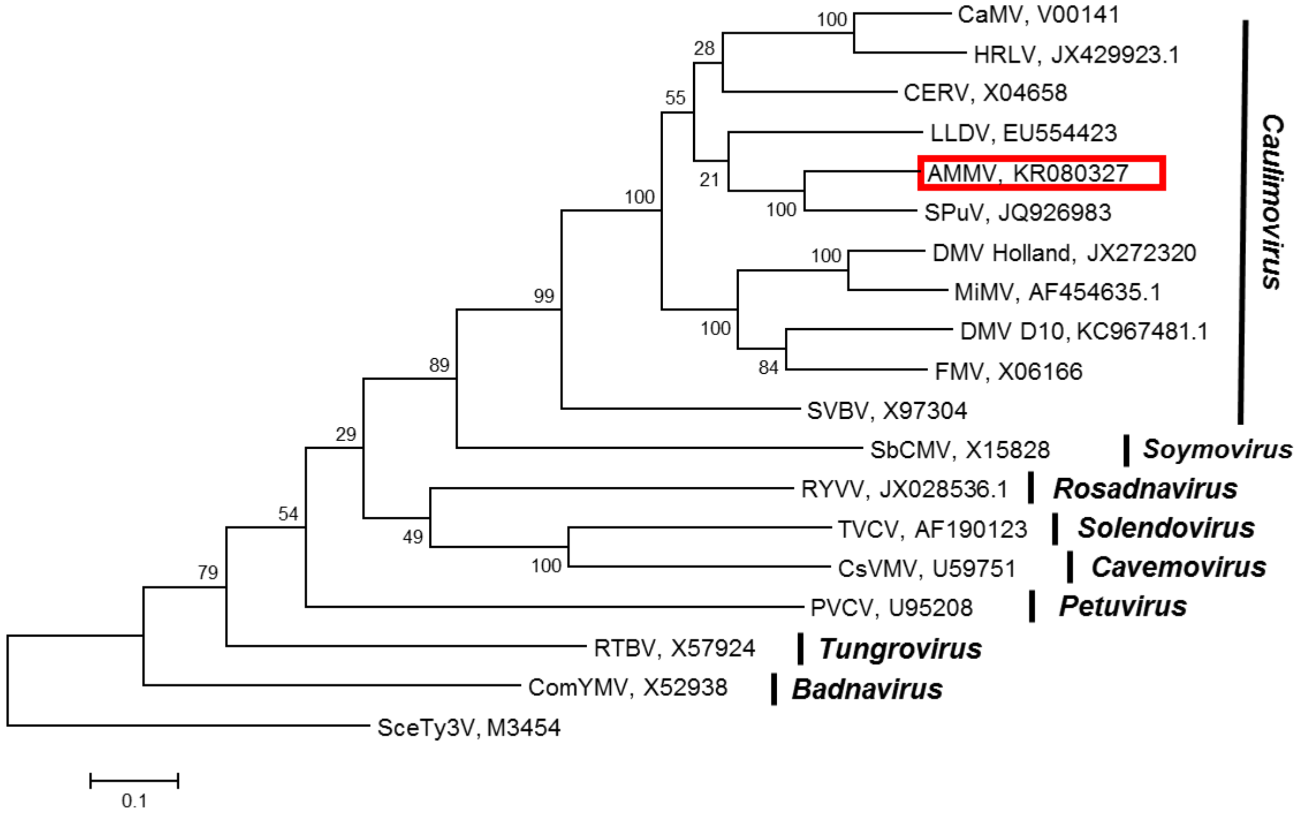

Fig. 1. Phylogenetic tree showing placement of *Atractylodes mild mottle virus* (AMMV) in the genus *Caulimovirus*, based on reverse transcriptase-RNase H gene sequences.

Evolutionary relationships were inferred using the maximum likelihood method, as implemented in MEGA v. 6.06. Bootstrap values from 1000 re-samplings are shown in the nodes of the branches. Type species of other genera in the *Caulimoviridae* are also included. The proposed new species is highlighted in the red box and accession numbers are provided next to each acronym. CaMV: *Cauliflower mosaic virus*; HRLV: *Horseradish latent virus*; CERV: *Carnation etched ring virus*; LLDV: *Lamium leaf distortion virus*; AMMV: *Atractylodes mild mottle virus*; SPuV: *Soybean Putnam virus*; DMV: *Dahlia mosaic virus*; MiMV: *Mirabilis mosaic virus*; FMV: *Figwort mosaic virus*; SVBV: *Strawberry vein banding virus*; SbCMV: *Soybean chlorotic mottle virus;* RYVV: *Rose yellow vein virus;* TVCV: *Tobacco vein clearing virus*; CsVMV*: Cassava vein mosaic virus*; PVCV: *Petunia vein clearing virus*; RTBV: *Rice tungro bacilliform virus*; ComYMV: *Commelina yellow vein mosaic virus*; SceTy3V: *Saccharomyces cerevisiae Ty3 virus*.

Table 1: Pairwise percent nucleotide identities for members of the genus *Caulimovirus* within the conserved reverse transcriptase-RNAseH domains of open reading frame 3. Data for the new species are highlighted in yellow. The sequences that were analysed corresponded to nucleotides 4437-5648 of *Cauliflower mosaic virus* (GenBank V00141.1)

	CaMV	AMMV	SPuV	HRLV	LLDV	CERV	MV_Hollar	MiMV	DMV_D10	FMV	SVBV	SbCMV	PVCV	TVCV	CsVMV	ComYMV	RTBV	SceTy3V	RYVV
CaMV																			
AMMV	67,9012																		
SPuV	68,4303	78,6596																	
HRLV	79,8942	67,3721	69,3122																
LLDV	67,5485	69,5767	69,4004	66,4021															
CERV	68,6067	69,6649	70,2822	67,1958	68,9594														
DMV_Holland	65,4321	67,1958	67,1958	63,4921	67,9012	66,843													
MiMV	64,7266	67,7249	67,9894	63,2275	67,1958	67,0194	82,8042												
DMV_D10	65,5203	66,7549	68,5185	63,1393	67,1076	67,5485	70,5467	70,4586											
FMV	64,8148	67,5485	67,1076	63,8448	66,5785	66,5785	72,3986	70,0176	72,6631										
SVBV	61,7284	64,1093	62,4339	59,1711	60,4938	60,8466	59,2593	61,1111	58,5538	61,8166									
SbCMV	53,4392	52,1164	54,321	52,6455	51,7637	52,2928	52,2046	51,1464	52,2046	52,7337	52,381								
PVCV	49,7354	49,1182	48,5009	47,5309	49,3827	50,3527	50,6173	49,03	48,4127	49,8236	47,2663	46,3845							
TVCV	52,2928	51,2346	51,2346	49,6473	50,8818	52,5573	53,6155	54,0564	54,1446	52,9101	52,2046	50,0882	48,6772						
CsVMV	49,1182	50,5291	52,2046	50,0882	52,0282	50,97	51,2346	51,4991	52,1164	51,5873	51,7637	49,9118	47,0899	62,6102					
ComYMV	47,5309	48,8536	48,5891	47,7072	45,679	46,4727	47,4427	48,6772	48,5891	48,06	47,7072	46,4727	45,3263	46,649	46,3845				
RTBV	50,2646	48,4127	48,4127	49,2945	47,5309	46,9136	49,4709	49,8236	49,03	49,6473	46,9136	47,8836	47,2663	53,8801	51,6755	49,9118			
SceTy3V	45,1499	46,4727	45,5026	44,2681	45,7672	44,5326	46,1199	44,3563	46,2963	45,5026	43,739	44,4444	43,5626	43,2099	43,739	46,0317	45,8554		
RYVV	50,2646	51,4991	50,3527	48,5891	51,5873	50,8818	53,2628	51,4109	51,4991	52,0282	53,7919	48,1481	47,5309	52,9101	53,9683	48,5891	50,3527	45,8554	