



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**

<b>Code assigned:</b>	<b>2015.017aP</b>	(to be completed by ICTV officers)			
<b>Short title:</b> Five new species in the genus <i>Sobemovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 10 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input type="checkbox"/>	10 <input checked="" type="checkbox"/>

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**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)

Sobemovirus

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

Date first submitted to ICTV: June 2015  
Date of this revision (if different to above):

**ICTV-EC comments and response of the proposer:**

EC comments: Correct mis-spelling of Rottboellia (not Roettboellia in various places). Check whether the use of *Artemisia chlorotic mosaic virus* rather than *Artemisia virus A* was really necessary.

Response: Rottboellia is now corrected and *Artemisia virus A* will keep its name.

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	<b>2015.017aP</b>	(assigned by ICTV officers)
<b>To create 5 new species within:</b>		
Genus:	<i>Sobemovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<i>unassigned</i>	
Order:		
<b>Name of new species:</b>	<b>Representative isolate: (only 1 per species please)</b>	<b>GenBank sequence accession number(s)</b>
<i>Artemisia virus A</i>	Switzerland	JN620802
<i>Cymbidium chlorotic mosaic virus</i>	Cym92-20	LC019764
<i>Papaya lethal yellowing virus</i>	26	JX123318
<i>Rottboellia yellow mottle virus</i>	Nigeria	KC577469
<i>Soybean yellow common mosaic virus</i>	South Korea	JF495127

**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

The members of the genus *Sobemovirus* have a linear monopartite, positive-sense, single stranded RNA genome, 4,003-4,575 nucleotides in length and non-enveloped icosahedral particles with a diameter of 25-33 nm. The genome is characterized by a viral genome-linked protein (VPg) covalently bound to its 5’ end, a non polyadenylated 3’ terminus, a polycistronic organization with five open reading frames and a frameshift signal UUUAAAC between ORF2a and 2b (see Figure 1).

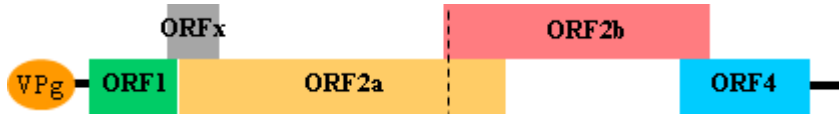


Figure 1: Diagram of the genome organization of the genus *Sobemovirus*

ORF1 encodes P1 a poorly conserved protein involved in the gene silencing suppression and systemic movement. ORF2a encodes a serine protease (motif H(X32)D(X62)TXXGWSK), VPg, the protein P10 with ATPase property and the protein P8 with RNA binding property. ORF2b encodes RNA-dependent RNA polymerase (motif T(X3)N(X19)GDD). ORF3 is translated to the coat protein (CP) from the subgenomic RNA (motif ACAAA). The translation of the ORFx of unknown function is initiated at a non-AUG site AUC. Another characteristic of the sobemoviruses is their narrow host range.

Current species demarcation criteria in the genus are: overall genome sequence identity less than 75%, host range and serological relatedness (Truve and Fargette, 2012).

The five new species share all these features, the phylogenetic relationships within the genus are depicted in Figure 2.

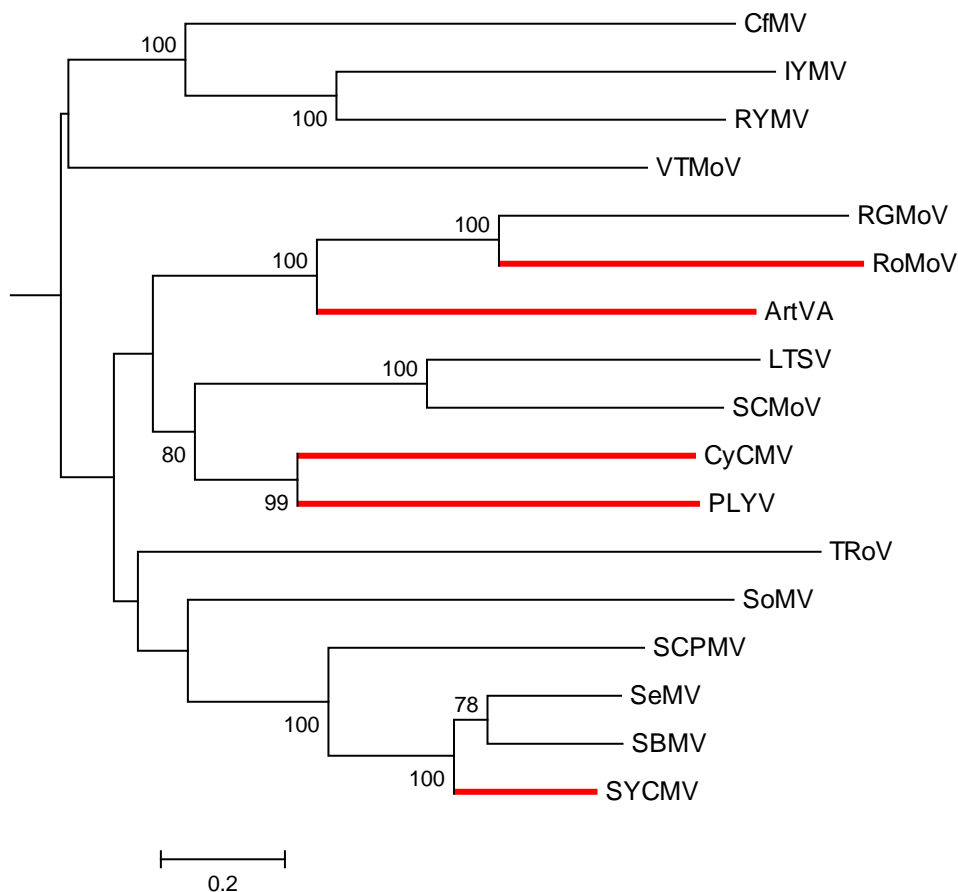


Figure 2: Phylogenetic tree inferred by maximum likelihood method from the full sequences of members of the genus *Sobemovirus*. Abbreviations: CfMV *Cocksfoot mottle virus* (accession number Z48630), IYMV *Imperata yellow mottle virus* (AM990928), RYMV *Rice yellow mottle virus* (L20893), VTMoV *Velvet tobacco mottle virus* (HM754263), RGMoV *Ryegrass mottle virus* (AB040446), RoMoV *Rottboellia yellow mottle virus* (KC577469), ArtVA *Artemisia*

virus A (JN620802), CyCMV Cymbidium chlorotic mosaic virus (LC019764), PLYV Papaya lethal yellowing virus (JX123318), LTSV *Lucerne transient streak virus* (U31286), SCMoV *Subterranean clover mottle virus* (AF208001), TRoV *Turnip rosette virus* (AY177608), SoMV *Sowbane mosaic virus* (AM940437), SCPMV *Southern cowpea mosaic virus* (M23021), SeMV *Sesbania mosaic virus* (AY004291), SBMV *Southern bean mosaic virus* (AF055887), SYCMV Soybean yellow common mosaic virus (JF495127).

#### **Artemisia virus A (ArtVA)**

This virus was isolated from sweet wormwood (*Artemisia annua*) (Ramel et al, 2013). The overall genome sequence identity of ArtVA is 70% with RoMoV and 72% with RGMoV.

#### **Cymbidium chlorotic mosaic virus (CyCMV)**

This virus was isolated from an orchid (*Cymbidium goeringii*) (Kondo et al, 2015). The overall genome sequence identity of CyCMV is 63% with PLYV and 74% with LTSV and SCMoV.

#### **Papaya lethal yellowing virus (PLYV)**

This virus was isolated from papaya (*Carica papaya*) (Peirera et al, 2012). The overall genome sequence identity of PLYV is 63% with CyCMV, 69% with LTSV and 70% with SCMoV.

#### **Rottboellia yellow mottle virus (RoMoV)**

Isolated from itchgrass (*Rottboellia cochinchinensis*) in Nigeria (Thottappilly et al., 1992), this virus infects also maize and congograss (*Imperata cylindrica*) (Somera and Truve, 2015). Proposed to be a member of the genus *Sobemovirus* (Thottappilly et al., 1992), entered to the list of the tentative species (Hull and Fargette, 2005), left out from the list of sobemovirus species (Truve and Fargette, 2012) because there were some similarities with *Imperata yellow mottle* (symptoms, virus particle size, host range) (Séréme et al, 2008) and there was no sequence data available. The overall genome sequence identity of RoMoV is 57% with RGMoV and 70% with ArtVA.

#### **Soybean yellow common mosaic virus (SYCMV)**

Isolated from soybean (*Glycine max*), the experimental host range includes also *Glycine soja* (Nam et al., 2012). The overall genome sequence identity of SYCMV is 31% with SBMV and 30% with SeMV.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

- Hull R and Fargette D. Genus Sobemovirus. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA (eds) *Virus Taxonomy*. Elsevier, Eighth Report of the International Committee on the Taxonomy of Viruses, 2005 pp 885–890.
- Kondo H, Takemoto S, Maruyama K, Chiba S, Andika IB, Suzuki N. Cymbidium chlorotic mosaic virus, a new sobemovirus isolated from a spring orchid (*Cymbidium goeringii*) in Japan. *Arch Virol*. 2015 May 31. [Epub ahead of print].
- Nam M, Kim JS, Park SJ, Park CY, Lee JS, Choi HS, Kim JS, Kim HG, Lim S, Moon JS, Lee SH. Biological and molecular characterization of Soybean yellow common mosaic virus, a new species in the genus Sobemovirus. *Virus Res*. 2012 Jan;163(1):363-7.
- Pereira AJ, Alfenas-Zerbini P, Cascardo RS, Andrade EC, Murilo Zerbini F. Analysis of the full-length genome sequence of papaya lethal yellowing virus (PLYV), determined by deep sequencing, confirms its classification in the genus Sobemovirus. *Arch Virol*. 2012 Oct;157(10):2009-11.
- Ramel ME, Gugerli P, Besse S, Simonnet X, Balmelli C. Molecular characterization of artemisia virus A, a new sobemovirus isolated from *Artemisia annua*. *Arch Virol*. 2013 Feb;158(2):463-6.
- Séréme D, Lacombe S, Konaté M, Pinel-Galzi A, Traoré VS, Hébrard E, Traoré O, Brugidou C, Fargette D, Konaté G. Biological and molecular characterization of a putative new sobemovirus infecting *Imperata cylindrica* and maize in Africa. *Arch Virol* 2008 153:1813–1820.
- Sõmera M, Truve E. Rottboellia yellow mottle virus is a distinct species within the genus Sobemovirus. *Arch Virol*. 2015 Mar;160(3):857-63.
- Thottappilly G, van Lent JWM, Rossel HW, Sehgal OP. Rottboellia yellow mottle virus, a new sobemovirus affecting *Rottboellia cochinchinensis* (Itch grass) in Nigeria. *Ann Appl Biol*. 1992 120:405–415.
- Truve E, Fargette D. Genus Sobemovirus. In: King AMQ, Carstens E, Adams M, Lefkowitz E (eds) *Virus Taxonomy*. Elsevier, Ninth Report of the International Committee on Taxonomy of Viruses, 2012 pp 1185–1189.

**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.