



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>	<i>2011.011aP</i>	(to be completed by ICTV officers)			
<b>Short title:</b> Create species <i>Imperata yellow mottle virus</i> in the genus <i>Sobemovirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

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

Drissa Sérémé (sereme@gmail.com), Séverine Lacombe, Moumouni Konaté, Agnès Pinel-Galzi, Valentin Stanislas Edgar Traoré, Eugénie Hébrard, Oumar Traoré, Christophe Brugidou, Denis Fargette, Gnissa Konaté

**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 Study Group**

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

---

---

Date first submitted to ICTV:

15 August 2011

Date of this revision (if different to above):

---

## 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>2011.011aP</b>	(assigned by ICTV officers)
<b>To create a new species within:</b>		
Genus:	<b><i>Sobemovirus</i></b>	Fill in all that apply. <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created (in a later module, below) write “<b>(new)</b>” after its proposed name.</li> <li>• If no genus is specified, enter “<b>unassigned</b>” in the genus box.</li> </ul>
Subfamily:		
Family:	<b><i>Unassigned</i></b>	
Order:		
<b>And name the new species:</b>		<b>GenBank sequence accession number(s) of reference isolate:</b>
<b><i>Imperata yellow mottle virus</i></b>		<b>AM990928</b>

### 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

A new virus was isolated from both the grass *Imperata cylindrica* and maize plants that had yellow mottle symptoms in Burkina Faso, West Africa [1]. Virus has isometric particles ca. 32 nm in diameter. Koch’s postulates were completed by mechanically inoculating uninfected *Imperata* or maize with either purified virus or sap from infected *Imperata* plants. The virions contain a single coat protein of 29.1 kDa. The genome consists of a single-stranded, positive-sense monopartite RNA of 4,547 nucleotides in length. These properties resembled those of members of the genus *Sobemovirus* [2].

The genome of the new virus was completely sequenced. The genomic RNA contained four ORFs (Fig. 1) flanked by 5' and 3' -untranslated sequences of 44 and 166 nt, respectively. The genome organization was typical of sobemoviruses. In addition, for the new virus, several amino acid motifs characteristic of sobemovirus group were identified. Indeed, ORF2a (713-2,509 nt) encodes a predicted serine protease and a viral genome-linked protein (VPg) including the two motifs H(X32)D(X62)TXXGWSG and WGD (1,868–1,876 nt) together with D- and E-rich sequences, characteristic of serine proteases and of VPgs, respectively [2]. ORF2b (2,176–3,768 nt) encodes the RNA-dependent RNA polymerase (RdRp) where the T(X3)N(X19)GDD typical motif of sobemovirus [3] was identified (see Fig. 1).

BLAST searches with the full genome of the new virus revealed matches with several members of the genus *Sobemovirus*. Then, we performed phylogenetic analysis

using all available sequences from the type isolates of members of the genus *Sobemovirus* and from *Potato leafroll virus*, a member of the genus *Polerovirus*, which was used as an outgroup. The analysis confirmed the grouping of the virus with other members of the genus *Sobemovirus* (Fig. 2).

The new virus was only distantly related to other sobemoviruses. Sequence identity when compared to other sobemoviruses was between 3.9 and 17.4% for the P1 amino acid sequence, 21.3 and 39.1% for the predicted serine protease and the viral genome-linked protein (VPg), 41.2 and 61.9% for the RdRp, and 19.9 to 43.5% for the CP amino acid sequence [1]. Based on similarity with sobemovirus RYMV, the proteolytic cleavage between the polyprotein and coat protein was suggested to occur at E322/S323 and Q418/S419 [1].

Current species demarcation criteria within the genus *Sobemovirus* (as defined in the Ninth Report) is that different species have overall genome sequence identity less than about 75%. Nucleotide identity shared between the new virus and *Rice yellow mottle virus* (RYMV) (56.5%), the virus most closely related to the new one, was lower than that between *Southern bean mosaic virus* (SBMV) and *Sesbania mosaic virus* (SeMV) (71.5%) the two most closely related sobemoviruses, and also lower than that between *Lucerne transient streak virus* (LTSV) and *Subterranean clover mottle virus* (SCMoV), another pair of sobemoviruses with 61.0% identity throughout their complete genomes (Table 1). Other useful criteria include serological reactions and host range. Similarly to other sobemoviruses, the host range of the new virus was narrow, restricted to *Imperata cylindrica*, *Rottboellia exaltata* and *maize*. This virus is also serologically distinct from RYMV. The new virus is mechanical transmitted but not seed-transmitted. Consistently, all sobemoviruses that infect monocotyledons, i.e., RYMV, *Cocksfoot mottle virus* (CfMV), *Ryegrass mottle virus* (RGMoV), are not seed-transmitted. The vector (if any) for this virus is not known.

Altogether, these data suggest that the new virus should be classified as a new species in the genus *Sobemovirus*. The name *Imperata yellow mottle virus* (IYMV) was proposed for this new virus species that differs from all previously described sobemoviruses.

MODULE 9: **APPENDIX**: supporting material

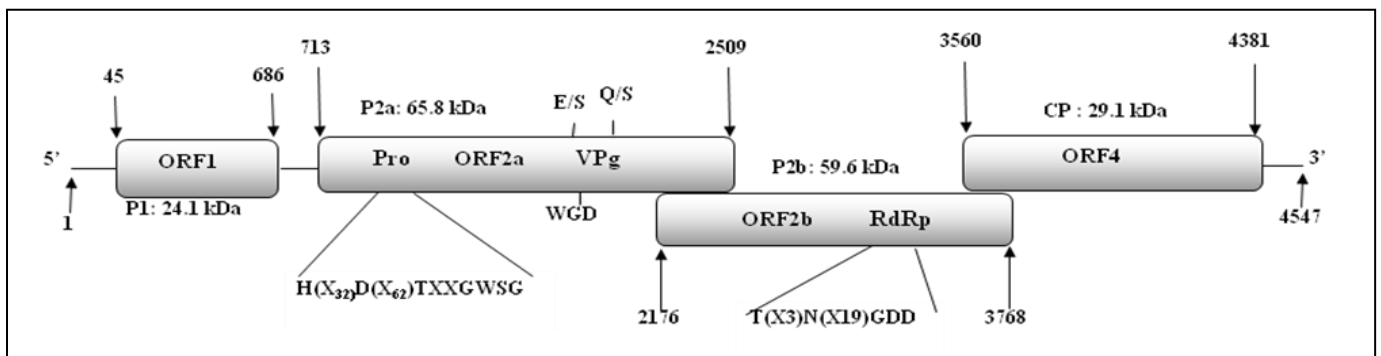
additional material in support of this proposal

**References:**

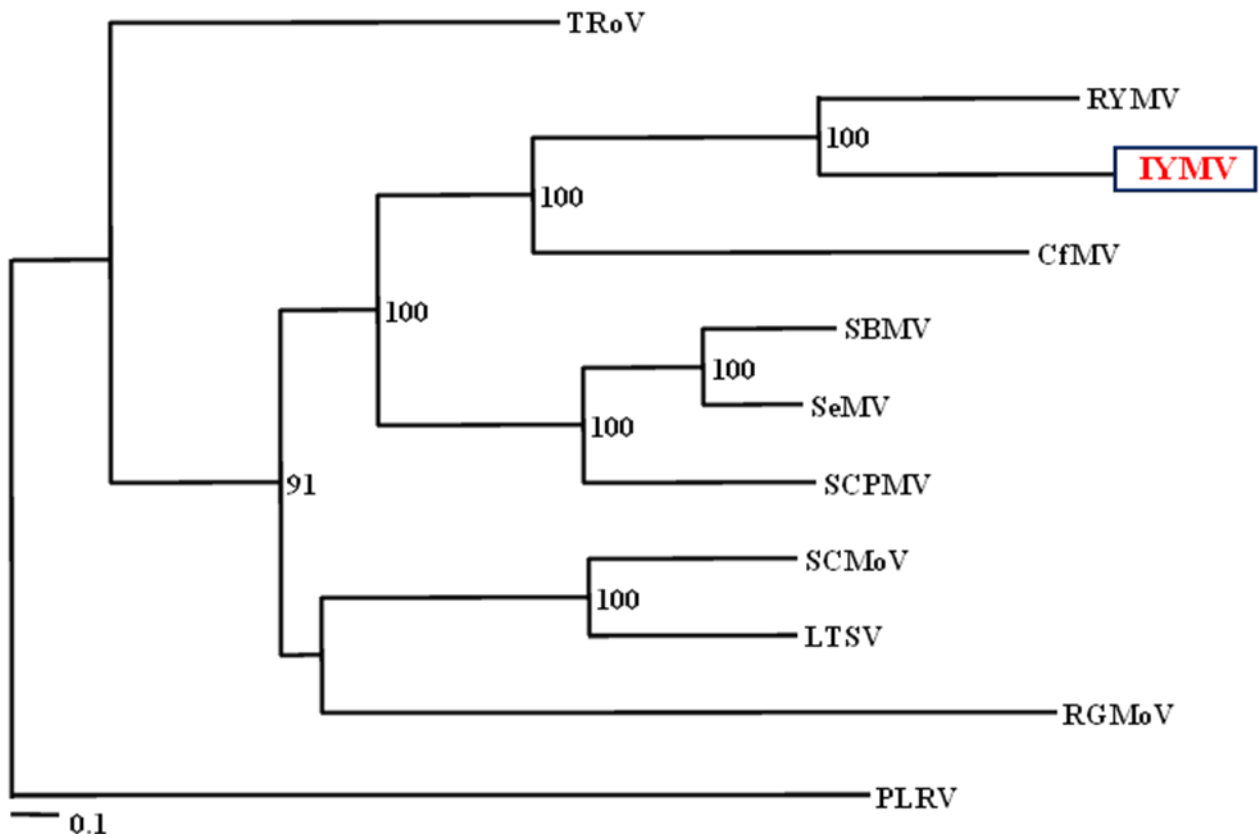
1. Sérémé, D., Lacombe, S., Konaté, M., Pinel-Galzi, A., Traoré, V. S. E., Hébrard, E., Traoré, O., Brugidou, C., Fargette, D., Konaté, K. (2008). Biological and molecular characterization of a new putative sobemovirus infecting *Imperata cylindrica* and maize in Africa. *Archives of virology*, 153:1813-20
2. Tamm, T., and Truve, E. (2000). Sobemoviruses. *Journal of virology*, 74:6231-6241
3. Balke, I., Resevica, G., Zeltins, A. (2007). The Ryegrass mottle virus genome codes for a sobemovirus 3C-like serine protease and RNA-dependent RNA polymerase translated via-1 ribosomal frameshifting. *Virus Genes* 35:395-398.

**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.



**Fig. 1** (from Sérémé et al., 2008). Organization of the IYMV genome. Grey rectangles indicate the open reading frames (ORFs) predicted for the IYMV RNA. The name and deduced size of the ORF1 to ORF4 gene products are indicated (P1 protein coded by ORF1, P2a protein coded by ORF2a, P2b protein coded by ORF2b, CP putative coat protein). The nucleotide position at the beginning and end of each ORF is indicated. Important motifs in the genome and coded proteins are shown, e.g., consensus sequences for protease (Pro), VPg in ORF2a, and RdRp in ORF2b. The locations of putative VPg cleavage sites are shown as vertical lines in the coding region, above which the peptide sequence at each site (E/S, Q/S) is indicated. Conserved motifs characteristic of a putative protease (H(X<sub>32</sub>) D(X<sub>62</sub>)TXXGWSG), VPg (WGD) and RdRp (T(X<sub>3</sub>)N(X<sub>19</sub>)GDD) are indicated.



**Fig. 2** (from Sérémé et al., 2008). Phylogenetic relationships of the new virus (*boxed*) and other sobemoviruses inferred by maximum likelihood from the full genome sequences. Sobemoviruses infecting monocotyledons include: cocksfoot mottle virus (CfMV, NC002618), ryegrass mottle virus (RGMoV, EF091714), rice yellow mottle virus (RYMV, AJ608218). Sobemoviruses infecting dicotyledons include: lucerne transient streak virus (LTSV, NC001696), southern bean mosaic virus (SBMV, L34672), subterranean clover mottle virus (SCMoV, NC004346), sesbania mosaic virus (SeMV, AY004291), southern cowpea mosaic virus (SCPMV, NC001625), and turnip rosette virus (TRoV, NC004553). Potato leafroll virus (PLRV, AF453394), a member of the genus *Polerovirus* was used as an outgroup. The bootstrap support of the branch nodes is given. Only bootstrap scores exceeding 75% are shown. The scale bar represents the number of nucleotide substitutions per site.

Table 1. Nucleotide sequence identities (in %) between IYMV and other sobemoviruses (from Sérémé et al., 2008)

	IYMV	CfMV	LTSV	RGMoV	SBMV	SCMoV	SeMV	SCPMV	TRoV
CfMV	45.4								
LTSV	41.8	44.1							
RGMoV	40.3	41.8	42.9						
SBMV	44.7	44.6	44.4	42.7					
SCMoV	41.7	43.7	61.0	43.1	45.1				
SeMV	44.3	45.0	46.7	44.0	71.5	46.5			
SCPMV	44.1	44.4	45.8	44.3	58.0	45.4	59.8		
TRoV	41.7	41.3	44.5	41.7	44.4	44.9	45.9	44.7	
RYMV	56.5	46	42.6	41.8	43.5	42.9	44.2	44.9	41.1