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:	***2015.008a-gM***	(to be completed by ICTV officers)

Short title: Establishment of one (1) new family (*Mymonaviridae*) including one (1) new genus with one (1) new species, in the order *Mononegavirales*
(e.g. 6 new species in the genus *Zetavirus*)

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

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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)	ICTV *Bornaviridae*, *Filoviridae*, *Nyamiviridae*, *Paramyxoviridae*, and *Rhabdoviridae* Study Groups

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

Date first submitted to ICTV:	June 15, 2015
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	***2015.008aM***	(assigned by ICTV officers)

To create one new species within:

Genus:	***Sclerotimonavirus*** **(new)**
Subfamily:	
Family:	***Mymonaviridae*** **(new)**
Order:	***Mononegavirales***

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)**
Sclerotinia sclerotimonavirus	Sclerotinia sclerotiorum negative-stranded RNA virus 1 (SsNSRV-1) AH-98	KJ186782

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

Sclerotinia sclerotiorum negative-stranded RNA virus 1 (SsNSRV-1) was originally isolated from hypovirulent strain AH-98 of *Sclerotinia sclerotiorum*, a fungal plant pathogen. Enveloped filamentous virion–like structures and nucleocapsids of SsNSRV-1 were observed in culture and are reminiscent of virions formed by filoviruses and certain rhabdoviruses. The SsNSRV-1 virion-like structures are 25–50 nm in width and ≈1000 nm in length; the nucleocapsids are long, flexible and helical, 22 nm in diameter and 200–2000 nm in length. Furthermore, nucleoprotein (NP) monomers that make up these coils could be observed (Figure 1a). The coding-complete genome of SsNSRV-1 is 10,002 nt in length and contains 6 non-overlapping and linearly arranged open reading frames (ORF I-VI) (Figure 1b; expression map is in Figure 1c). Both genome length and overall ORF organization are reminiscent of those of mononegaviruses. The gene-junction sequences [(A/U)(U/A/C)UAUU(U/A)AA(U/G)AAAACUUAGG(A/U)(G/U)] of SsNRSV-1 fit those of other mononegavirues. Finally, ORF V encodes an RNA-dependent RNA polymerase (RdRp, L) containing the mononegaviral RdRp domain (pfam00946). Together, these data indicate that SsNSRV-1 is a novel member of the order *Mononegavirales*.

However, SsNSRV-1 differs significantly from all members of currently established mononegaviral families. Phylogenetical analysis of the RdRp domain of SsNSRV-demonstrated that SsNSRV-1 is very distantly related to viruses of mononegaviral families *Bornaviridae* and *Nyamiviridae* (Figure 2). The genome of SsNSRV-1 contains 6 ORFs, but

ORF II encodes NP, whereas members of other mononegavirus families encode this protein via ORF1. Furthermore, the SsNSRV-1 contains an additional ORF (ORF VI) downstream of ORF V (RdRp), whereas the RdRp-encoding ORF is the final ORF in all other known mononegaviruses (Figure 3). Finally, SsNSRV-1 infects fungi, whereas no other fungus-infecting mononegaviruses have been described.

Based on the unique characteristics, SsNSRV-1 represents a new mononegavirus species to be included in a new genus and family within the order *Mononegavirales*.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2015.008bM***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	
Family:	***Mymonaviridae***
Order:	***Mononegavirales***

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	***2015.008cM***	(assigned by ICTV officers)

To name the new genus: *Sclerotimonavirus*

Assigning the type species and other species to a new genus

Code	***2015.00d8M***	(assigned by ICTV officers)

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

Sclerotinia sclerotimonavirus

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

See Module 2

Origin of the new genus name:

Sclerotimonavirus: sigil of Sclerotinia sclerotiorum, *Mononegavirales*, and *virus*

Reasons to justify the choice of type species:

Only one species is proposed to be included in this genus, making it the type species by default.

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.

See Module 3

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2015.008eM***	(assigned by ICTV officers)

To create a new family containing the subfamilies and/or genera listed below within the Order: ***Mononegavirales***

Code	***2015.008fM***	(assigned by ICTV officers)

To name the new family: ***Mymonaviridae***

assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)

To assign the following subfamilies (if any) to the new family:

N/A

Code	***2015.008gM***	(assigned by ICTV officers)

To assign the following genera to the new family:

You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family

Sclerotimonavirus

The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):**

N/A

Reasons to justify the creation of the new family:

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

- See Module 2

Origin of the new family name:

Mymonaviridae: sigil of Mycota (fungi), *Mononegavirales*, and the family-specific suffix *viridae*

Figure 1

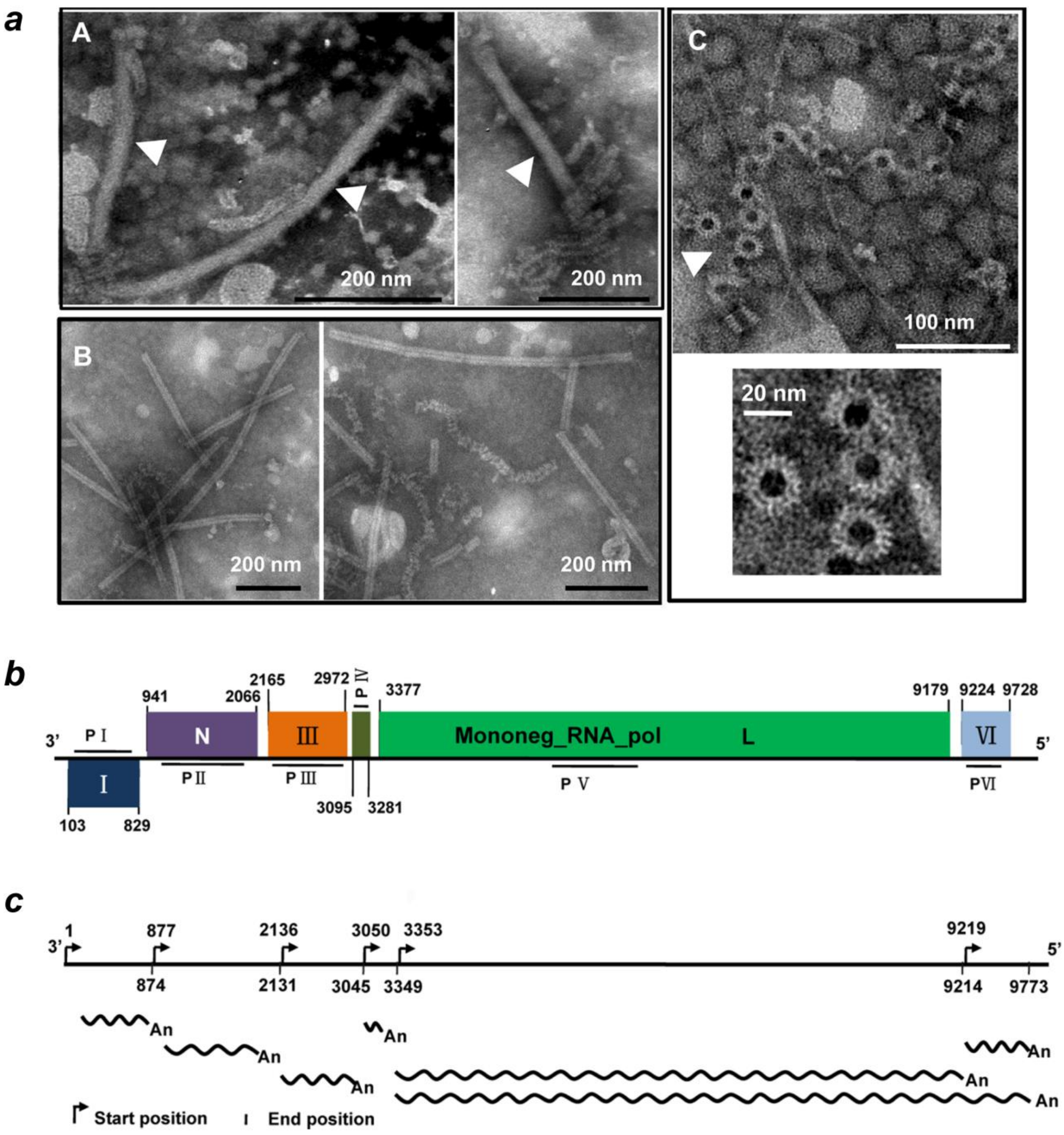

Figure 1. Virion morphology and genome organization and expression map of Sclerotinia sclerotiorum negative-stranded RNA virus 1 (SsNSRV-1). (*a*) Morphology and structure of SsNSRV-1 virions and nucleoprotein–RNA complexes (RNPs). Particles and RNPs were purified from mycelia of strain AH98 and Ep-1PNA367-PT2 and negatively stained with 2 % PTA (W/V, pH 7.4) (scale bars are shown at the bottom). (A) Filamentous, possibly enveloped virions and RNPs. (B) Purified tight or loose coils of RNPs. (C) Rings that make up the coils and NP monomers. **(b)** Genomic organization of SsNSRV-1 showing all six ORFs. **(*c*)** Deduced transcription map of SsNSRV-1 based on 5'- and 3'-RACE. This figure was modified from Liu *et al*.

Figure 2

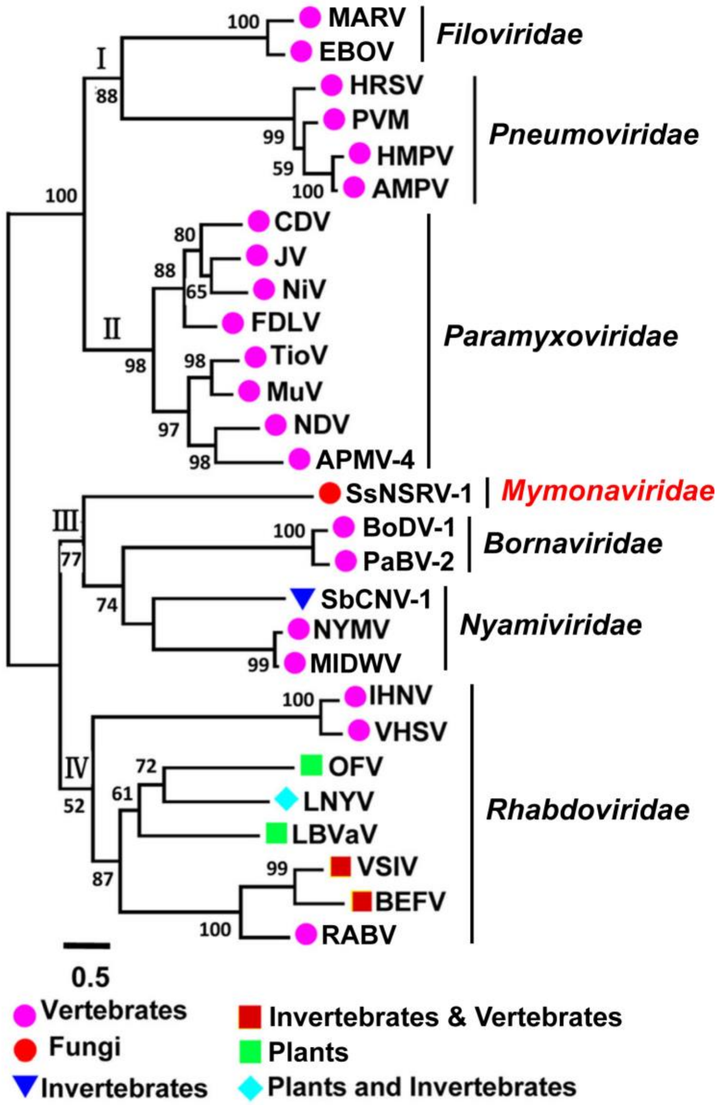

Figure 2. Phylogram of the core RdRP motifs of SsNSRV-1 and the selected mononegaviruses. The selected mononegaviruses were Ebola virus (EBOV), Marburg virus (MARV), human respiratory syncytial virus (HRSV), pneumonia virus of mice (PVM), avian metapneumovirus (AMPV), human metapneumovirus (HMPV), canine distemper virus (CDV), Nipah virus (NiV), Mumps virus (MuV), avian parainfluenza virus type 4 (APMV-4), Tioman virus (TioV), Newcastle disease virus (NDV), Fer-de-Lance virus (FDLV), J virus (JV), Borna disease virus 1 (BoDV-1), parrot bornavirus 2 (PaBV-2), infectious hemorrhagic necrosis virus (IHNV), viral hemorrhagic septicemia virus (VHSV), rabies virus (RABV), vesicular stomatitis Indiana virus (VSIV), bovine ephemeral fever virus (BEFV), lettuce necrotic yellows virus (LNYV), soybean cyst nematode virus 1 (SbCNV-1), Midway virus (MIDWV), Nyamanini virus (NYMV), orchid fleck virus (OFV), and lettuce big-vein associated virus (LBVaV). This figure was modified from Liu *et al*.

Figure 3

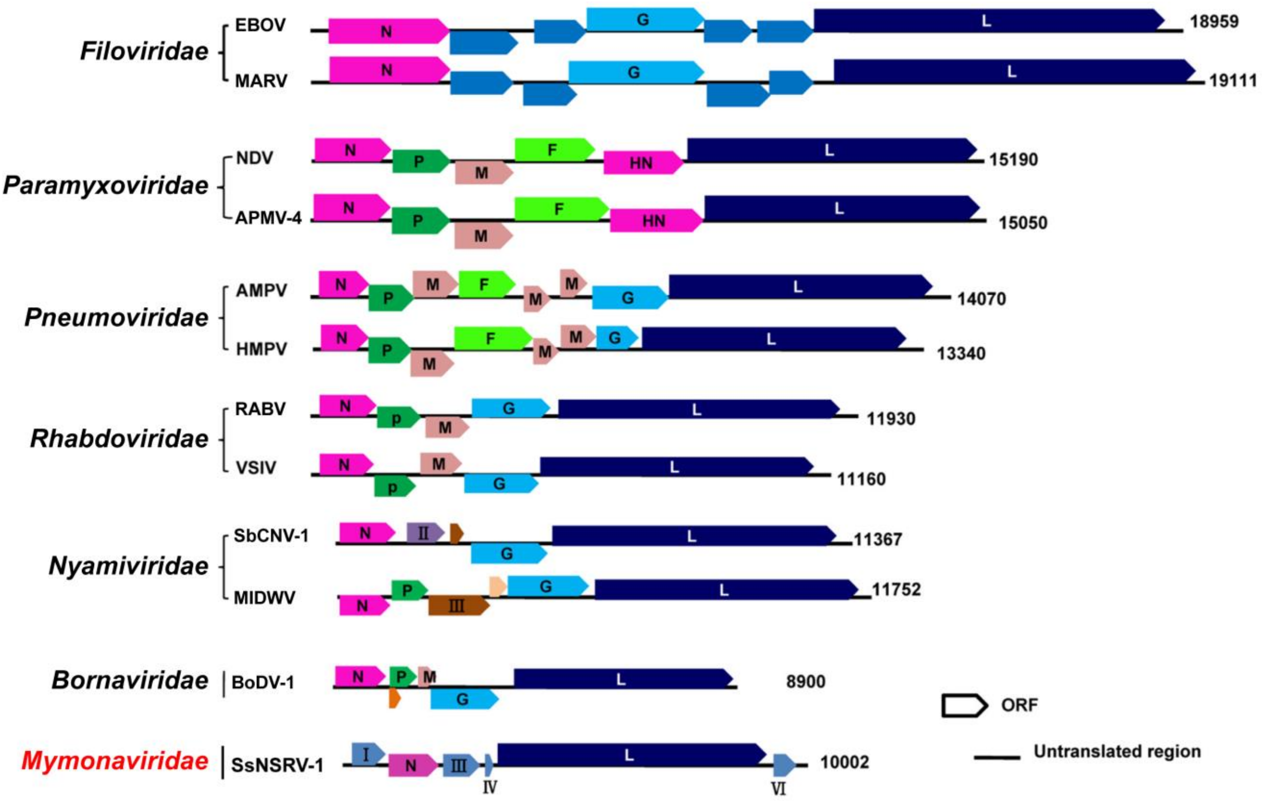

Figure 3. Comparison of the genome organization of Sclerotinia sclerotiorum negative-stranded RNA virus 1 (SsNSRV-1) and other selected mononegaviruses (abbreviations as in Figure 2). This figure was modified from Liu *et al*.

References:

Liu L, Xie J, Cheng J, Fu Y, Li G, Yi X and Jiang D. 2014. Fungal negative-stranded RNA virus that is related to bornaviruses and nyaviruses. Proc. Natl. Acad. Sci. USA 111(33): 12205-12210.