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:	***2013.002a-hV***	(to be completed by ICTV officers)

Short title: Create a family named *Nyamiviridae*, with 1 genus and 3 species, in the order *Mononegavirales*
(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** ☒	

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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 *Mononegavirales* Study Group Chairs of ICTV *Bornaviridae*, *Filoviridae*, *Rhabdoviridae*, and *Paramyxoviridae* Study Groups

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

Date first submitted to ICTV:	June, 2013
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	***2013.002aV***	(assigned by ICTV officers)

To create 2 new species within:

Genus:	***Nyavirus* (new)**
Subfamily:	**N/A**
Family:	***Nyamiviridae* (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Midway nyavirus	FJ554525= NC_012702
Nyamanini nyavirus	FJ554526= NC_012703

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

Nyamanini virus (NYMV) and Midway virus (MIDWV) are listed as unassigned viruses in the 9th ICTV Report ("form a distinct lineage in the order *Mononegavirales*") (Adams *et al*. 2011). NYMV was discovered in 1957 and isolated repeatedly thereafter in land birds and *Argas* soft ticks. It is endemic in South Africa, Egypt, Thailand, Nigeria, Nepal, and Sri Lanka. MIDWV was discovered in 1966 and isolated repeatedly thereafter in sea birds and *Ornithodoros* soft ticks. It is endemic in Hawaii, USA, and Japan. NYMV and MIDWV are serologically related, but clearly distinct from each other and not related serologically to any other virus tested (Taylor, Henderson *et al*. 1966; Taylor, Hurlbut *et al*. 1966; reviewed in Kuhn *et al*. 2013). Since both NYMV and MIDWV proofed also to be genomically distinct from other known viruses, and due to the different geographic distribution, different host spectrum, it is proposed to assign both viruses to separate novel species.

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	***2013.002bV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	**Unassigned**
Subfamily:	**N/A**
Family:	***Nyamiviridae* (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.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Soybean cyst nematode virus	HM849038

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

Soybean cyst nematode virus 1 (SbCNV-1, previously named soybean cyst nematode nyavirus) is a newly discovered agent that has thus far not been classified by the ICTV. It has been found in an inbred laboratory culture of the plant-parasitic soybean cyst nematode and in contrast to NYMV and MIDWV is not associated with ticks or birds (Bekal *et al*. 2011). The virus differs from NYMV and MIDWV in that its genome encodes one less ORF. SbCNV-1 ORF1, ORF4, and ORF5 are significantly similar to the N/ORF1, G/ORF5, and L/ORF6 proteins of MIDWV and NYMV. The ORF5 polymerase core module firmly places SbCNV-1 into the NYMV/MIDWV clade (Table 1, Figure 1). Consequently, a new species is proposed for SbCNV-1. Due to the different genome structure, and the overall clearer relationship between NYMV and MIDWV, it is proposed to leave this novel species unassigned to a genus, but assign to the same new family as NYMV and MIDWV.

MODULE 3: **NEW GENUS**

creating a new genus

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

Code	***2013.002cV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	**N/A**
Family:	***Nyamiviridae* (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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2013.002dV***	(assigned by ICTV officers)

To name the new genus: *Nyavirus*

Assigning the type species and other species to a new genus

Code	***2013.002eV***	(assigned by ICTV officers)

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

Nyamanini nyavirus (new)

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:**

2

Reasons to justify the creation of a new genus:

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

NYMV and MIDWV are clearly related (but distinct) serologically, have the same genome organization, show clear but distinct protein profile amino acid similarity, cluster together in nucleotide sequence analyses, and both infect ticks (albeit of different species) and birds (albeit of different species) (Mihindukulasuriya *et al*. 2009; Takahashi *et al*. 1980; Takahashi *et al*. 1982; reviewed in Kuhn *et al*. 2013; Table 1, Figure 1). These data justify the inclusion of the two proposed species into one novel genus.

Origin of the new genus name:

Sigil of the first three letters of geo. *Nya*manini Pan (place of isolation of Nyamanini virus in South Africa); and *-virus* – ending denoting a virus genus → Neo-Lat. n. neut. sg. *Nyavirus* – the genus of nyaviruses.

Reasons to justify the choice of type species:

Nyamanini virus (NYMV), the sole member of the proposed species *Nyamanini nyavirus*, was the first virus discovered among the group of viruses discussed here. It is also the best-characterized of the three viruses both ecologically and molecular-biologically.

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.

Members of the species *Midway nyavirus* are characterized by having the properties of nyaviruses (members of the proposed genus *Nyavirus*); having a full-length genomic sequence different from the "type virus" of the type species of the proposed genus *Nyavirus* (*Nyamanini virus*) by >30% and that of Midway virus <30%; and infecting soft ticks and/or seabirds (Kuhn *et al*. 2013).

Members of the species *Nyamanini nyavirus* are characterized by having the properties of nyaviruses (members of the proposed genus *Nyavirus*); having a full-length genomic sequence different from the "type virus" of the type species of the proposed genus *Nyavirus* (*Nyamanini virus*) by <30%; and infecting soft ticks and/or land birds (Kuhn *et al*. 2013).

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2013.002fV***	(assigned by ICTV officers)

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

If there is no Order, write "**unassigned**" here.
If the Order has yet to be created (in Module 6) please write **"(new)"** after the proposed name.

Code	***2013.002gV***	(assigned by ICTV officers)

To name the new family: *Nyamiviridae*

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:
You may list several subfamilies here. For each subfamily, please state whether it is new or existing.

- If the subfamily is new, it must be created in Module 4
- If the subfamily already exists, please complete Module 7 to 'REMOVE' it from its existing family

N/A

Code	***2013.002hV***	(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

***Nyavirus* (new)**

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):**

1

Reasons to justify the creation of the new family:
Additional material in support of this proposal may be presented in the Appendix, Module 9

MIDWV, NYMV, and SbCNV-1 clearly fulfill all the major criteria outlined in the 9th ICTV Report as members of the order *Mononegavirales*. However, their properties are clearly distinct from those of members of the established mononegaviral families *Bornaviridae*, *Filoviridae*, *Paramyxoviridae*, and *Rhabdoviridae* and they are in contradiction to the member inclusion criteria for these families (reviewed in (Kuhn *et al*. 2013; Table 2). Consequently, a new mononegaviral family needs to be established.

Origin of the new family name:

Sigil of the first three letters of geo. *Nya*manini Pan (place of isolation of Nyamanini virus in South Africa) and the first two letters of geo. *Mi*dway Atoll (place of isolation of Midway virus in the USA); and suff. -*viridae* – ending denoting a virus family → Neo-Lat. n. fem. pl.

Nyamiviridae – the family of nyamiviruses.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adams MJ, Christian P, Ghabrial SA, Knowles NJ, Lavigne R (2011) Unassigned Viruses. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Virus Taxonomy - Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, London, United Kingdom, pp 1199-1207

Bekal S, Domier LL, Niblack TL, Lambert KN (2011) Discovery and initial analysis of novel viral genomes in the soybean cyst nematode. J Gen Virol 92:1870-1879

Easton AJ, Pringle CR (2011) Order *Mononegavirales*. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ (eds) Virus Taxonomy - Ninth Report of the International Committee on Taxonomy of Viruses. Elsevier/Academic Press, London, United Kingdom, pp 653-657

Herrel M, Hoefs N, Staeheli P, Schneider U (2012) Tick-borne Nyamanini virus replicates in the nucleus and exhibits unusual genome and matrix protein properties. J Virol 86:10739-10747

Herrel M, Haag L, Nilsson J, Staeheli P, Schneider U (2013) Reverse genetics identifies the product of open reading frame 4 as an essential particle assembly factor of Nyamanini virus. J Virol [Epub May 22, 2013]

Kondo H, Chiba S, Toyoda K, Suzuki N (2013) Evidence for negative-strand RNA virus infection in fungi. Virology 435:201-209

Kuhn JH, Bekal S, Caì Y, Clawson AN, Domier LL, Herrel M, Jahrling PB, Kondo H, Lambert KN, Mihindukulasuriya KA, Nowotny N, Radoshitzky SR, Schneider U, Staeheli P, Suzuki N, Tesh RB, Wang D, Wang LF, Dietzgen RG (2013) Nyamiviridae: Proposal for a new family in the order *Mononegavirales*. Arch Virol [Epub May 1, 2013]

Mihindukulasuriya KA, Nguyen NL, Wu G, Huang HV, da Rosa AP, Popov VL, Tesh RB, Wang D (2009) Nyamanini and Midway viruses define a novel taxon of RNA viruses in the order *Mononegavirales*. J Virol 83:5109-5116

Takahashi M, Nii S, Casals J (1980) Hirota virus: A new tick-borne arbovirus related to Nyamanini. In: Vesenjak-Hirjan J (ed) Arboviruses in the Mediterranean countries: 6th FEMS symposium held under the auspices of the Yugoslav Academy of Sciences and Arts in Zagreb Zentralblatt für Bakteriologie, Mikrobiologie und Hygiene - 1. Abteilung Supplement 9. Gustav Fischer Verlag, Stuttgart, Germany

Takahashi M, Yunker CE, Clifford CM, Nakano W, Fujino N, Tanifuji K, Thomas LA (1982) Isolation and characterization of Midway virus: a new tick-borne virus related to Nyamanini. J Med Virol 10:181-193

Taylor RM, Henderson JR, Thomas LA (1966) Antigenic and other characteristics of

additional material in support of this proposal

References:

Quaranfil, Chenuda, and Nyamanini arboviruses. Am J Trop Med Hyg 15:87-90

Taylor RM, Hurlbut HS, Work TH, Kingston JR, Hoogstraal H (1966) Arboviruses isolated from *Argas* ticks in Egypt: Quaranfil, Chenuda, and Nyamanini. Am J Trop Med Hyg 15:76-86

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.

Table 1. Properties of NYMV, MIDWV, and SbCNV-1 expression products (taken from Kuhn *et al*. 2013; based on Bekal *et al*. 2011; Herrel *et al*. 2012; Herrel *et al*. 2013; Mihindukulasuriya *et al*. 2009; Takahashi *et al*. 1980; Takahashi *et al*. 1982)

Analogouys gene in other mononegavirus genomes	**NYMV / MIDWV / SbCNV-1 expression products**	**Presence of signal peptide**	**Percent amino acid similarity**
N gene analog of bornaviruses, paramyxoviruses, rhabdoviruses; *NP* analog of filoviruses	NYMV ORF1: 370 aa (42.0 kD/pI=6.95) MIDWV ORF1: 370 aa (41.4 kD/pI=7.36) SbCNV-1 ORF1: 412 aa (44.6 kD/pI=6.55)	No No No	NYMV-MIDWV: 80.3 NYMV-SbCNV-1: 18.9 MIDWV-SbCNV-1: 17.1
X gene analog of bornaviruses; *VP24* gene analog of filoviruses	NYMV ORF2: 214 aa (24.5 kD/pI=4.15) MIDWV ORF2: 230 aa (25.7 kD/pI=4.08)	No No	NYMV-MIDWV: 54.2 NYMV-SbCNV-1: N/A MIDWV-SbCNV-1: N/A
P gene analog of bornaviruses, paramyxoviruses, and rhabdoviruses; *VP35* gene analog of filoviruses	NYMV ORF3: 382 aa (44.6 kD/pI=9.03) MIDWV ORF3: 425 aa (49.1 kD/pI=8.40) SbCNV-1 ORF2: 281 aa (29.4 kD/pI=4.59)	No No No	NYMV-MIDWV: 56.3 NYMV-SbCNV-1: 14.6 MIDWV-SbCNV-1: 19.2
M gene analog of bornaviruses, paramyxoviruses, and rhabdoviruses; *VP40* gene analog of filoviruses	NYMV ORF4: 131 aa (15.1 kD/pI=9.84) MIDWV ORF4: 132 aa (15.3 kD/pI=9.11) SbCNV-1 ORF3: 80 aa (9.0 kD/pI=9.56)	No No No	NYMV-MIDWV: 68.2 NYMV-SbCNV-1: 20.0 MIDWV-SbCNV-1: 25.0
G gene analog of bornaviruses, paramyxoviruses, and rhabdoviruses; *GP* gene analog of	NYMV ORF5: 658 aa (74.1 kD/pI=6.83) MIDWV ORF5: 597 aa (67.4 kD/pI=7.46) SbCNV-1 ORF4: 561 aa (61.4 kD/pI=6.17)	Yes Yes Yes	NYMV-MIDWV: 66.2 NYMV-SbCNV-1: 17.1 MIDWV-SbCNV-1: 17.1

filoviruses			
L gene analog of bornaviruses, filoviruses, paramyxoviruses, and rhabdoviruses	NYMV ORF6: 1,936 aa (217.1 kD/pI=7.94) MIDWV ORF6: 1,935 aa (218.1 kD/pI=8.24) SbCNV-1 ORF5: 2,086 aa (236.3 kD/pI=8.30)	No No No	NYMV-MIDWV: 77.9 NYMV-SbCNV-1: 25.9 MIDWV-SbCNV-1: 25.5

N/A, not applicable. All values were calculated with the DNAStar Lasergene Suite, version 8.1.4.

Table 2. Overview of data justifying the need for a novel mononegavirus family for NYMV, MIDWV, and SbCNV-1 (taken from Kuhn *et al*. 2013; based on Bekal *et al*. 2011; Herrel *et al*. 2012; Herrel *et al*. 2013; Mihindukulasuriya *et al*. 2009; Takahashi *et al*. 1980; Takahashi *et al*. 1982; Taylor, Henderson *et al*. 1966; Taylor, Hurlbut et al. 1966)

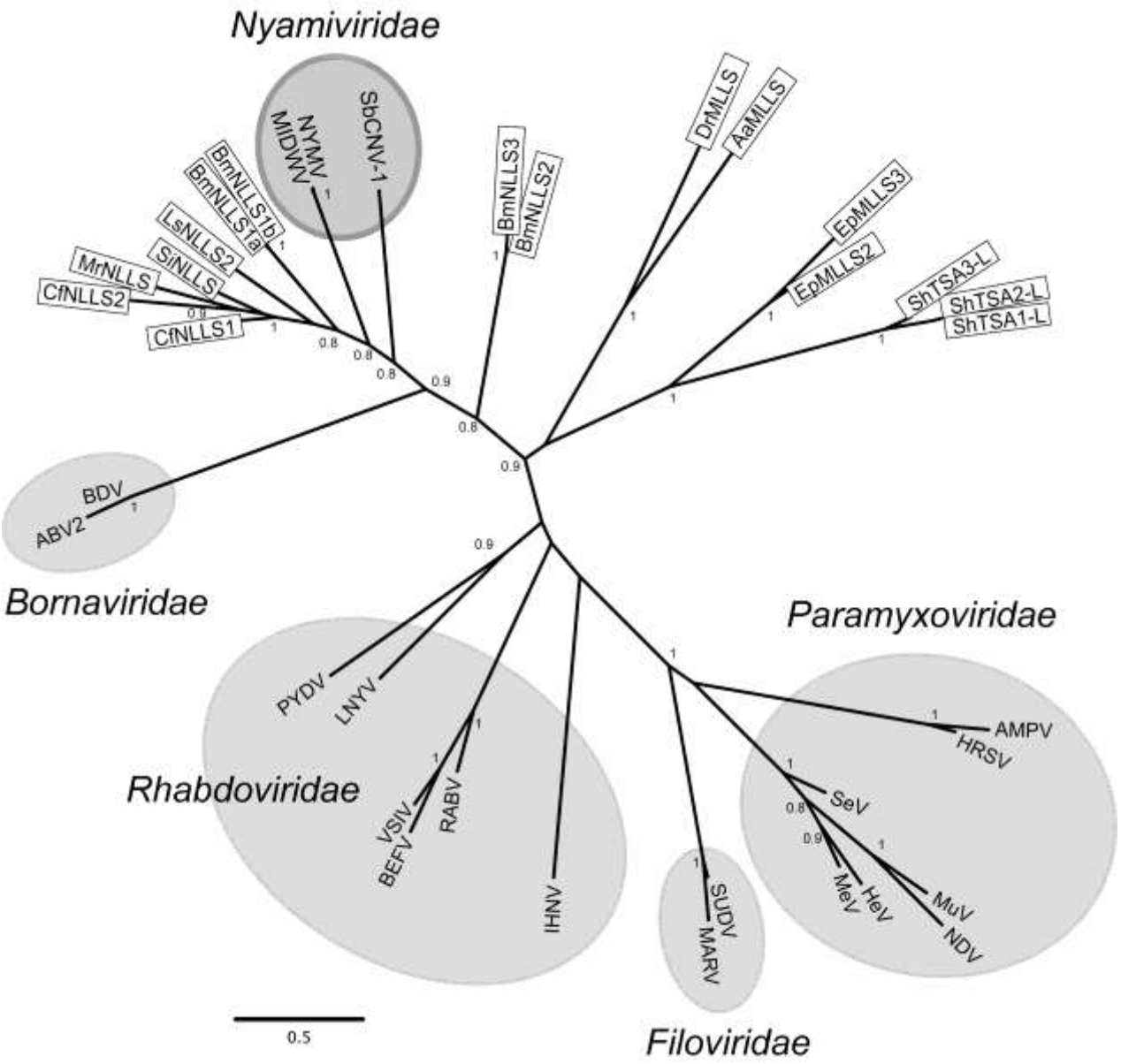
Mononegavirus family	**Member inclusion criteria as defined by the ICTV**	**Contradictory properties of NYMV, MIDWV, and SbCNV-1**
Bornaviridae		
	Genomes ≈9 kb in length	Genomes ≈11 kb in length
	Overlapping genes	No overlapping genes
	Gene splicing	unlikely
	Single matrix protein	NYMV and MIDWV: two matrix proteins
	N-glycosylated matrix protein	NYMV, MIDWV, and SbCNV-1 matrix proteins not *N*-glycosylated
	Spherical virions ≈90 nm in diameter	NYMV and MIDWV particles spherical and ≈ 130 nm in diameter
	Infect mammals and birds, but not arthropods or nematodes	NYMV and MIDWV infect ticks; SbCNV-1 infects nematodes
Filoviridae		
	Genomes ≈19 kb in length	Genomes ≈11 kb in length
	Overlapping genes	No overlapping genes
	RNA editing of the *GP* gene	no evidence of a slippery sequence in NYMV, MIDWV, or SbCNV-1 *G* genes
	3’ and 5’ genomic ends are fully complimentary	NYMV 3’ end protruding
	Replication exclusively in the cytoplasm	NYMV replication in the nucleus
	Formation of branched, 6-shaped, or filamentous virions ≥ 800 nm in length	NYMV and MIDWV particles spherical and ≈ 130 nm in diameter
	Infect nonhuman primates, pigs, and bats, but not arthropods or nematodes	NYMV and MIDWV infect ticks; SbCNV-1 infects nematodes
	Endemic in sub-Saharan Africa, Spain, and the Philippines	Not known to be endemic in these areas
	Cause viral hemorrhagic fever in humans and nonhuman primates	Not known to cause any disease in humans or nonhuman primates
Rhabdoviridae		
	3’ and 5’ genomic ends are fully complimentary	NYMV 3’ end protruding
	Single matrix protein	NYMV and MIDWV: two matrix proteins
	Replication exclusively in the cytoplasm (all rhabdoviruses except nucleorhabdoviruses)	NYMV replication in the nucleus
	Bullet-shaped, cone-shaped or bacilliform virions	NYMV and MIDWV particles spherical
	Infect all kinds of animals, plants, and arthropods, but not nematodes	NYMV and MIDWV infect ticks; SbCNV-1 infects nematodes
Paramyxoviridae		
	Genomes ≈15 kb in length	Genomes ≈11 kb in length

	3’ and 5’ genomic ends are fully complimentary	NYMV 3’ end protruding
	RNA editing of the *P* gene	no evidence of a slippery sequence in NYMV, MIDWV, or SbCNV-1 *P* genes
	Replication exclusively in the cytoplasm	NYMV replication in the nucleus
	Single matrix protein	NYMV and MIDWV: two matrix proteins
	At least two envelope proteins constituting the fusion machinery	One envelope protein
	Virions ≥150 nm	NYMV and MIDWV particles spherical and ≈ 130 nm in diameter
	Not known to infect ticks or nematodes	NYMV and MIDWV infect ticks; SbCNV-1 infects nematodes

Table 3. Proposed Virus Taxonomy (as outlined here and in Kuhn *et al*. 2013)

Order	**Family**	**Genus**	**Species**	**Virus (Abbreviation)**
Mononegavirales				
	Nyamiviridae (new)			
		Nyavirus (new)		
			Nyamanini nyavirus (new)	
				Nyamanini virus (NYMV)
			Midway nyavirus (new)	
				Midway virus (MIDWV)
		Unassigned (new)	*Soybean cyst nematode virus* (new)	
				soybean cyst nematode virus 1 (SbCNV-1)

Figure 1. Phylogenetic relationship of NYMV, MIDWV, and SbCNV-1 to other mononegaviruses (taken from Kuhn *et al*. 2013; based on Kondo *et al*. 2013)



A maximum likelihood tree was constructed using PhyML 3.0 based on a multiple amino acid sequence alignment of the RdRp polymerase core module. Virus names and GenBank/RefSeq accession numbers: bornaviruses - Borna disease virus (BDV; NP_042024), avian bornavirus genotype 2 (ABV2; ADU05398); filoviruses - Sudan virus (SUDV; YP_138527), Marburg virus (MARV; YP_001531159); paramyxoviruses - Newcastle disease virus (NDV; NP_071471), Hendra virus (HeV; NP_047113), measles virus (MeV; NP_056924), Sendai virus (SeV; NP_056879), mumps virus (MuV; NP_054714), avian metapneumovirus (AMPV; YP_443845), human respiratory syncytial virus (HRSV; NP_056866); rhabdoviruses - rabies virus (RABV; NP_056797), bovine ephemeral fever virus (BEFV; NP_065409), vesicular stomatitis Indiana virus (VSIV; NP_041716), infectious hematopoietic necrosis virus (IHNV; NP_042681), potato yellow dwarf virus (PYDV; YP_004927971), lettuce necrotic yellows virus (LNYV; YP_425092); nyamiviruses - Nyamanini virus (NYMV; YP_002905337), Midway virus (MIDWV; YP_002905331), soybean cyst nematode virus 1 (SbCNV-1; AEF56729). Obtained and aligned partial or fragment sequences are depicted in boxes. Mononegavirus L-like protein

sequences (MLLSs) in pea powdery mildew fungus (*Erysiphe pisi*) (EpMLLS), yellow fever mosquito (*Aedes aegypti*) (AaMLLS), zebrafish (*Danio rerio*) (DrMLLS); nyamivirus L-like protein sequences (NLLSs) in lettuce (*Lactuca sativa*) (LsNLLS), silkworm (*Bombyx mori*) (BmNLLS), leafcutter bee (*Megachile rotundata*) (MrNLLS), black carpenter and fire ants (*Camponotus pennsylvanicus* and *Solenopsis invicta*) (CfNLLS and SiNLLS); transcriptome shotgun assembly mononegavirus L-like protein sequences (ShTSA-L) in an ascomycete fungus causing dollar spot (*Sclerotinia homoeocarpa*) (ShTSA-L). Numbers at the nodes represent aLRT values derived using an SH-like calculation (only values greater than 0.7 are shown). Note that the zebra fish (*Danio rerio*) sequence was first reported as another NLLS, but is has very poor sequence similarity (≈20%) to MIDWV L and clusters more with MLLSs from fungi. The sequence is therefore listed as an MLLS (DrMLLS) in the figure.