



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:	2014.007aVv2	(to be completed by ICTV officers)			
Short title: create species <i>Sierra Nevada nyavirus</i> in the genus <i>Nyavirus</i> , family <i>Nyamiviridae</i> , order <i>Mononegavirales</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (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"/>

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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

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

Date first submitted to ICTV:

July 2014

Date of this revision (if different to above):

August 2014

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	2014.007aV	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Nyavirus</i>	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.
Subfamily:		
Family:	<i>Nyamiviridae</i>	
Order:	<i>Mononegavirales</i>	
Name of new species:	Representative isolate:	GenBank sequence accession number(s)
<i>Sierra Nevada nyavirus</i>	Sierra Nevada virus isolate BA-T	KF530058

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

Based on its genomic structure and phylogeny, Sierra Nevada virus (SNVV) is closely related to Nyamanini virus (NYMV) and Midway virus (MIDWV), indicating that it is a third member of the *Nyavirus* genus (Rogers et al., 2014). The SNVV genome is about 50% similar to NYMV and MIDWV, which is less than the identity between NYMV and MIDWV (≈63%) (see results of PASC analysis posted at <http://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?cmdresult=main&id=458> and APPENDIX]. SNVV is antigenically distinct from MIDWV and NYMV [see APPENDIX]. Antigen reactivity and virion size indicate that SNVV represents a distinct nyaviral group. Although NYMV and MIDWV have been isolated from birds of different species and their ticks, it is unclear whether SNVV can also infect birds. SNVV was originally isolated at the University of California/Davis in Vero cell cultures inoculated with a homogenate of *O. coriaceus* ticks collected in northern California (exact site unknown). The virus caused a viral cytopathic effect in both Vero and BHK cells within 48 hours after inoculation, and intracranial inoculation of newborn mice with SNVV leads to illness and death within 2–3 days.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Rogers, M.B., Cui, L., Fitch, A., Popov, V., Travassos da Rosa, A.P.A., Vasilakis, N., Tesh, R.B., and Ghedin, E. (2014) Short Report: Whole Genome Analysis of Sierra Nevada Virus, a Novel *Mononegavirus* in the Family *Nyamiviridae*. *Am. J. Trop. Med. Hyg.*, 91(1), pp. 159–164

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. Results of complement fixation tests comparing Nyamanini, Midway, and Sierra Nevada viruses.

		Immune serum			
		NYMV	MIDWV	SNVV	Control
Antigen	NYMV	512*/128	32/32	0	0
	MIDWV	128/512	1024/≥512	0	0
	SNVV	0	0	64/≥2	0
	Control	0	0	0	0

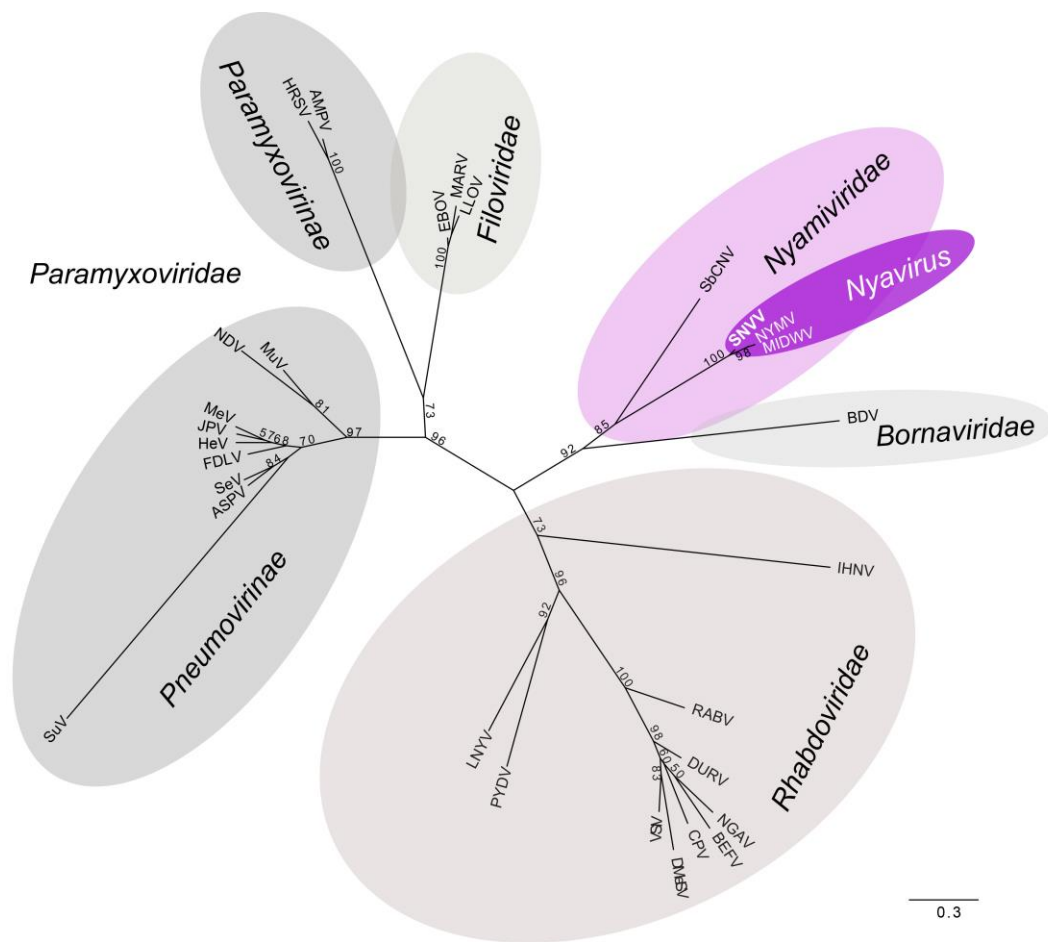


Figure 1. Maximum likelihood phylogenetic tree of mononegavirus RdRP protein sequences. The tree was generated with RAxML-HPC, using the GTR substitution model, rates across sites modeled on a gamma distribution and 1,000 bootstrap replicates. This analysis indicates Sierra Nevada virus (SNVV) branches within a clade of *Nyamiviridae* and branches closely with Nyamanini virus (NYWV) and Midway virus (MIDWV), thereby being in agreement with whole-genome PASC analysis. Adapted from Rogers et al. 2014

Figure 1a. Enlargement of area of Figure 1

