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:	***2012.015aP***	(to be completed by ICTV officers)

Short title: Remove (abolish) the species *Narcissus symptomless virus* in the genus *Carlavirus*, family *Betaflexiviridae*

(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** ☒	

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

Steve Wylie, s.wylie@murdoch.edu.au

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

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

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- *Either* to abolish a taxon entirely (when only part (a) needs to be completed)
- *Or* to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	***2012.015aP***	(assigned by ICTV officers)

To remove the following taxon (or taxa) from their present position:

Narcissus symptomless virus

The present taxonomic position of these taxon/taxa:

Genus:	***Carlavirus***	Fill in all that apply.
Subfamily:		
Family:	***Betaflexiviridae***	
Order:	***Tymovirales***	

If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write “yes” in the box on the right	

Reasons to justify the removal:
Explain why the taxon (or taxa) should be removed

1. Nerine latent virus was first described in 1972 (Hakkaart FA (1972) Virusziekten van Nerine. Jversl Inst Plziektenk Onderz, Wageningen 1971:105–106) and further characterized in 1978 (Maat DZ, Huttinga H, Hakkaart FA (1978) Nerine latent virus, some properties and serological detectability in *Nerine bowdenii*. Neth J Plant Pathol 84:47–59).

2. Seven nucleotide sequences from Nerine latent virus isolates IVT80054 (HM119498), 281299 (HM119496), 191191 (HM119495, HM119499), EXT07 (HM119497, HM119501), and 281299 (HM119500) were made available June 2010 by Pham K.T.K., Lemmers M.E.C. and de Kock M.J.D. These isolates were collected in the Netherlands 1991-1999 from plants of *Nerine*, *Hippeastrum*, and *Ismene*. Year of collection is given in the GenBank summaries. The sequences are partial sequences of replicase and coat protein (CP).

3. Narcissus symptomless virus was first described in 2006 (Chen J, Shi YH, Lu YW, Adams MJ, Chen JP (2006) Narcissus symptomless virus: a new carlavirus of daffodils. Arch Virol 151:2261–2267) from narcissus in China. The complete genome sequence was obtained (NC_008552) and named Hangzhou-2005. This isolate is the type isolate of the species. Subsequently, six sequences of narcissus symptomless virus from New Zealand representing coat proteins and partial replicases have become available (FJ606452, GQ205442, FJ546720, FJ546718, FJ546721, FJ546719).

4. In the taxonomic description of Narcissus symptomless virus, Chen et al (2006) provide Fig 2**,** which describes the phylogenetic relationships of the 13 carlavirus genomes available. Included is a sequence described as Nerine latent virus and the

GenBank accession given is DQ098905. In fact, DQ098905 corresponds to Hippeastrum latent virus; no sequence of Nerine latent virus was available in 2006.

5. Resemblances in serology and experimental host responses led Maat et al. 1978 to propose that Nerine latent virus and Hippeastrum latent virus were probably the same virus.

6. Adams et al (2004) list Hippeastrum latent virus as a synonym of Nerine latent virus.
(Adams MJ, Antinow JF, Bar-Joseph M, Brunt AA, Candresse T, Foster GD, Martelli GP, Milne RG, Fauquet CM (2004) The new plant family Flexiviridae and assessment of molecular criteria for species demarcation. Arch Virol 149:1045–1060)

7. Hippeastrum latent virus is listed as a synonym of Nerine latent virus in the Springer Index of Viruses 2nd Ed (Tidona C, & Darai G, eds, 2011).

8. Nucleotide pairwise alignment of the complete genomes of Hippeastrum latent virus and Narcissus symptomless virus reveal they share 54% identity, below the species demarcation limit for flexiviruses (Adams et al 2004).

9. Nucleotide sequence identities between Narcissus symptomless virus Hangzhou-2005 and the partial genome sequences (above) of Nerine latent virus and Narcissus symptomless virus are 94-97% for CP and replicase sequences. These figures are above the species demarcation point for flexiviruses (72% for CPs) (Adams et al, 2004).

Summary:

- No sequence information for Nerine latent virus was available when the genome sequence of narcissus symptomless virus was revealed.
- Hippeastrum latent virus and Nerine latent virus are clearly distinct viruses. There is confusion in the literature on this point.
- Sequence identities of isolates described as those of Narcissus symptomless virus and Nerine latent virus show that they belong to the same taxon.
- The name Nerine latent virus has priority over the name Narcissus symptomless virus, and as such, the taxon Narcissus symptomless virus should be abolished.
- The type isolate of Narcissus symptomless virus should be made the type isolate of Nerine latent virus.

MODULE 9: **APPENDIX**: supporting material

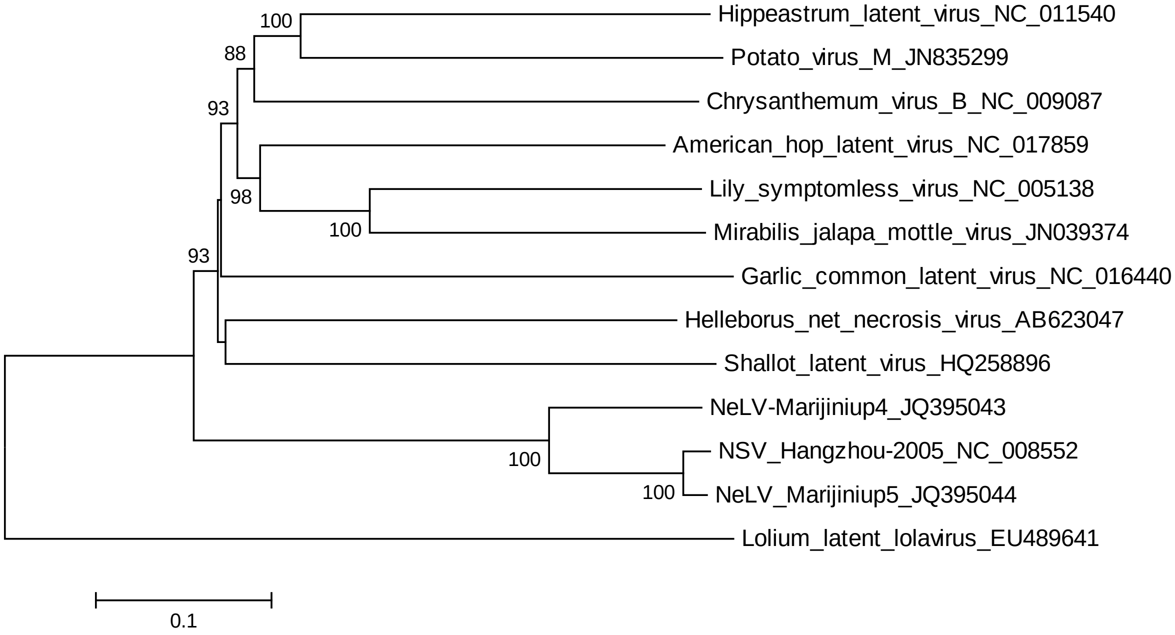
additional material in support of this proposal

References:

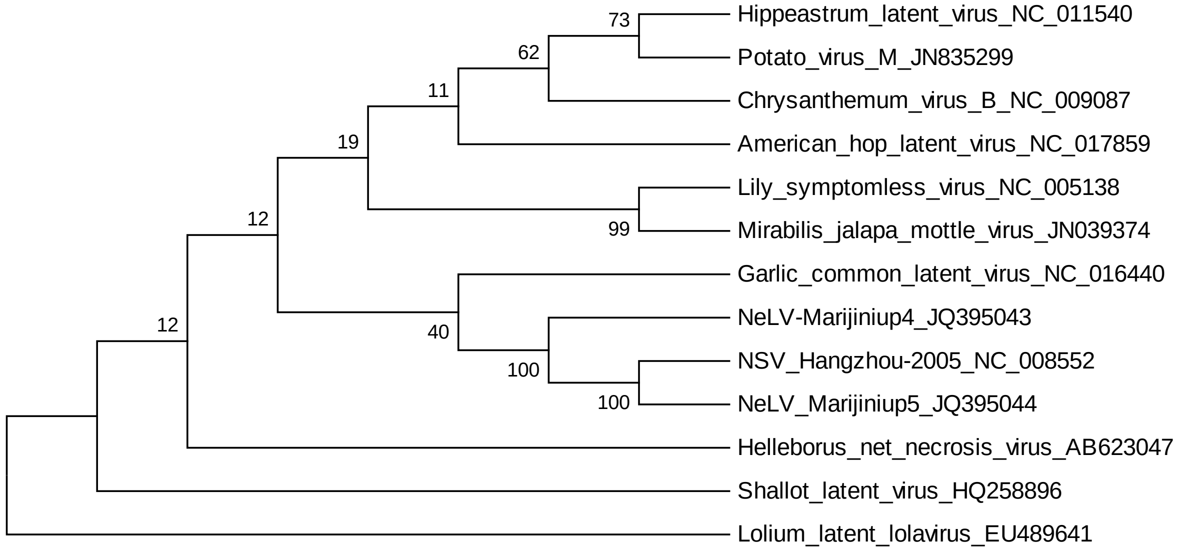
Wylie SJ, Jones MGK (2012) Complete genome sequences of seven carlavirus and potyvirus isolates on *Narcissus* and *Hippeastrum* plants in Australia, and proposals to clarify their naming. *Archives of Virology* (available online 12 May 2012. DOI: 10.1007/s00705-012-1319-6)

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.



NJ Replicase proteins



MP Replicase proteins

Phylogenies of complete replicase protein sequences done in Mega5 with 1000 bootstrapped replications. NJ, Neighbor-joining; MP, Maximum parsimony methods used. LoLV provided as the outgroup.