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:	***2011.009aV***	(to be completed by ICTV officers)

Short title: create species named *Obodhiang virus* in the genus *Ephemerovirus*, family *Rhabdoviridae*
(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:

Peter J Walker (Peter.Walker@csiro.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)	Rhabdoviridae Study Group

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

Date first submitted to ICTV:	31 July 2011
Date of this revision (if different to above):	26th October 2012 (SGS)

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	***2011.009aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Ephemerovirus***
Subfamily:	
Family:	***Rhabdoviridae***
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:**
Obodhiang virus	HM856902

Reasons to justify the creation and assignment of the new species:

Obodhiang virus (OBOV) is a member of the *Rhabdoviridae*, genus *Ephemerovirus* according to electron microscopy, general genome organization, phylogenetic analysis of the sequence of each of the structural proteins (N, P, M, G and L) and the presence of multiple additional genes between G and L, including a second glycoprotein (G_{NS}) gene that appears to have been generated by gene duplication.

OBOV has been isolated on three occasions from mosquitoes (*Mansonia uniformis*) collected near Malakal in southern Sudan in 1963 (Schmidt et al., 1965; Shope, 1975). By negative contrast electron microscopy, the OBOV virion is cone- or bullet-shaped with a helical nucleocapsid and length of approximately 180 nm (Bauer & Murphy, 1975).

The genome sequence of OBOV (14,717 nt) has been determined (Genbank HM856902). The gene order is 3'-N-P-M-G-G_{NS}-α1-α2-β-L-5' (Fig. 1), where N, P, M, G and L are common rhabdoviruses nucleoprotein, phosphoprotein, matrix protein, glycoprotein and polymerase protein genes, respectively. The genome organization is similar to that of Adelaide River virus (ARV) with which is shares the same number and order of genes. The genome organization is also similar to BEFV (the type species of the genus *Ephemerovirus*) but lacks an additional gene (γ) between the β and L genes and the absence of alternative ORFs in the P and α2 genes (designated P' and α3 in BEFV). There is identifiable amino acid sequence homology between the OBOV G_{NS}, α1, α2, β genes and those of other ephemerovirus species [i.e., BEFV, ARV, *Kotonkan virus* (KOTV) and *Berrimah virus* (BRMV)].

Phylogenetic analysis of the complete N, G and L proteins indicates that OBOV clusters with viruses of the genus *Ephemerovirus* (Figs. 2, 3 and 4). The OBOV gene sequences are more closely related to ARV than to BEFV, KOTV or BRMV. Similar results have been obtained by phylogenetic analysis of smaller sequence domains within the OBOV N gene (Kuzmin et al., 2006).

OBOV cross-reacts weakly with ARV but is distinct from BEFV, BRMV, KOTV and Kimberley virus (KIMV) in neutralization tests using hyperimmune antisera (Table 1). OBOV cross-reacts strongly with ARV and KOTV in group-specific complement-fixation (CF) and indirect fluorescent antibody (IFA) tests. Like other ephemeroviruses, OBOV has also been shown to cross-react weakly in IFA CF tests with lyssaviruses and several other unclassified insect-borne rhabdoviruses (Bauer & Murphy, 1975; Tesh et al., 1983; Calisher et al., 1989).

Species demarcation criteria:

Species cross-react in complement fixation and/or indirect immunofluoresence tests but exhibit low to no cross-neutralization. They exhibit similar but distinct genome organizations with the common feature of a non-structural glycoprotein (Gns) gene but variations in the number of accessory protein genes and the location of transcriptional control sequences. Different species may share up to 91% identity in N protein amino acid sequence

The new species fits these criteria. The level of identity of the N protein of the new species to its closest relative is 87%

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Bauer, S. P. & Murphy, F. A. (1975). Relationship of two arthropod-borne rhabdoviruses (kotonkan and Obodhiang) to the rabies serogroup. Infection and Immunity 12, 1157-1172.

Calisher, C. H., Karabatsos, N., Zeller, H., Digoutte, J.-P., Tesh, R. B., Shope, R. E., Travassos da Rosa, A. P. A. & St. George, T. D. (1989). Antigenic relationships among rhabdoviruses from vertebrates and hematophagous arthropods. Intervirology 30, 241-257.

Kuzmin, I. V., Hughes, G. J. & Rupprecht, C. E. (2006). Phylogenetic relationships of seven previously unclassified viruses within the family Rhabdoviridae using partial nucleoprotein gene sequences. J Gen Virol 87, 2323-2331.

Schmidt, J. R., Williams, M. C., Lulu, M., Mivule, A. & Mujombe, E. (1965). Viruses isolated from mosquitoes collected in the Southern Sudan and Western Ethiopia. East African Virus Research Institute Report 15, 24.

Shope, R. E. (1975). Rabies virus antigenic relationships. In The natural history of rabies, pp. 141-152. Edited by G. M. Baer. New York: Academic Press.

Tesh, R. B., Travassos da Rosa, A. P. A. & Travassos da Rosa, J. S. (1983). Antigenic relationship among rhabdoviruses infecting terrestrial vertebrates. Journal of General Virology 64, 169-176.

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.

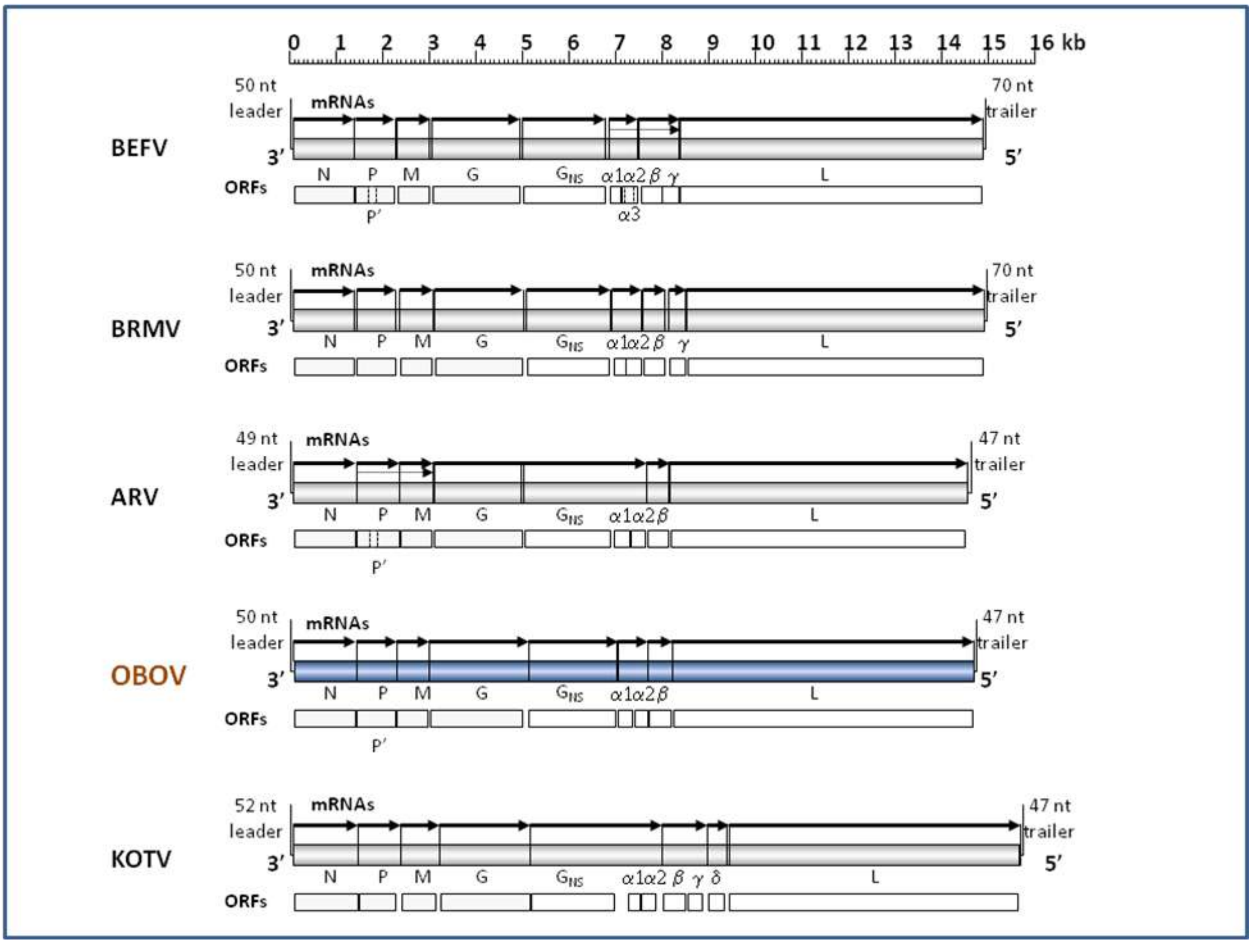

Figure 1. Comparison of the OBOV genome organisation and deduced transcription strategy with those of recognised members of the genus *Ephemerovirus*.

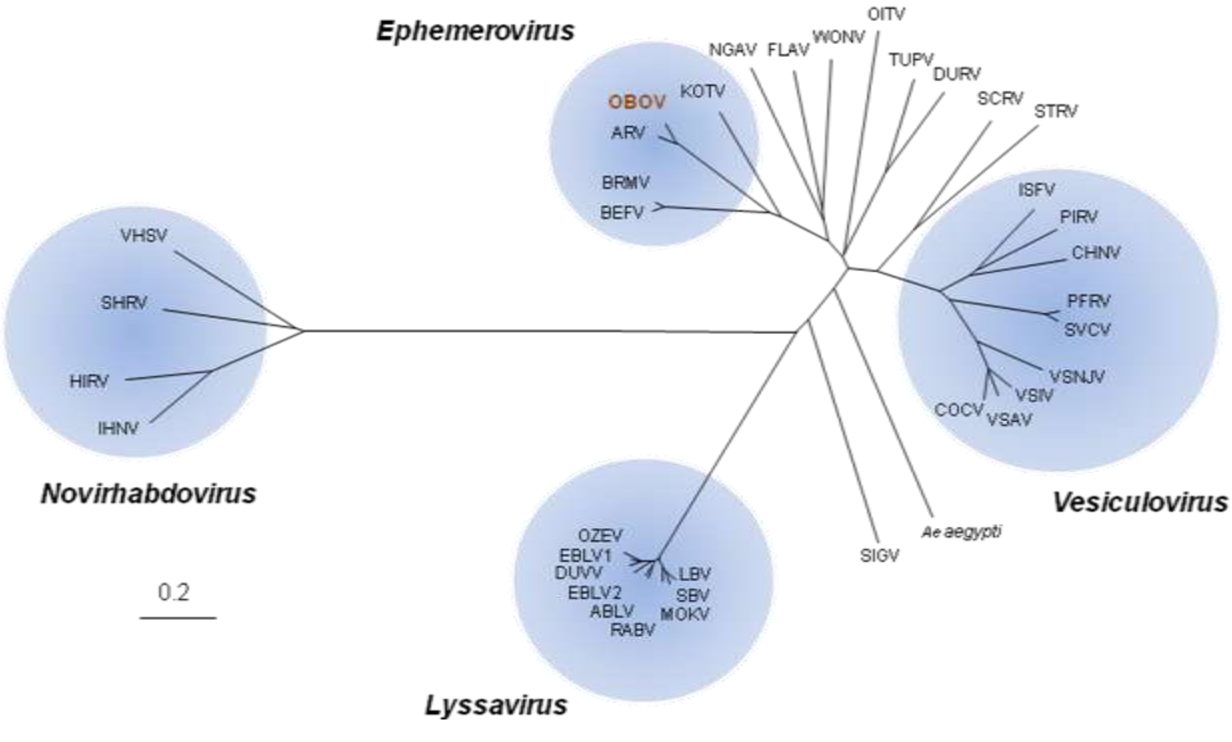

Figure 2. Phylogenetic relationship of rhabdovirus N protein complete amino acid sequences. The tree was generated in Mega 4.0 by the neighbour-joining method from a ClustalW multiple sequence alignment using default parameters. Branch lengths are proportional to the genetic distance between the sequences.

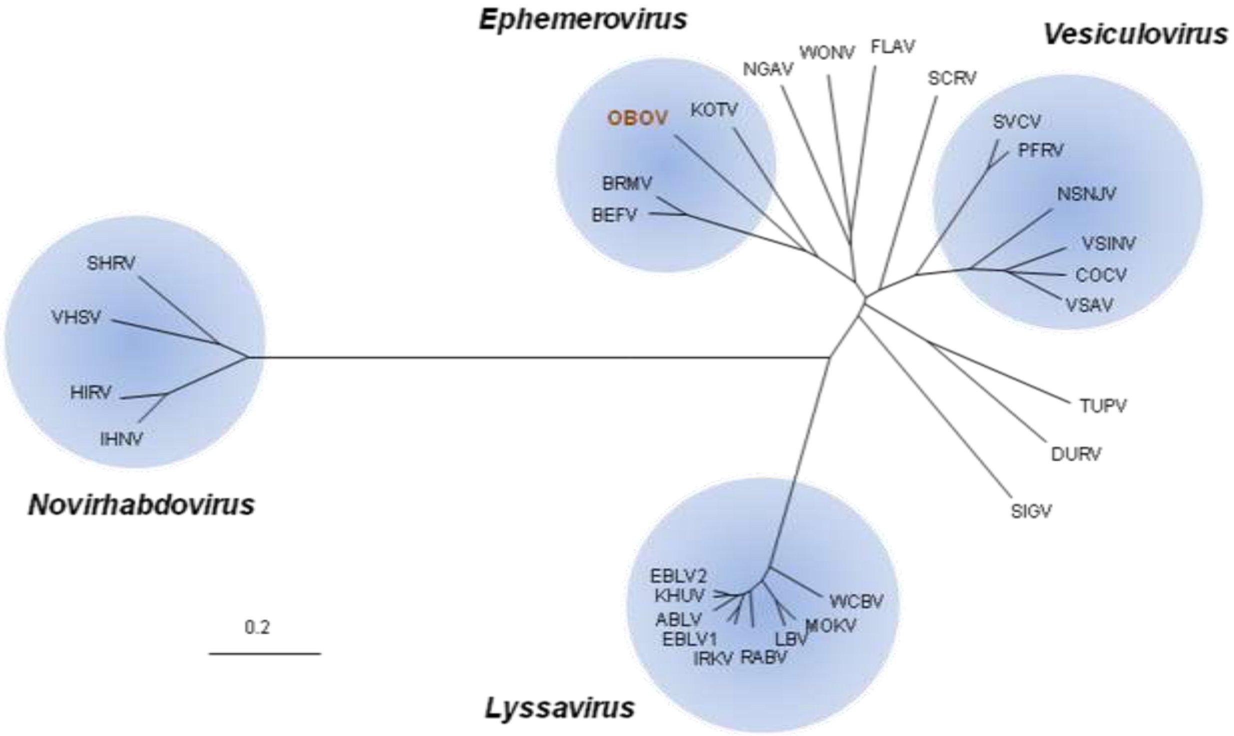

Figure 3. Phylogenetic relationship of rhabdovirus L protein complete amino acid sequences. The tree was generated in Mega 4.0 by the neighbour-joining method from a ClustalW multiple sequence alignment using default parameters. Branch lengths are proportional to the genetic distance between the sequences.

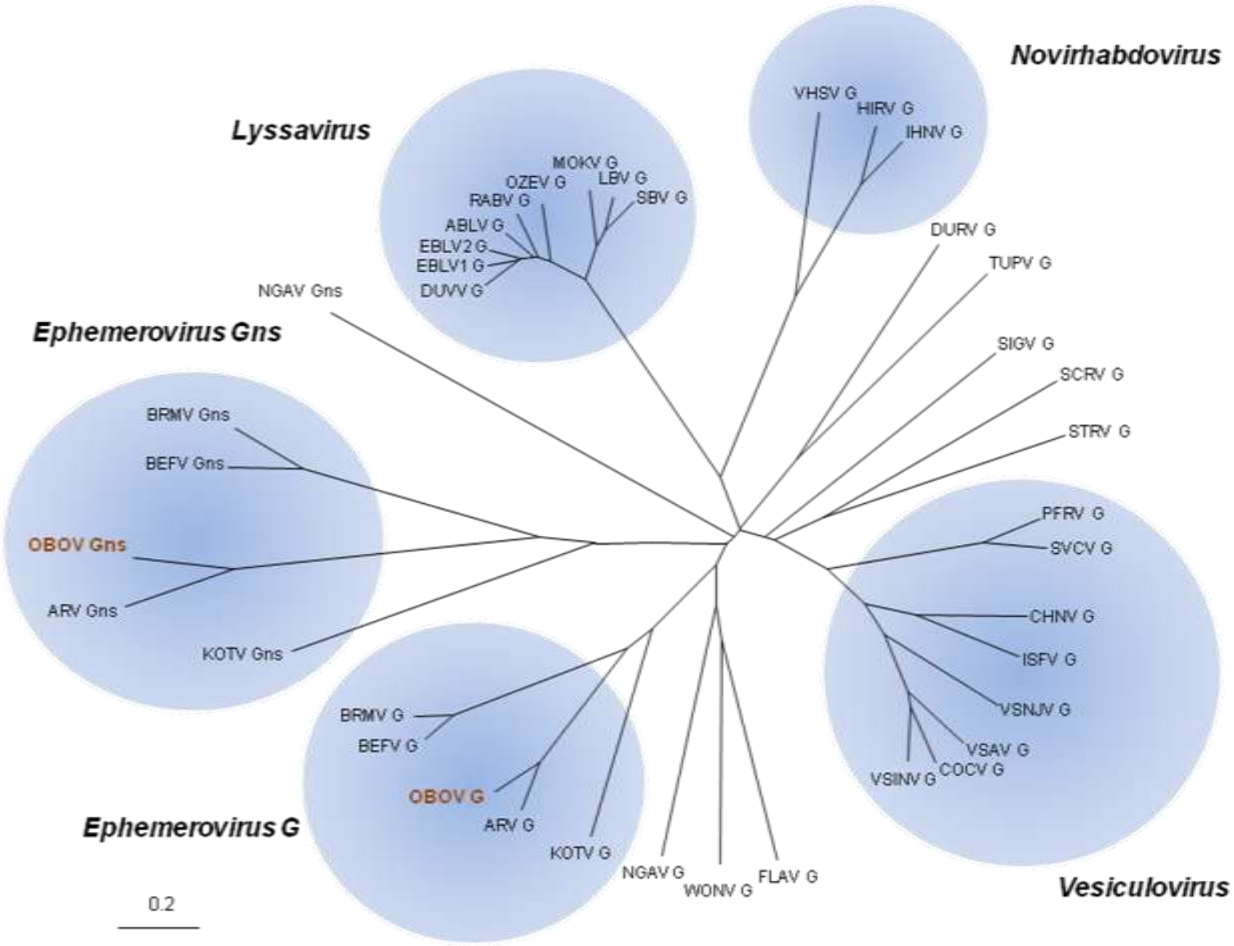

Figure 4. Phylogenetic relationship of rhabdovirus G and G_{NS} protein complete amino acid sequences. The tree was generated in Mega 4.0 by the neighbour-joining method from a ClustalW multiple sequence alignment using default parameters. Branch lengths are proportional to the genetic distance between the sequences.

Table 1. Serum neutralisation tests between kotonkon virus, Obodhiang virus and four other ephemeroviruses.

Virus	Titre of antibody					
	ARV	BEFV	BRMV	KIMV	KOTV	OBOV
ARV	*640*	-	-	-	-	40
BEFV	-	*1280*	20	-	-	-
BRMV	-	80	*40*	-	-	-
KIMV	-	-	-	*80*	-	-
KOTV	-	-	-	-	*640*	-
OBOV	40	-	-	-	-	*1280*