



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:	2009.017a,bV	(to be completed by ICTV officers)			
Short title: Create new species named Ngaingan virus to be unassigned in the family Rhabdoviridae (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>
	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>	

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

Peter Walker, Peter.Walker@csiro.au

Has this proposal has been seen and agreed by the relevant study group(s)?
Please select answer in the box on the right

Yes

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

Approved by EC41 and checked by SGS

Date first submitted to ICTV: 26.05.09
Date of this revision (if different to above): 23.06.09

MODULE 2: **NEW SPECIES**

Part (a) to create and name one or more new species.

If more than one, they should be a group of related species belonging to the same genus (see Part b)

Code	2009.017aV	(assigned by ICTV officers)
To create 1 new species with the name: <i>Ngaingan virus</i>		

Part (b) assigning new species to higher taxa

All new species must be assigned to a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family.

Code	2009.017bV	(assigned by ICTV officers)
To assign the species listed in section 2(a) as follows:		
Genus:	unassigned	Fill in all that apply. <ul style="list-style-type: none">• 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:	Rhabdoviridae	
Order:	Mononegavirales	

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.
- Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Ngainingan virus (NGAV) is a member of the *Rhabdoviridae* according to electron microscopy, general genome organization, and phylogenetic analysis of the sequence of each of the structural proteins (N, P, M, G and L). The available information is sufficient to establish a new species within the family but several unique characteristics do not allow assignment of this virus into any of the existing genera.

NGAV was isolated in 1970 from a pool of biting midges collected at Kowanyama in northern Queensland, Australia. The midge pool was thought to consist of only *Culicoides brevitarsis* but later studies suggested that *C. actoni* may also have been present. Neutralizing antibodies have been detected in wallabies, wallaroos and kangaroos, and possibly cattle and buffaloes.

Complete genome sequence of NGAV (15, 764 nt) has been deposited in Genbank (FJ_715959). It is the largest genome yet described for any rhabdovirus, containing 13 ORFs in the order 3'-N-P-U1-U2-U3-M-U4-G-G_{NS}-U5-U6-U7-L-5' (Fig. 1), where N, P, M, G and L are common rhabdovirus nucleoprotein, phosphoprotein, matrix protein, glycoprotein and polymerase protein genes. The NGAV P gene contains two alternative ORFs (designated P1' and P2'). Although similar alternative P ORFs (referred to as either C or P') occur in several other rhabdoviruses, they lack significant aa sequence identity with NGAV P1' or P2'. The NGAV G_{NS} gene encodes a non-structural glycoprotein (568 aa) that is homologous to the non-structural, type 1 transmembrane glycoproteins of ephemeroviruses. Like the ephemerovirus G_{NS} proteins, NGAV G_{NS} has similar structural features and significant aa sequence identity to the NGAV G protein and those of other animal rhabdoviruses. NGAV contains 7 additional genes between the P- and M-genes (U1, U2 and U3), the M- and G-genes (U4) and the G_{NS}- and L-genes (U5, U6 and U7) encoding small proteins of unknown function. Although similar in size (81 aa - 153 aa) to proteins encoded ORFs located in similar positions in several other rhabdoviruses, they lack significant sequence similarity or significant structural similarity to any known protein. None of the small unique NGAV proteins has yet been detected in infected cells.

Each NGAV ORF is flanked by conserved transcription termination and termination/polyadenylation sequences. The NGAV putative transcription initiation sequence occurs in two forms (UUGUC or UCGUC), the second of which differs substantially from those of other rhabdoviruses. The consensus transcription termination/polyadenylation sequence (GWWC[U]₇) is common to all genes except the G_{NS} gene which occurs in an unusual form (GTAC[U]₈).

Phylogenetic analysis (Fig. 2) of the N, G and proteins places NGAV amongst other rhabdoviruses associated with insects, mammals and birds and most closely related to Flanders virus (FLAV) and Wongabel virus (WONV). Phylogenetic analysis using a portion of the L protein also places NGAV closely related to FLAV and WONV, as well as Parry Creek virus (PCV). FLAV is a member of the Hart Park serogroup and antigenic cross-reactions have been reported between NGAV and other insect-transmitted rhabdoviruses including Tibrogargan virus and Biven's Arm virus. However, none of these viruses has been assigned to a genus. Phylogenetic analysis of the G_{NS} protein indicates an evolutionary relationship to ephemeroviruses for which the non-structural glycoprotein has been considered a defining characteristic. The placement of NGAV is therefore ambiguous according to current taxonomic criteria and so it cannot be considered as a member of any established genus at this time.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Doherty, R. L., J. G. Carley, H. A. Standfast, A. L. Dyce, B. H. Kay, W. A. Snowdon. (1973). Isolation of arboviruses from mosquitoes, biting midges, sandflies and vertebrates collected in Queensland, 1969 and 1970. *Trans. R. Soc. Trop. Med. Hyg.* 67:536-43.

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

Bourhy, H., Cowley, J.A., Larrous, F., Holmes, E.C., Walker, P.J. (2005). Phylogenetic relationships among rhabdoviruses inferred using the L polymerase gene. *J. Gen. Virol.* 86:2849-2858.

Gubala, A.J., Davis, S., Weir, R., Melville, L., Cowled, C.J., Walker, P.J., Boyle, D.B. (submitted). Ngaingan virus, a macropod-associated rhabdovirus, encodes a second glycoprotein and seven novel proteins.

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.

Figure 1. WONV genome organization (from Gubala et al., submitted).

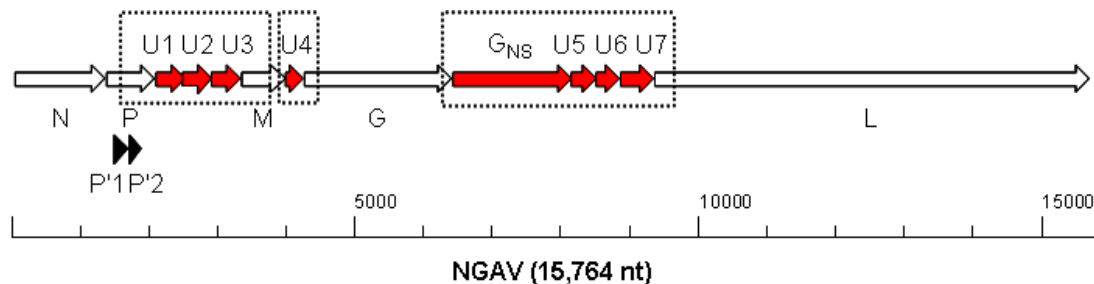


Figure 2. Phylogenetic position of NGAV within the *Rhabdoviridae* based on the alignment of (A) complete nucleoprotein and (B) complete glycoprotein (G and G_{NS}) sequences (from Gubala et al., submitted).

