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:	***2009.018a,bV***	(to be completed by ICTV officers)

Short title: Create new species named Wongabel virus to be unassigned in the 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 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	***2009.018aV***	(assigned by ICTV officers)

To create 1 new species with the name:

Wongabel virus

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	***2009.018bV***	(assigned by ICTV officers)

To assign the species listed in section 2(a) as follows:

Genus:	**unassigned**
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.

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

Wongabel virus (WONV) 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.

WONV was isolated in 1979 from biting midges (*Culicoides austropalpalis*) collected from the Atherton Tablelands, northern Queensland, Australia. Low levels of neutralizing antibodies have been detected in sea birds, cattle and wallabies.

The complete genome sequence of WONV (13, 196 nt) is available (EF_612701). The gene order is 3'-N-U4-P-U1-U2-U3-M-G-U5-L-5' (Fig. 1), where N, P, M, G and L are common rhabdoviruses nucleoprotein, phosphoprotein, matrix protein, glycoprotein and polymerase protein genes. WONV lacks an alternative ORF in the P gene which encodes the C or P' protein in some other rhabdoviruses. However, WONV contains 3 additional genes between the P and M genes and 2 additional open reading frames overlapping the N and G genes (U4 and U4, respectively), each of which encodes a protein that lacks significant amino acid sequence identity with other known proteins. The U1 protein (179 aa; calculated mass = 21.2 kDa) is hydrophilic with numerous potential phosphorylation sites, an N-glycosylation site, and amidation site and two N-myristoylation sites. The U2 protein (192 aa; calculated mass = 21.9 kDa) contains a two N-myristoylation sites and a highly hydrophobic domain of 10 amino acids followed by a mitochondrial energy transfer signature that is characteristic of carrier and transport proteins. The U3 protein (142 aa; calculated mass = 16.5 kDa) contains 5 putative phosphorylation sites and an 18-aa alpha helix and presently has no assigned function. The U4 protein (49 aa; calculated mass = 5.8 kDa) contains a single putative N-myristoylation site and shares overall 49% identity of GTP-binding proteins of several bacteria. The U5 protein (127 aa; calculated mass = 14.9 kDa) contains predicted N-terminal extracellular domain, 22-aa transmembrane domain and highly basic cytoplasmic tail, and has overall structural similarity to the alpha-1 proteins of ephemeroviruses which have been suggested to be viroporins. Proteins of similar size to the U1, U2, U3 and U5 proteins have been detected in WONV-infected cells by immunoblot analysis using polyclonal mouse ascitic fluid.

The WONV putative transcription initiation sequence (UCAUC) is conserved in all WONV genes and is the same as that reported in Flanders virus (FLAV). The predicted transcription termination/polyadenylation sequence is also conserved (G(U/A)AC[U_7]). Transcription of the U4 and U5 ORFs appears to be possible only by internal initiation on the N- and G-mRNA, respectively. In each case, the termination codon overlaps the predicted polyadenylation sequence (GUACUUUUUUU).

Phylogenetic analysis of the N and G proteins places WONV most closely related to FLAV and amongst other rhabdoviruses associated with insects, mammals and birds. Phylogenetic analysis using a portion of the L gene also places WONV closely related to FLAV as well as Parry Creek virus (PCV) and Ngaingan virus (NGAV). FLAV is a member of the Hart Park serogroup but none of these viruses has been assigned to a genus. Therefore, WONV cannot be considered as a member of any established genus at this time (Fig. 2).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Gubala, A.J., Proll, D.F, Barnard, R.T., Cowled, C.J., Crameri, S.G., Hyatt, A.D., Boyle, D.B. (2008). Genomic characterisation of Wongabel virus reveals novel genes within the Rhabdoviridae. Virology 376: 13-23.

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.

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., 2008).

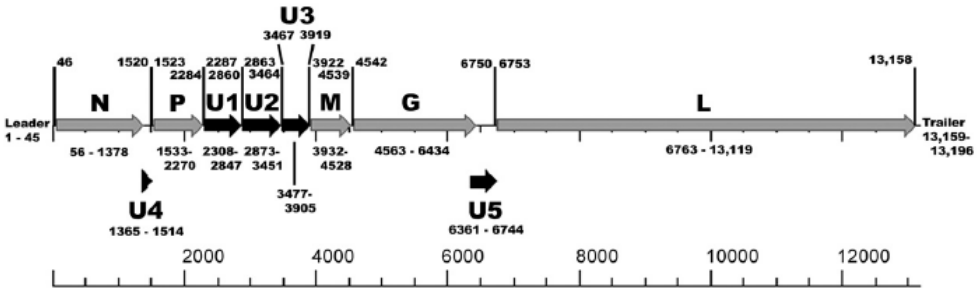

Figure 2. Phylogenetic position of WONV within the *Rhabdoviridae* based on the alignment of complete nucleoprotein (A) and glycoprotein (B) sequences (from Gubala et al., 2008).