



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: | 2010.013aV | (to be completed by ICTV officers) |
| Short title: Create species named Kotonkan virus in the genus Ephemerovirus (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 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 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)

Rhabdovirus

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 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 | 2010.013aV | (assigned by ICTV officers) |
| To create 1 new species within: | | |
| Genus: | <i>Ephemerovirus</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>Rhabdoviridae</i> | |
| Order: | <i>Mononegavirales</i> | |
| And name the new species: | | GenBank sequence accession number(s) of reference isolate: |
| <i>Kotonkan virus</i> | | HM474855 |

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

Kotonkan virus (KOTV) 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.

KOTV was isolated from a mixed pool of biting midges (*Culicoides* spp.) collected in Ibadan, Nigeria in 1967 (Kemp et al., 1973). A high prevalence of neutralizing antibodies has been detected in African cattle, hedgehog (*Atelerix albiventris*) and the giant rat (*Cricetomys gambianus*). There is also some evidence of antibody in sheep, horses and possibly humans. Seroconversion to KOTV neutralising antibody has been associated with a bovine ephemeral fever-like illness in cattle and mild signs of disease have been reported in cattle following experimental infection (Tomori et al., 1974). By negative contrast electron microscopy, the KOTV virion is cone- or bullet-shaped with a helical nucleocapsid and length of approximately 180 nm (Bauer & Murphy, 1975).

The genome sequence of KOTV (15.8 kb) has been determined (accession number to be advised). The gene order is 3'-N-P-M-G- G_{NS} - $\alpha 1$ - $\alpha 2$ - β - γ - δ -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 BEFV (the type species of the genus *Ephemerovirus*), with the exception of the insertion of an additional gene (δ) between the γ and L genes and the absence of alternative ORFs in the P and $\alpha 2$ genes (designated P' and $\alpha 3$ in BEFV). There is identifiable amino acid sequence homology between the KOTV G_{NS} , $\alpha 1$, $\alpha 2$, β and γ genes and those of other ephemeroviruses [i.e., BEFV, Berrimah virus (BRMV) and Adelaide River virus (ARV)].

Phylogenetic analysis of the complete N, G and L proteins indicates that KOTV clusters with viruses of the genus *Ephemerovirus* (Figs. 2, 3 and 4). The KOTV N gene sequence is more closely related to that of BEFV and BRMV than is ARV, the third currently recognized member of the genus. Similar results have been obtained by phylogenetic analysis of smaller sequence domains within the KOTV L and N genes (Bouhry et al., 2005; Kuzmin et al., 2006).

KOTV has not been shown to cross-react antigenically with BEFV, BRMV or ARV. However, like other ephemeroviruses, KOTV has been shown to cross-react weakly in indirect fluorescent antibody (IFA) tests with lyssaviruses and several other unclassified insect-borne rhabdoviruses (Bauer & Murphy, 1975; Calisher et al., 1989).

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.
- Bourhy, H., Cowley, J. A., Larrous, F., Holmes, E. C. & Walker, P. J. (2005). Phylogenetic relationships among rhabdoviruses inferred using the L polymerase gene. *Journal of General Virology* 86, 2849-2858.
- 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.
- Kemp, G. E., Lee, V. H., Moore, D. L., Shope, R. E., Causey, O. R. & Murphy, F. A. (1973). Kotonkan, a new rhabdovirus related to Mokola virus of the rabies serogroup. *American Journal of Epidemiology* 98, 43-49.
- 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. *Journal of General Virology* 87, 2323-2331.
- Tomori, O., Fagbami, A. & Kemp, G. (1974). Kotonkan virus: experimental infection of white Fulani calves. *Bulletin of Epizootic Diseases of Africa* 22, 195-200.

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.

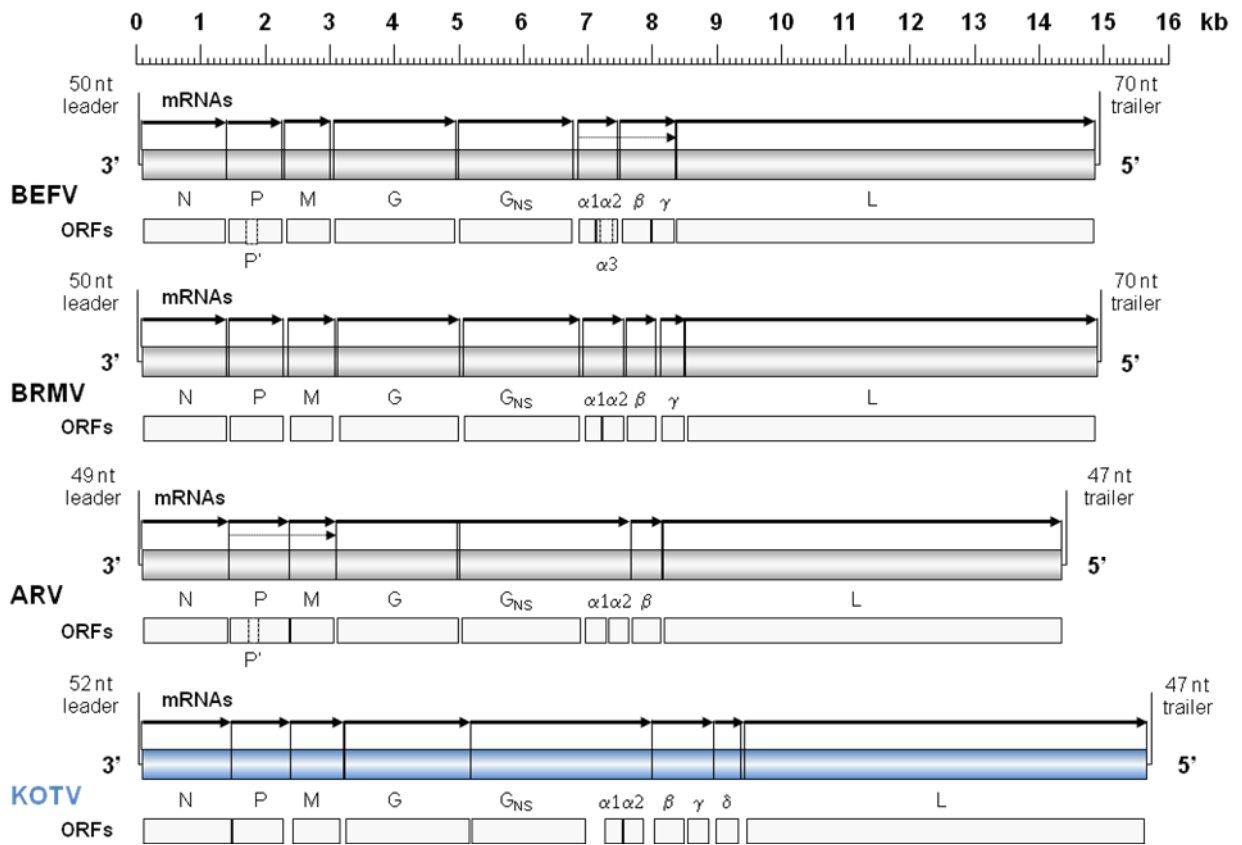


Figure 1. Comparison of the KOTV genome organisation and deduced transcription strategy with those of recognised members of the genus *Ephemerovirus*.

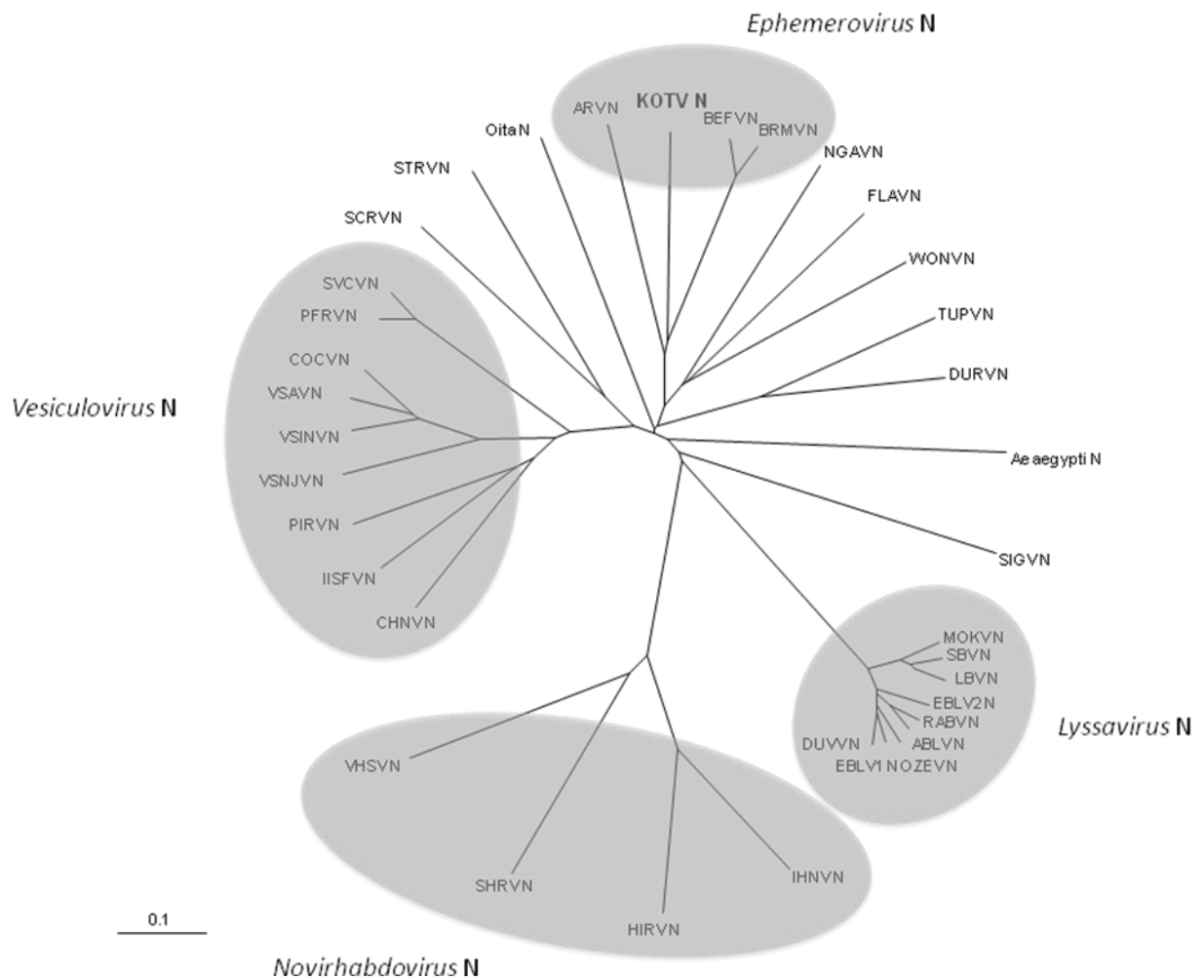


Figure 2. Phylogenetic relationship of rhabdovirus N protein complete amino acid sequences. The tree was generated by the neighbour-joining method from a Clustal X multiple sequence alignment using default parameters and visualised using Treeview. Branch lengths are proportional to the genetic distance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

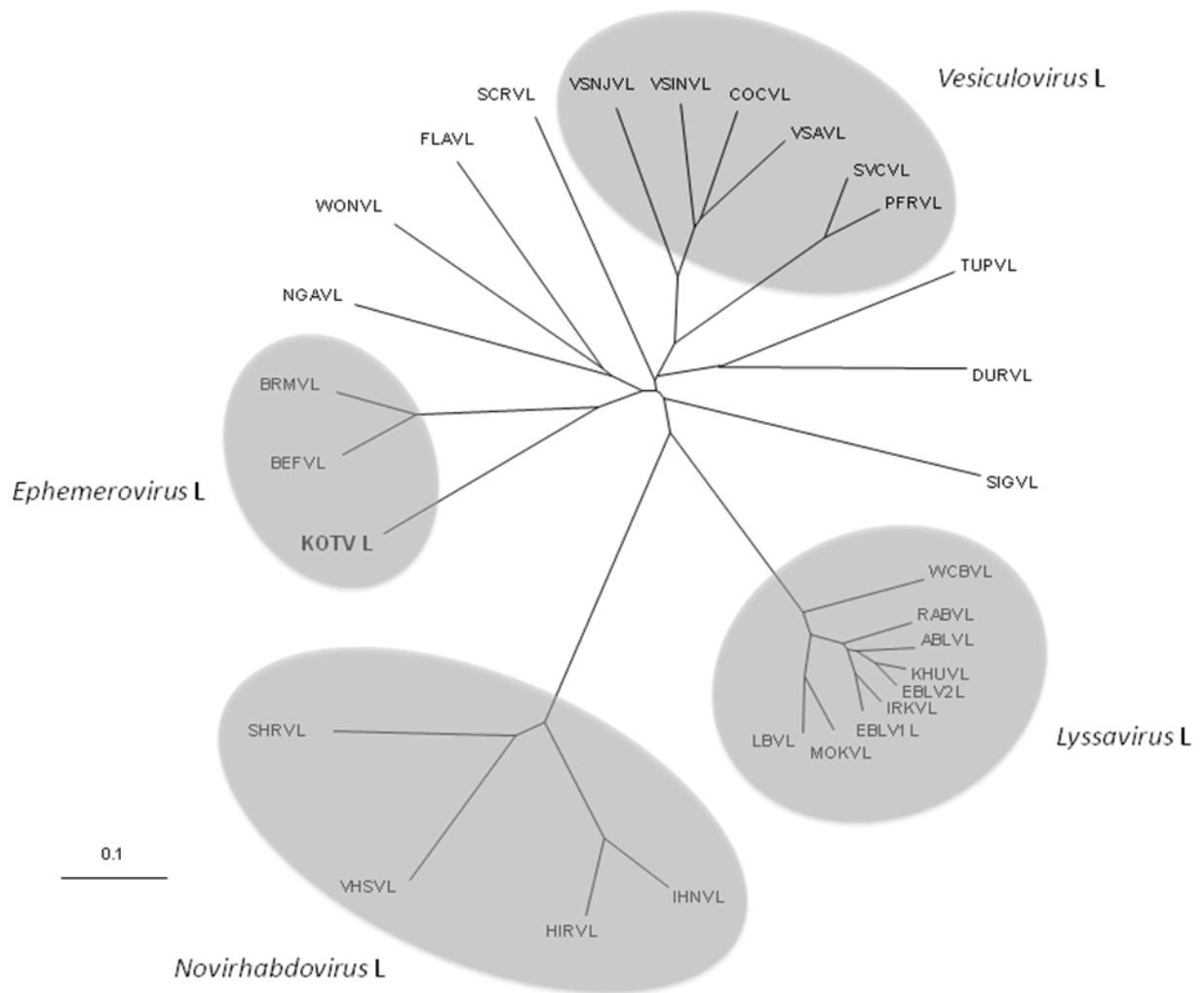


Figure 3. Phylogenetic relationship of rhabdovirus L protein complete amino acid sequences. The tree was generated by the neighbour-joining method from a Clustal X multiple sequence alignment using default parameters and visualised using Treeview. Branch lengths are proportional to the genetic distance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

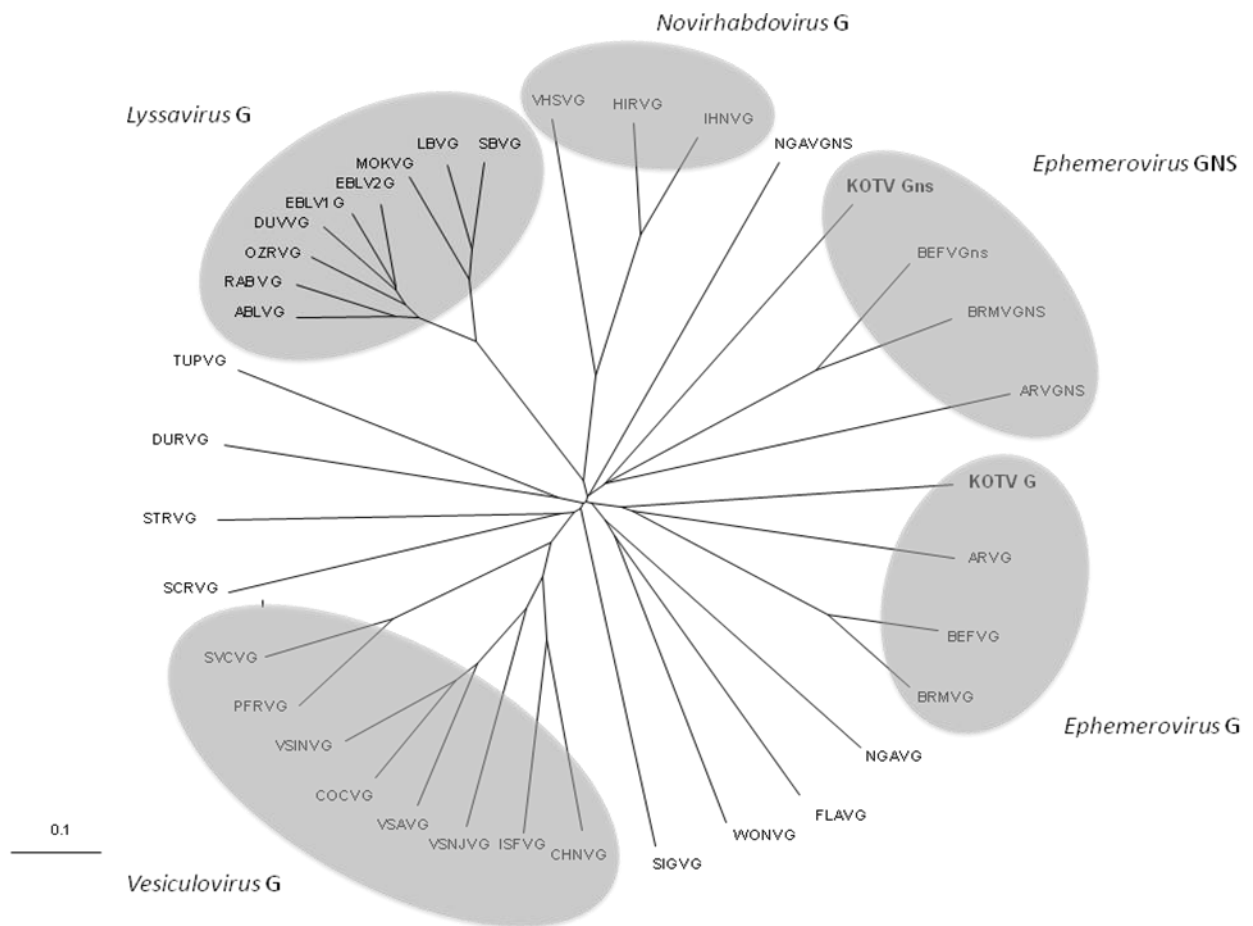


Figure 4. Phylogenetic relationship of rhabdovirus G and G_{NS} protein complete amino acid sequences. The tree was generated by the neighbour-joining method from a Clustal X multiple sequence alignment using default parameters and visualised using Treeview. Branch lengths are proportional to the genetic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