



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**

<b>Code assigned:</b>	<b><i>2009.013a,bV</i></b> (to be completed by ICTV officers)
<b>Short title:</b> Create a species named Tupaia virus, unassigned in the family Rhabdoviridae in the order Mononegavirales (e.g. 6 new species in the genus <i>Zetavirus</i> )	
<b>Modules attached</b> (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:**

Ivan Kuzmin, [ibk3@cdc.gov](mailto:ibk3@cdc.gov)

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:**

1. No abbreviation is needed for a species, only for a virus. If it was needed, it wouldn't be italicized. Delete abbreviation.
2. No need to italicize the word "unassigned".
3. Change "to assign" (page 3, line 3) to "assignment of"
4. Correct spelling of "Sandjimba"
5. Second reference (do not center): correct spelling of "Flugel" (umlaut over the "u").

Other than some grammatical changes, the rest looks okay to me.

Approved by EC41 and checked by SGS

Date first submitted to ICTV: 26.05.09  
Date of this revision (if different to above): 22.06.09

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	<b>2009.013aV</b>	(assigned by ICTV officers)
<b>To create 1 new species with the name:</b>		
<i>Tupaia 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	<b>2009.013bV</b>	(assigned by ICTV officers)
<b>To assign the species listed in section 2(a) as follows:</b>		
Genus:	<b>unassigned</b>	Fill in all that apply. <ul style="list-style-type: none"> <li>• If the higher taxon has yet to be created (in a later module, below) write "<b>(new)</b>" after its proposed name.</li> <li>• If no genus is specified, enter "<b>unassigned</b>" in the genus box.</li> </ul>
Subfamily:		
Family:	<b>Rhabdoviridae</b>	
Order:	<b>Mononegavirales</b>	

<b>Reasons to justify the creation and assignment of the new species:</b>	
<ul style="list-style-type: none"> <li>• Explain how the proposed species differ(s) from all existing species.               <ul style="list-style-type: none"> <li>○ If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.</li> <li>○ 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.</li> </ul> </li> <li>• Provide Genbank accession numbers (not RefSeq accessions) for genomic sequences</li> <li>• Further material in support of this proposal may be presented in the Appendix, Module 9</li> </ul>	

*Tupaia virus* (TUPV) belongs to *Rhabdoviridae* according to electron microscopy, general genome organization, and phylogenetic placement within the family. However, several unique characteristics do not allow assignment of this virus into any of the existing genera, and the available information is sufficient to establish a new species within the family.

TUPV was isolated from spontaneously degenerating hepatocellular carcinoma cells from a tree shrew (*Tupaia belangeri*), imported from Thailand and kept in captivity for about 6 years. The host range of the virus in vitro appears to be restricted to tupaia cells.

Complete genome of TUPV (about 11.5 kb) is available: [NC\\_007020](#); [AY840978](#). The gene order is 3'-N-P/C-M-SH-G-L-5' (Fig. 1), where N, P, M, G and L are common for rhabdoviruses nucleoprotein, phosphoprotein, matrix protein, glycoprotein and polymerase protein genes. In addition, TUPV genome contains the unique small hydrophobic (SH) transcription unit between M and G genes, and the corresponding transcript was found in the infected cells. A Kyte-Doolittle hydrophobicity plot of the SH protein shows two hydrophobic amino acid stretches, one at the amino terminus and one in the center of the sequence. The combined transmembrane topology and signal peptide prediction algorithms identified a type I transmembrane protein with a signal peptide (amino acids 1 to 20), a small extracellular domain, a transmembrane region (amino acids 30 to 51), and a cytoplasmic tail of 42 amino acids. Furthermore, the overlapping ORF in the TUPV P mRNA (nucleotides 57 to 719) has the potential to code for a 221-amino-acid C protein that is therefore more than 3 times larger than the vesicular stomatitis virus proteins and slightly larger than the paramyxovirus proteins. The TUPV C protein has a predicted pI of approximately 10, similar to the paramyxovirus and vesicular stomatitis virus proteins. Except for a high content in the basic amino acids arginine, lysine, and histidine no significant sequence similarity was found between the TRV and vesicular stomatitis virus C proteins.

Phylogenetically, TUPV is placed within the rhabdoviruses, associated with insects, mammals and birds however, can not be considered as a member of any established genus (Fig 2). Based on the N gene phylogeny, TUPV is mostly related to the unassigned African viruses *Kolongo virus* (KOLV) and *Sandjimba virus* (SJAV), both isolated from birds. In other analyses, where limited fragments of L gene were compared, TUPV demonstrated relatedness to *Humpty Doo virus* (HDOOV), isolated from gnats in Australia. Therefore, viruses related to TUPV may be distributed quite broadly.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Springfeld, C., Darai, G., Cattaneo, R. (2005). Characterization of the Tupaia rhabdovirus genome reveals a long open reading frame overlapping with P and a Novel gene encoding a small hydrophobic protein. *J. Virol.* 79, 6781–6790.

Kurz, W., H. Gelderblom, R. M. Fluegel, and G. Darai. 1986. Isolation and characterization of a tupaia rhabdovirus. *Intervirology.* 25:88–96.

Kuzmin, I.V., Novella, I.S., Dietzgen, R.G., Padhi, A., Rupprecht, C.E. (2009) The rhabdoviruses: Biodiversity, phylogenetics and evolution. *Infection, Genetics and Evolution* (in press)

**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. TUPV genome organization (from Springfield et al., 2005).

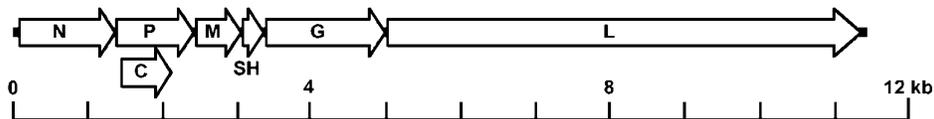


Figure 2. Phylogenetic position of TUPV within *Rhabdoviridae* based on the alignment of partial nucleoprotein (A) and polymerase (B) gene sequences (from Kuzmin et al., 2009).

