



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>2009.012a,bV</i></b>	(to be completed by ICTV officers)			
<b>Short title:</b> Create a species named Flanders 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

Has this proposal has been seen and agreed by the relevant study group(s)? Please select answer in the box on the right	<b>Yes</b>
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**ICTV-EC or Study Group comments and response of the proposer:**

1. In my previous message I neglected to mention that the word Rhabdoviridae should be italicized. Here also.
2. No abbreviation is needed for a species, only for a virus. If it was needed, it wouldn't be italicized. Delete abbreviation.
3. No need to italicize the word "unassigned".
4. Page 3, line 1: Change 1964 to 1961
5. Change "to assign" (page 3, line 3) to "assignment of"
6. Page 3, paragraph 2: You might consider mentioning that Flanders virus is found mostly in eastern North America and Hart Park virus found mostly in western North America. Some overlap is found at the geographic extremes but, for the most part, these viruses have been found where their mosquito hosts occur, *Culiseta melanura* in the east (FLAV), *Culex tarsalis* in the west (HPV).
4. The meaning of "further to ephemeroviruses" is unclear to me.

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

Approved by ICTV at 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>2009.012aV</b>	(assigned by ICTV officers)
<b>To create 1 new species with the name:</b>		
<i>Flanders 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>2009.012bV</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>	

**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

*Flanders virus* (FLAV) was discovered in 1961. It 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. The available information is sufficient to establish a new species within the family.

FLAV is associated with mosquitoes and birds in North America. Initial serologic neutralization, complement fixation, and double-diffusion tests demonstrated that FLAV is related to Hart Park virus (HPV). Further serologic studies demonstrated that FLAV isolates from different states of the USA were close related to each other but different from the Hart Park virus. Furthermore, FLAV was found mostly in eastern North America, whereas HPV was found mostly in western North America. Some overlap is found at the geographic extremes but, for the most part, these viruses have been found where their mosquito hosts occur, *Culiseta melanura* in the east (FLAV), *Culex tarsalis* in the west (HPV).

FLAV genome is about 13 kb negative-sense, single-stranded RNA. The gene order with intergenic regions is: 3'-N-(tc)-P-(tc)-pseudogene1-(tc)-19K-(tc)-pseudogene2-(tt)-M-G-(tt)-L-5', where N, P, M, G and L are common for rhabdoviruses nucleoprotein, phosphoprotein, matrix protein, glycoprotein and polymerase protein genes. The unique features include the additional 19K gene (which codes for the 19 kDa protein), surrounded by two pseudogenes, about 500 nucleotides each, situated between the P and M genes.

Phylogenetically, FLAV can not be assigned into any of the existing genera of *Rhabdoviridae* (Fig 1). According to the N and L gene sequences, FLAV demonstrates limited relatedness to Wongabel and Ngaingan viruses, that circulate in Australia, and further this cluster is distantly related to ephemeroviruses (with long genetic distance but substantial bootstrap support).

GenBank accession numbers: AF523199, AF523197, AF523196, AF523195, AF523194, AH012179.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Boyd KR. (1972). Serological comparisons among Hart Park virus and strains of Flanders virus. *Infect Immunol.* 5: 933-937.

Murphy FA, Coleman PH, Whitfield SG. (1966). Electron microscopic observations of Flanders virus. *Virology.* 30: 314-317.

Boyd KR, Whitaker-Dowling P. (1988). Flanders virus replication and protein synthesis. *Virology.* 163(2):349-358.

Kokernot RH, Hayes J, Will RL, Radivojevi B, Boyd KR, Chan DHM. (1969). Arbovirus Studies in the Ohio-Mississippi Basin, 1964–1967. III. Flanders virus. *Am. J. Trop. Med. Hyg.* 18: 762-767.

Whitney E. (1964) Flanders Strain, an arbovirus newly isolated from mosquitoes and birds of New York State. *Am. J. Trop. Med. Hyg.*, 13: 123-131.

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



