



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:	2015.005a,bM	(to be completed by ICTV officers)
Short title: Assign the free-floating genus <i>Varicosavirus</i> to the family <i>Rhabdoviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 10 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 checked="" type="checkbox"/> 8 <input type="checkbox"/> 9 <input type="checkbox"/> 10 <input checked="" type="checkbox"/>	

Author(s):

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List the ICTV study group(s) that have seen this proposal:

<p>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)</p>	<p>ICTV <i>Bornaviridae</i>, <i>Filoviridae</i>, <i>Nyamiviridae</i>, and <i>Paramyxoviridae</i> Study Groups</p>
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ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 15, 2015

Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	2015.005aM	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Varicosavirus</i>		
The present taxonomic position of these taxon/taxa:		
Genus:		Fill in all that apply.
Subfamily:		
Family:	unassigned	
Order:	unassigned	
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

Based on recent phylogenetic evidence, the free-floating genus *Varicosavirus* should be assigned to the family *Rhabdoviridae*

Part (b) re-assign to a higher taxon

Code	2015.005bM	(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
Genus:		Fill in all that apply. • If the higher taxon has yet to be created write " (new) " after its proposed name and complete relevant module to create it. If no genus is specified, enter " unassigned " in the genus box.
Subfamily:		
Family:	<i>Rhabdoviridae</i>	
Order:	<i>Mononegavirales</i>	

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please 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 accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 10

The genus *Varicosavirus* is recognized by the ICTV, but has not yet been assigned to a family. Phylogenetic analysis of the viral polymerase gene consistently places the genus with its type species *Lettuce big-vein associated virus* and virus representative LBVaV with viruses in the family *Rhabdoviridae*, most closely related to, but distinct from the genera *Cytorhabdovirus* and *Nucleorhabdovirus*.

The similarity LBVaV with rhabdoviruses is best summarized in [1]: The genome structure and probable transcription mechanism of LBVaV indicates that it has a close relationship with rhabdoviruses. The amino acid sequences of both the CP/N and L protein of LBVaV have significant similarities with those of rhabdoviruses. LBVaV also resembles rhabdoviruses in possessing conserved transcription termination/polyadenylation signal-like poly(U) tracts and in transcribing monocistronic RNAs. The presence of poly(U) tracts in the noncoding region (NCR) of LBVaV RNA-1 and RNA-2 suggest that transcription of LBVaV is regulated by a mechanism similar to that of rhabdoviruses. However, whereas rhabdoviruses contain a single negative sense ssRNA, LBVaV has two such RNAs.

Although varicosaviruses are structurally and phylogenetically related to rhabdoviruses, the deep evolutionary history and host adaptation processes that have led to genome segmentation and gene loss are less clear. However, phylogenetic analysis of L genes clearly indicates that LBVaV falls well within the extent of genetic diversity currently represented in the family *Rhabdoviridae*, supporting the assignment of the genus *Varicosavirus* as new genus in the family.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Walsh, J.A., Verbeek, M. (2012) Genus *Varicosavirus*. In: Virus Taxonomy: Ninth Report of the International Committee on Taxonomy of Viruses, Elsevier Inc., pp. 777-781.
- Palacios, G., Forrester, N.L., Savji, N., Travassos da Rosa, A.P.A., Guzman, H., DeToy, K., Popov, V.L., Walker, P.J., Lipkin, I.W.I., Vasilakis, N., Tesh, R.B. (2013). Characterization of Farmington virus, a novel virus from birds that is distantly related to members of the family *Rhabdoviridae*. *Virology* 460:219.
- Li, C.X., Shi, M., Tian, J.H., Lin, X.D., Kang, Y.J., Chen, L.J., Qin, X.C., Xu, J., Holmes, E.C., Zhang, Y.Z. (2015). Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-strand RNA viruses. *eLife* 4:e05378.

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.

Appendix 1: Comparison of the genome organization of LBVaV, type member of the genus *Varicosavirus*, and representative members of other genera harboring plant-infecting viruses, such as *Nucleorhabdovirus* and *Cytorhabdovirus* (both family *Rhabdoviridae*) and “*Dichorhavirus*” (newly proposed genus in the family *Rhabdoviridae*).

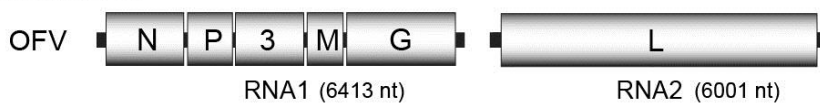
Appendix 2: Comparison of genome size and encoded proteins of varicosaviruses and selected plant (-) ssRNA viruses.

Appendix 3: Phylogenetic relationship of LBVaV to selected mononegaviruses.

Appendix 1

Comparison of the genome organization of LBVaV, type member of the genus *Varicosavirus*, and representative members of other genera harboring plant-infecting (-) RNA viruses, such as *Nucleorhabdovirus* and *Cytorhabdovirus* (both family *Rhabdoviridae*) and “*Dichorhavirus*” (newly proposed genus in the family *Rhabdoviridae*). OFV RNA1 encodes 49 kDa (ORF1: nucleocapsid protein N), 26 kDa (ORF2: putative phosphoprotein P), 38 kDa (ORF3: putative movement protein), 20 kDa (ORF4: putative matrix protein M) and 61 kDa (ORF5: putative glycoprotein G) proteins, and RNA2 encodes a single protein of 212 kDa (ORF6: large polymerase protein L). Virus names and GenBank/Refseq accession numbers are as follows: proposed genus “*Dichorhavirus*” - orchid fleck virus (OFV; RNA1: NC_009608, RNA2: NC_009609), *Nucleorhabdovirus* - potato yellow dwarf virus (PYDV; NC_016136), *Cytorhabdovirus* - lettuce necrotic yellows virus (LNYV; NC_007642), *Varicosavirus* - lettuce big-vein associated virus (LBVaV; NC_011558, RNA2: NC_011568). The genomic locations in the 3’-5’ negative-sense arrangement are shown, as well as the relative sizes of the viral genes.

Dichorhavirus



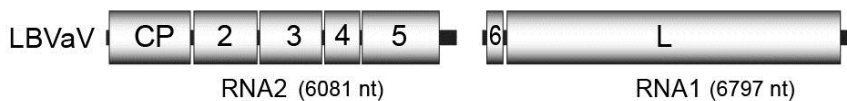
Nucleorhabdovirus



Cytorhabdovirus



Varicosavirus



3' ← Genome organization → 5'

Appendix 2: Comparison of genome size and encoded proteins of varicosaviruses and selected plant (-) ssRNA viruses

Genus	Virus name (abbreviation)	Genome size (nt)	Proteins (kDa) ORF # (putative function/denomination)						
			1 (N/CP)*	X*	2 (P)	3 (MP)	4 (M)	5 (G)	6 (L)
<i>Varicosavirus</i>	lettuce big vein-associated virus (LBVaV)	RNA 1: 6797 RNA 2: 6081	44	-	36	32	19	41	232
<i>Nucleorhabdovirus</i>	potato yellow dwarf virus (PYDV)	Non-segmented 12,875	52	9.7	31	33	29	70	220
" <i>Dichorhavirus</i> "	orchid fleck virus (OFV)	RNA 1: 6413 RNA 2: 6001	49	-	26	38	20	61	212

* A protein of unknown function; N/CP indicates the different naming of ORF #1 in the listed genera; -: not present.

Appendix 3

Phylogenetic relationships of LBVaV to selected mononegaviruses. A maximum-likelihood tree was constructed using PhyML 3.0 (<http://www.atgc-montpellier.fr/phyml/>) based on a multiple amino acid sequence alignment of the entire L polymerase. Ambiguously aligned regions were removed using Gblocks 0.91b (http://molevol.cmima.csic.es/castresana/Gblocks_server.html) with the all options of less stringent selection. The best-fit model LG+I +G+F was selected using ProtTest ver. 2.4 (http://darwin.uvigo.es/software/prottest2_server.html). Virus names and GenBank/Refseq accession numbers of the L polymerase sequences are shown. The members of the proposed genus “*Dichorhavirus*” and the genus *Varicosavirus* are indicated by black bold letters. Numbers at the nodes represent aLRT values derived using an SH like calculation (only values greater than 0.9 are shown).

