



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"

Code assigned:	2007.027a-f.P	(to be completed by ICTV officers)
Short title: Creation of new order Tymovirales (e.g. 6 new species in the genus <i>Zetavirus</i> ; re-classification of the family <i>Zetaviridae</i> etc.)		
Modules attached (please check all that apply):	1 <input checked="" type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input type="checkbox"/>
	5 <input type="checkbox"/>	6 <input checked="" type="checkbox"/>
	7 <input type="checkbox"/>	

Author(s) with e-mail address(es) of the proposer:

Mike Adams (mike.adams@bbsrc.ac.uk) on behalf of the Flexiviridae SG and
Jan Kreuze (j.kreuze@cgiar.org)

If the proposal has been seen and agreed by the relevant study group(s) write "yes" in the box on the right

YES

ICTV-EC or Study Group comments and response of the proposer:

The original (2007) proposal was to split the family Flexiviridae into three subfamilies and then to assign the families Flexiviridae and Tymoviridae to the new order Tymovirales. As a result of EC discussion and comments, the Study Group has agreed to split the Flexiviridae into three families and thus create an order with four families. This makes it necessary for a set of formal decisions to dismantle the old family and these have to be taken in connection with the entire series of proposals 2007.006-026P to create new genera and families prior to assignment to the new order.

Date first submitted to ICTV: 08 June 2007
Date of this revision (if different to above): 20 Aug 2008

MODULE 1: REMOVE and MOVE

Code	2007.027aP	(assigned by ICTV officers)
To remove the following genera from their present position in the family <i>Flexiviridae</i>:		
(1) <i>Allxivirus</i> , <i>Mandarivirus</i> , <i>Potexvirus</i>		
(2) <i>Carlavirus</i> , <i>Citrivirus</i> , <i>Capillovirus</i> , <i>Foveavirus</i> , <i>Trichovirus</i> , <i>Vitivirus</i>		
Reasons to justify the removal:		
The existing family is being split into two: see proposals 2007.018-20P.A.Alphaflexiviridae [genera listed under (1)] and 2007.021-023P.A.Betaflexiviridae [genera listed under (2)] which give further details.		
Code	2007.027bP	(assigned by ICTV officers)
To remove the following species from their present position unassigned in the family <i>Flexiviridae</i>:		
<i>Banana mild mosaic virus</i>		

<i>Cherry green ring mottle virus</i> <i>Cherry necrotic rusty mottle virus</i> <i>Potato virus T</i> <i>Sugarcane striate mosaic-associated virus</i>	
Reasons to justify the removal:	
The existing family is being split into two: These species are being re-assigned to the new family <i>Betaflexiviridae</i> (see proposal 2007.021-023P.A.Betaflexiviridae)	
Code	2007.027cP (assigned by ICTV officers)
To remove the family <i>Flexiviridae</i>	
If this taxon is to be completely removed write "yes" in the box on the right	YES
Reasons to justify the removal:	
The existing family is being split into two: see proposals 2007.018-20P.A.Alphaflexiviridae and 2007.021-023P.A.Betaflexiviridae	

MODULE 6: **NEW ORDER**

Code	2007.027dP (assigned by ICTV officers)
To create a new order containing families resembling: <i>Tymoviridae</i> and <i>Alphaflexiviridae</i>	

Code	2007.027eP (assigned by ICTV officers)
To name the new order: <i>Tymovirales</i>	

Code	2007.027fP (assigned by ICTV officers)
<p>To assign the following as families in the order created in section 6(a): You may list several families here. For each family, please state whether it is new or existing. If the family is new, there must be a proposal to create it.</p> <p><i>Alphaflexiviridae</i> (new family: see proposal 2007.018-20P.A.Alphaflexiviridae) <i>Betaflexiviridae</i> (new family: see proposal 2007.021-023P.A.Betaflexiviridae) <i>Gammaflexiviridae</i> (new family: see proposal 2007.024-026P.A.Gammaflexiviridae) <i>Tymoviridae</i> (existing family not assigned to an order)</p>	
Reasons to justify the creation of a new order:	
<p>Phylogenetic analysis of the replication proteins shows a close relationship within the "alpha-like" supergroup between the (current) <i>Flexiviridae</i> and the <i>Tymoviridae</i>. In fact flexivirid members of the proposed family <i>Alphaflexiviridae</i> appear to be slightly more closely related to the <i>Tymoviridae</i> than to the other members of the (current) <i>Flexiviridae</i> in this gene. The proposed new order recognizes these substantial similarities and also provides a framework for the classification of some mycoviruses.</p> <p>The following paragraphs provide a more detailed justification for the proposed division of the family <i>Flexiviridae</i> into families and for the creation of the order <i>Tymovirales</i>.</p> <p>The family <i>Flexiviridae</i> was recognized in 2004, and included a number of previously "floating" genera of plant viruses that had a monopartite ssRNA polyadenylated genome encapsidated in flexuous filamentous particles. Genome organization differed between genera but all had an alpha-like replication</p>	

polyprotein as the 5'-proximal ORF while the final or penultimate ORF encoded the single coat protein (Adams et al., 2004). Within the family, the major differences were in (i) the replication polyprotein – these clearly fall into two distinct lineages (Potexvirus-like and Carlavirus-like; see Figure 1), (ii) the type of cell-to-cell movement protein(s), which were either of the “Triple gene block” (TGB) type (Morozov & Solovyev, 2003) or a single protein of the ‘30K’ family (Melcher, 2000) and (iii) the coat protein – these fall into two groups (Figure 2) but do not coincide with the groups of the replication polyprotein.

A recent analysis has re-examined the position of the family *Flexiviridae* in relation to other virus groups, particularly the family *Tymoviridae*. Tymovirids have icosahedral particles, some have a polyadenylated genome and the single cell-to-cell movement (where present) is not related to those found in the (current) family *Flexiviridae*. However, the replication proteins are quite closely related and in phylogenetic analyses the potexvirus-like replicases are more closely related to tymovirids than to carlaviruses. A common evolutionary ancestor for the family *Tymoviridae* and the two distinct evolutionary clusters of the *Flexiviridae* has been postulated that would be a plant virus with a polyadenylated genome, filamentous virions, and a triple gene block of movement proteins (Figure 3; Martelli et al., 2007). The analyses also identified three mycoviruses that need to be classified within the *Tymoviridae-Flexiviridae* grouping.

The set of proposals divides the existing family *Flexiviridae* into two families corresponding to potexvirus-like (*Alphaflexiviridae*) and carlavirus-like (*Betaflexiviridae*) lineages. A third genus and family appears advisable to accommodate one of the mycoviruses, *Botrytis virus F* (proposed new genus *Mycoflexivirus* [2007.006-009P.A.Mycoflexivirus] and new family *Gammaflexiviridae* [2007.024-026P.A.Gammaflexiviridae]). To recognize the relationship of flexivirids to the family *Tymoviridae*, a new order *Tymovirales* embracing all families is also proposed. The phylogenetic trees in Figures 1-3 support and illustrate these conclusions.

Origin of the new order name:

Derived from the family name *Tymoviridae*. It would be inappropriate to base the order name on the family *Flexiviridae* since this implies flexuous particles

References:

- Adams MJ, Antoniw JF, Bar-Joseph M, Brunt AA, Candresse T, Foster GD, Martelli GP, Milne RG, Zavriev SK, Fauquet CM (2004) The new plant virus family Flexiviridae and assessment of molecular criteria for species demarcation. *Archives of Virology* 149, 1045-1060.
- Martelli G, Adams MJ, Kreuze JF, Dolja VV (2007) Family Flexiviridae: a case study in virion and genome plasticity. *Annual Review of Phytopathology* 45, 73-100.
- Melcher U (2000) The ‘30K’ superfamily of viral movement proteins. *Journal of General Virology* 81, 257-266.
- Morozov SY, Solovyev AG (2003) Triple gene block: modular design of a multifunctional machine for plant virus movement. *Journal of General Virology* 84, 1351-1366.

Annex

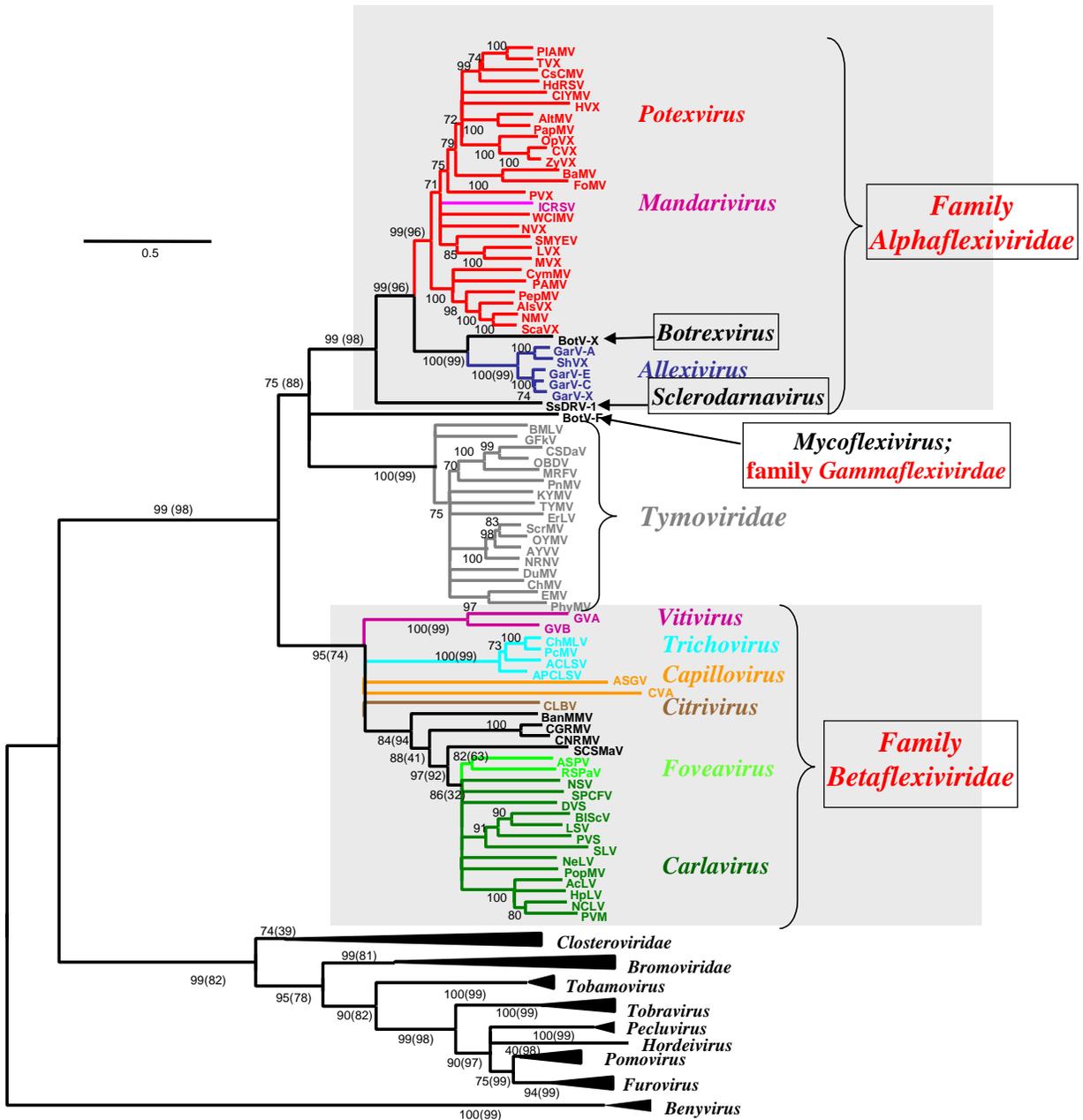


Figure 1. Phylogenetic tree of the replicase amino acid sequences adapted from Martelli et al., 2007. Genera within the (current) family *Flexiviridae* are indicated in different colors. Proposed new genera and families are shown in boxes. The tree was created from the fused alignments of methyl-transferase, helicase, and polymerase conserved core domains of plant infecting “Alpha” like viruses. Deletion of the variable regions between the conserved domains was required to obtain a robust alignment. trees were created by neighbor joining using the JTT matrix and pair-wise gap deletion. Numbers on branches indicate percentage of bootstrap support out of 1000 bootstrap replications. Branches with less than 70% bootstrap support were collapsed. Similar phylogenies were obtained using the Maximum Parsimony method, and the corresponding bootstrap values are indicated between brackets in branches above the genus level. Scales indicate JTT amino acid distances. Distantly related genera and families that formed well-supported monophyletic clades were collapsed into a triangle, the size of which corresponds to the variation found within the clade.

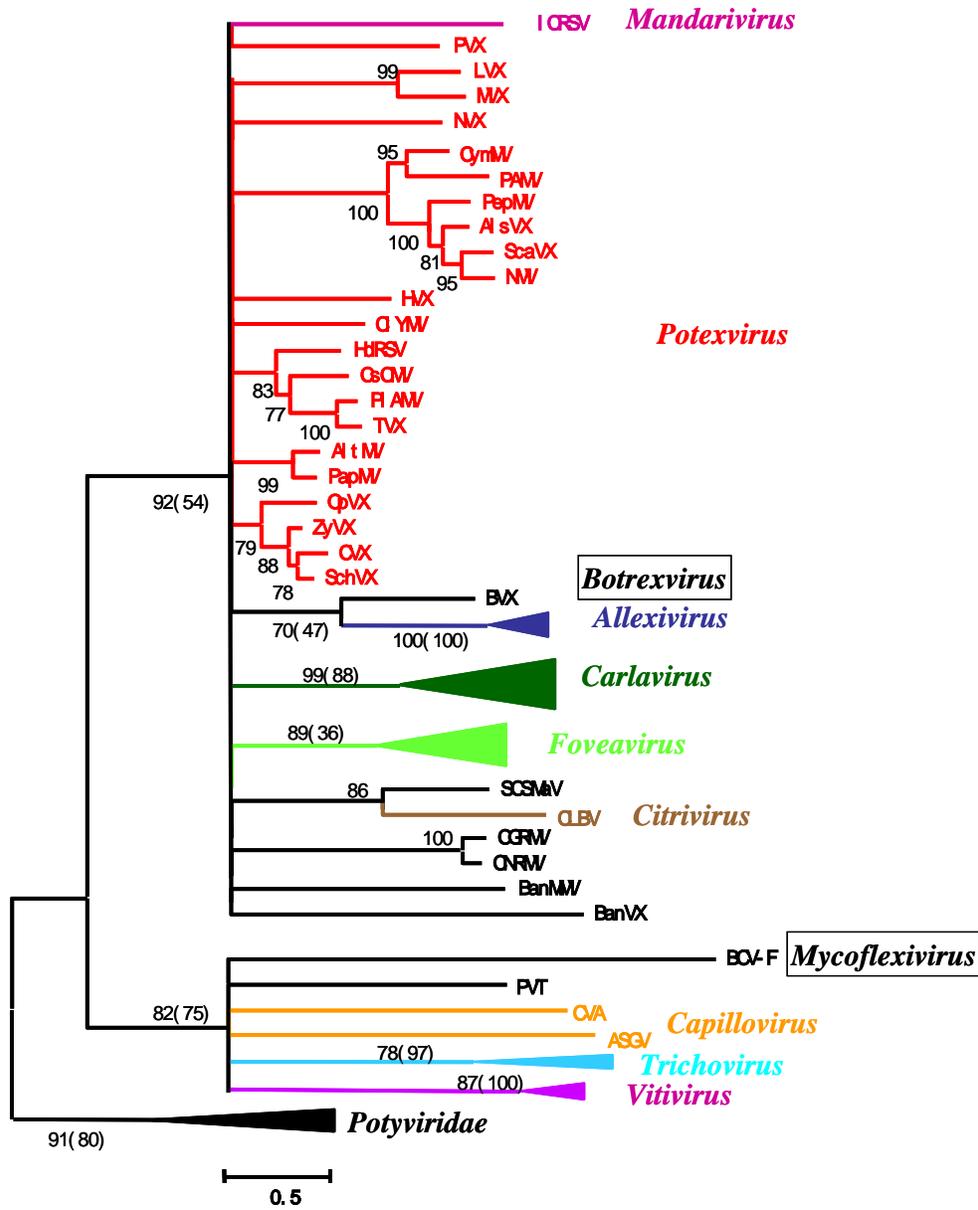


Figure 2. Phylogenetic tree of the flexivirus capsid protein sequences adapted from Martelli et al., 2007. Colors and methods are as in Figure 1.

Figure 3. Projected evolutionary scenario and taxonomy within the proposed order *Tymovirales*. Boxes represent open reading frames: in shades of blue, replicase gene; in shades of red, CP genes. 30K-like movement proteins in orange, triple gene block (TGB) proteins in yellow, coat proteins in red and RNA-binding proteins in purple. Other ORFs are white. The methyltransferase (M), AlkB (A), OTu-like peptidase (O), papain-like protease (P), RNA helicase (H), and RNA-dependent RNA polymerase (R) domains of the replicase are also shown. Genus names in boxes are the proposed new mycovirus genera. Adapted from Martelli et al., 2007.

