



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:	2010.004aP	(to be completed by ICTV officers)			
Short title: A new species in the genus Cucumovirus (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

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

Simon Scott(sscott@clemson.edu) on behalf of the Bromoviridae SG

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)

Bromoviridae

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	2010.004aP	(assigned by ICTV officers)
To create 1 new species within:		
Genus:	<i>Cucumovirus</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>Bromoviridae</i>	
Order:		
And name the new species:		GenBank sequence accession number(s) of reference isolate:
<i>Gayfeather mild mottle virus</i>		FM881899, FM881900, FM881901

<p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ 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. • Further material in support of this proposal may be presented in the Appendix, Module 9
<p>Species demarcation criteria in the genus are serological relatedness, and sequence similarity.</p> <p>Weak cross reaction with antibodies against CMV in ELISA</p> <p>Gayfeather mild mottle virus (GMMV) was isolated from <i>Liatris spicata</i> (common name Gayfeather). Complete genomic sequence and phylogenetic analysis indicated it to be a member of the genus <i>Cucumovirus</i> (Adams et al., 2009).</p> <p>Data presented within the reference (extracted below) clearly demonstrate the relationships of this virus with other cucumoviruses. Comparison of 1a protein sequences and full genome sequences show GMMV to be most closely related to, but distinct from, tomato aspermy virus and as such should be considered a new species of cucumovirus.</p>

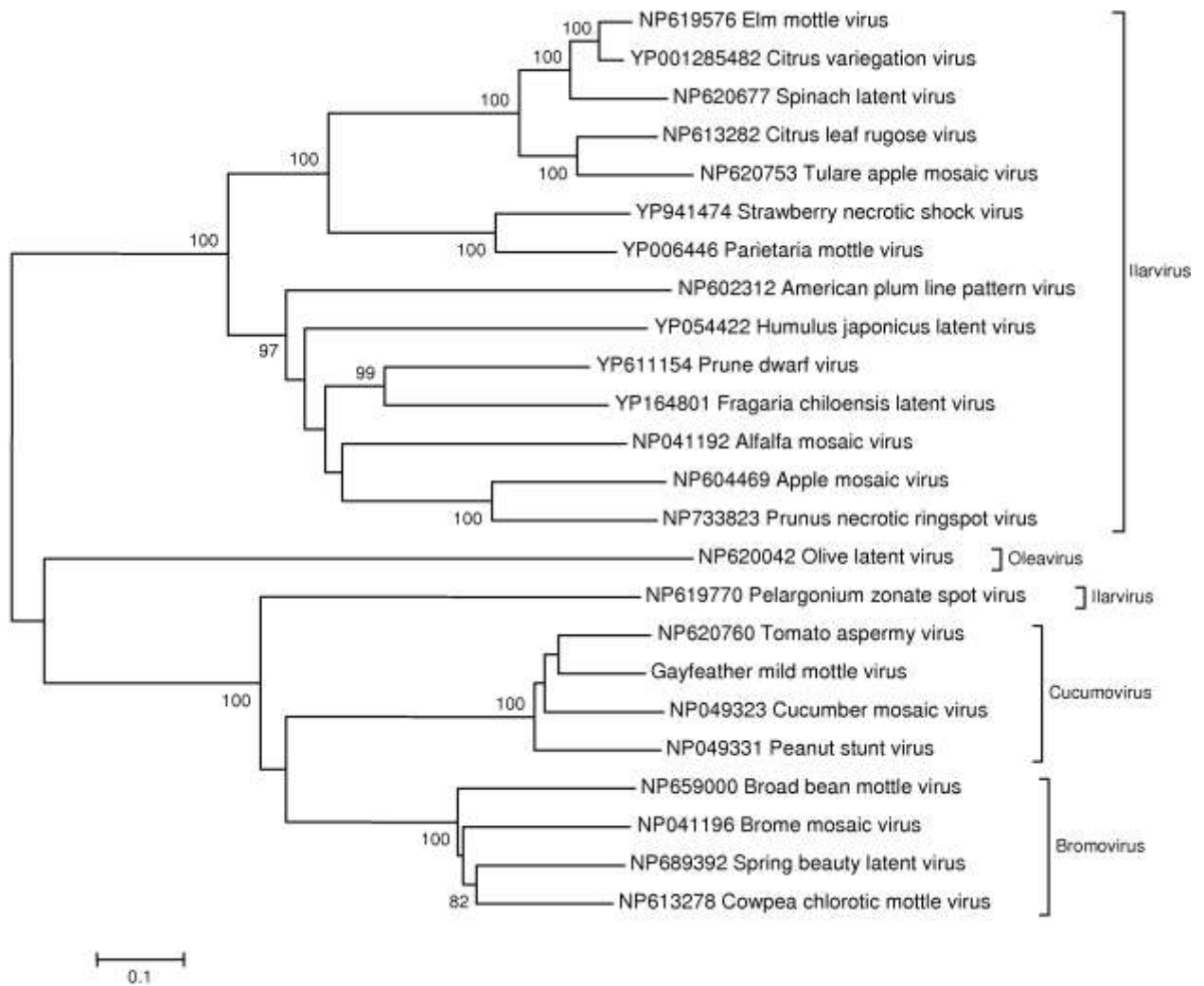


Fig. 2 Bootstrapped neighbour-joining tree (1000 replicates) constructed from an alignment of 1a protein sequences from the Bromoviridae family. Gayfeather mild mottle virus (GMMV) is placed within the Cucumovirus genus.



Fig. 3 Bootstrapped neighbour-joining tree (1000 replicates) constructed using uncorrected P distances derived from an alignment of the full reference genomes of all known cucumoviruses [Cucumber mosaic virus (CMV), Peanut stunt virus (PSV) and Tomato aspermy virus (TAV)], Gayfeather mild mosaic virus and a Bromovirus, Broad bean mottle virus (BBMV). Reference genome accession numbers: PSV (NC_002038, NC_002039, NC_002040); CMV (NC_002035, NC_002034, NC_001440); TAV (NC_003837, NC_003838, NC_003836); BBMV (NC_004008, NC_004007, NC_004006).

Table 2 Percentage nucleotide differences between the whole genomes of the currently recognized cucumoviruses [Cucumber mosaic virus (CMV), Peanut stunt virus (PSV) and Tomato aspermy virus (TAV)], Gayfeather mild mottle virus (GMMV) and a bromovirus, Broad bean mottle virus (BBMV).

	GMMV	PSV	TAV	CMV
PSV	43.19%	—		
TAV	40.06%	35.88%	—	
CMV	41.19%	34.97%	35.16%	—
BBMV	55.50%	55.19%	54.24%	54.26%

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adams IP, Glover RH, Monger WA, Mumford R, Jackeviciene J, Navalinskiene, Samuitiene, M and Boonham, N (2009) Next-Generation sequencing and Metagenomic analysis: a universal diagnostic tool in plant virology. <i>Molecular Plant Pathology</i> 10: 537-545
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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.

