



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	2008.004P	<small>(to be completed by ICTV officers)</small>
Short title: 1 new species in the genus <i>Vitivirus</i> <small>(e.g. 6 new species in the genus <i>Zetavirus</i>; re-classification of the family <i>Zetaviridae</i> etc.)</small>		
Modules attached <small>(please check all that apply):</small>	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input type="checkbox"/>
	5 <input checked="" type="checkbox"/>	6 <input 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

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

MODULE 5: **NEW SPECIES**

Code	2008.004P	<small>(assigned by ICTV officers)</small>
To create 1 new species assigned as follows:		
Genus:	<i>Vitivirus</i>	Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)
Subfamily:		
Family:	proposed family <i>Betaflexiviridae</i> (formerly <i>Flexiviridae</i>)	
Order:		

Name(s) of proposed new species:

Mint virus 2

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Species demarcation criteria published in the 8th report are:

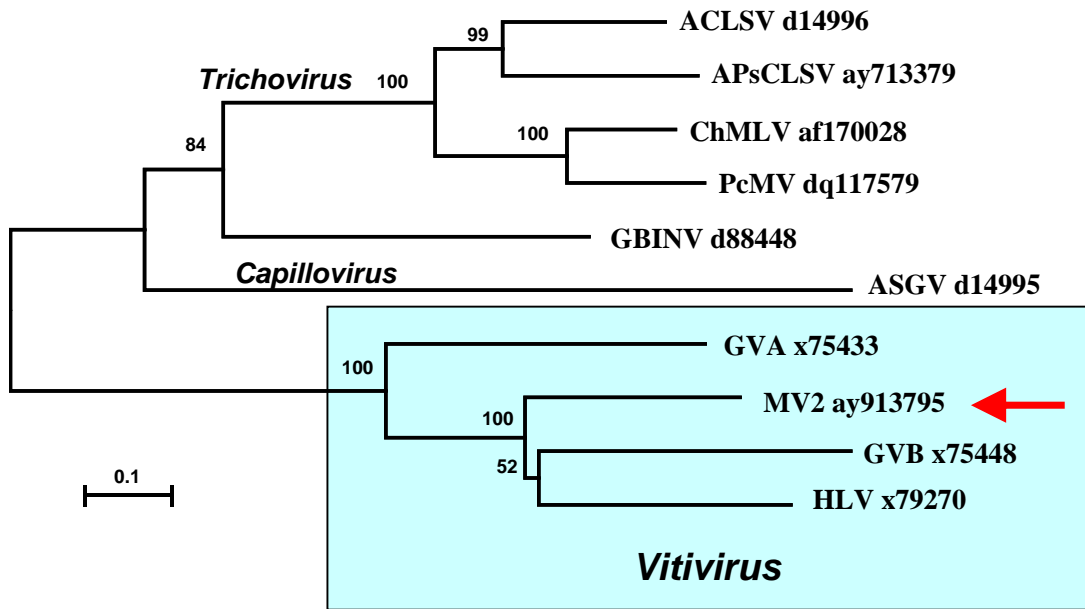
Each distinct species usually has a specific natural host range. Distinct species do not cross-protect in infected common host plant species. Distinct species are readily differentiated by serological procedures; strains of individual species are often distinguishable in reactions with polyclonal antisera, but more readily so with monoclonal antibodies. Distinct species have less than ca. 72% identical nt or 80% identical aa between their CP or polymerase genes.

This is one of several viruses that interferes with the variegated phenotype of the ornamental clone

Argument to justify the creation of the new species:

Mentha x gracilis 'Variegata'. The nucleotide sequence of the 3'-half of the virus (AY913795) indicates that the virus is related to members of the genus *Vitivirus* (Tzanetakis et al., 2007). It could be transmitted by the mint aphid (*Ovatus crataegarius*) in the presence of a helper virus. Phylogenetic analyses (Fig. 1) and sequence comparisons justify its status as a distinct species within the genus *Vitivirus*: coat protein amino acid identities with other members of the genus are 66% (HLV), 62% (GVB) and 57% (GVA).

Fig. 1. Phylogenetic (NJ) tree of the nucleotide sequences of the concatenated movement and coat protein genes of members of the genera *Vitivirus*, *Capillovirus* and *Foveavirus*. From MEGA4 using maximum composite likelihood and 10,000 bootstrap replicates.



References:

Tzanetakis I.E., Postman J.D., Martin R.R. (2007). Identification, detection and transmission of a new vitivirus from *Mentha*. Arch. Virol. 152:2027-2033