



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:	2009.003a,bV	(to be completed by ICTV officers)			
Short title: Create a species named <i>Lettuce yellow mottle virus</i> in the genus <i>Cytorhabdovirus</i> in the family <i>Rhabdoviridae</i> in the order <i>Mononegavirales</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)					
Modules attached (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:

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Has this proposal has been seen and agreed by the relevant study group(s)?
Please select answer in the box on the right

Yes

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

Proposers are members of the study group

Date first submitted to ICTV: 08.05.2009
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	2009.003aV	(assigned by ICTV officers)
To create 1 new species with the name(s): <i>Lettuce yellow mottle 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	2009.003bV	(assigned by ICTV officers)
To assign the species listed in section 2(a) as follows:		
Genus:	<i>Cytorhabdovirus</i>	Fill in all that apply. <ul style="list-style-type: none">• 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>Rhabdoviridae</i>	
Order:	<i>Mononegavirales</i>	

Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.

A new lettuce-infecting cytorhabdovirus that is serologically unrelated to lettuce necrotic yellows virus (LNYV) has been isolated near Valence, France, by Dr. H. Lot (INRA Avignon, France). Since this virus produces typical chlorotic spots and yellow leaf mottling on infected lettuce leaves, the name *lettuce yellow mottle virus* (LYMoV) was suggested (photos of purified viral particles and particles found in the cytoplasm, as well as symptoms on lettuce shown in Heim et al. 2008).

The full-length nucleotide sequence of the genomic RNA has been determined (Genbank accession EF687738). Six open reading frames were found in the antigenomic sequence of the 12,926 nt negative-sense viral RNA genome. The genomic organisation was same as that of LNYV, the type species of the genus Cytorhabdovirus: 3'-N-P-3-M-G-L-5', where N is the capsid protein gene, P the putative phosphoprotein gene, 3 a gene coding for a putative protein of unknown function, M the putative matrix protein gene, G the glycoprotein gene, and L the putative polymerase gene.

Deduced amino acid sequence comparison with the corresponding sequences of other rhabdoviruses revealed the closest relationship to LNYV, with identities ranging from 41% for the matrix proteins and 65% for the L polymerase proteins (Heim et al. 2008).

- If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria.

Although LYMoV is most similar to LNYV on the basis of both genomic organisation (both have 6 ORFs, while SCV and NCMV have 7 and 9 ORFs, respectively) and sequence identities in the different rhabdovirus proteins, the two viruses are serologically unrelated. Species demarcation with plant-infecting rhabdoviruses is currently based on serological similarity, host range and vector specificity, sequence identity being considered as “not presently sufficient” for discrimination of species by the International Committee of Virus Taxonomy, due to the low number of completely sequenced viral genomes in the genus Cytorhabdovirus. However, the differences observed between LYMoV and LNYV appear to be sufficient to classify LYMoV as a new species. While LNYV is transmitted in a persistent, propagative manner by the aphid *Hyperomyzus lactucae*, the vector of LYMoV is still unknown.

Available biological data and the complete genome sequence of LYMoV support its assignment as species in the genus *Cytorhabdovirus*.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Heim, F., Lot, H., Delecalle, B., Bassler, A., Krczal, G., and Wetzel, T. (2008) Complete nucleotide sequence of a putative new cytorhabdovirus infecting lettuce. Arch. Virol. 153, 81-92

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.

Table 1: Sequence comparisons between the deduced LYMoV proteins and the corresponding sequences of other plant rhabdoviruses. The results are shown in % of identity. The sequence comparisons were done using the clustalw program (<http://www.ebi.ac.uk/clustalw/>).

	N	P	3	M	G	L
LNyV	56	48	58	41	49	65
NCMV	20	11	8	9	15	25
SCV						51*
SYNV	16	6	9	2	12	17
MMV	15	7	4	7	6	18
MFSV	15	9	2	1	10	19
RYSV	12	6	5	3	11	18
TaVCV	16	3	7	6	5	19

LNyV : *Lettuce necrotic yellows virus*, NCMV : *Northern cereal mosaic virus*, SCV*: *Strawberry crinckle virus* (partial sequence only, Genbank Accession number AY250986), SYNV : *Sonchus yellow net virus*, MMV : *Maize mosaic virus*, MFSV: *Maize fine streak virus*, RYSV : *Rice yellow stunt virus*, TaVCV : *Taro vein chlorosis virus*.

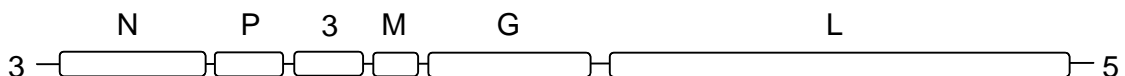


Figure 1: LYMoV genomic organisation