



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**

<b>Code assigned:</b>	<b>2010.019aP</b>	(to be completed by ICTV officers)			
<b>Short title:</b> To create a new species in the genus Tymovirus of the family Tymoviridae (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (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:**

Dreher, Theo W. theo.dreher@oregonstate.edu (on behalf of Tymoviridae Study Group)

**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)

Tymoviridae

**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	<b><i>2010.019aP</i></b>	(assigned by ICTV officers)
<b>To create 1 new species within:</b>		
Genus:	<b><i>Tymovirus</i></b>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<b><i>Tymoviridae</i></b>	
Order:	<b><i>Tymovirales</i></b>	
<b>And name the new species:</b>		<b>GenBank sequence accession number(s) of reference isolate:</b>
<i>Chiltepin yellow mosaic virus</i>		FN563123 = NC_014127

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

- 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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Key characteristics of the family *Tymoviridae* are (see 8<sup>th</sup> ICTV Report, Dreher et al., 2005):

- 30 nm non-enveloped icosahedral particles showing the presence of both full and empty (stain-penetrating) particles when observed by negative staining EM;
- 6-7.5 kb positive strand RNA viral genome.

Within the family, members of the genus *Tymovirus*:

- have 6.0-6.7 kb genome and a single c. 0.6 kb subgenomic RNA (sgRNA);
- have genomes encoding 3 proteins: (1) RP, a c. 200 kDa replication polyprotein with methyltransferase (MTR), papain-like protease (PRO), helicase (HEL) and RNA-dependent RNA polymerase (RdRp, POL) domains; (2) OP, a 50-80 kDa proline-rich protein encoded by an almost entirely overlapping ORF that serves as movement protein and RNAi suppressor; (3) a c. 20 kDa coat protein encoded near the 3’ end that is expressed from the sgRNA;
- have a 16 nt Tymobox sequence (GAGUCUGAAUUGCUUC) involved in subgenomic RNA synthesis;
- have a nonpolyadenylated genome, typically with a tRNA-like structure at the 3’ end;
- mechanically transmissible
- spread to all main tissues of the host
- associated with the formation of double-membrane vesicles at the peripheries of chloroplasts in infected leaves.

The criteria demarcating species in the genus are:

- Overall sequence identity of less than 80%
- Capsid protein sequences less than 90% identical
- Differential host range
- Differences in the 3’-terminal structure
- Serological specificity

## Chiltepin yellow mosaic virus (ChiYMV) properties

### Origin:

Isolated from *Capsicum annuum* var. *aviculare*, known commonly as chiltepin, in Tula (Tamaulipas, Mexico (22° 59'N, 99° 38'W) during 2001. The type isolate is ChiYMV-20.5; another isolate also from Tula is ChiYMV-20.8. Ref.: Pagan et al., 2010.

ChiYMV produces yellow mosaic in leaves of systemically infected chiltepin plants; the virus is mechanically transmissible.

**Host range:** is almost entirely limited to the *Solanaceae*, with systemic infections (mostly mosaic or yellow mosaic symptoms) produced in *Capsicum annuum*, *Capsicum chinense*, *Capsicum frutescens*, *Datura stramonium*, *Nicotiana benthamiana*, *N. clevelandii*, *N. glutinosa*, *N. tabacum*, *N. rustica*, *Physalis floridana*, *Solanum lycopersicum*. Asymptomatic systemic infections were observed in *Gomphrena globosa* (*Amaranthaceae*). No local lesion hosts have been identified.

**Genome organization:** is typical of tymoviruses, with extensively overlapping RP and OP ORFs beginning 7 nucleotides apart, a downstream CP ORF encoded by a 6.5 kb (6517 nt) positive strand RNA genome. The nucleotide composition has the typical skewed composition with high C (35%). The RP has the typical MTR, PRO, HEL and POL domains. The 16-nt tymobox typical of tymoviruses is present at the 3' end of the RP ORF. Typical predicted secondary structures are present in the 5' UTR (hairpins with characteristic C-C and C-U mismatches) and 3' UTR (tRNA-like structure with valine-specific anticodon).

**Phylogenetic relationships:** ChiYMV is clearly placed within the tymovirus clade, with closest relationship to eggplant mosaic virus based on comparisons of genomic RNA sequence and sequence of all predicted proteins (Annex Figure 1). The predicted proteins encoded by ChiYMV and EMV are only 60-68% identical, while the genomic RNAs are only 65% identical.

***The above data indicate convincingly that ChiYMV is a tymovirus, and that it is distinct from other known tymoviruses, justifying classification as a new species.***

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

- Dreher T.W., Edwards M.C., Gibbs A.J., Haenni A-L., Hammond R.W., Jupin I., Koenig R., Sabanadzovic S., Abou Ghanem-Sabanadzovic N., Martelli G.P. (2005). Family Tymoviridae. In Fauquet C.M., Mayo M., Maniloff J., Desselberger U., Ball L.A. (Eds.): Virus Taxonomy (Eight Report of the ICTV). Elsevier/Academic Press, London pp 1061-1074.
- Pagan, I, Betancourt, M., de Miguel, J., Pinero, D., Fraile, A and Garcia-Arenal, F. (2010) Genomic and biological characterization of chiltepin yellow mosaic virus, a new tymovirus infecting Capsicum annum var. aviculare in Mexico. Arch Virol 155:675-84.

**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.

---

**Figure 1.** Phylogenetic trees showing the relationship of ChiYMV to other species and genera of the family *Tymoviridae*. Unrooted trees constructed with polymerase and CP sequences. Assigned and putative members of the three *Tymoviridae* genera are shown in colour: *Tymovirus*, black; *Maculavirus*, red; *Marafivirus*, blue.

