

# Template for Taxonomic Proposal to the ICTV Executive Committee To create a new Unassigned Genus

Code<sup>†</sup> **2007.031P** To create a new genus\*

Code<sup>†</sup> **2007.032P** To name the new genus\* ***Cilevirus***

Code<sup>†</sup> **2007.033P** To create and designate the species  
As the type species of the new genus\* ***Citrus leprosis virus C***

Code<sup>†</sup> **2007.034P** To designate the following as species of the new genus\*:

***Citrus leprosis virus C***

<sup>†</sup> Assigned by ICTV officers

\* repeat these lines and the corresponding arguments for each genus created in the family

## Author(s) with email address(es) of the Taxonomic Proposal

Dr. E. C. Locali-Fabris, Centro APTA Citros Sylvio Moreira/ IAC, Cordeirópolis/SP, Brazil – eliane@centrodecitricultura.br  
Dr. J. Freitas-Astua, EMBRAPA Mandioca e Fruticultura Tropical/ BA, Brazil and Centro APTA Citros Sylvio Moreira/IAC, Cordeirópolis/SP, Brazil – jfastua@centrodecitricultura.br  
Dr. A. A. Souza, Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis/SP, Brazil – alessandra@centrodecitricultura.br  
Dr. M. A. Takita, Centro de Recursos Genéticos Vegetais/IAC, Campinas/SP, Brazil – takita@centrodecitricultura.br  
Dr. G. Astua-Monge, Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis/SP, Brazil – gamo@centrodecitricultura.br  
R. Antonioli-Luizon, Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis/SP, Brazil – renataal@centrodecitricultura.br  
V. Rodrigues, Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis/SP, Brazil – rodrigues@centrodecitricultura.br  
Dr. M. L. P. N. Targon, Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis/SP, Brazil – luisa@centrodecitricultura.br  
Dr. M. A. Machado, Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis/SP, Brazil – marcos@centrodecitricultura.br

## Old Taxonomic Order

**Order**

**Family** *Rhabdoviridae*

**Genus** Unassigned

**Type Species** Unassigned

**Unassigned tentative species in the family** *Citrus leprosis virus (CiLV)*

## New Taxonomic Order

**Order**

**Family**

**Genus** *Cilevirus*

**Type Species** *Citrus leprosis virus C*

**Species in the Genus**

## ICTV-EC comments and response of the SG

## Argumentation to choose the type species in the genus

This bacilliform, rhabdo-like virus is the first *Brevipalpus* transmitted-virus (BrTV) of the cytoplasmic type to have its genome completely sequenced. Also, this is the best studied virus within the group, with available information on its host range, epidemiology, symptomatology, and interaction with its vector. It is the only one being proposed as a definitive species at this time.

## Species demarcation criteria in the genus

Not applicable: only one species at present.

## List of Species in the created genus

<i>Citrus leprosis virus C</i>		
Citrus leprosis virus C	(CiLV-C)	DQ352194 (RNA1), DQ352195 (RNA2)

## Argumentation to create a new genus:

Since the first micrographs of leprosis-infected citrus cells showed the resemblance between Citrus leprosis virus and members of the *Rhabdoviridae* family, this and other *Brevipalpus*-transmitted viruses (BrTV) have been considered tentative members of this family (ICTV 01.062.0.00.359 (CiLV) at <http://www.ncbi.nlm.nih.gov/ICTVdb/Ictv/index.htm>). However, despite the morphology and cytopathic effects they induce in infected cells, there is little additional information supporting this classification. With the complete sequencing of the CiLV cytoplasmic type (CiLV-C) genome, it was evident that this virus does not share any sequence similarity with rhabdoviruses. While rhabdoviruses have monopartite genomes, the CiLV-C's genome is bipartite, with 8,745 nucleotides [nt] in RNA 1 and 4,986 nt in RNA 2. RNA 1 contains two open reading frames (ORFs), which correspond to 286 kDa and 29 kDa proteins. The 286 kDa protein is a polyprotein putatively involved in viral replication, which contains four conserved domains: methyltransferase, protease, helicase and polymerase. RNA 2 contains four ORFs corresponding to 15 kDa, 61 kDa, 32 kDa and 24 kDa proteins, respectively. The 32 kDa protein is putatively involved in cell-to-cell movement of the virus, but none of the other putative proteins exhibit any conserved domain. The 5' regions of the two genomic RNAs contain a 'cap' structure and in the 3' terminals there were identified polyA tails. Sequence analyses and searches for structural and non-structural protein similarities revealed conserved domains corresponding to the movement protein and replication-associated proteins with members of various ssRNA+ genera, such as *Furovirus*, *Bromovirus*, *Tobravirus* and *Tobamovirus*. Phylogenetic analyses strongly suggest that CiLV-C is a member of a distinct, novel virus genus and family, since no similarity was found between sequences of this virus and other cyto- or nucleorhabdoviruses available at the GenBank, indicating that it does not belong to the family *Rhabdoviridae*, as tentatively proposed. In a recent review on plant rhabdoviruses, it was reported that more than 75 viruses (including CiLV) are tentatively classified as rhabdoviruses solely because of their morphology. They do not belong to a specific genus since there is no available information on their molecular properties which, along with their biological properties, could unequivocally classify them as members of this or other virus families. Considering the ICTV key for classification of rhabdoviruses and the genomic information on CiLV-C obtained in this study, it is possible to conclude that CiLV-C should not be considered a member of the family *Rhabdoviridae*. According to the Committee, all rhabdoviruses share similar biochemical composition of the virions [ssRNA (-)], replication strategy, nature of the particle structure and genome organization (monopartite). Not only is the CiLV-C genome bipartite and of ssRNA positive sense, but there is a complete lack of sequence similarity between this virus and actual rhabdoviruses, which clearly excludes it from the family. The phylogenetic analyses clearly demonstrate that CiLV's putative proteins exhibit similarity with those of ssRNA (+) viruses from several genera and families. However, they also show that it is not possible to taxonomically classify the virus within any currently accepted genus or family, since it appears to be a unique virus (see Annex). When considered all of the available information presented, it becomes clear that it belongs to a novel virus genus. It is transmitted by a tenuipalpid mite, *Brevipalpus* sp., its morphology resembles that of rhabdoviruses, but is significant smaller than members of that family, the particular organization of its bipartite genome and the lack of sequence similarity among most of its ORFs and the sequences available in the GenBank clearly suggest that this virus cannot be classified within any of the genera currently accepted by the ICTV. Hence, we propose that *Citrus leprosis virus C* be considered as the type species of a new genus, *Cilevirus*, which would possibly include other members of the bacilliform, cytoplasmic viruses transmitted by *Brevipalpus* sp. that share sequence similarity with CiLV-C, such as Solanum violae-folium ringspot virus (SvRSV), Passionfruit green spot virus (PFGSV), and Ligustrum ringspot virus (LigRSV).

## Origin of the proposed genus name

*Cilevirus* is based on the genus of the natural host (Ci - *Citrus*) and on the name of the disease caused by the type member virus (le – leprosis).

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**Annex:**

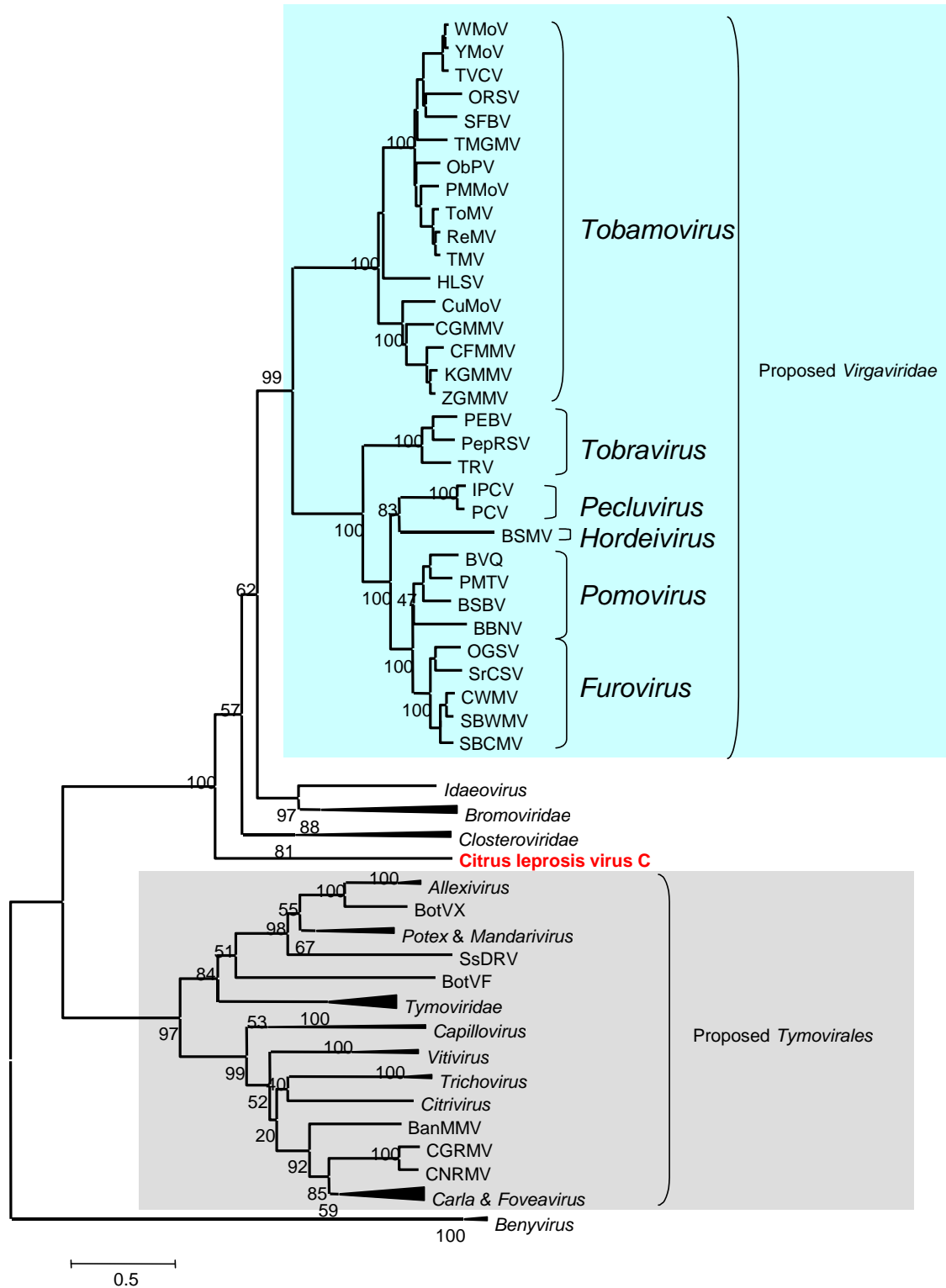


Figure: Phylogenetic (Neighbor-joining) tree of the amino acid sequences of the fused Met-Hel-RdRp domains of the members of the genera proposed for inclusion in the family *Virgaviridae* (pale blue) and the order *Tymovirales* (grey) together with other related viruses to show the distinctive position of *Citrus leprosis virus C*. Numbers on branches indicate percentage of bootstrap support out of 1000 bootstrap replications. Scales indicate JTT amino acid distances. The figure is taken from the Annex to the family *Virgaviridae* proposal and has been added by Mike Adams.