

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

Code<sup>†</sup>  To create a new genus

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

Code<sup>†</sup>  To designate the species   
As the type species of the new genus

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

Code<sup>†</sup>  To designate the following as tentative species in the new genus\*:

<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

Le Gall, O. (legall@bordeaux.inra.fr)  
Wellink, J. (Joan.Wellink@wur.nl)  
Ikegami, M. (ikegami@nashi.nodai.ac.jp)  
Iwanami, T. (tiwsw37@affrc.go.jp)  
Jones, A. T. (tjones@scri.sari.ac.uk)  
Karasev, A. V. (Alexander.Karasev@mail.tju.edu)  
Lehto, K. (kirsi.lehto@utu.fi)  
Sanfacon, H. (SanfaconH@agr.gc.ca)  
Yoshikawa, N. (yoshikawa@iwate-u.ac.jp)  
Wetzel, T. (twetzel.sifa-nw@agrarinfo.rlp.de)

## Old Taxonomic Order

Order  
 Family *Comoviridae*  
 Genus *Nepovirus* (tentative)  
 Type Species *Tobacco ringspot virus*  
 Species in the Genus  
 Tentative Species in the Genus

## New Taxonomic Order

Order  
 Family  
 Genus *Cheravirus*  
 Type Species *Cherry rasp leaf virus (CRLV)*  
 Species in the Genus *Apple latent spherical virus (ALSV)*  
*Cherry rasp leaf virus (CRLV)*  
 Tentative Species in the Genus *Arracacha virus B (AVB)*  
*Artichoke vein banding virus (AVBV)*

## ICTV-EC comments and response of the SG

### Argumentation to choose the type species in the genus

*Cherry rasp leaf virus* is one of the best known viruses in this genus biologically speaking. Biological studies have been conducted for years, and strains have been characterized. The entire nucleotide sequence of its RNA-2 has recently been determined.

The full nucleotide sequence of *Apple latent spherical virus* is known, but otherwise not sufficient biological data on this newly described virus is available.

### Species demarcation criteria in the genus

- Type of biological vector
- Host range
- Absence of serological cross-reaction
- Absence of cross-protection
- Sequence similarity:
  - less than 80% amino-acid sequence identity in the Large CP within a species.
  - less than 80% amino-acid sequence identity in the proteinase-polymerase region.

### List of Species in the created genus

*Cherry rasp leaf virus* (CRLV)  
*Apple latent spherical virus* (ALSV)

### List of Tentative Species in the created genus

**Arracacha virus B (AVB)**  
**Artichoke vein banding virus (AVBV)**  
(so far “tentative nepoviruses” but with 3 CP subunits).

## Argumentation to create a new genus:

There was a good level of homogeneity among nepoviruses when this group was created, historically in the first session of creation of plant virus groups and with *Strawberry latent ringspot virus* as one of the founding members: they were all nematode-transmitted and icosahedral, all had a positive-sense single-stranded RNA genome with a poly-A tail and probably a VPg, and their genome encoded polyproteins. However it soon became evident that some nepoviruses were atypical in several respects, for instance in the number of different CP subunits (one in typical nepoviruses, 2 to 3 in some tentative members). These viruses were then considered “tentative nepoviruses” [1]. Their atypical character was further confirmed when sequence data became available and suggested first that they were distinct from other members of the genus *Nepovirus* [2], and even of the family *Comoviridae* [3]. Instead, the recent availability of the full-length (or partial in some instances) sequence of the genome of several of these “tentative nepoviruses” suggested that they all were closer to members of the family *Sequiviridae* [3-8].

*Sequiviridae* are icosahedral plant picorna-like viruses that have a ssRNA genome encoding polyproteins with a “replication block” showing sequence motifs, in this order from the N-terminus to the C-terminus of the polyprotein, typical of a NTP-binding protein, a Cysteine trypsin-like proteinase and an RNA-dependent RNA polymerase. This is a property shared by viruses in the family *Comoviridae*. Unlike nepoviruses but like the “tentative nepoviruses”, they also have more than one CP subunit (3 CP subunits in the genera *Sequivirus* and *Waikavirus*).

However, unlike the “tentative nepoviruses”, viruses in the family *Sequiviridae* typically have a monopartite genome and are transmitted by insects when their biological vector is known. This is considered as of secondary importance for the cohesion of the family (and providing demarcation criteria within the family) since:

- the family *Potyviridae* also contains genera that differ in the number of their genome RNAs,
- the families *Potyviridae* and *Comoviridae*, for instance, also contains viruses that differ in the type of biological vector,
- the genus *Nepovirus* is now known to contain at least one virus transmitted by mites, and specific transmission by insects of its type member *Tobacco ringspot virus* has also been described.

Thus, the creation of two new genera (*Sadwavirus* and *Cheravirus*) is proposed. *Sadwaviruses* and *cheraviruses* differ from genera in the family *Sequiviridae* in having a bipartite genome. They differ from *Comoviridae* in sequence clustering analysis. Specifically, in addition they differ from nepoviruses by the number of CP subunits (2 in *sadwaviruses* as in *comoviruses* and *fabaviruses*, and 3 in *cheraviruses* unlike any member of the family *Comoviridae*). Tentative *sadwaviruses* and *cheraviruses* have been designated among other tentative nepoviruses that had 2 or 3 CPs, respectively.

The distinguishing features of *sadwaviruses* are therefore:

- A bipartite ssRNA genome encoding polyproteins, with a 3' poly-A
- A “replication block” typical of picorna-like viruses
- Sequences clustering close to the family *Sequiviridae*
- 3 distinct CP subunits of about 25 kDa

The difficulty that we see at this point is that the level of sequence divergence within each of these genera is higher than within other related genera of plant viruses (see figure), leaving a risk that either or both of these genera will have to be divided when more data becomes available. However the situation in this respect is not notably worse than that found in picornaviruses. At this stage we are hopeful that this proposal will offer a global clarification of the situation regarding these viruses, and hopeful that it will promote further characterization of some of these viruses (for instance sequence data on SLRSV and *Cherry rasp leaf virus* RNA-1, and on so-far tentative *Cheraviruses* would be valuable, as well as further biological characterization of several of these viruses, for example the identification of the vectors of SDV, *Apple latent spherical virus* etc).

## Origin of the proposed genus name

“Chera” derives its name from that of the type member species, *Cherry rasp leaf virus*.

## References

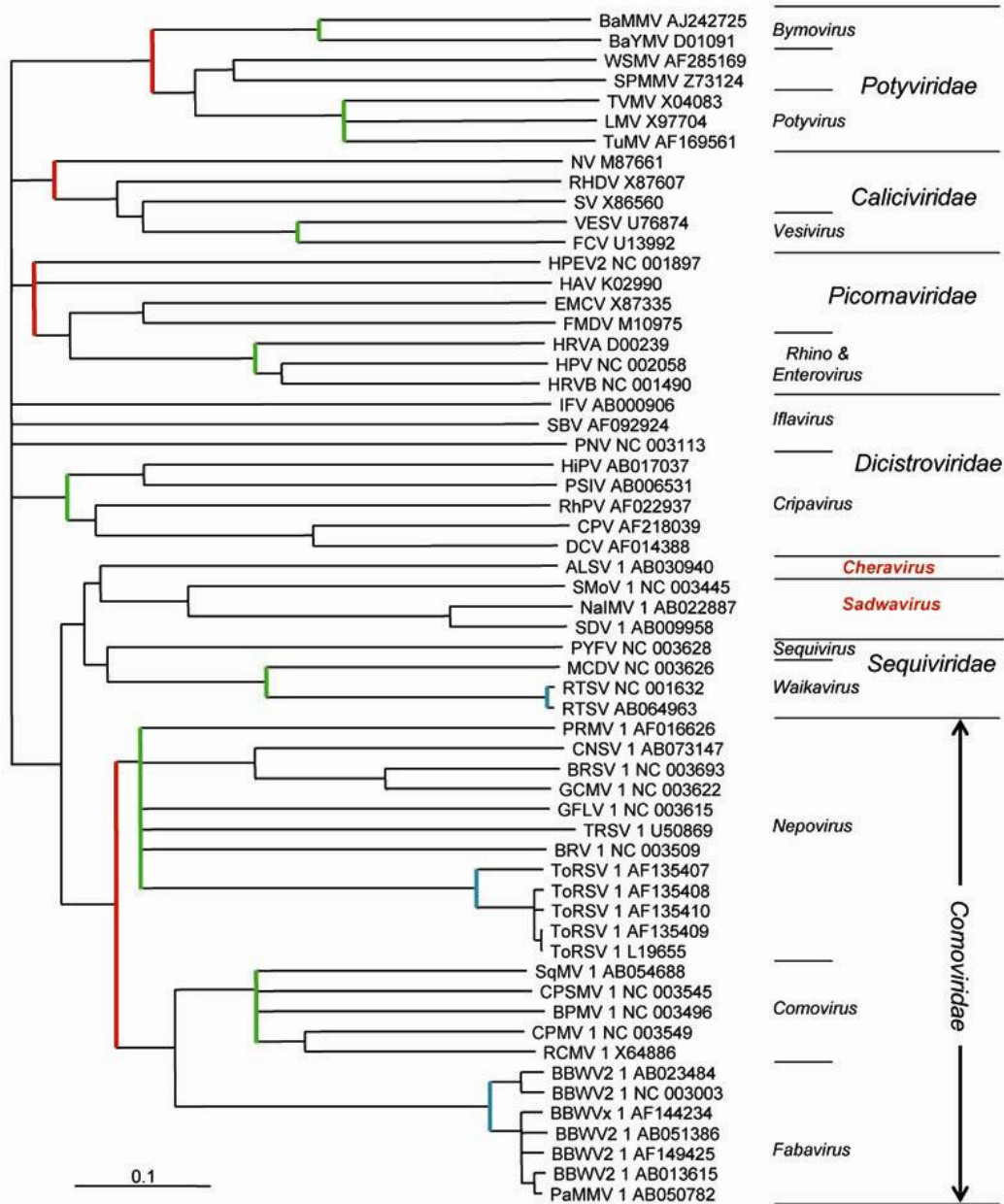
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2. Le Gall O, Candresse T & Dunez J. 1995. A multiple alignment of the capsid protein sequences of nepoviruses and comoviruses suggests a common structure. *Arch Virol* **140**, 2041-53.
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5. James D & Upton C. 2002. Nucleotide sequence analysis of RNA-2 of a flat apple isolate of Cherry rasp leaf virus with regions showing greater identity to animal picornaviruses than to related plant viruses. *Arch Virol* **147**, 1631-41.
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## Annex:

A dendrogram (proposed on a poster at the 2002 IUMS meeting in Paris) based on neighbor-joining analysis of an amino-acid sequence covering a portion of the proteinase and polymerase genes shows the level of sequence relatedness within plant and animal picorna-like viruses (annotations to the right of this dendrogram were not updated regarding the taxonomical status of insect picorna-like viruses).

Similar analysis using other regions of the viral genome produce similar clusterings, although usually with a lower significance due to less sequence conservation. Nevertheless, analysis of the CP coding region is the only one available for some viruses including a sadwavirus (SLRSV) and a cheravirus (CRLV), and confirm the proposed clustering.



### Pro-Pol region

(with new sequences & branches collapsed when supported by bootstrap values <75%)

/ Family-level nodes     
 / Genus-level nodes     
 / Species-level nodes