

# 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\*:

*Satsuma dwarf virus (SDV)*  
*Strawberry latent ringspot virus (SLRSV)*  
*Strawberry mottle virus (SMoV)*

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

**Lucerne Australian symptomless virus (LASV)**  
**Rubus Chinese seed-borne virus (RCSBV)**

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

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

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## Old Taxonomic Order

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

## New Taxonomic Order

Order  
Family  
Genus *Sadwavirus*  
Type Species *Satsuma dwarf virus*  
Species in the Genus *Satsuma dwarf virus (SDV)*  
*Strawberry latent ringspot virus (SLRSV)*  
*Strawberry mottle virus (SMoV)*

Tentative Species in the Genus

## ICTV-EC comments and response of the SG

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

*Satsuma dwarf virus* is one of the best known viruses in this genus. Biological studies have been conducted for years, and strains have been characterized. The entire nucleotide sequence of SDV has been determined, as well as that of one RNA of a strain, and extensive sequence information is also available for other strains and isolates. No information on the biological vector of SDV is available, but there does not seem to be a typical type of vector in the genus since from the two species for which data is available one is transmitted by soil nematodes (*Strawberry latent ringspot virus*) and the other (*Strawberry mottle virus*) is transmitted by aphids.

### 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

*Satsuma dwarf virus* (SDV)  
*Strawberry latent ringspot virus* (SLRSV)  
*Strawberry mottle virus* (SMoV)

### List of Tentative Species in the created genus

**Lucerne Australian symptomless virus (LASV)**  
**Rubus Chinese seed-borne virus (RCSBV)**  
(so far were “tentative nepoviruses” but with 2 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*
- 2 distinct CP subunits of about 40 and 20 kDa respectively

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

“Sadwa” derives its name from that of the type member species, *Satsuma dwarf virus*. Satsuma is a typical citrus in Japan, and dwarfing is one of the symptoms induced by this virus.

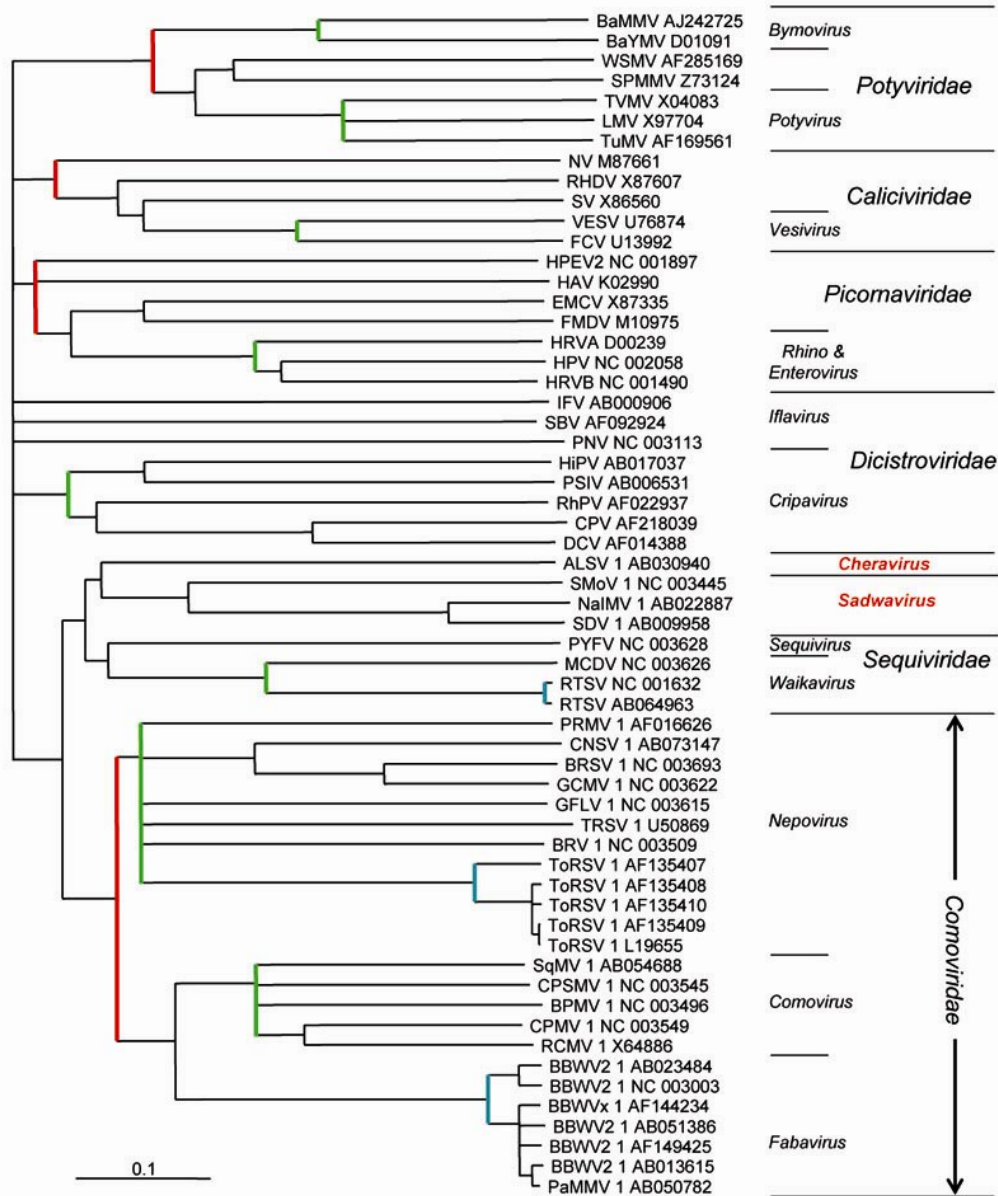
## References

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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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7. Li C, Yoshikawa N, Takahashi T, Ito T, Yoshida K & Koganezawa H. 2000. Nucleotide sequence and genome organization of apple latent spherical virus: a new virus classified into the family Comoviridae. *J Gen Virol* **81**, 541-7.
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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.

Similar analysis using other regions of the viral genome produced similar clusterings, although usually with a lower significance due to a lower level of 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 although it was less resolute it confirmed 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