

# Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code †  To designate the following as species in the genus:

belonging to the family° :

† Assigned by ICTV officers

° leave blank if inappropriate or in the case of an unassigned genus

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

## Old Taxonomic Order

Order

Family Luteoviridae

Genus

Type Species

Species in the Genus

Tentative Species in the Genus

Unassigned Species in the family Sugarcane yellow leaf virus

## New Taxonomic Order

Order

Family Luteoviridae

Genus Polerovirus

Type Species

Species in the Genus Sugarcane yellow leaf virus

Tentative Species in the Genus

Unassigned Species in the family

## ICTV-EC comments and response of the SG

## Species demarcation criteria in the genus

- Virions are icosahedral particles with diameters of approximately 27 nm; buoyant density in CsCl is 1.39-1.42; S<sub>20w</sub> is 115-127S.
- Genome sizes range from 5641 nt for *Beet western yellows virus* to 5882 nt for *Potato leafroll virus* (PLRV).
- The polerovirus genome has a VPg linked to the 5'-end of the genome RNA.
- Poleroviruses possess an ORF0.
- The non-coding region between ORF2 and ORF3 is about 200 nt.
- Translation products of ORF1 and ORF2 form replication-related proteins, which are most similar to those of the *Sobemovirus* genus.
- Frameshift from ORF1 into ORF2 occurs upstream of the termination of ORF1.
- ORF4 is present within ORF3.
- ORF5 is about 1400 nt.

## Argumentation to justify the designation of new species in the genus

Recombination likely has played an important role in the generation of new species within the *Luteoviridae*. The recombinational histories of some members of the family are more discernable than others. The properties of the coat proteins (virion structure, antigenicity and amino acid sequence similarities) are one of the primary defining features of the *Luteoviridae*. Consequently, the coat proteins of the *Luteoviridae* are more similar to other members of the family than they are to the coat proteins of viruses from other families. The same is not true for the nonstructural proteins, which divide the *Luteoviridae* into two broad groups (luteoviruses and polero- and enamoviruses). The nonstructural proteins of luteoviruses are tombusvirus-like, while the nonstructural proteins of the polero- and enamoviruses are more similar to those of the sobemoviruses. Even though the predicted amino acid sequences of the coat proteins of ScYLV show closer affinities with luteo- and enamoviruses, the nonstructural proteins of ScYLV are most similar to those of poleroviruses, which resemble sobemoviruses. Based on the properties listed below, it is proposed that ScYLV be classified as a species within the genus *Polerovirus*.

- ScYLV virions are icosahedral particles with diameters of approximately 27 nm.
- The RNA genome of ScYLV is 5899 nt (AF157029, AJ249447).
- ORF0 is present (absent in luteoviruses).
- Translation products of ORF1 and ORF2 form replication-related proteins, which are most similar to those of the *Sobemovirus* genus (tombusvirus-like in luteoviruses).
- The predicted amino acid sequence of ScYLV ORF 1 contains regions similar to the serine protease and VPg identified in PLRV (luteoviruses lack a VPg).
- The non-coding region between ORF2 and ORF3 is about 216 nt (usually less than 100 nt for luteoviruses).
- Frameshift from ORF1 into ORF2 occurs 261 nt upstream of the termination of ORF1 (less than 20 nt for luteoviruses).
- ORF4 is present within ORF3 (absent in enamoviruses).
- ORF5 is about 1440 nt (less than 800 nt in enamoviruses).

## List of created Species in the genus

Sugarcane yellow leaf virus

## References

- Moonan, F., Molina, J. and Mirkov, T.E. (2000). *Sugarcane yellow leaf virus: An emerging virus that has evolved by recombination between luteoviral and poleroviral ancestors. Virology, 269*, 156-171.
- Smith, G.R., Borg, Z., Lockhart, B.E., Braithwaite, K.S. and Gibbs, M.J. (2000). *Sugarcane yellow leaf virus: a novel member of the Luteoviridae that probably arose by inter-species recombination J. Gen. Virol. 81*, 1865-1869.

## Annexes: