

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[°] :

Bean leafroll virus
Soybean dwarf virus

† Assigned by ICTV officers

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

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Old Taxonomic Order

Order

Family *Luteoviridae*

Genus

Type Species

Species in the Genus

Tentative Species in the Genus

Unassigned Species in the family *Bean leafroll virus and Soybean dwarf virus*

New Taxonomic Order

Order

Family *Luteoviridae*

Genus *Luteovirus*

Type Species

Species in the Genus *Bean leafroll virus and Soybean dwarf 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 1.39-1.40 g/cm³; S_{20w} is 106-118S.
- Genome sizes are 5273 nt *Barley yellow dwarf virus* –MAV (BYDV-MAV) (partial sequence), 5677 nt (BYDV-PAV), and 5697 nt (BYDV-PAS).
- The genome RNA does not have a VPg.
- There is no ORF0 and frameshift from ORF1 into ORF2 occurs at the termination codon of ORF1.
- The translation products of ORF1 and ORF2 form replication-related proteins, which are most similar to those of the *Tombusviridae*.
- The length of the non-coding sequence between ORF2 and ORF3 is about 100 nt.
- There is no evidence for the presence of a genome-linked protein and translation is by a cap-independent mechanism.
- ORF4 is present and contained within ORF3.

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 BLRV and SbDV show closer affinities with poleroviruses, the nonstructural proteins of these two viruses are most similar to those of the *Tombusviridae*. Based on the properties listed below, it is proposed that BLRV and SbDV be classified as a species within the genus *Luteovirus*.

- The nucleotide sequence of the BLRV and SbDV genomes (AF441393 and L24049) are 5964 and 5708-5853nt in length, respectively and contain five large ORFs, similar to members of the *Luteovirus* genus.
- There is no evidence of an ORF0, which is found only in polero- and enamoviruses.
- BLRV and SbDV lack an ORF6. The sizes and sequences of ORF6s among BYDVs can be highly variable and ORF6 expression is not required for virus infectivity.
- ORFs 1 and 2 overlap by just 15 nt for BLRV and 9 nt for SbDV compared to over 400 nt for members of the *Polerovirus* and *Enamovirus* genera.
- The conceptual translation of ORFs 1 and 2 is predicted to encode a tombusvirus-like RdRp.
- Like poleroviruses, ORFs 2 and 3 are separated by 211 nt for BLRV and 208 nt for SbDV. Other luteoviruses have intergenic regions of about 100 nt, while poleroviruses possess intergenic regions of more than 200 nt. The length of the intergenic region is not necessarily a stable character of division of species into genera.

List of created Species in the genus

Bean leafroll virus
Soybean dwarf virus

References

- Domier, L.L., McCoppin, N.K., Larsen, R.C. and D'Arcy, C.J. (2002). Nucleotide sequence shows that *Bean leafroll virus* has a Luteovirus-like genome organization. *J. Gen. Virol.*, 83, 1791-1798.
- Rathjen J.P., Karageorgos L.E., Habili N., Waterhouse P.M., and Symons R.H. (1994). Soybean dwarf luteovirus contains the third variant genome type in the luteovirus group. *Virology*, **198**, 671-679.
- Terauchi, H., Kanematsu, S., Honda, K., Mikoshiba, Y., Ishiguro, K. and Hidaka, S. (2001). Comparison of complete nucleotide sequences of genomic RNAs of four *Soybean dwarf virus* strains that differ in their vector specificity and symptom production. *Arch. Virol.*, **146**, 1885-1898.

Annexes: