Template for Taxonomic Proposal to the ICTV Executive Committee
Creating Unassigned Species in an existing Family

Code[†] 2005.015P.04 To designate the following as unassigned species in the family:

Luteoviridae

Tobacco vein distorting 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
Unassigned Species in the family

New Taxonomic Order

Order
Family
Unassigned Species in the family

ICTV-EC comments and response of the SG

Species demarcation criteria in the genera

Species demarcation criteria for the Polerovirus genus

- Particles are thought to have 180 subunits arranged in a T=3 icosahedron. Virion buoyant density in CsCl is 1.39-1.42; S20w is 115-127S.
- Genome sizes range from 5,641 nt for BWYV to 5,882 nt for PLRV.
- The polerovirus genome has a VPg linked to the 5'-end of the genome RNA.
- Poleroviruses possess an ORF0 and a non-coding region between ORF2 and ORF3 of about 200 nt.
- The translation products of ORF1 and ORF2 form replication-related proteins, which are most similar to those of sobemoviruses.
- Frameshift from ORF1 into ORF2 occurs upstream of the termination of ORF1.
- Polerovirus genomes differ from those of enamoviruses in that ORF4 is present within ORF3 and ORF5 is about 1400 nt.

Argumentation to justify the designation of unassigned species in the family

Approximately 30% to the TVDV genome sequence has been reported. This highly informative sequence showed that TVDV likely is a member of the Polerovirus genus. However, because the sequence is incomplete, it is not possible to determine whether the TVDV genome contains an ORF0 or other features that might further differentiate it from other members of the genus.

Below is a list of features derived from the partial TVDV sequence that are consistent with the Polerovirus genus species demarcation criteria:

- The TVDV genome contains an ORF 4, which is found only in luteo- and poleroviruses.
- Conceptual translation of ORF 2 of TVDV is predicted to encode a sobemovirus-like RdRp.
- Like poleroviruses, ORFs 2 and 3 of TVDV were separated by 202. Poleroviruses possess intergenic regions of more than 200 nt, while luteoviruses typically have intergenic regions of about 100 nt.

List of created Unassigned Species in the family

Tobacco vein distorting virus **(TVDV)**

References

Li, F., Ma, K.L., Robinson, D., Ndowora, T. and Chen, H. (2004) cDNA cloning and sequence analysis of the RNA-dependent RNA polymerase gene of tobacco bushy top virus isolate A2. GenBank AJ704819.

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Li ,F., Qian, N., Zhou, X., Wu, J. and Chen, H. (2003) DNA cloning and sequence analysis of the RdRp gene of a Yunnan isolate of tobacco vein-distorting virus. Yunnan Nongye Daxue Xuebao 18, 212-212 (TVE459320).

Li, F., Qian, N., Yang, G., Wu, J., Zhou, X. and Chen, H. (2002) cDNA cloning and sequence analysis of the coat protein gene of tobacco vein-distorting virus. Yunnan Nongye Daxue Xuebao 17, 440-441 (TVE457176).

Annexes: