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

Code <sup>†</sup> 2005.014P.04	To designate the following as species in the genus:	
	Polerovirus	
	belonging to the family <sup>°</sup> : <i>Luteoviridae</i>	
	Carrot red leaf virus Carrot red leaf virus-UK1 (CRLV-UK1) AY695933	
<sup>†</sup> Assigned by ICTV officers		

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

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#### **Old Taxonomic Order**

**Tentative Species in the Genus** 

Order		
Family Luteoviridae		
Genus		
Type Species		
Species in the Genus		
Tentative Species in the G	enus	
Unassigned Species in the	family Carrot	red leaf virus
New Taxonomic Orde	r	
Order		
Family Luteoviridae		
Genus	Polerovirus	
Type Species		
Species in the Genus	Carrot red leaf	virus

Unassigned Species in the family ICTV-EC comments and response of the SG

### Species demarcation criteria in the 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 new species in the genus

- The nucleotide sequence of the CRLV genome (NC\_006265) is 5723 nt in length and contains six large ORFs, similar to members of the Polerovirus genus.
- The CLRV genome contains an ORF0, which is found only in polero- and enamoviruses and an ORF 4, which is found only in luteo- and poleroviruses.
- ORFs 1 and 2 overlapped by 475 nt compared to less than 100 nt for members of the Luteovirus genus.
- Conceptual translation of ORFs 1 and 2 is predicted to encode a sobemovirus-like RdRp.
- Like poleroviruses, ORFs 2 and 3 were separated by 228. Poleroviruses possess intergenic regions of more than 200 nt, while luteoviruses typically have intergenic regions of about 100 nt.
- ORF5 of CLRV is 1473 nt in length compared to less than 800 nt for enamoviruses.

## References

- Huang, L., Naylor, M., Pallet, D.W., Reeves, J., Cooper, J.I. and Wang, H. (2005) *Carrot red leaf virus* complete genome sequence. GenBank NC\_006265.
- Huang, L.F., Naylor, M., Pallett, D.W., Reeves, J., Cooper, J.I. and Wang, H. (2005) The complete genome sequence, organization and affinities of carrot red leaf virus. Arch. Virol. DOI: 10.1007/s00705-005-0537-6..

Annexes: