This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.030-032P***	(to be completed by ICTV officers)

Short title: One new species in the genus Luteovirus; two new species in the genus Polerovirus; move one unassigned species to the genus Polerovirus.
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☒
	6 ☒	**7** ☐			

Author(s) with e-mail address(es) of the proposer:

Leslie Domier for Luteoviridae SG

ICTV-EC or Study Group comments and response of the proposer:

MODULE 5: **NEW SPECIES**

Code	***2008.030P***	(assigned by ICTV officers)

To create one new species assigned as follows:

Genus:	***Luteovirus***
Subfamily:	
Family:	***Luteoviridae***
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Rose spring dwarf-associated virus

Argument to justify the creation of the new species:
If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Criteria used to demarcate species of the family *Luteoviridae* include:

- Differences in breadth and specificity of host range;
- Failure of cross protection in either one-way or two-way relationships;
- Differences in serological specificity with discriminatory polyclonal or monoclonal antibodies;
- Differences in aa sequences of any gene product of greater than 10%.

Argument to justify the creation of the new species:

Rose spring dwarf-associated virus (RSDaV) has been proposed as a new species within the *Luteovirus* genus. It was identified in multiflora rose with spring dwarf disease using degenerate PCR primers (Salem et al 2008a). The complete nucleotide sequence of RSDaV (EU024678) shows a luteovirus-like genome organization (Salem et al 2008b). The predicted amino acid sequence of CpCSV ORF2 (RdRp) is most similar to the ORF2 product of Soybean dwarf virus (SbDV; 63% identity) and the product of ORF3 (coat protein) is most similar to ORF3 of Sugarcane yellow leaf virus (ScYLV; 40% identity; Figure 1).

Given its genome organization and low levels of amino acid sequence identity to other members of the genus, RSDaV represents a new species within the genus *Luteovirus*.

References:

Salem, N., Golino, D. A., Falk, B. W., and Rowhani, A. (2008a) Identification and partial characterization of a new luteovirus associated with rose spring dwarf disease. Plant Dis. 92:508-512.

Salem,N.M., Miller,W.A., Rowhani,A., Golino,D.A., Moyne,A.L. and Falk,B.W. (2008b) Rose spring dwarf-associated virus has RNA structural and gene-expression features like those of *Barley yellow dwarf virus*. Virology 375:354-360.

MODULE 5: **NEW SPECIES**

Code	***2008.031P***	(assigned by ICTV officers)

To create two new species assigned as follows:

Genus:	***Polerovirus***
Subfamily:	
Family:	***Luteoviridae***
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Chickpea chlorotic stunt virus
Melon aphid-borne yellows virus

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Criteria used to demarcate species of the family *Luteoviridae* include:

- Differences in breadth and specificity of host range;
- Failure of cross protection in either one-way or two-way relationships;
- Differences in serological specificity with discriminatory polyclonal or monoclonal antibodies;

Argument to justify the creation of the new species:

- Differences in aa sequences of any gene product of greater than 10%.

Chickpea chlorotic stunt virus (CpCSV) was identified in chickpea and faba bean plants with yellowing and stunting symptoms in Ethiopia. CpCSV isometric particles are about 28 nm in diameter and show close serological relationships with virus species of the BWYV subgroup. CpCSV is transmitted by *Aphis craccivora*, but not by *Acyrthosiphon pisum*, *Aphis fabae*, or *Myzus persicae*. The complete nucleotide sequence of CpCSV (AY956384) shows a polerovirus-like genome organization (Abraham et al., 2006). The predicted amino acid sequence of CpCSV ORF2 is most similar to that of TuYV (59% identity) and the coat protein ORF3 is most similar to that of Groundnut rosette assistor virus (GRAV; 78% identity; Figure 1).

Melon aphid-borne yellows virus (MABYV was identified from diseased cucurbits in China using degenerate PCR primers specific for poleroviruses. A complete nucleotide sequence (EU000534) shows that MABYV has a polerovirus-like genome organization (Xiang et al., 2008). The predicted amino acid sequences of ORF2 and ORF3 are most similar to those of Cucurbit aphid-borne yellows virus (CABYV) at 75% and 82% amino acid sequence identity, respectively (Figure 1). No information about the pathogenicity, serological specificity, transmission specificity and geographical distribution of MABYV has been published to date.

Given their genome organizations and low levels of amino acid sequence identity with other members of the genus, CpCSV and MABYV represent new species within the genus *Polerovirus*.

References:

Abraham, A. D., Menzel, W., Lesemann, D.-E., Varrelmann, M., and Vetten, H. J. (2006) Chickpea chlorotic stunt virus: A new polerovirus infecting cool-season food legumes in Ethiopia. Phytopathology 96:437-446.

Xiang, H.Y., Shang, Q.X., Han, C.G., Li, D.W., and Yu, J.L. (2008) Complete sequence analysis reveals two distinct poleroviruses infecting cucurbits in China. Arch. Virol. 153:1155-1160.

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

MODULE 6: **REMOVE and MOVE**

- To remove an existing taxon entirely, complete section (a)
- To remove a taxon from one position and re-assign it elsewhere (e.g. to move an existing species from its current position into a genus THAT ALREADY EXISTS) complete BOTH sections (a) and (b). Please note that if an existing species is being moved into a NEW genus (or family) then you should complete only section (a) in this module but ALSO module 4 (for a new genus) or module 2 (for a new family)

SECTION (a)

Code	***2008.032aP***	(assigned by ICTV officers)

To remove (abolish) the following taxon(s):

Tobacco vein distorting virus

Old and new composition of the higher taxon that will be depleted by the removal:

Currently one of 9 species unassigned in the family *Luteoviridae* so number of species will become 8

Argument to justify the removal:

To be re-assigned to genus *Polerovirus* in view of sequence data now available (see below)

SECTION (b)

Code	***2008.032bP***	(assigned by ICTV officers)

To re-assign the following taxon(s):

Tobacco vein distorting virus

Proposed new position of these taxon(s):

Assign to genus *Polerovirus*

Argument to justify the re-assignment:

If it is proposed to re-assign species to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Tobacco vein distorting virus (TVDV) is currently a species within the *Luteoviridae* that has not been assigned to a genus. TVDV was identified in diseased tobacco in China using degenerate PCR primers specific for poleroviruses. A complete nucleotide sequence (EF529624) now shows that TVDV has a polerovirus-like genome organization (Mo et al., 2007). The predicted amino acid sequence of TVDV ORF2 is most similar to the ORF2 product of Turnip yellows virus (TuYV) (65% identity) and the product of ORF3 is most similar to ORF3 of CABYV (57% identity; Figure 1). TVDV is a helper virus for the umbravirus Tobacco bushy top virus. Together, the viruses cause tobacco bushy top disease, which has produced severe tobacco losses in western Yunan Province.

Given its genome organization and low levels of amino acid sequence identity to other members of the genus, TVDV represents a new species within the genus *Polerovirus*.

References:

Mo,X., Chen,Z., and Chen,J. (2007) Complete nucleotide sequence and genome organization of a Chinese isolate of tobacco vein distorting virus. Unpublished, Direct Submission (29-MAR-2007).

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

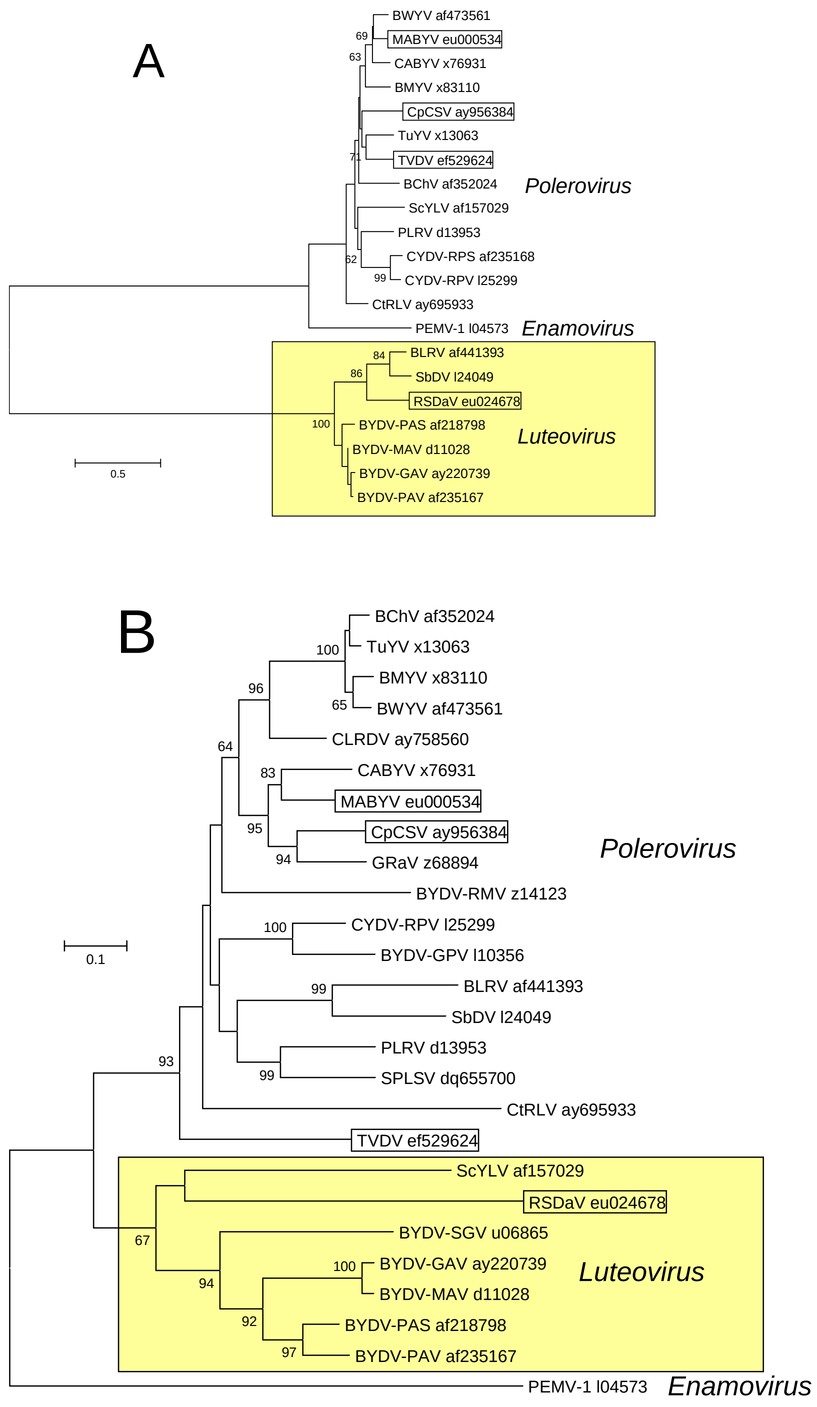

Figure 1. Phylogenetic analyses of the (**A**) ORF2 (RNA-dependent RNA polymerase) and (**B**) ORF3 (coat protein) predicted amino acid sequences of species within the family *Luteoviridae*. Amino acid sequences were aligned with CLUSTALX and analyzed in MEGA4 (NJ, JTT algorithm). The values at the forks indicate the percentage of trees in which this grouping occurred after bootstrapping (100 replicates; shown only when >60%). The scale bar shows the number of substitutions per base.