



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

| | | | | | |
|---|---|---|--|---|----------------------------|
| Code assigned: | 2013.017aP | (to be completed by ICTV officers) | | | |
| Short title: Three new species in the genus <i>Polerovirus</i> , family <i>Luteoviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i>) | | | | | |
| Modules attached (modules 1 and 9 are required) | 1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/> | 2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/> | 3 <input type="checkbox"/> 8 <input type="checkbox"/> | 4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/> | 5 <input type="checkbox"/> |

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

Leslie Domier leslie.domier@ars.usda.gov

List the ICTV study group(s) that have seen this proposal:

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

Luteoviridae

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

Date first submitted to ICTV:

09/27/2011

Date of this revision (if different to above):

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

| | | |
|--|----------------------------|--|
| Code | 2013.017aP | (assigned by ICTV officers) |
| To create three new species within: | | |
| Genus: | <i>Polerovirus</i> | Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ (new) ” after its proposed name. • If no genus is specified, enter “ unassigned ” in the genus box. |
| Subfamily: | | |
| Family: | <i>Luteoviridae</i> | |
| Order: | | |
| And name the new species: | | GenBank sequence accession number(s) of reference isolate: |
| Cotton leafroll dwarf virus | | GU167940 |
| Pepper vein yellows virus | | AB594828 |
| Suakwa aphid-borne yellows virus | | JQ700308 |

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| <p>Reasons to justify the creation and assignment of the new species:</p> <ul style="list-style-type: none"> • Explain how the proposed species differ(s) from all existing species. <ul style="list-style-type: none"> ○ If species demarcation criteria (see module 3) have previously been defined for the genus, explain how the new species meet these criteria. ○ If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria. • Further material in support of this proposal may be presented in the Appendix, Module 9 |
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Complete genome nucleotide sequences of Cotton leafroll dwarf virus (CLRDV, NC_014545) (Distefano et al., 2010), Pepper vein yellows virus (PeVYV, NC_015050) (Murakami et al., 2011), and Suakwa aphid-borne yellows virus (SABYV, NC_018571) (Knierim et al., 2012) have been reported and/or deposited in GenBank. The genome organizations of CLRDV, PeVYV, and SABYV are polerovirus-like. The genomes contain an ORF0, and the non-coding region between ORF2 and ORF3 is about 200 nt. For each virus, ORF1 and ORF2 encode replication-related proteins that are most similar to those of sobemoviruses (see phylograms below). The frameshift from ORF1 into ORF2 occurs upstream of the termination of ORF1, and ORFs 1 and 2 overlap by more than 400 nt. ORF4 is present within ORF3, and ORF5 is greater than 1200 nt.

The products of ORFs 3 (CP) and 5 (RTD) are highly conserved among luteovirids. The products of ORFs 2 and 3 of CLRDV share the highest levels of amino acid sequence identity with the corresponding proteins from Turnip yellows virus (52% and 80% identity, respectively). PeVYV had the highest amino acid sequence identities in ORF0 to ORF3 (76 - 92%) with Tobacco vein distorting virus (TVDV). The predicted product of ORF5 was only 25% identical to the predicted ORF5 product of TVDV. The predicted amino acid sequence of SABYV ORF0 did not show significant homology to any previously described members of the Luteoviridae. The amino acid sequences derived from ORFs 1 and 2 of SABYV were most similar to the corresponding proteins from Turnip yellows virus at 38% and 61% identity, respectively. The products of ORFs 3, 4 and 5 of SABYV were most similar to those of Melon aphid-borne yellows virus at 99%, 79%, and 76% identical, respectively. Because the amino acid sequences of all three viruses are predicted to encode proteins that differ by more than 10% from the most closely related virus species, CLRDV, PeVYV and SABYV represent new species within the genus *Polerovirus*.

MODULE 9: **APPENDIX**: supporting material

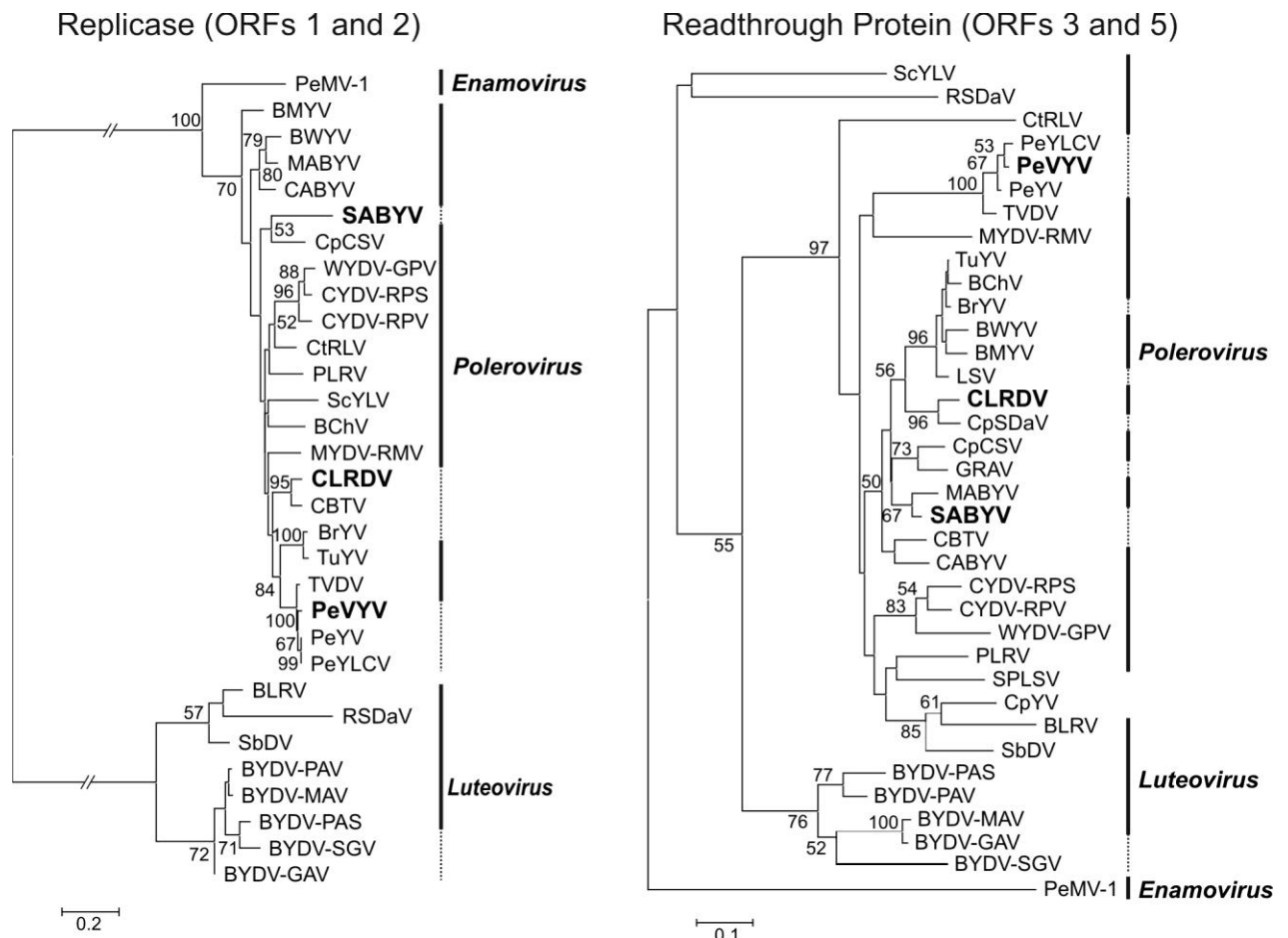
additional material in support of this proposal

References:

- Distefano A.J., Kresic, I.B., Hopp, H.E. 2010. The complete genome sequence of a virus associated with cotton blue disease, cotton leafroll dwarf virus, confirms that it is a new member of the genus Polerovirus. Arch. Virol. 155, 1849-1854.
- Knierim,D., Tsai,W.S., Deng,T.C., Green,S. and Kenyon,L. 2012. Full-length genome analysis of four polerovirus isolates infecting cucurbits in Taiwan determined from total RNA extracted from field samples. NCBI Direct Submission. NC_018571.
- Murakami R., Nakashima, N., Hinomoto, N., Kawano, S., Toyosato, T. 2011. The genome sequence of pepper vein yellows virus (family Luteoviridae, genus Polerovirus). Arch. Virol. 156, 921-923.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.



Phylogenetic analyses of the predicted amino acid sequences of the replicase (ORFs 1 and 2) (Left) and readthrough proteins (ORFs 3 and 5) (Right) of virus species associated with the family *Luteoviridae*. Amino acid sequences were aligned with CLUSTALX and neighbour-joining trees were constructed with MEGA 5.2. Bootstrap values above 50% are indicated. New virus species are shown in bold lettering. Solid vertical lines indicate recognized species within the indicated genus. Dotted lines indicate potential new members of the genus. Abbreviations and GenBank accession numbers for sequences used in the construction of the trees are: Barley yellow dwarf virus GAV (BYDV-GAV, NC_004666), Barley yellow dwarf virus MAV (BYDV-MAV, NC_003680), Barley yellow dwarf virus PAS (BYDV-PAS, NC_002160), Barley yellow dwarf virus PAV (BYDV-PAV, NC_004750), Barley yellow dwarf virus-SGV (BYDV-SGV, BYU06865), Bean leafroll virus (BLRV, NC_003369), Beet chlorosis virus (BChV, NC_002766), Beet mild yellowing virus (BMYV, NC_003491), Beet western yellows virus (BWYV, NC_004756), Brassica yellows virus (BrYV, JN015068), Carrot red leaf virus (CtRLV, NC_006265), Cereal yellow dwarf virus-RPV (CYDV-RPS, NC_002198), Cereal yellow dwarf virus-RPV (CYDV-RPV, NC_004751), Chickpea chlorotic stunt virus (CpCSV, NC_008249), Chickpea stunt disease-associated virus (CpSDaV, Y11530), Chickpea yellows virus (CpYV, GQ118150), Cotton bunchy top virus (CBTV, JF803842), Cotton leafroll dwarf virus (CLRDV, NC_014545), Cucurbit aphid-borne yellows virus (CABYV, NC_003688), Groundnut rosette assistor virus (GRAV, Z68894), Lentil stunt virus (LSV, GQ118152), Maize yellow dwarf virus-RMV (MYDV-RMV, NC_021484), Melon aphid-borne yellows virus (MABYV, NC_010809), Pea enation mosaic virus 1 (PEMV1, NC_003629), Pepper vein yellows virus (PeVYV, NC_015050), Pepper yellow leaf curl (PeYLCV, HM439608), Pepper yellows virus (PeYV, FN600344), Potato leafroll virus (PLRV, NC_001747), Rose spring dwarf-associated virus (RSDaV, NC_010806), Soybean dwarf virus (SbDV, NC_003056), Suakwa aphid-borne yellows virus (SABYV, NC_018571), Sugarcane yellow leaf virus (ScYLV, NC_000874), Sweet potato leaf speckling virus (SPLSV, DQ655700), Tobacco vein distorting virus (TVDV, NC_010732), Turnip yellows virus (TuYV, NC_003431), and Wheat yellow dwarf virus-GPV (WYDV-GPV, NC_012931).