



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:	2013.016a-cP	(to be completed by ICTV officers)
Short title: move species <i>Barley yellow dwarf virus-RMV</i> from its current position as unassigned species in the family <i>Luteoviridae</i> to the genus <i>Polerovirus</i> , family <i>Luteoviridae</i> and to rename the species <i>Maize yellow dwarf virus-RMV</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"/> 2 <input type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 6 <input type="checkbox"/> 7 <input checked="" type="checkbox"/> 8 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	

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

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

Comment of the ICTV EC to the SG:

1. Change format of proposal to a rename and move proposal. This will allow the ICTV to better track the history of changes to the taxonomy on the website. In fact, the species does not disappear, it is simply renamed and moved to a different taxa. Please use Module 7 for the move action and Module 8 for the rename action.
2. Consider changing name of virus to Maize yellow dwarf virus RMV (without the dash) and consider in the future, renaming other Luteoviridae species in a similar manner (eliminating dashes)

Response of the SG:

1. This has been done
2. I prefer to retain the hyphen in MYDV-RMV and all of the YDVs (both in spelled-out and abbreviated forms) for the following reasons:
 - a. If it were called MYDV RMV, that looks like two viruses and is very confusing.
 - b. It's extremely useful to have MYDV-RMV as one string for search purposes. Search engines would search for MYDV or RMV if the hyphen were absent.
 - c. Precedence. The hyphen has been used since Rochow first named the YDVs. All other YDVs have similarly hyphenated names. They would have to be changed and plant virologists would be confused.

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1. Changes should be made in taxonomy to correct misclassifications or to clarify things.
Removing the hyphen does neither.
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Date first submitted to ICTV:

June 3, 2013

Date of this revision (if different to above):

MODULE 7: **REMOVE and MOVE**

Use this module whenever an existing taxon needs to be removed:

- Either to abolish a taxon entirely (when only part (a) needs to be completed)
- Or to move a taxon and re-assign it e.g. when a species is moved from one genus to another (when BOTH parts (a) and (b) should be completed)

Part (a) taxon/taxa to be removed or moved

Code	2013.016aP	(assigned by ICTV officers)
To remove the following taxon (or taxa) from their present position:		
<i>Barley yellow dwarf virus-RMV</i>		
The present taxonomic position of these taxon/taxa:		
Genus:	<i>Unassigned</i>	Fill in all that apply.
Subfamily:		
Family:	<i>Luteoviridae</i>	
Order:		
If the taxon/taxa are to be abolished (i.e. not reassigned to another taxon) write "yes" in the box on the right		

Reasons to justify the removal:

Explain why the taxon (or taxa) should be removed

Barley yellow dwarf virus-RMV is currently unassigned in the family *Luteoviridae*. This virus was first described as one of the first four "isolates" of barley yellow dwarf virus (BYDV) (Rochow, 1969). However, our recent determination of the complete genome sequence of BYDV-RMV isolate RMV MtFE87 revealed that it is unrelated to the other BYDVs which are in the genus *Luteovirus* (Krueger *et al.*, 2013). It has the genome organization of a polerovirus and is most closely related to these viruses, but it is not very closely related to any polerovirus species, including *Cereal yellow dwarf virus* or *Wheat yellow dwarf virus*, which were once considered isolates of BYDV. Current species demarcation criteria used by the ICTV Luteoviridae study group state that if one gene differs by 10% from all other species then the virus can be considered as a potential new species. The percent identity of each gene of proposed MYDV-RMV to each gene's closest relative is as follows: P0, 23%; P1, 39%; P2, 64%; P3, 61%; P4, 41%; P5, 33%. Thus, all of the genes differ by >10% from all other viruses. See module 9 (Appendix) for more details. Moreover, BYDV-RMV has been shown to be serologically distinct from the other BYDVs and from CYDV-RPV (Rochow & Carmichael, 1979). Because of its relationship to poleroviruses we propose to remove the taxon from its current position as unclassified and to move it to the genus *Polerovirus*. We also propose to rename the virus *Maize yellow dwarf virus-RMV* (see Module 8).

Part (b) re-assign to a higher taxon

Code	2013.01bP	(assigned by ICTV officers)
To re-assign the taxon (or taxa) listed in Part (a) as follows:		
Genus:	<i>Polerovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created write “ (new) ” after its proposed name and complete relevant module to create it. If no genus is specified, enter “ unassigned ” in the genus box.
Subfamily:		
Family:	<i>Luteoviridae</i>	
Order:		

Reasons to justify the re-assignment:

- If it is proposed to re-assign species to an existing genus, please explain how the proposed species differ(s) from all existing species.
 - 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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

Genus Polerovirus is appropriate because IBYDV-RMV has the genome organization of a polerovirus and is most closely related to these viruses, but it is not very closely related to any other known polerovirus species (Fig. 2). Accession number:

MODULE 8: **NON-STANDARD**

Template for any proposal not covered by modules 2-7. This includes proposals to change the name of existing taxa (but note that stability of nomenclature is encouraged wherever possible).

non-standard proposal

Code	2013.016cP	(assigned by ICTV officers)
Rename the species Barley yellow dwarf virus-RMV as <i>Maize yellow dwarf virus-RMV</i>		

Text of proposal:

The proposed new name, Maize yellow dwarf virus-RMV (MYDV-RMV), (i) acknowledges that the virus is a strikingly different new species, (ii) is consistent with observations that BYDV-RMV often infects maize (Brown et al., 1984;Beuve et al., 1999;Itnyre et al., 1999a;Itnyre et al., 1999b), (iii) retains the RMV notation for the predominant vector, *Rhopalosiphum maidis* (although aphids in other species can be efficient vectors), and (iv) retains the YDV descriptor long used for luteovirids that infect cereals.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

- Beuve, M., Naïbo, B., Foulgocq, L., and Lapierre, H. (1999). Irrigated Hybrid Maize Crop Yield Losses Due to Barley Yellow Dwarf Virus-PAV Luteovirus. *Crop Sci.* 39, 1830-1834.
- Brown, J.K., Wyatt, S.D., and Hazelwood, D. (1984). Irrigated corn as a source of barley yellow dwarf virus and vector in eastern Washington. *Phytopathology* 74, 46-49.
- Gasteiger, E., Gattiker, A., Hoogland, C., Ivanyi, I., Appel, R.D., and Bairoch, A. (2003). ExPASy: The proteomics server for in-depth protein knowledge and analysis. *Nucleic Acids Res.* 31, 3784-3788.
- Itnyre, R.L.C., D'arcy, C.J., Pataky, J.K., and Pedersen, W.L. (1999a). Symptomatology of Barley Yellow Dwarf Virus-RMV Infection in Sweet Corn. *Plant Disease* 83, 781-781.
- Itnyre, R.L.C., D'arcy, C.J., Pedersen, W.L., and Sweets, L.E. (1999b). Reaction of Sweet Corn to Inoculation with Barley Yellow Dwarf Virus RMV-IL. *Plant Disease* 83, 566-568.
- Krueger EN, Beckett RJ, Gray SM, Miller WA (2013) The complete nucleotide sequence of the genome of Barley yellow dwarf virus-RMV reveals it to be a new Polorovirus distantly related to other yellow dwarf viruses. *Frontiers in Virology* (under review).
- Rochow, W.F. (1969). Biological properties of four isolates of barley yellow dwarf virus. *Phytopathology* 59, 1580-1589.
- Rochow, W.F., and Carmichael, L.E. (1979). Specificity among barley yellow dwarf viruses

additional material in support of this proposal

References:

in enzyme immunosorbent assays. *Virology* 95, 415-420.
Zhang,W., Cheng,Z., Xu,L., Wu,M., Waterhouse,P., Zhou,G. and Li,S. (2009). The complete nucleotide sequence of the barley yellow dwarf GPV isolate from China shows that it is a new member of the genus *Polerovirus*. *Arch. Virol.* 154, 1125-1128.

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.

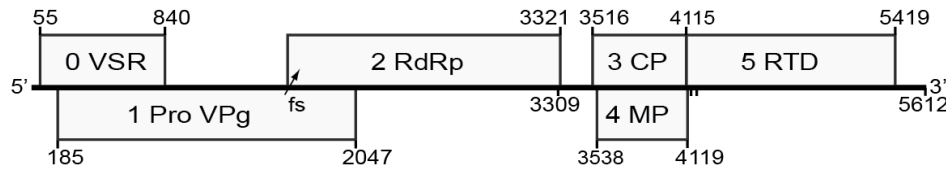


Fig. 1. Genome organization of proposed MYDV-RMV. Numbers in small font indicate genomic positions of each ORF (numbered in large font) and the position of the predicted subgenomic RNA 5' end and the readthrough sequence. VPg, viral genome-linked protein; VSR, putative viral suppressor of RNA silencing; RdRp, RNA dependent RNA polymerase; CP, coat protein; MP,

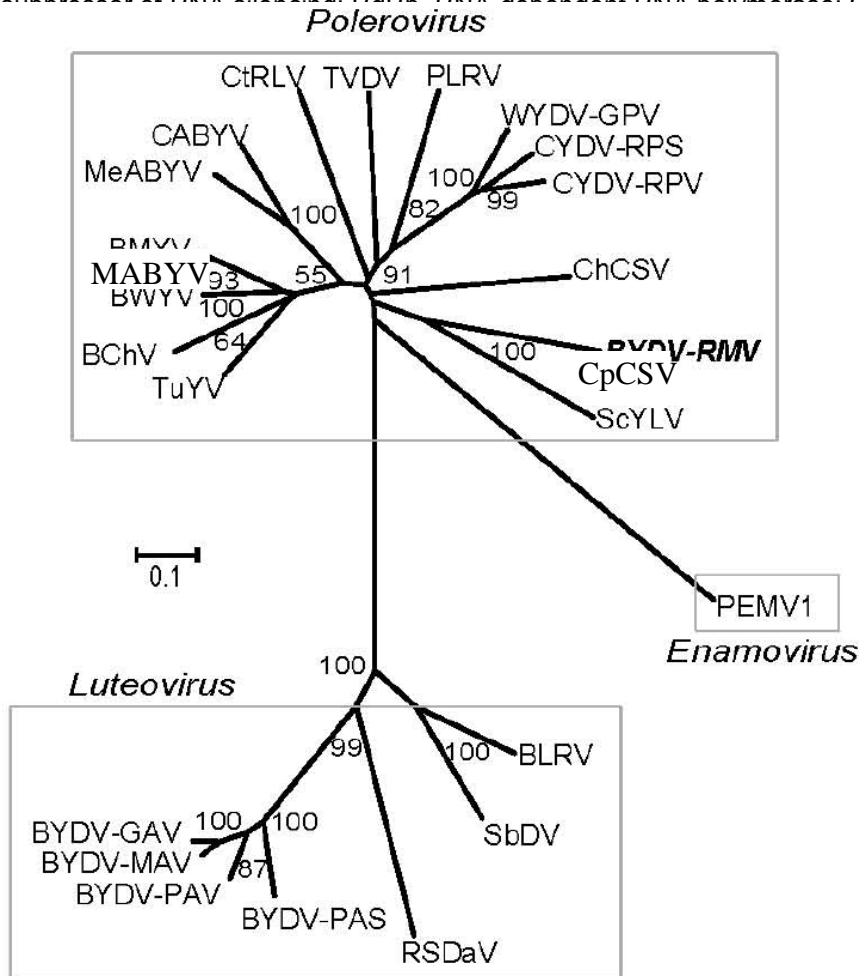


Fig. 2. Neighbor-joining tree of Clustal W-aligned whole genome sequences of luteovirids generated in the MEGA 4 software package. Numbers representing bootstrap values when greater than 50% for 1000 replicates are shown. The proposed new virus MYDV-RMV is indicated by its current official name, BYDV-RMV in bold.

Table 1. Sequence identity (%)^a of BYDV-RMV proteins to those of other luteovirids.

Virus^a	Accession no.	P0	P1	P2	P3	P4	P5
PEMV1	NC_003629	23	18	37	30	NA ^b	30
BLRV	NC_003369	NA ^b	7	14	51	31	26
BYDV-GAV	NC_004666	NA ^b	10	16	45	28	31
BYDV-MAV	NC_003680	NA ^b	9	15	45	26	29
BYDV-PAS	NC_002160	NA ^b	7	14	42	19	31
BYDV-PAV	NC_004750	NA ^b	10	15	45	21	31
RSDaV	NC_010806	NA ^b	2	19	32	25	31
SbDV	NC_003056	NA ^b	7	14	51	38	26
BChV	NC_002766	15	27	57	60	37	25
BMYV	NC_003491	20	33	59	60	39	25
BWYV	NC_004756	22	31	57	61	38	24
CABYV	NC_003688	22	34	57	59	43	33
CpCSV	NC_008249	18	30	60	59	37	29
CtRLV	NC_006265	17	32	62	48	28	30
CYDV-RPS	NC_002198	19	30	52	58	32	28
CYDV-RPV	NC_004751	20	29	51	61	33	27
MABYV	NC_010809	23	33	58	55	41	31
PLRV	NC_001747	11	30	56	55	35	25
ScYLV	NC_000874	18	30	56	40	29	37
TuYV	NC_003431	21	39	64	61	38	26
TVDV	NC_010732	23	32	62	53	31	26
WYDV-GPV	NC_012931	20	30	53	59	35	27

^aThe identity of the sequences to BYDV-RMV was determined with the EMBOSS Needle global pairwise alignment algorithm. Molecular weights for the BYDV-RMV proteins were estimated using the ExPASy Server (Gasteiger et al., 2003). Virus abbreviations are as listed in the Luteoviridae chapter of the Ninth ICTV Report. Additional abbreviations: BYDV-GAV, GAV isolate of BYDV; WYDV-GPV, GPV isolate of Wheat yellow dwarf virus (Zhang et al., 2009).

^bNA, not applicable.