



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.

MODULE1: **TITLE, AUTHORS, etc**

<b>Code assigned:</b>	<b>2013.014aP</b>	(to be completed by ICTV officers)										
<b>Short title:</b> create two new species in the genus <i>Luteovirus</i> , family <i>Luteoviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )												
<b>Modules attached</b> (modules 1 and 9 are required)	<table border="0"> <tr> <td>1 <input checked="" type="checkbox"/></td> <td>2 <input checked="" type="checkbox"/></td> <td>3 <input type="checkbox"/></td> <td>4 <input type="checkbox"/></td> <td>5 <input type="checkbox"/></td> </tr> <tr> <td>6 <input type="checkbox"/></td> <td>7 <input type="checkbox"/></td> <td>8 <input type="checkbox"/></td> <td>9 <input checked="" type="checkbox"/></td> <td></td> </tr> </table>	1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>	6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>		
1 <input checked="" type="checkbox"/>	2 <input checked="" type="checkbox"/>	3 <input type="checkbox"/>	4 <input type="checkbox"/>	5 <input type="checkbox"/>								
6 <input type="checkbox"/>	7 <input type="checkbox"/>	8 <input type="checkbox"/>	9 <input checked="" type="checkbox"/>									

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

Armelle Marais : <a href="mailto:amarais@bordeaux.inra.fr">amarais@bordeaux.inra.fr</a> Thierry Candresse : <a href="mailto:tc@bordeaux.inra.fr">tc@bordeaux.inra.fr</a> Laurence Svanella-Dumas : <a href="mailto:svanella@bordeaux.inra.fr">svanella@bordeaux.inra.fr</a>
---

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

A list of study groups and contacts is provided at <a href="http://www.ictvonline.org/subcommittees.asp">http://www.ictvonline.org/subcommittees.asp</a> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	ICTV <i>Luteoviridae</i> Study Group
--	--------------------------------------

**ICTV-ECor Study Group comments and response of the proposer:**

**Comments of the EC to the SG:**

1. For *Barley yellow dwarf virus kerII* , choose a single isolate as the type isolate and provide a single accession number in the table.
2. Consider changing name of the virus to eliminate the dash and the capital letter (i.e. *Barley yellow dwarf virus kerII*). Note also that the kerII and kerIII abbreviation should be italicized. In the future, consider changing the name of other luteoviridae species in a similar manner to eliminate unnecessary dashes.

**Response of the SG:**

1. Done
2. Capital letter removed. Hyphen moved to be consistent with other yellow dwarf virus names.

Date first submitted to ICTV:

June 2013

Date of this revision (if different to above):

MODULE2: **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	<b>2013.004aP</b>	(assigned by ICTV officers)
<b>To create 2 new species within:</b>		
Genus:	<i>Luteovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:		
Family:	<i>Luteoviridae</i>	
Order:		
<b>And name the new species:</b>		<b>GenBank sequence accession number(s) of reference isolate:</b>
<i>Barley yellow dwarf virus-kerII</i>		KC571999
<i>Barley yellow dwarf virus-kerIII</i>		KC559092

**Reasons to justify the creation and assignment of the new species:**

- 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.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Characterization of grass-infecting viruses in the Kerguelen archipelago has provided information about the presence of members of the *Barley yellow dwarf virus* (BYDV) species complex (Svanella-Dumas *et al.* 2013). The authors have determined the complete or near complete sequence of two divergent agents, KerII and KerIII, and discussed their phylogenetic relationships with other BYDV species and other *Luteovirus* members.

The species demarcation criteria in the *Luteovirus* genus are

- 1) differences in breadth and specificity of host range
- 2) differences in serological specificity with discriminatory polyclonal or monoclonal antibodies
- 3) differences in amino acid sequence identity of any gene product of greater than 10%

(Domier, 2005)

1/ Genome structure and phylogeny place the KerII and KerIII agents in the *Luteovirus* genus (absence of a P0 ORF, presence of a P6 ORF, phylogeny of the P2 polymerase...) (Domier, 2005) (**Figures 1 and 2**)

2/ Comparisons of KerII isolates (K465 and K439 isolates) and KerIII isolate (K460) with other sequenced *Luteovirus* members showed that whatever the ORF considered, at least 23% and 32% of amino acid divergence was observed with the KerII isolates and KerIII isolates, respectively. The divergence is similarly high between the KerII and KerIII agents (at least 22% in the P1-P2, the less divergent region). These values are clearly outside the species demarcation criteria of 10% (**Table 1**).

3/ The KerII and KerIII agents are grass-infecting Luteoviruses as BYDV (Svanella-Dumas *et al.*, 2013; Miller and Rosachova, 1997).

4/ The KerII and KerIII agents showed highest overall nucleotide identity levels with representative members of the BYDV species complex (values comprised between 62.9 and 63.8 %). The corresponding values obtained for BYDV species for which only partial sequences are available are between 65.6 and 66.5%. Full genome phylogeny also supports an affinity with other BYDV species (**Figure 3**).

In conclusion, the KerII and KerIII agents have *Luteovirus* genomes but their divergence from all other sequences *Luteovirus* members falls clearly outside of the species demarcation criteria. Their natural host range and their sequence affinities position them as new *Luteovirus* species within the BYDV species complex, so that the names BYDV-kerII and BYDV-kerIII are proposed for these new species.

MODULE9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

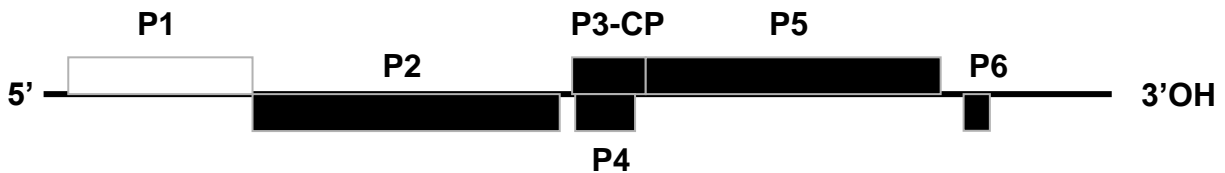
Domier LL (2005) Family *Luteoviridae*. In: King AMQ, Adams MJ, Carstens EB, Lefkowitz EJ, editors. *Virus Taxonomy*, ninth Report of International Committee on Taxonomy of Viruses. Amsterdam, The Netherlands: Elsevier Academic Press. pp. 1045-1053.

Miller MA, Rosachova L (1997) Barley yellow dwarf viruses. *Annu Rev Phytopathol* 35: 167-190.

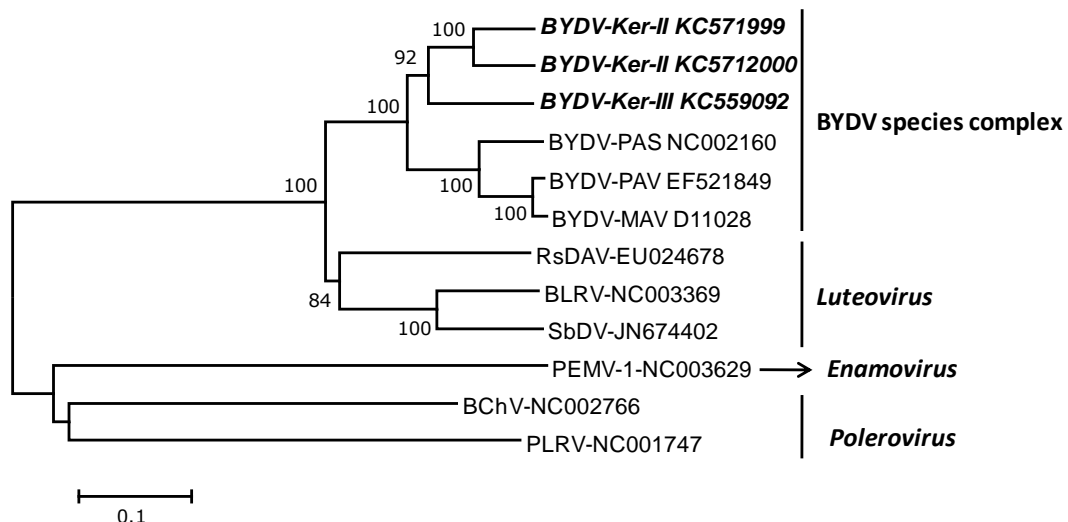
Svanella-Dumas L, Candresse T, Hullé M, Marais A (2013) Distribution of *Barley yellow dwarf virus-PAV* in the sub-Antarctic Kerguelen Islands and characterization of two new Luteovirus species. *PLOS One*, in press.

**Annex:**

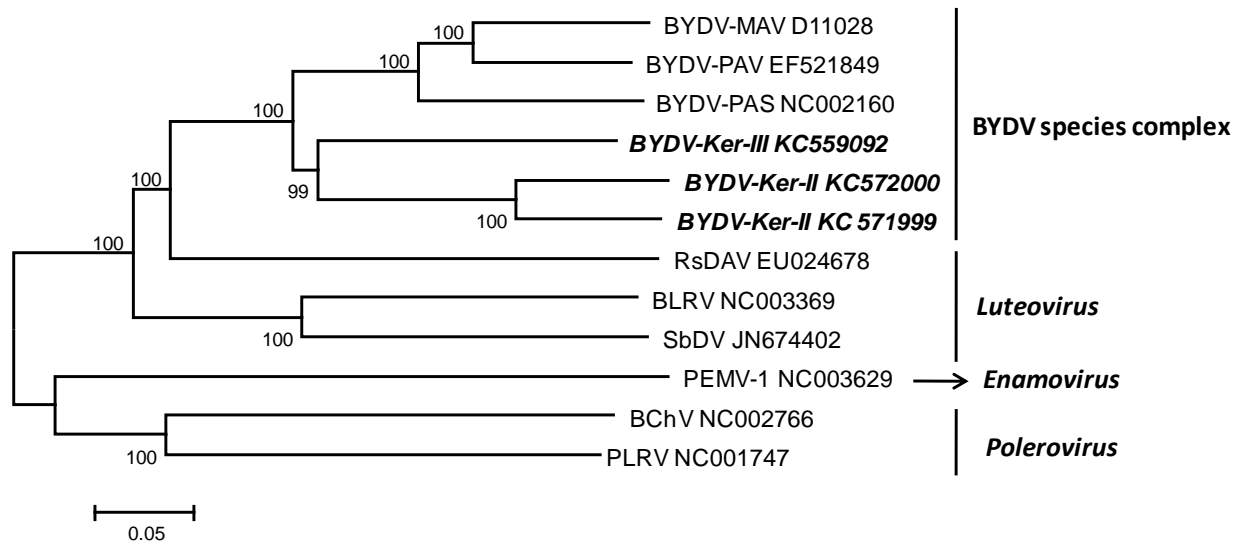
Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate 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.



**Figure 1: Schematic representation of the RNA genome of KerII and KerIII agents**



**Figure 2: Phylogenetic analysis of the polymerase (ORF2) sequences of representatives of species in the family *Luteoviridae*.** The abbreviations followed by the accession numbers are: BYDV, *Barley yellow dwarf virus*, RSDaV, *Rose spring dwarf-associated virus*; BLRV, *Bean leafroll virus*; SbDV, *Soybean dwarf virus*; PEMV, *Pea enation virus*; PLRV, *Potato leafroll virus*; BChV, *Beet chlorosis virus*. The proposed new BYDV species are in bold italics. The genera to which the particular viruses belong are indicated on the right. Amino acids were aligned with CLUSTALW and neighbor-joining trees were reconstructed with MEGA 5.0. Bootstrap values (1,000 replicates) above 70% are indicated. The scale bar represents 10% amino acid divergence.



**Figure 3: Phylogenetic tree reconstructed using the complete genome sequences of *Luteoviridae* members.** The abbreviations followed by the accession numbers are: BYDV, *Barley yellow dwarf virus*; RSDaV, *Rose spring dwarf associated virus*; BChV, *Beet chlorosis virus*; SbDV, *Soybean dwarf virus*; BLRV, *Bean leaf roll virus*; PLRV, *Potato leaf roll virus*; PEMV, *Pea enation mosaic virus*. The proposed new BYDV species are in bold italics. The genera to which the particular viruses belong are indicated on the right. The tree was reconstructed by neighbor-joining method using the p-distance model and was bootstrapped with 1,000 replications. Numbers at nodes indicate bootstrap values higher than 70%. The scale bar represents 5% nucleotide divergence.

**Table 1: Average amino acid divergence between the KerII and KerIII agents and *Luteovirus* members in the P3P5 region.**

	<b>BYDV-kerIII KC559092</b>	<b>BYDV-kerII KC572000</b>	<b>BYDV-kerII KC571999</b>	<b>BYDV-PAV EF521849</b>	<b>BYDV-MAV D11028</b>	<b>BYDV-PAS NC002160</b>	SbDV JN674402	BLRV NC003369
<b>BYDV-kerII KC572000</b>	<b>39.2</b>							
<b>BYDV-kerII KC571999</b>	<b>40.1</b>	<b>1.3</b>						
<b>BYDV-PAV EF521849</b>	<b>40.4</b>	<b>39.3</b>	<b>39.5</b>					
<b>BYDV-MAV D11028</b>	<b>40.6</b>	<b>38.7</b>	<b>40.0</b>	<b>36.1</b>				
<b>BYDV-PAS NC002160</b>	<b>38.3</b>	<b>39.3</b>	<b>39.4</b>	<b>12.8</b>	<b>36.1</b>			
SbDV JN674402	70.1	72.4	71.5	69.8	7.0	69.7		
BLRV NC003369	67.5	71.9	71.0	68.4	7.1	70.7	4.7	
RsDAV EU024678	66.2	67.3	68.2	68.3	6.8	68.8	7.2	7.2

Members of BYDV species complex are in bold.