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:	***2010.021a-gV***	(to be completed by ICTV officers)

Short title: Create family Bidnaviridae
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☒	**3** ☒	**4** ☐	**5** ☒
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

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

Peter Tijssen for the Parvoviridae Study Group (peter.tijssen@iaf.inrs.ca)

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)	Parvoviridae

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

Date first submitted to ICTV:
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.

Code	***2010.021aV***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Bidensovirus (new)***
Subfamily:	***Unassigned***
Family:	***Bidnaviridae (new)***
Order:	***Unassigned***

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.

And name the new species:

Bombyx mori bidensovirus

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.
- Provide accession numbers for genomic sequences
- Further material in support of this proposal may be presented in the Appendix, Module 9

The two *Bombyx mori* bidensoviruses (BmDNV-2 and BmDNV-3) have virtually identical nt sequences (98%) and are unique among ssDNA viruses.

a. The segmented genome consists of two parts of about 6 and 6.5 kb, respectively, that are packaged separately. The complementary strands are also packaged, so that there are 4 different types of full particles. The total genome length is almost 13 kb (instead of 4-6 kb for parvoviruses).

b. The DNAs have ITRs (about 225 nt for VD1 and 525 nt for VD2), as do parvoviruses. This is unlike other ssDNA virus familes.

c. Segment VD2 codes for a structural protein in one sense (1160 amino acids) and an NS at the other end on the complementary strand (222 amino acids).

d. Segment VD1 codes also for a structural protein in one sense (1115 amino acids) and 3 NSs at the 5'-end (126, 316 and 499 amino acids, respectively) of the complementary strand, and thus has also an ambisense organization.

e. The viruses code for a protein that is homologous to DNA polymerase, unlike parvoviruses.

f. The viruses do not code for the typical ORFs found in densoviruses and there is no sequence identity.

g. In contrast to parvoviruses, the viruses code for two different structural proteins.

h. The transcription strategy has been analyzed and is different from that of parvoviruses or other ssDNA viruses.

MODULE 3: **NEW GENUS**

creating a new genus

Ideally, a genus should be placed within a higher taxon.

Code	***2010.021bV***	(assigned by ICTV officers)

To create a new genus within:

Subfamily:	***Unassigned***
Family:	***Bidnaviridae***
Order:	***Unassigned***

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 family is specified, enter "**unassigned**" in the family box

naming a new genus

Code	***2010.021cV***	(assigned by ICTV officers)

To name the new genus: *Bidensovirus*

Assigning the type species and other species to a new genus

Code	***2010.021dV***	(assigned by ICTV officers)

To designate the following as the type species of the new genus

Bombyx mori bidensovirus

Every genus must have a type species. This should be a well characterized species although not necessarily the first to be discovered

The new genus will also contain any other new species created and assigned to it (Module 2) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of species (including the type species) that the genus will contain:**

1

Reasons to justify the creation of a new genus:

Additional material in support of this proposal may be presented in the Appendix, Module 9

First genus in new family, to accommodate a single new species.

Origin of the new genus name:

From name of first species in this genus.

Reasons to justify the choice of type species:

Only species classified in this genus.

Species demarcation criteria in the new genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

MODULE 5: **NEW FAMILY**

creating and naming a new family

Code	***2010.021eV***	(assigned by ICTV officers)

To create a new family containing the subfamilies and/or genera listed below within the Order: ***Unassigned***

If there is no Order, write "**unassigned**" here.
If the Order has yet to be created (in Module 6) please write **"(new)"** after the proposed name.

Code	***2010.021fV***	(assigned by ICTV officers)

To name the new family: ***Bidnaviridae***

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assigning subfamilies, genera and unassigned species to a new family

Code		(assigned by ICTV officers)

To assign the following subfamilies (if any) to the new family:
You may list several subfamilies here. For each subfamily, please state whether it is new or existing.

- If the subfamily is new, it must be created in Module 4
- If the subfamily already exists, please complete Module 7 to 'REMOVE' it from its existing family

Code	***2010.021gV***	(assigned by ICTV officers)

To assign the following genera to the new family:
You may list several genera here. For each genus, please state whether it is new or existing.

- If the genus is new, it must be created in Module 3
- If the genus already exists, please state whether it is currently unassigned or is to be removed from another family. If the latter, complete Module 7 to 'REMOVE' it from that family

Bidensovirus

The new family will also contain any other new species created and assigned to it (Module 3) and any that are being moved from elsewhere (Module 7b). **Please enter here the TOTAL number of unassigned species that the family will contain (those NOT within any of the genera or subfamilies listed above):**

0

Reasons to justify the creation of the new family:
Additional material in support of this proposal may be presented in the Appendix, Module 9

See module 2.

Origin of the new family name:

Bisegmented ssDNA viruses).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

E.g.:

1. Wang YJ, Yao Q, Chen KP, Han X. 2006 [Organization and transcription strategy of genome of Bombyx mori bidensovirus (China isolate) VD1] Sheng Wu Gong Cheng Xue Bao. 22:707-12. Chinese.
2. Wang YJ, Yao Q, Chen KP, Wang Y, Lu J, Han X. 2007 Characterization of the genome structure of Bombyx mori densovirus (China isolate). Virus Genes. 35:103-8.
3. Ito K, Kidokoro K, Sezutsu H, Nohata J, Yamamoto K, Kobayashi I, Uchino K, Kalyebi A, Eguchi R, Hara W, Tamura T, Katsuma S, Shimada T, Mita K, Kadono-Okuda K. 2008 Deletion of a gene encoding an amino acid transporter in the midgut membrane causes resistance to a Bombyx parvo-like virus. Proc Natl Acad Sci U S A. 105:7523-7.

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.